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Investigating venom composition and variation in West European vipers

Ignazio Avella

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Ignazio Avella
PhD Thesis presented to the
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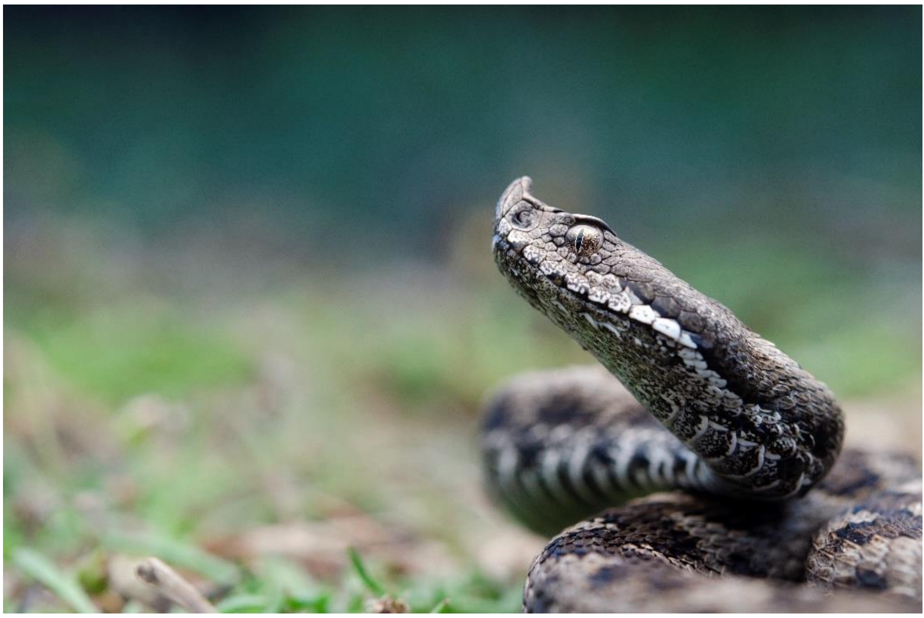

Investigating venom composition and variation in West European vipers

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Doutoramento em Biodiversidade, Genética e Evolução

Departamento de Biologia, Faculdade de Ciências da Universidade do Porto

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Declaração de Honra

Eu, Ignazio Avella, natural de Nola, residente em Nola com o telefone +39 3479917204, nacional de Italia, portador do Cartão de Cidadão nº AX7866202, inscrito no Programa Doutoral em Biodiversidade, Genética e Evolução da Faculdade de Ciências da Universidade do Porto declaro, nos termos do disposto na alínea a) do artigo 14.º do Código Ético de Conduta Académica da U.Porto, que o conteúdo da presente tese reflete as perspetivas, o trabalho de investigação e as minhas interpretações no momento da sua entrega.

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Ignazio Avella

Ignazio Avella
Porto, 14 de junho de 2023

Foreword

Four scientific articles were published in indexed, peer-reviewed international journals as a result of the work developed in the scope of the present thesis. As these works were performed in collaboration with other authors, the candidate clarifies that, in all of them, he actively participated in obtaining and analysing the data, discussing the results, and in writing their final, published versions. The articles in question are:

1. Di Nicola, M. R., Pontara, A., Kass, G. E. N., Kramer, N. I., Avella, I., Pampena, R., Mercuri, S. R., Dorne, J. L. M., & Paolino, G. (2021). Vipers of major clinical relevance in Europe: taxonomy, venom composition, toxicology and clinical management of human bites. *Toxicology*, 453, 152724. https://doi.org/10.1016/j.tox.2021.152724

2. Avella, I., Calvete, J. J., Sanz, L., Wüster, W., Licata, F., Quesada-Bernat, S., Rodríguez, Y., & Martínez-Freiría, F. (2022) Interpopulational variation and ontogenetic shift in the venom composition of Lataste's viper (*Vipera latastei*, Boscá 1878) from northern Portugal. *Journal of Proteomics*, 263, 104613. https://doi.org/10.1016/j.jprot.2022.104613

3. Avella, I., Wüster, W., Luiselli, L., & Martínez-Freiría, F. (2022) Toxic habits: an analysis of general trends and biases in snake venom research. *Toxins*, 14(12), 884. https://doi.org/10.3390/toxins14120884

4. Avella, I., Damm, M., Freitas, I., Wüster, W., Lucchini, N., Zuazo, Ó., Süssmuth, R., & Martínez-Freiría, F. (2023). One Size Fits All—Venomics of the Iberian adder (*Vipera seoanei*, Lataste 1878) reveals low levels of venom variation across its distributional range. *Toxins*, 15(6), 371. https://doi.org/10.3390/toxins15060371

The thesis was developed at BIOPOLIS-CIBIO/InBIO – Research Centre in Biodiversity and Genetic Resources, Vairão, Portugal, and at IBV – Institute of Biomedicine of Valencia, CSIC – Spanish National Research Council, Valencia, Spain. The Faculty of Sciences of the University of Porto was the institution awarding the degree.

The candidate's work was supervised by Dr. Fernando Martínez-Freiría (BIOPOLIS-CIBIO – Research Center in Biodiversity and Genetic Resources, Vairão, Portugal), and co-supervised by Prof. Dr. Wolfgang Wüster (Molecular Ecology and Evolution at Bangor, School of Natural Sciences, Bangor University, Bangor, United Kingdom) and Prof. Dr. Juan J. Calvete

(Evolutionary and Translational Venomics Laboratory, IBV – Institute of Biomedicine of Valencia, CSIC – Spanish National Research Council, Valencia, Spain).

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To my parents Anna and Luigi

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Resumo

Nos últimos anos, a aplicação de metodologias de alto rendimento (“high-throughput”) no campo da venómica veio revolucionar e renovar o interesse na investigação de venenos de cobras, levando, em pouco tempo, à produção de nova informação sobre o veneno de inúmeras espécies e fornecendo uma visão abrangente sobre a sua composição e propriedades. Este avanço metodológico permitiu acesso detalhado a alguns dos processos subjacentes à origem e evolução do veneno de cobra, com a identificação de compostos com potencial relevância médica e o desenvolvimento de ferramentas terapêuticas para mitigar o impacto de mordidas a nível mundial. No entanto, lacunas consideráveis existem na investigação de venenos de cobras, particularmente em determinadas espécies ou tópicos de estudo. Esta tese tem como principal objetivo aumentar o conhecimento atual sobre os venenos produzidos por víboras europeias, com especial ênfase em espécies do género *Vipera* da Península Ibérica, contribuindo desta forma para colmatar as lacunas detetadas neste campo de investigação.

Um total de 267 estudos em venenos de cobras, publicados entre 1964 e 2021, foram revistos com o intuito de avaliar, pela primeira vez de forma quantitativa e qualitativa, as tendências e vieses na investigação neste campo. Apesar da tendência positiva no número de artigos publicados anualmente, esta análise também revelou uma desconsideração generalizada no estudo de famílias de cobras com relevância médica supostamente reduzida (e.g., Atractaspididae), sub-representação de algumas das áreas geográficas mais afetadas por mordidas de cobra (i.e., ecozonas Indomalaia e Afrotrópicas), bem como interesse limitado nos contextos funcionais e ecológicos do veneno de cobras. De facto, cobras da família Viperidae foram mais representadas do que qualquer outro taxon, os Neotrópicos foram a região biogeográfica mais representada em termos de número de espécies estudadas e a maioria das publicações focou-se na caracterização de veneno de cobra, ao passo que tópicos mais relacionados com ecologia raramente foram considerados.

Apesar de cobras da família Viperidae serem as mais estudadas no geral, víboras da subfamília Crotalinae foram duas vezes mais representadas do que as da subfamília Viperinae (i.e., víboras verdadeiras), com relevância médica crítica em todo o Velho Mundo. Na Europa, a maioria dos acidentes ofídicos é causada por víboras verdadeiras do género *Vipera*, constituido por mais de 20 espécies. Entre estas, seis espécies de maior relevância médica são distinguidas, considerando a sua difusão na Europa e elevado número de acidents ofíficos registados: *Vipera ammodytes*, *Vipera aspis*, *Vipera berus*, *Vipera latastei*, *Vipera seoanei* and *Vipera ursinii*. De uma forma geral, os médicos europeus não têm treino específico para identificar mordidas de cobra, reconhecer os seus sintomas e manifestações clínicas nem aplicar tratamento adequado, pelo que beneficiariam de ferramentas disponíveis para auxiliar na gestão de envenenamento por *Vipera.* Para tal, foram definidas chaves taxonómicas para a identificação das seis espécies *Vipera* acima mencionadas, bem como para a sua distinção de outras cobras europeias não pertencentes ao género *Vipera.* Os dados atualmente disponíveis sobre a composição dos seus venenos e sintomas causados pela sua mordida foram revistos e sumariados. Foi possível obter informação sobre a composição e atividade dos venenos de *V. ammodytes*, *V.aspis*, *V. berus* e *V. ursinii*, que parecem ser caracterizados por poucas famílias de toxinas muito abundantes, responsáveis pela maior parte da sua composição (i.e., SVMP, PLA_2, SVSP, CTL) em conjunto com componentes menos abundantes (e.g., DISI, CRISP, LAAO). Estes resultados estão de acordo com o padrão de composição geralmente reportado em venenos de víboras verdadeiras e com os efeitos maioritariamente hemorrágicos e citotóxicos associados a envenenamentos por viperídeos. De facto, a revisão das manifestações clínicas relacionadas com as espécies *Vipera* em questão mostrou que estas variam de locais requerendo apenas tratamento tópico (por exemplo, dor e inchaço) a sistémicas, potencialmente letais com necessidade de antídoto (por exemplo, insuficiência renal, alterações hematológicas). Por fim, foi definido um protocolo uniformizado para gestão clínica de mordidas de *Vipera*, abordando detalhadamente o tratamento dos sintomas locais e sistémicos, bem como a administração de antídoto.

Notavelmente, as informações disponíveis sobre a composição e atividade dos venenos de *V. latastei* e *V. seoanei* eram bastante reduzidas, impedindo a avaliação detalhada e compreensiva destas duas espécies pouco estudadas. Assim, e com o objetivo de preencher esta lacuna, foi conduzido o primeiro estudo detalhado sobre a composição e variação dos venenos de *V. latastei* e *V. seoanei,* baseado na aplicação de metodologias proteómicas “bottom-up”. Relativamente a *V. latastei*, foram analisados os venenos de espécimes juvenis e adultos de duas localidades do norte de Portugal sob condições ambientais diferentes. Foram produzidos seis proteomas de venenos (três por população) provenientes de víboras de ambas as idades (i.e., dois juvenis e quatro adultos), bem como perfis RP-HPLC de 54 venenos provenientes de espécimes selvagens. Os perfis cromatográficos e abundâncias relativas das suas toxinas variaram entre os venenos de juvenis e adultos, sugerindo a ocorrência de alterações ontogenéticas na composição do veneno. Especificamente, metaloproteinase de veneno de cobra (SVMP) foi a família de toxinas mais abundante em venenos juvenis, enquanto proteases de serina de veneno de cobra (SVSPs), fosfolipases A_2 (PLA_2s) e proteínas tipo-lectina tipo-C (CTLs) foram as principais toxinas em venenos adultos. Verificou-se que os perfis RP-HPLC de veneno variam significativamente entre as localidades amostradas, indicando variabilidade geográfica. Além disso, a presença/ausência de certos picos nos perfis cromatográficos parece estar significativamente correlacionada com fatores como o tamanho e sexo das víboras. Os resultados mostram que o veneno de *V. latastei* é um fenótipo variável, em que diferenças intraespecíficas na sua composição provavelmente refletem diferenças na ecologia alimentar desta espécies em diferentes fases de vida e sob diferentes pressões ambientais.

Relativamente a *V. seoanei*, foram analisados venenos de 49 espécimes adultos provenientes de 20 localidades ao longo da área de distribuição da espécie na Península Ibérica. O proteoma de referência do veneno de *V. seoanei* foi gerado com base num "pool" de venenos individuais; perfis SDS-PAGE foram produzidos para todas as amostras de venenos e os padrões de variação foram visualizados com Non-metric Multidimensional Scaling (NMDS). A presença e natureza da variação nos venenos entre localidades, bem como o efeito de 14 previsores (biológicos, ecogeográficos, genéticos) na sua ocorrência, foram avaliados com a aplicação de regressão linear. O veneno incluiu pelo menos12 famílias diferentes de toxinas, das quais cinco (i.e., PLA_2, SVSP, DISI, CTL, SVMP) representavam cerca de 75% de todo o proteoma. As análises comparativas do perfis SDS-PAGE mostraram semelhanças consideráveis entre as localidades amostradas, sugerindo baixa variabilidade geográfica. Análises de regressão sugeriram efeitos significativos de previsões biológicos e de habitat na reduzida variação detetada nos venenos de *V. seoanei* analisados. Outros fatores foram também significativamente associados à presença/ausência de bandas individuais nos perfis SDS-PAGE. Os baixos níveis de variabilidade detetados em *V. seoanei* podem ser o resultado de expansão populacional recente ou de outros processos além de forças seletivas positivas direcionais que atuam na manutenção do veneno como fenótipo conservado.

A análise das tendências e vieses em estudos em venenos de cobras detetou a desconsideração consistente de determinadas grupos de cobras e tópicos de estudo. De forma similar, a revisão dos dados atualmente disponíveis sobre as seis espécies *Vipera* de elevada importância médica na Europa deixou a descoberto lacunas de conhecimento, em especial sobre a composição e variação intraespecífica dos seus venenos. Com esta tese, a aplicação de metodologias de venómica "bottom-up" nos venenos de *V. latastei* e *V. seoanei* permitiu dar o primeiro passo para colmatar estas lacunas e complementar o conhecimento na área. De facto, os resultados destas análises permitiram caracterizar os venenos destas víboras pouco estudadas e detetar variação intraespecífica nos seus venenos a diferentes níveis (i.e., variação ontogenética em *V. Latastei*; variação geográfica a diferente magnitude em *V. latastei* e *V. seoanei*), abrindo portas para estudos futuros na variação do venenos destas duas espécies. Expandir as análises proteómicas conduzidas nesta tese a outras espécies *Vipera* pouco estudadas, em conjunto com a implementação de análises genómicas, trancriptómicas e funcionais, de certo permitirá obter uma visão mais completa da evolução e variação do veneno de víboras europeias.

Palavras-chave

Vipera, *Vipera latastei*, *Vipera seoanei*, Viperidae, Viperinae, verdadeiras víboras, Europa, Península Ibérica, veneno de cobra, toxinas, venômica, proteômica de baixo para cima, variabilidade geográfica, mudança ontogenética

Abstract

The application in recent years of the high-throughput methodologies constituting snake venomics has provided snake venom research with renewed interest and enthusiasm, leading to the rapid production of a remarkable amount of information on a multitude of snake venoms, and providing a comprehensive view of their compositions and properties. This has allowed to obtain a detailed insight into some of the processes underlying snake venom origin and evolution, and has led to the identification of compounds of potential medicinal relevance, and to the development of powerful therapeutic tools to mitigate the global burden of snakebite. Nonetheless, considerable knowledge gaps exist in snake venom research, especially concerning the attention paid to certain topics and snake species. The main goal of this thesis is to contribute to this research field, increasing the current knowledge on the venoms produced by European vipers, focusing on species of the genus *Vipera* from the Iberian Peninsula.

Aiming to provide the first qualitative and quantitative estimate of the trends and biases in snake venom research, we reviewed a total of 267 snake venom studies published between 1964 and 2021. While our analysis showed an overall positive trend in the number of articles published yearly, it also underlined severe neglect of snake families of supposedly minor medical relevance (e.g., Atractaspididae), underrepresentation of some of the areas most impacted by snakebite (i.e., Indomalayan and Afrotropic realms), and limited interest in the ecological and functional context of snake venom. Indeed, snakes of the family Viperidae were significantly more represented than any other snake taxon retrieved, the Neotropics were the most represented biogeographic realm for number of studied species, and the vast majority of the publications focused on snake venom characterisation, whereas more ecology-related topics were rarely considered.

Although snakes of the family Viperidae were the most studied overall, the subfamily Crotalinae (i.e., pit vipers) was twice as represented than Viperinae (i.e., true vipers), of critical medical relevance across the Old World. In Europe, most snakebite accidents are caused by true vipers of the genus *Vipera*, comprising more than 20 species. Amongst these, the species of major medical relevance due to their greater diffusion across Europe and the high number of registered snakebites are six, namely *Vipera ammodytes*, *Vipera aspis*, *Vipera berus*, *Vipera latastei*, *Vipera seoanei* and *Vipera ursinii*. Generally not trained to identify snakebites, recognise their clinical manifestations, and apply appropriate treatment, European physicians need tools to help them with the management of European *Vipera* envenomations. To this end, we defined taxonomic keys for the identification of the abovementioned six *Vipera* species, and to distinguish them from European non-viperid snakes. We then reviewed and resumed the data currently available on the composition of their venoms and the symptoms

they can cause. We were able to retrieve several information concerning composition and activities of the venoms of *V. ammodytes*, *V.aspis*, *V. berus* and *V. ursinii*, which appear to be characterised by few very abundant toxin families accounting for most of their compositions (i.e., SVMP, PLA_2, SVSP, CTL) together with several less abundant components (e.g., DISI, CRISP, LAAO). This is concordant with the compositional pattern generally reported for true viper venoms, and with the mainly haemorrhagic and cytotoxic effects of viperid envenomations. Indeed, when reviewing the clinical manifestations caused by the *Vipera* species in question, we found these to range from local and only requiring topical treatment (e.g., algesia, swelling) to systemic, potentially lethal, and requiring antivenom therapy (e.g., renal failure, haematological alterations). Finally, we defined a standardised protocol for the clinical management of *Vipera* snakebite, addressing in detail the treatment of local and systemic symptoms and antivenom administration procedures.

Notably, information available on composition and activity of *V. latastei* and *V. seoanei* venoms was extremely reduced, and did not allow the development of a comprehensive assessment for this two inadequately studied species. We thus aimed to fill this knowledge gap by providing the first detailed investigation on composition and variation of *V. latastei* and *V. seoanei* venoms, performed by the application of bottom-up proteomics. Concerning *V. latastei*, we analysed the venoms of juvenile and adult specimens from two environmentally different localities from northern Portugal. We thus produced six venom proteomes (three per population) from vipers belonging to both age classes (i.e., two juveniles and four adults), and RP-HPLC profiles of 54 venoms collected from wild specimens. Venoms from juveniles and adults differed in their chromatographic profiles and relative abundances of their toxins, suggesting the occurrence of ontogenetic changes in venom composition. Specifically, snake venom metalloproteinase (SVMP) was the most abundant toxin family in juvenile venoms, while snake venom serine proteinases (SVSPs), phospholipases A_2 (PLA_2s), and C-type lectin-like proteins (CTLs) were the main toxins comprising adult venoms. The RP-HPLC venom profiles were found to vary significantly between the two sampled localities, indicating geographic variability. Furthermore, the presence/absence of certain peaks in the venom chromatographic profiles appeared to be significantly correlated also to factors like body size and sex of the vipers. Our findings show that *V. latastei* venom is a variable phenotype, with intraspecific differences in its composition likely mirroring changes in the feeding ecology of this species, taking place during different life stages and under different environmental pressures.

Concerning *V. seoanei*, we analysed the venoms of 49 adult specimens from 20 localities across the species' Iberian distribution. We used a pool of all individual venoms to generate a *V. seoanei* venom reference proteome, produced SDS-PAGE profiles of all venom

samples, and visualised patterns of variation using Non-metric Multidimensional Scaling (NMDS). By applying linear regression, we then assessed presence and nature of venom variation between localities, and investigated the effect of 14 predictors (biological, eco-geographic, genetic) on its occurrence. The venom comprised at least 12 different toxin families, of which five (i.e., PLA_2, SVSP, DISI, CTL, SVMP) accounted for about 75% of the whole proteome. The comparative analyses of the SDS-PAGE venom profiles found them to be remarkably similar across the sampled localities, suggesting low geographic variability. Regression analyses suggested significant effects of biological and habitat predictors on the little variation we detected across the analysed *V. seoanei* venoms. Other factors were also significantly associated with the presence/absence of individual bands in the SDS-PAGE profiles. The low levels of venom variability we detected within *V. seoanei* might be the result of a recent population expansion, or of other processes than directional positive selection acting to maintain a conserved venom phenotype.

The analysis of trends and biases in snake venom studies allowed to detect the consistent neglect of some research topics and snake taxa. Similarly, reviewing the data currently available on the six *Vipera* species of major medical importance in Europe uncovered a severe lack of information on some of them, especially in terms of venom composition and intraspecific variation. The development of bottom-up venomics on the venoms of *V. latastei* and *V. seoanei* made it possible to make a first step towards filling this knowledge gap. Indeed, the results of these analyses led to the characterisation of these greatly overlooked viper venoms, detecting intraspecific venom variation at different levels (i.e., ontogenetic variation in *V. latastei*; geographic variation of different magnitude in *V. latastei* and *V. seoanei*), and paved the way for investigating the occurrence of venom variation in these two species. Expanding the performed proteomic analyses to other so far neglected *Vipera* species, together with the implementation of genomic, transcriptomic, and functional analyses, would certainly provide a more complete insight into evolution and variation of European viper venoms.

Keywords

Vipera, *Vipera latastei*, *Vipera seoanei*, Viperidae, Viperinae, true vipers, Europe, Iberian Peninsula, snake venom, toxins, venomics, bottom-up proteomics, venom characterisation, geographic variability, ontogenetic shift

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List of Abbreviations

3FTx	Three-finger toxin
5'NT	5'-nucleotidase
ALT	Alanine transaminase
AP	Aminopeptidase
AspPs	Aspartic proteinases
AST	Aspartate aminotransferase
BIP	Bradykinin-inhibitory peptide
BPP	Bradykinin-potentiating peptide
C-NAP	C-type natriuretic peptides
CK	Creatin kinase
CNS	Central nervous system
CPR	Cardiopulmonary resuscitation
CRISP	Cysteine-rich secretory protein
CTL	C-type lectin-like protein
DC-domain	Disintegrin-like/cysteine-rich domain released from PIII-SVMP
DIC	Disseminated Intravascular Coagulation
DISI	Disintegrin
D49-PLA$_2$	D49-phospholipase A$_2$
ECG	Electrocardiogram
Fab	Fragment antigen-binding
Hyal	Hyaluronidase
IgG	Immunoglobulin G
INR	International Normalized Ratio
K49-PLA$_2$	K49-phospholipase A$_2$
(K/R)TS-DISI	Disintegrin of class KTS or RTS
KUN	Kunitz-type inhibitor
LAAO	L-amino-acid oxidase
MS	Mass spectrometry
NP	Natriuretic peptide
PI-SVMP	Snake venom metalloproteinase of class PI
PII-SVMP	Snake venom metalloproteinase of class PII
PIII-SVMP	Snake venom metalloproteinase of class PIII
PCC	Poison control center
PDE	Phosphodiesterase
PLA$_2$	Phospholipase A$_2$
PLB	Phospholipase B
PT	Prothrombin time
QC	Glutaminyl cyclase
SVMP	Snake venom metalloproteinase
SVMP Frag	Fragment of SVMP
SVMPi	Inhibitor of SVMP
SVSP	Snake venom serine proteinase
VEGF	Vascular endothelial growth factor
VNGF	Venom nerve growth factor
WHO	World Health Organization

Chapter 1

General Introduction

General Introduction

1.1 Snake venom: origin and evolution

Venoms can broadly be defined as secretions produced in specialised glands by an organism delivered to another organism through the infliction of a wound, containing molecules able to disrupt the physiological and/or biochemical processes of the envenomated target (Arbuckle, 2017; Fry et al., 2009a). These complex mixtures of highly bioactive compounds (i.e., toxins) have evolved independently several times in different animal taxa (e.g., Gastropoda, Cephalopoda, Hymenoptera, Arachnida, Reptilia, Mammalia) (Arbuckle, 2017; Jenner and Undheim, 2017; Sunagar and Moran, 2015), and are thought to serve three main functions: i) prey subjugation, ii) defence from predators/attackers, and iii) intraspecific interaction (Arbuckle, 2017; Casewell et al., 2013; Jenner and Undheim, 2017; Schmidt, 2019).

In reptiles, the presence of a core set of highly expressed toxin-related genes has been dated up to approximately 170 million years ago, at the base of a clade termed Toxicofera (Greek for “those who bear toxins”), composed of snakes, iguanian lizards, and anguimorph lizards (Fry et al., 2006; Vidal and Hedges, 2005), and supported by several phylogenetic studies (e.g., Pyron et al., 2013; Wiens et al., 2012; Zheng and Wiens, 2016). A number of extant members of these three lineages present protein-secreting oral glands of different complexity and share some basal toxin families, regardless of whether or not they are used to perform a venomous function. This suggests that such toxin families were possibly recruited before diversification and separation of the toxicoferan lineages, thus supporting the hypothesis that the reptilian venom system had a single origin at the base of the Toxicofera, and successively underwent diversification and/or specialisation, or loss (Calvete et al., 2023; Fry et al. 2006; Fry et al., 2012; Li et al., 2005; see Figure 1.1).

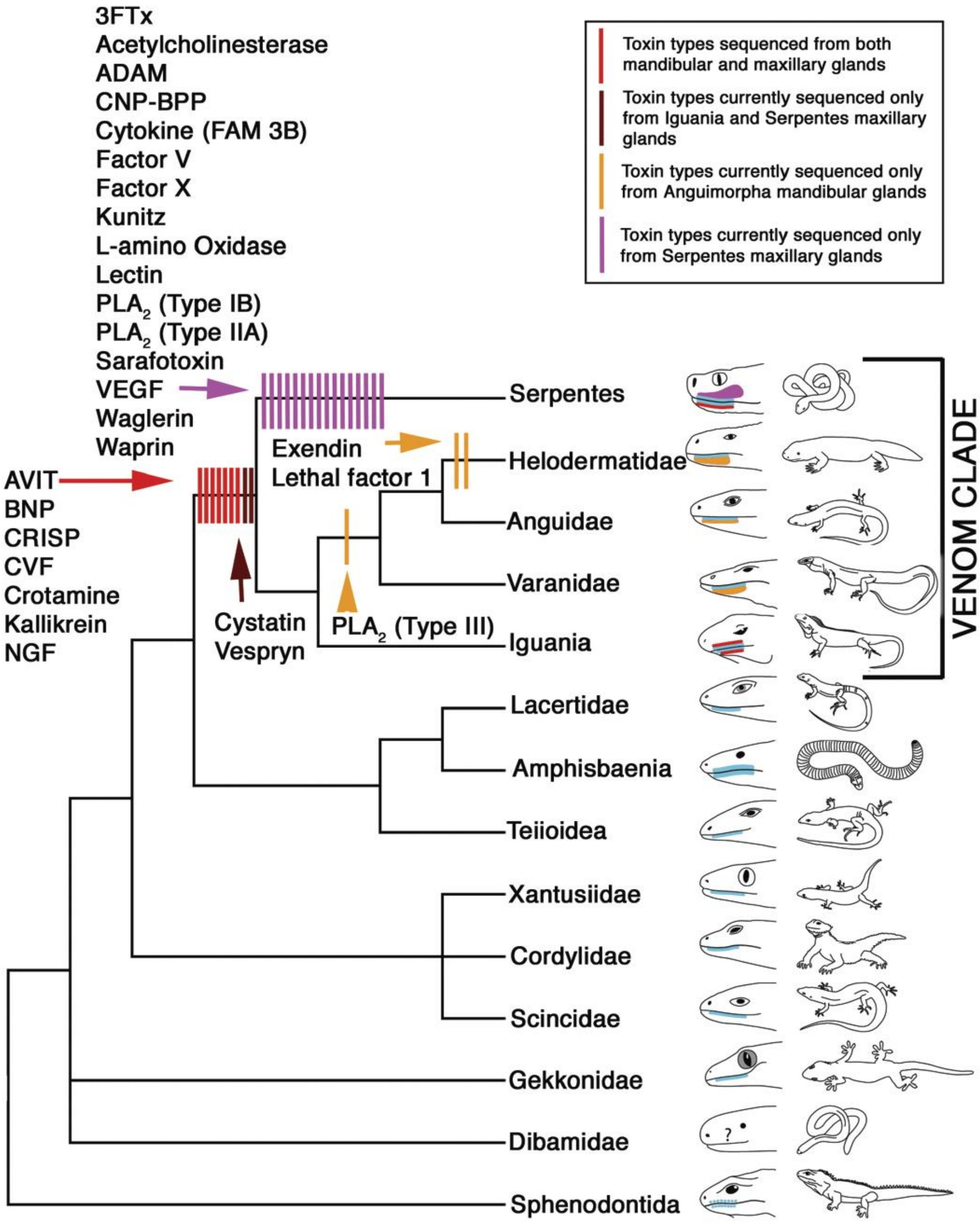

Figure 1.1 Relative glandular development and timing of toxin recruitment events mapped over the squamate reptile phylogeny. Mucus-secreting glands are coloured blue; the ancestral form of the protein-secreting gland (serial, lobular and non-compound) red; the complex, derived form of the upper snake-venom gland (compound, encapsulated and with a lumen) fuchsia, and the complex, derived form of the anguimorph mandibular venom gland (compound, encapsulated and with a lumen) orange. Toxin family key: 3FTx, three-finger toxins; ADAM, a disintegrin and metalloproteinase; CNP-BPP, C-type natriuretic peptide-bradykinin-potentiating peptide; CVF, cobra venom factor; NGF, nerve growth factor; VEGF, vascular endothelial growth factor (from Fry et al., 2006).

Among all venomous reptiles currently known to science, snakes are arguably the most notorious ones. Venomous snakes (all belonging to the clade Caenophidia, i.e., “advanced snakes”) inject venom into the body of their prey or attacker through specialised fangs or grooved teeth (Broeckhoven and du Plessis, 2017; Vonk et al., 2008). Species belonging to the families Viperidae, Elapidae and Atractaspididae use an advanced high-pressure, front-fanged venom delivery system (Kerkkamp et al., 2017). In these snakes, the compression of the primary venom gland by a skeletal muscle propels the venom originating from it through the primary venom duct, the secondary/accessory venom gland, and into specialised hollow fangs, which act like hypodermic needles (Jackson, 2003; Young and Kardong, 2007). Conversely, non-front-fanged colubroid snakes present a low-pressure venom delivery system. In these snakes, venom is slowly released from the venom glands (commonly referred to as Duvernoy’s glands, lacking compressor muscles) near maxillary fangs, typically enlarged and grooved, through which it flows into the bitten organism (Jackson, 2003; Weinstein, 2017; see Figure 1.2).

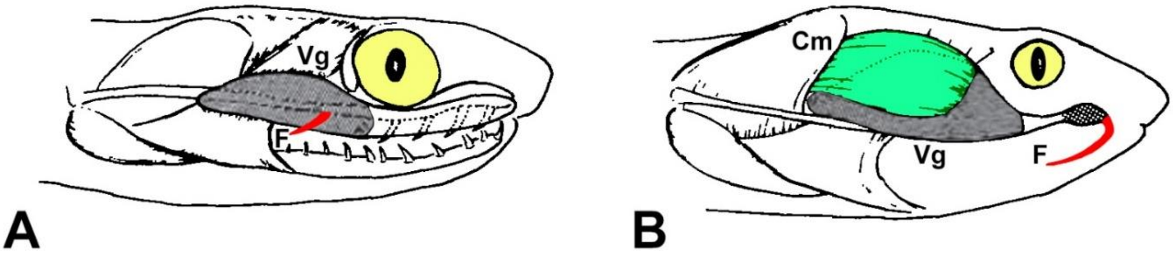

Figure 1.2 Comparison of non-front-fanged colubroid snake (A) and front-fanged (viperid) snake (B) venom delivery systems. Vg = venom gland (grey area); F = venom fang (red area); Cm = compressor muscle (green area) (modified from Weinstein and Kardong, 1994).

Snake venom is a mixture of proteins and peptides, organic molecules (e.g., carbohydrates, lipids) and salts in an aqueous medium (Casewell et al., 2013; Chan et al., 2016), thought to serve the main function of aiding predation (Arbuckle, 2017; Daltry et al., 1996), although selection on venom composition resulting from it being used for defensive purposes has been demonstrated for some species (i.e., spitting elapids of the genera *Naja* and *Hemachatus*; Kazandjian et al., 2021). Once injected into the prey/attacker, the toxins it comprises become systemic via dispersal by the bloodstream and lymphatic system, interacting with the physiological proteins and receptors of the envenomated organism, disrupting its homeostasis by targeting nervous system, blood coagulation cascade, and/or cardiovascular and neuromuscular system (Kerkkamp et al., 2017).

Through the analysis of compositional studies focusing on the venom proteomes of 132 different elapid and viperid snake species, Tasoulis and Isbister (2017) were able to identify more than 60 protein families comprising them. Excluding four protein families, each unique to a single genus, the authors classified them based on compositional abundance and frequency of occurrence into dominant, secondary, minor, and rare. The four dominant protein families were phospholipases A_2 (PLA_2s), snake venom metalloproteinases (SVMPs), snake venom serine proteinases (SVSPs) and three-finger toxins (3FTxs). The six secondary protein families included cysteine-rich secretory proteins (CRISPs), L-amino acid oxidases (LAAOs), Kunitz-type inhibitors (KUNs), C-type lectin-like proteins (CTLs), disintegrins (DISIs) and natriuretic peptides (NPs). The last two categories comprised nine minor and 36 rare protein families, respectively. In total, 63 protein families composing snake venoms were thus proposed.

This impressive diversity of venom components is considered to predominantly be a result of the so-called ‘birth and death’ process of gene evolution (Fry et al., 2003; Nei et al., 1997; see Figure 1.2). According to this model, genes encoding physiological body proteins (e.g., salivary, immunological, pancreatic) undergo frequent duplications, leading to the creation of duplicate copies. These copies are free from the functional constraints to which the original genes are subjected, and while most of them undergo pseudogenisation into dysfunctional forms over time, others are retained (Ohno, 1970). Once a retained duplicate copy is selectively expressed in the venom gland, it often undergoes additional gene duplications and neofunctionalisation (i.e., gain of novel functions), typically leading to the birth of large multi-locus gene families encoding toxins exhibiting formidable structural and functional diversity (Casewell et al., 2013; Chang and Duda Jr., 2012; Fry et al., 2003; Kordiš and Gubenšek, 2000). Recent studies have also highlighted the importance of alternative splicing and trans-splicing in driving the diversification of certain snake venom toxins, particularly snake venom metalloproteinases (SVMPs), snake venom serine proteinases (SVSPs) and vascular endothelial growth factors (VEGFs) (Ogawa et al., 2019; Shibata et al., 2018).

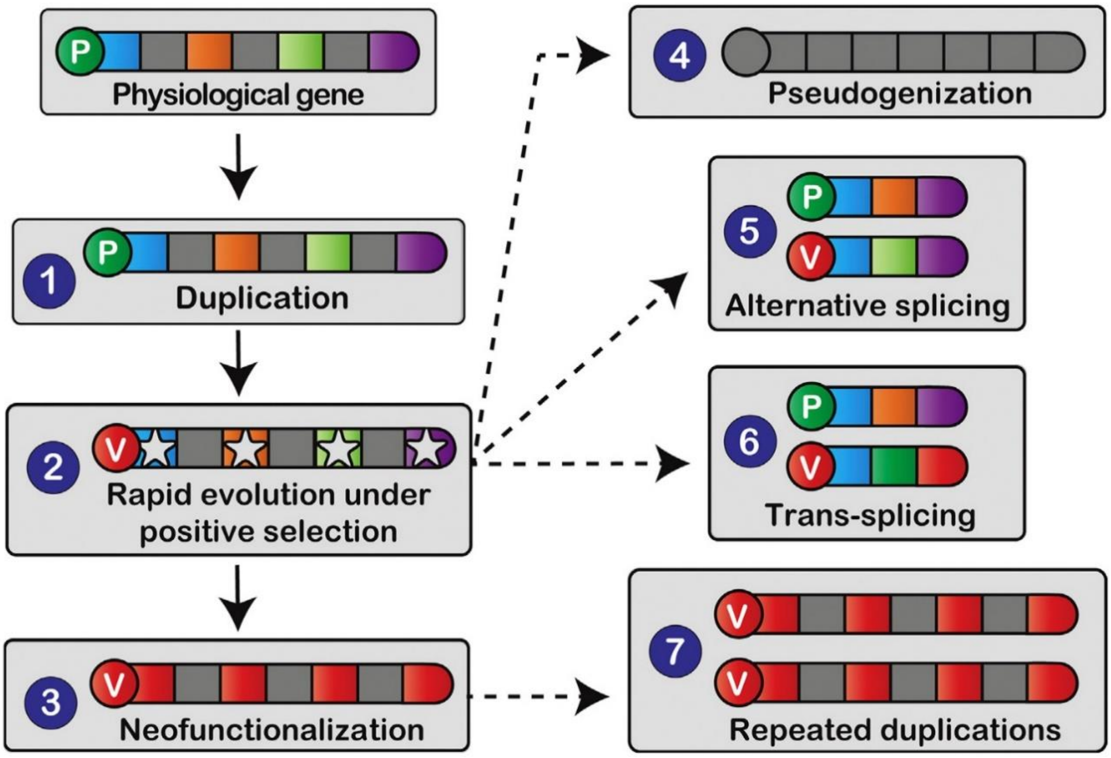

Figure 1.3 The molecular and evolutionary mechanisms that underpin the origin and diversification of snake venom toxins. This figure depicts various evolutionary mechanisms that underpin the origin and diversification of snake venom coding genes. Here, introns are shown in grey, while exons are depicted in various colours. Following their origin from (endo)physiological homologues (P) via (1) duplication, snake venom coding genes (V) rapidly accumulate variation under the influence of (2) positive Darwinian selection. On rare occasions, this process results in (3) the origin of novel functions, while it more commonly leads to (4) pseudogenization/degeneration. Snake venom diversity can also be generated via (5) alternative- and (6) trans-splicing, while increased expression can be achieved through (7) repeated gene duplications (from Casewell et al., 2020).

The ‘birth and death’ model of evolution of snake venom toxin families is often accompanied by evidence of accelerated evolution and positive selection (Sunagar and Moran, 2015). This has been demonstrated to mainly act by accumulating variations on surface-exposed amino acid residues, while retaining a largely stable protein macromolecular structure, thus promoting rapid toxin neofunctionalisation by modification of protein-target interactions (Casewell et al., 2011; Kordiš and Gubenšek, 2000). The evolution and diversification of snake venoms thus appear to be the result of the synergistic action of gene duplication, positive selection, and protein neofunctionalisation.

1.2 Variation in snake venom

The complexity of snake venom composition harbours the potential for extreme variation, which has been found to occur frequently and at all taxonomic levels (see Chippaux et al., 1991), as a consequence of both the evolutionary histories of divergent lineages and selection on the deployment of specific toxins (Casewell et al., 2020). The analysis of electrophoretic patterns of venoms obtained from different members of the families Viperidae and Elapidae, for example, highlighted substantial variation in venom composition both between and within families (Bertke et al., 1966). Indeed, elapid and viperid venoms present major compositional differences, with the first being generally less diverse in number of protein families, and presenting high abundances of 3FTxs. In turn, these toxins are virtually absent in viperid venoms, which are generally richer in SVMPs (Tasoulis and Isbister, 2017; see Figure 1.4). The reasons why certain toxin families have become central components of the venom of one lineage rather than the other are probably linked to their evolutionary histories and the ecological pressures they were subjected to, but are not fully understood (Fry et al., 2012).

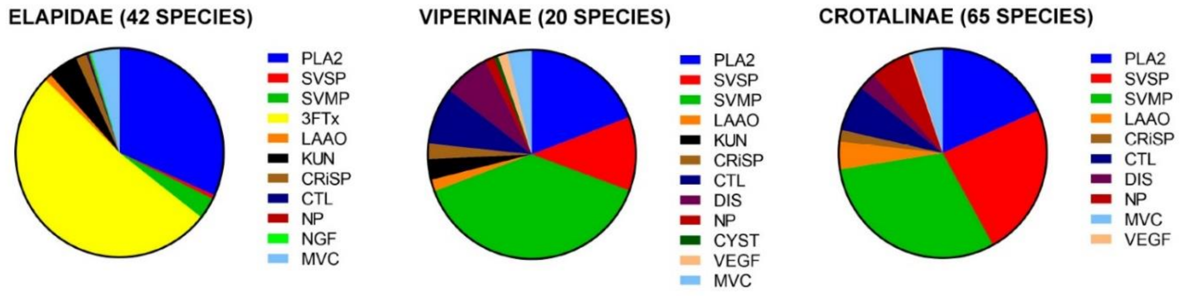

Figure 1.4 Relative proportions of different protein families for the venoms of: Elapidae (left); Viperinae (middle); and Crotalines (right), averaged from the number of species noted in the brackets. Toxin family key: PLA2, phospholipase A2; SVSP, snake venom serine proteinase; SVMP, snake venom metalloproteinase; LAAO, L-amino-acid oxidase; 3FTx, three-finger toxin; KUN, kunitz peptide; CRiSP, cysteine-rich secretory protein; CTL, C-type lectin; DIS, disintegrin; NP, natriuretic peptide; NGF, nerve growth factor; CYST, cystatin; VEGF, vascular endothelial growth factor; MVC, minor venom component (modified from Tasoulis and Isbister, 2017).

Broad differences in venom compositions can also be found between different genera belonging to the same family and between congeneric species. For instance, the analysis of the venom gland transcriptomes of several species of Australian elapids belonging to 11 different genera unravelled extensive variation for 3FTxs, CTLs, NPs, PLA$_2$s, and other toxin types (Jackson et al., 2013). At a finer scale, the analysis of more than 10 species of the genus *Bothrops* highlighted the existence of a large range of variation in their toxic activities, as well as in number and intensity of bands of the corresponding electrophoretic profiles (Queiroz et al., 2008). Similarly, the analysis of the venoms of different species of arboreal pit vipers of the genus *Bothriechis* found that while *Bothriechis thalassinus* and *Bothriechis aurifer* venoms presented a prevalence of SVMPs, CTLs and bradykinin potentiating peptides (BPPs), and a lack of PLA_2s, the latter were the predominant components of *Bothriechis bicolor* venom. The same study also found that, while the composition of *Bothriechis marchi* venom was similar to that of *B. thalassinus* and *B. aurifer*, being rich in SVMPs and BPPs, it also resembled *B. bicolor* venom in that it also contained considerable amounts of PLA_2s (Pla et al., 2017).

Notably, variation in venom composition and activity has been found to occur also at intra-specific level. This is for example the case of the South American rattlesnake *Crotalus durissus*, presenting two distinct venom phenotypes between different populations: one, belonging to the subspecies *C. d. cumanensis*, characterised by high levels of SVMPs and low lethal potency to lab mice, and the other, belonging to the subspecies *C. d. durissus*, *C. d. ruruima*, and *C. d. terrificus*, characterised by low levels of SVMP activity and high lethal potency to mice (Calvete et al., 2010). Similarly, the venoms of spectacled cobra *Naja naja* specimens from Punjab and West Bengal have been found to possess higher toxicities and greater amounts of neurotoxic 3FTxs than venoms of specimens originating from Rajasthan, characterised instead by higher abundances of cytotoxic/cardiotoxic 3FTXs and relatively lower lethal potencies (Senji Laxme et al., 2021).

Extensive evidence of venom variation occurring within the same population has also been presented. For example, through the analysis of proteomes and activities of venoms collected from 18 juvenile *Bothrops jararaca* specimens, Menezes et al. (2006) found considerable levels of individual variability and detected sex-related differences between siblings born and raised in controlled conditions, suggesting genetic inheritance. Similarly, compositional and functional variation between the venoms of juvenile and adult conspecifics (i.e., ontogenetic variation) has been documented for numerous snake species. For instance, Andrade and Abe (1999) found that the venom of juvenile *B. jararaca* specimens had a higher toxicity on anurans than that of adults, while Mackessy et al. (2018) found that venoms from adult specimens of *Crotalus polystictus* had higher SVMP activity than neonate venoms, which in turn presented a much higher PLA_2 activity and increased relative toxicity.

The evidence gathered so far suggests that one of the main factors contributing to such a dynamic scenario where snake venom composition varies at interspecific, intraspecific, and individual level is selection on the deployment of specific toxins for predatory purposes.

1.2.1 Diet as main driver of snake venom variation

Predatory venoms are typically more complex and variable in composition and physiological effects than defensive ones (Fry et al., 2009b). Concerning snake venoms, recent reports suggest the presence of a correlation between high prey diversity and a higher variety of toxic components. Indeed, different venom compositions are likely required to effectively subjugate prey items with different physiologies (Lyons et al., 2020). Support for this hypothesis, defined as "food availability hypothesis" (Siqueira-Silva et al., 2021), has been provided by a recent study focusing on the functional activities of the venoms of 258 snake species, which found that venoms of snakes with generalist diets showed higher venom complexity (Davies and Arbuckle, 2019). Consistently with this, in a comprehensive study focusing on 46 species of American pit vipers belonging to the genera *Agkistrodon*, *Crotalus*, and *Sistrurus*, Holding et al. (2021) suggested that venom complexity evolves in response to the phylogenetic breadth of the prey spectrum. In the presence of natural selection, such diversity likely has the potential to result in critical variation in venom composition, toxicity and mode of action.

Considering prey subjugation as the primary function of snake venom, therefore directly linked to the snake's fitness and survival, it stands to reason that snake venom composition is under strong natural selection for diet. First formal evidence supporting this hypothesis was provided by Daltry et al. (1996), who performed multivariate analyses on the electrophoretic patterns of venoms produced by several specimens of the pit viper *Calloselasma rhodostoma* collected from different populations, and found a significant relationship between venom composition and variation in diet. The authors suggested that the compositional differences detected between the analysed *C. rhodostoma* venoms could be adaptive, with venom compositions having been shaped by natural selection in response to differences in prey availability between the sampled populations.

Several other studies have provided results supporting the correlation between snake venom variation and diet. For example, Creer et al. (2003) found correlation between variation in venom phospholipases and adaptation to different diets in *Trimeresurus stejnegeri* specimens sampled from geographically different localities on the main island of Taiwan and two offshore Pacific islands. Accordingly, several studies detected increased prey-specific lethality to natural prey types. For instance, Barlow et al. (2009) found strong association between the toxicity of venoms collected from vipers of the genus *Echis* to a natural scorpion prey and degree of arthropod feeding. Additionally, studies on the venoms of different pigmy rattlesnake species of the genus *Sistrurus* showed correlation between venom diversity and proportion of mammals found in the diet, and strong prey-specific effects on amphibian, reptile, and mammal prey (Gibbs and Mackessy, 2009; Sanz et al., 2006).

Further support for diet as a driving factor in snake venom evolution has also been provided by research developed on snake species which shifted to a new prey-capture technique (e.g., constriction), or adapted to prey types that do not require venom to be subdued (e.g., eggs, worms, snails). The atrophied venom glands, significantly reduced fangs, and inactivity of the only three-finger toxin expressed in the venom of the sea snake *Aipysurus eydouxii*, for example, appear to be secondary results of the adaptation to feeding exclusively on fish eggs, which made venom unnecessary (Gopalakrishnakone and Kochva, 1990; Li et al., 2005; Voris and Voris, 1983). Loss or degeneration of the venom system due to it no longer being subjected to selection appears to have taken place also in other snake species feeding on defenceless prey (e.g., the bird egg specialist *Dasypeltis scabra*), and in some species which evolved constriction as a novel strategy of prey capture (e.g., *Pituophis guttatus*; Fry et al., 2008).

In light of the critically adaptive value and fast evolution rates of snake venom (Barua and Mikheyev, 2020; Casewell et al., 2011), the occurrence of venom variation between specimens originating from different areas (i.e., geographic/regional variation) might reasonably be associated with environmental pressures varying across geography, likely determining changes in prey communities, and ultimately influencing the feeding ecology of snake populations. This has been recently shown by Holding et al. (2018), who found that differences in prey community composition and genetic differentiation among populations accounted for roughly 70% of the variation in venom composition detected between 127 *Crotalus oreganus* venom samples from 13 locations across California.

Similarly, the occurrence of venom variation between individuals belonging to different age classes has frequently been correlated with differences in diet and/or foraging strategies. As an example, the fact that juveniles of *Bothrops asper* and *Crotalus viridis* present more SVMPs in their venoms than the adults has been associated with the fact that both species undergo a marked ontogenetic dietary shift, from a mainly ectotherm-based diet to a diet including mostly endotherm prey (Saldarriaga et al., 2003; Saviola et al., 2015). In some cases, ontogenetic variation in venom composition has been found to lead to differential venom effectiveness against different prey items, and taxa-specific effects. For instance, Mackessy et al. (2006) found significant variation in venom composition between neonate and adult *Boiga irregularis* specimens, mirrored by an ontogenetic shift in enzyme activities and toxicity. Specifically, neonate venoms were more than twice as toxic to reptile prey than adult venoms, which is concordant with the mostly ectotherm-based diet of *B. irregularis* juveniles. Conversely, no stark ontogenetic differences in venom composition and taxa-specific effects were found in the monocled cobra *Naja kaouthia* (Modahl et al., 2016), a generalist species with no apparent ontogenetic shift in prey preference (Chaitae, 2011).

The development of venom resistance in several animal species preying on venomous snakes (Khan et al., 2020; Perales et al., 2005; van Thiel et al., 2022), the innate avoidance of some colour patterns characteristic of certain venomous snake species (Smith, 1975, 1977), and the evolution of Batesian mimicry of some front-fanged taxa (Davis Rabosky et al., 2016; Greene and McDiarmid, 1981) suggest that snake venom can frequently provide an effective defence against predators/attackers. In this scenario, it appears plausible that selection might act on the venom composition of at least some snake species as a result of it being used for defensive purposes, other than predation. A recent work from Kazandjian et al. (2021) proved this to be the case for the venom-spitting elapids currently known. Using gene, protein, and functional analyses, the authors showed that African and Asian spitting *Naja* species and the rinkhals *Hemachatus haemachatus* possess venoms characterised by a significant up-regulation of PLA_2, which potentiate the effects of pre-existing cytotoxins widespread among cobras on mammalian sensory neurons, making the venom of spitting elapid species more effective than their non-spitting counterparts in (rapidly) causing pain, associated with defensive venom use (Chahl and Kirk, 1975; Eisner and Camazine, 1983). Similarly, Bohlen et al. (2011) discovered in the venom of the Texas coral snake *Micrurus tener* the first snake venom toxin (i.e., MitTx) unambiguously serving the sole purpose of causing pain. This toxin has later been found also in the venoms of *Micrurus mosquitensis* and *Micrurus nigrocinctus* (Fernández et al., 2015), and its presence has been strongly suggested also in the venoms of other *Micrurus* species (Aird et al., 2017; Rey-Suárez et al., 2016; Sanz et al., 2019). Additionally, Zhang et al. (2017) found in the venom of the Brazilian lancehead *Bothrops moojeni* the Lys49 myotoxin BomoTx, inducing inflammatory pain, thermal hyperalgesia, and mechanical allodynia through the promotion of ATP release and the consequent activation of the P2X2 and/or P2X3 purinergic receptors. Despite the proven strongly algesic activity of the toxins MitTx and Lys49, however, the role they might be playing in antipredator defence was actually never explored, and the relevance of defence in shaping snake venom evolution remains widely understudied.

1.2.2 Snake venom variation and the snakebite problem

Current, conservative estimates suggest that snakebite envenoming affects up to about 2 million people annually, and causes between 20,000 and 125,000 deaths per year worldwide (GBD 2019 Snakebite Envenomation Collaborators, 2022; Gutiérrez et al., 2017; Kasturiratne et al. 2008). Due to the high variability of snake venom composition, a wide variety of symptoms can arise following envenomation, depending on the occurrence and abundance of the toxin families, and on their molecular targets and enzymatic activities (Casewell et al., 2020; Chippaux et al., 1991; Gutiérrez et al., 2017; Tasoulis and Isbister, 2023). As a general rule, for instance, viperids tend to cause haemotoxic (e.g., haemorrhage, blood clots) and local (e.g., swelling, necrosis) effects, consistent with the predominance of SVSPs and SVMPs in their venoms (Damm et al., 2021; Slagboom et al., 2017; Warrell, 2010), whereas neurotoxic symptoms (e.g., ptosis, ataxia, paralysis) are more commonly elicited by elapid venoms, in which PLA_2s and 3FTxs are usually the dominant toxins (Silva et al., 2017; Warrell, 2010). Nonetheless, it must be noted that there are reports of local tissue damage and coagulopathy caused by elapid venoms (Warrell, 2010; White, 2005) and of neurotoxicity arsing following viperid bites (Kularatne and Ratnatunga, 1999; Shelke et al., 2002).

Defining snakebite symptomatology based on the snake lineages involved in the envenomations is in fact often very complex, and can lead to wrong assumptions regarding the therapeutic approach to apply, with potentially severe consequences (Fry et al. 2008; Junqueira de-Azevedo et al. 2006; Warrell, 2010). In the light of the very common occurrence of snake venom variation, it stands to reason that alterations in venom composition can impact the clinical manifestations observed following envenoming. A number of medically important species have indeed been found to exhibit substantial variation in the composition of their venoms, the symptoms these can elicit, and the efficacy of antivenom therapy. For example, Senji Laxme et al. (2019) found significant differences between proteomic, biochemical/pharmacological and toxicity profiles of the venom of some of India’s most medically relevant snake species (i.e., common krait *Bungarus caeruleus*, banded krait *Bungarus fasciatus*, Sind krait *Bungarus sindanus*, Russell’s viper *Daboia russelii*, saw-scaled viper *Echis carinatus*, monocled cobra *Naja kaouthia*, spectacled cobra *Naja naja*), and detected the alarmingly poor cross-neutralising capabilities of several commercial Indian antivenoms. Similarly, venoms of *D. russelii* specimens from different areas within the Indian Peninsula present marked concentration-dependent differences in procoagulant and anticoagulant activities (Prasad et al. 1999), and antivenoms manufactured using the venoms of Indian specimens exhibit low neutralising potencies against venoms of Bangladeshi origin (Pla et al., 2019).

Snake antivenoms are made starting from the hyperimmune serum collected from a large mammal (typically a horse) injected with increasing doses of venom over several months, in order to produce a progressive rise in neutralising antibodies (IgG) specific to the venoms used for immunisation (Lalloo and Theakston, 2003; Silva and Isbister, 2020). In this scenario, it is clear that the production of effective antivenoms depends on the knowledge of venom variation. Indeed, the characterisation of snake venom and its variation is of central relevance for both primary venom research and snakebite management, enabling the identification of the toxins to be neutralised, the prediction of the efficacy of existing antivenoms against untested snake species, and the targeted selection of the most appropriate species and specimens for the production of new ones (Calvete et al., 2021; Casewell et al., 2020; Gutiérrez et al., 2017).

1.3 The genus *Vipera*

1.3.1 Phylogenetic context

The genus *Vipera* Laurenti, 1768 comprises a group of venomous snakes belonging to the family Viperidae, subfamily Viperinae (i.e., Old World vipers, or "true vipers"). Despite the development of several studies on the phylogenetic and phylogeographic relationships between members of this family (e.g., Garrigues et al., 2005; Lenk et al., 2001; Wüster et al., 2008), and specifically within the genus *Vipera* (e.g., Ursenbacher et al., 2006; Velo-Antón et al., 2012), phylogeny and taxonomy of this group are still partially unresolved. A recent work aiming at assessing the validity of species belonging to the genera *Daboia*, *Macrovipera*, *Montivipera* and *Vipera* as independently evolving lineages (Freitas et al., 2020) analysed the relationships between the 26 *Vipera* species described at the time. By estimating phylogenetic relationships and time of divergence between species using a Bayesian Inference method implemented on the concatenated dataset of seven mtDNA markers (i.e., CR, control region; COI, Cytochrome c oxidase subunit I; cyt b, cytochrome b; ND2, NADH dehydrogenase subunit 2; ND4, NADH dehydrogenase subunit 4; ND5, NADH dehydrogenase subunit 5; 16S, mitochondrial gene coding for 16S rRNA), the authors recovered that the genus *Vipera* forms three well-supported monophyletic groups, named *Vipera* 1, *Vipera* 2, and *Pelias* (as originally defined by Zerova, 1992). While both *Vipera* 1 (including *Vipera aspis*, *Vipera latastei,* and *V. monticola*) and Vipera 2 (including *Vipera ammodytes* and *Vipera transcaucasiana*) presented deep phylogenetic structure and high levels of divergence between and within taxa, *Pelias* was the most diversified group in terms of described species, but the genetic divergence between them was overall shallow. The *Pelias* clade resulted divided into two subclades: one including *Vipera barani*, *Vipera berus*, *Vipera nikolskii*, and *Vipera seoanei*, and the other including the remaining 18 species considered (for details, see Freitas et al., 2020). In light of the phylogenetic reconstruction produced, several species did not match the recognised relevant evolutionary units and some of them were paraphyletic, thus signalling the presence of taxonomic inflation within *Vipera*. Despite the results obtained by Freitas et al. (2020), 21 species belonging to this genus are currently recognised by the most recent and complete list of reptile species available (i.e., The Reptile Database): *Vipera altaica*, *V. ammodytes*, *Vipera anatolica*, *V. aspis*, *V. berus*, *Vipera darevskii*, *Vipera dinniki*, *Vipera eriwanensis*, *Vipera graeca*, *Vipera kaznakovi*, *V. latastei*, *Vipera lotievi*, *Vipera monticola*, *V. nikolskii*, *Vipera* *orlovi*, *Vipera renardi*, *Vipera sakoi*, *V. seoanei*, *V. transcaucasiana*, *Vipera ursinii*, and *Vipera walser* (see Uetz et al., 2023).

1.3.2 Ecological overview

Snakes of the genus *Vipera* are spread across the Old World, and can be found predominantly in Europe from Portugal to Turkey, Mediterranean islands (i.e., Sicily, Elba, Montecristo), and the United Kingdom (Phelps, 2010; Sindaco et al., 2013). Nevertheless, *Vipera* species also occur in Africa (i.e., *V. monticola*, in Morocco, Algeria, and probably Tunisia; Martínez-Freiría et al., 2021), Western Asia (e.g., *V. eriwanensis* in Turkey, Georgia, Armenia, Azerbaijan, and Iran; Iankoshvili and Tarkhnishvili, 2021; Kukushkin et a., 2012; Kutrup et al., 2005; Rajabzadeh et al., 2011), and East Asia (i.e., *V. berus*, reaching up to North Korea; Mallow et al., 2003; Phelps, 2010; Sindaco et al., 2013; Ursenbacher et al., 2006).

Members of this genus are typically small to medium-sized, with a maximum total length for adult specimens ranging from about 400 mm (i.e., *V. monticola*; Brito et al., 2006; Martínez-Freiría et al 2021) up to roughly one metre (i.e., *V. ammodytes*; Mallow et al., 2003; Phelps, 2010). Depending on the species, the head is markedly triangular or not very distinct from the body, which in turn can be more or less slender or thickset, but invariably covered with keeled scales (Mallow et al., 2003; Phelps, 2010). Vipers belonging to this genus are generally distinguishable for their dorsal pattern, typically comprising of a conspicuous zigzag, in some cases highly variable (e.g., *V. aspis*, Ducrest et al., 2014; *V. seoanei*, Lucchini et al., 2020; see Figure 1.5). Several studies have shown that this characteristic zigzag pattern might function as a warning signal against predators (Martínez-Freiría et al., 2017; Valkonen et al., 2011; Wüster et al., 2004), while others have suggested that variation in it might be driven by its cryptic role, as the zigzag pattern could decrease a viper's detectability on certain backgrounds, and/or its thermal role, as larger zigzag bands might provide higher thermoregulatory efficiency (Martínez-Freiría et al., 2020; Santos et al., 2014).

Figure 1.5 Dorsal pattern of some *Vipera* species in European snakebites: *V. ammodytes* (A); *V. aspis* (B); *V. berus* (C); *V. latastei* (D); *V. seoanei* (E); *V. ursinii* (F). Photo credits: Matteo R. Di Nicola (A, B, C, F); Matthieu Berroneau (D, E) (from Paolino et al., 2020).

Snakes of the genus *Vipera* mainly prey on vertebrates, both ectotherms (e.g., amphibians, reptiles) and endotherms (e.g., rodents; Anđelković et al., 2021; Brito, 2004; Espasandín et al., 2022; Luiselli and Agrimi, 1991), although some members of the *Pelias* clade are known to mainly feed on invertebrates (e.g., *V. usinii*, Baron, 1992; *V. graeca*, Mizsei et al., 2019). Notably, several *Vipera* species undergo a marked ontogenetic shift in diet composition, with juvenile vipers switching from an ectotherm-based to an endotherm-based diet as they grow (e.g., *V. latastei*, Brito, 2004; *V. seoanei*, Espasandín et al., 2022). For a number of them, changes in prey consumption due to factors such as seasonality and/or environmental variability have also been reported (e.g., Mizsei et al., 2019; Santos et al., 2007, 2008; Tomović et al., 2022).

1.3.3 Venom and envenoming

A recent work providing a comprehensive compilation of venom compositions of snakes belonging to the subfamily Viperinae reports that the venoms produced by snakes of this subfamily appear to comprise of four major toxin families, accounting on average for about 75% of their compositions: snake venom metalloproteinases (SVMPs), phospholipases A_2 (PLA_2s), snake venom serine proteinases (SVSPs), and C-type lectin-like proteins (CTLs) (Damm et al., 2021). Less abundant toxin families, accounting for about 17% of the considered venom compositions, are disintegrins (DISIs), cysteine-rich secretory proteins (CRISPs), vascular endothelial growth factors (VEGFs), Kunitz-type inhibitors (KUNs) and L-amino-acid oxidases (LAAOs). Among the minor components, observed less frequently and at low abundances across the venom compositions reported, are nerve growth factors (NGFs), 5′-nucleotidases (5Ns), phosphodiesterases (PDEs), hyaluronidases (HYALs), phospholipases B (PLBs), cystatins (CYSs), glutaminyl cyclotransferases (QCs), aminopeptidases (APs), SVMP-inhibitors (SVMPis) and bradykinin-potentiating peptides (BPPs) (see Damm et al., 2021). These components are concordant with the mainly haemorrhagic and cytotoxic effects of viper envenomation (Gutiérrez et al., 2017; Warrell, 2010).

Among the subfamily Viperinae, the genus *Vipera* is the most frequently involved one in snakebite accidents in Europe (Chippaux, 2012; Paolino et al., 2020; Zanetti et al., 2018). Specifically, from a recent analysis of 3574 reports of snakebite accidents caused by *Vipera* species in Europe, *V. ammodytes*, *V. aspis*, *V. berus*, *V. latastei*, *V. seoanei* and *V. ursinii* resulted to be the six *Vipera* species of highest medical relevance in Europe, on the basis of their wide distribution and the high number of reported envenomations caused by them (Paolino et al., 2020). Particularly, *V. ammodytes*, *V. aspis*, and *V. berus* were accountable for the highest number of ophidic accidents, followed by *V. latastei*, *V. seoanei*, and *V. ursinii*.

Clinical symptoms caused by envenoming by members of this genus range from minimal and local (e.g., algesia, swelling) to systemic and potentially life-threatening (e.g., haematological, neurological; Chippaux, 2012; Paolino et al., 2020). From the analysis by Paolino et al. (2020), the local symptoms most frequently observed were oedema (73.6%), ecchymosis (68.3%), and erythema (56.6%), while systemic symptoms like haemorrhage, disseminated intravascular coagulation, and low platelet count were reported but rarer (11%, 3.1%, and 7.0% of the cases, respectively). Hypotension, a known dangerous effect of *Vipera* envenoming, was detected in more than half (55.2%) the analysed reports. Neurotoxic effects, typically documented only for few species of this genus (e.g., *V. ammodytes*, Logonder et al., 2008; *V. aspis*, Zanetti et al., 2018; *V. berus*, Malina et al., 2017) were not prevalent, but neurological symptoms affecting cranial nerves were reported in 14.8% of the considered cases (Paolino et al., 2020).

Notably, despite the medical relevance of *Vipera* envenomations, the venom of species belonging to this genus appears to receive limited attention from snake venom research. Particularly, a recent review of Old World viper venom proteomes found that only 13 of the 89 Viperinae venom proteomes analysed focused on the composition of *Vipera* venoms, encompassing only 10 species (Damm et al., 2021). In this work, *V. ammodytes* and *V. berus* seemingly received more attention than the other *Vipera* species. Indeed, the venoms of *V. ammodytes* and *V. berus*, together with *V. aspis* and *V. ursinii*, have been characterised and analysed with different levels of detail (e.g., Georgieva et al., 2008; Giribaldi et al., 2020; Lang Balija et al., 2020; Latinovic et al., 2016), probably because of the major medical relevance of these species in Europe (Paolino et al., 2020). Nonetheless, *V. latastei* and *V. seoanei*, the other two European species of highest medical importance (Paolino et al., 2020), have so far been minimally investigated (see Damm et al., 2021). Providing a first characterisation of the venoms of these two species would be crucial, not only to reach a more comprehensive knowledge on properties and variability of European viper venoms, but also to help improve the clinical management of the envenomations they can cause.

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Chapter 2

Objectives and Thesis Structure

2.1 General objectives

The main goal of this thesis is to increase the current knowledge on the venoms produced by vipers belonging to the genus *Vipera*, focusing on species from the Iberian Peninsula. General goals are defined as follows: 1) provide a formal description of the general trends and biases in snake venom studies in terms of species and research topics; 2) provide a resume of the current knowledge on the species of the genus *Vipera* of major medical importance in Europe; 3) provide the first characterisation of the venoms of the species *Vipera latastei* and *Vipera seoanei*, with an assessment of their intraspecific variation.

2.2 Thesis outline

This dissertation is divided into seven chapters, as follows:

Chapter 1 comprises of a resume of topics relevant to the following chapters, starting with a brief introduction on snake venom origin and evolution, and the molecular mechanisms involved. Then, a description of snake venom variation, the taxonomic levels at which it can occur, and its relationship with snake diet is provided. Emphasis is given to evidence supporting the role of diet as main driver of snake venom variation, and to the supposed adaptive value of the latter. Finally, phylogenetic and ecological context of species belonging to the genus *Vipera*, together with some of the information available about their venoms and the envenomations they can cause, is presented.

In Chapter 2, the main objectives of this thesis and its outline are described.

Chapter 3 investigates trends and biases in snake venom studies through the analysis of relevant articles published over the past 57 years. Information on taxonomy, realm of origin, and harmful potential of the studied snake species is provided, and used as factors to test whether or not they can influence the popularity of a species in snake venom research. Information on the most investigated topics in this field of study is also presented.

This study was published as:

- Avella, I., Wüster, W., Luiselli, L., & Martínez-Freiría, F. (2022) Toxic habits: an analysis of general trends and biases in snake venom research. *Toxins*, 14(12), 884. https://doi.org/10.3390/toxins14120884

Chapter 4 focuses on the study of the six *Vipera* species of major medical relevance in Europe, namely *Vipera ammodytes*, *Vipera aspis*, *Vipera berus*, *Vipera latastei*, *Vipera seoanei* and *Vipera ursinii*. A key to their identification, information about the composition of their venoms and their toxicity, as well as guidelines for first aid and clinical treatment of the envenomation symptoms they can cause are provided.

This study was published as:

- Di Nicola, M. R., Pontara, A., Kass, G. E. N., Kramer, N. I., Avella, I., Pampena, R., Mercuri, S. R., Dorne, J. L. M., & Paolino, G. (2021). Vipers of major clinical relevance in Europe: taxonomy, venom composition, toxicology and clinical management of human bites. *Toxicology*, 453, 152724. https://doi.org/10.1016/j.tox.2021.152724

Chapter 5 provides the first proteomic characterisation of the venom of Lataste's viper (*Vipera latastei*). Through the analysis of proteomes and chromatographic profiles obtained from venoms of both adult and juvenile specimens collected in two environmentally distinct localities in northern Portugal, an assessment of the ontogenetic and geographic variation in the composition of this species' venom is presented.

This study was published as:

- Avella, I., Calvete, J. J., Sanz, L., Wüster, W., Licata, F., Quesada-Bernat, S., Rodríguez, Y., & Martínez-Freiría, F. (2022) Interpopulational variation and ontogenetic shift in the venom composition of Lataste's viper (*Vipera latastei*, Boscá 1878) from northern Portugal. *Journal of Proteomics*, 263, 104613. https://doi.org/10.1016/j.jprot.2022.104613

Chapter 6 provides the first proteomic characterisation of the venom of the Iberian adder (*Vipera seoanei*). Through the analysis of electrophoretic profiles obtained from venoms of adult specimens collected across the species' distributional range in northern Iberian Peninsula, an assessment of the geographic variation in *V. seoanei* venom composition is presented. The study also includes an investigation on biological, genetic, and eco-geographic factors potentially involved in the occurrence of such variation.

This study was published as:

- Avella, I., Damm, M., Freitas, I., Wüster, W., Lucchini, N., Zuazo, Ó., Süssmuth, R., & Martínez-Freiría, F. (2023). One Size Fits All—Venomics of the Iberian adder (*Vipera seoanei*, Lataste 1878) reveals low levels of venom variation across its distributional range. *Toxins*, 15(6), 371. https://doi.org/10.3390/toxins15060371

In Chapter 7, a discussion of the topics and interpretations drawn in this thesis is presented, with an emphasis on the major findings and future research challenges arising from it.

Chapter 3

Analysis of general trends and biases in snake venom research

Introduction

About 200,000 species of venomous animals belonging to many different taxa (e.g., cnidarians, arthropods, reptiles, fishes, mammals) are currently known to science (Jenner and Undheim, 2017). Among them, snakes are arguably the most notorious ones. Of more than 3900 snake species currently recognised (Uetz et al., 2022), about 300, mainly belonging to the families Viperidae (e.g., adders, rattlesnakes, palm pit vipers), Elapidae (e.g., cobras, coral snakes, sea snakes), and Colubridae (e.g., vine snakes, twig snakes, boomslangs) are considered of medical importance by the World Health Organization (WHO) (Longbottom et al., 2018; Uetz et al., 2022; WHO, 2020).

Snake venom is a complex mixture of peptides, proteins, small organic molecules, and salts (Calvete, 2013; Chan et al., 2016), able to disrupt the general homeostasis of the envenomated organism, affecting it in different ways and with different levels of specificity and potency (Cohen et al., 2005; Herzig et al., 2005; Lyons et al., 2020). Snake venom has long been and remains in the spotlight for researchers from all over the world, mostly because of the medical importance of snakebites for human health (Gutiérrez et al., 2006, 2017; Kasturiratne et al., 2008). For many years, it has been studied through traditional biochemical and pharmacological approaches, often focusing mainly on abundant toxins present in venoms produced by the most common medically relevant species (e.g., *Daboia russelii*, Kasturi and Gowda, 1989; *Bothrops jararaca*, Nishida et al., 1994), and neglecting the venoms of a large number of rarer and/or generally less studied species (Jackson et al., 2019; Lomonte and Calvete, 2017; Mackessy and Saviola, 2016).

Advances in the so-called “omic” technologies, defined as the application of highthroughput methodologies (Fuzita et al., 2016), and their inclusion in the conventional analysis procedures, completely revolutionised snake venom studies. The term “venomics” currently describes the comprehensive study and characterisation of the whole venom profile of a toxic organism by the means of integrated “omic” methodologies, namely proteomics, transcriptomics, and genomics (Calvete, 2013; Fuzita et al., 2016; Oldrati et al., 2016). Specifically, modern snake venomics allow for the identification of venom components both directly, through the analysis of the protein content of crude venom (i.e., proteomics), and indirectly, through the sequencing of venom gland mRNA or cDNA (i.e., transcriptomics), or of the full genome (i.e., genomics) of the analysed species (Oldrati et al., 2016). By allowing the rapid characterisation of all venom components of a growing number of snake species from all over the world, the deployment of snake venomics is gradually filling the knowledge gap left by the application of previous, less comprehensive approaches. The remarkable amount of information produced by venomics about composition and properties of different snake venom phenotypes, together with its implementation in functional studies, is helping to elucidate the processes underlying snake venom origin and evolution, and is driving the development of powerful therapeutic tools to be used to mitigate the global burden of snakebite (Post et al., 2019; Sajevic et al., 2011) and successfully treat different types of diseases (e.g., Azim et al., 2016; King, 2011, and references within).

Despite the growing attention snake venom studies have received since the rise of venomic approaches, it has been noted that, in this line of research, some topics tend to be investigated more frequently than others (Arbuckle, 2020; Calvete, 2013; Stern, 2019). Questions regarding snake ecology (e.g., interactions between snakes and their prey), for example, are seldom addressed in venomic studies, despite being relevant for both evolutionary biology and the development of effective snakebite mitigation strategies (Gutiérrez, 2020; Jackson et al., 2019; Murray et al., 2020). Similarly, research efforts seem to be greatly biased towards species belonging to the families Elapidae and Viperidae, whereas other snake families (e.g., Psammophiidae, Pseudoxyrophiidae, Atractaspididae, Homalopsidae) tend to be overlooked (Jackson et al., 2019). Although these tendencies in snake venom studies have long been recognised (e.g., Diz and Calvete, 2016; Jackson et al., 2019), they have never been formally quantified.

In the present stduy, we aim to provide formal categorisation and quantification of the current biases in snake venom research. To this end, we (i) present an estimation and description of the prevailing trends in snake venom studies published between 1964 and 2021, (ii) analyse whether and how the focus of the retrieved studies changed in terms of topics and taxa covered across the defined time frame, and (iii) test whether potential biases in terms of number of articles dedicated to each retrieved snake species could be related to specific factors (e.g., taxonomy, biogeographic realm of origin). We expect our findings to uncover the taxonomic and topic imbalances present in this field of study, and potentially help identify their origin and define the directions to follow to redress them.

Materials and Methods

Article selection

Publications considered for the current study were gathered and organised using the Google Scholar (Google Inc. (Menlo Park, CA, USA)) web search engine (https://scholar.google.com), between the months of December 2018 and March 2022. To perform the search, the following query was used, applying every possible combination of the ten selected keywords: (<venom> OR <venomics>) AND (<toxin> OR <composition> OR <profile>) AND (<snake> OR <viper> OR <elapid> OR <colubrid> OR <atractaspid>). The evaluation timeframe we defined went from 1964 to 2021. Search results were sorted by relevance following Google Scholar default search options, with the quality of the result search match being higher on top of the result list and progressively decreasing. We thus reviewed for consideration the first 200 articles obtained for each keyword combination searched, checking their suitability for inclusion in the final dataset. Articles focusing on the study of snake venom composition and variation, presenting either a protein-centred venom approach or an indirect approach based on different techniques (e.g., transcriptomics, bioinformatics, toxicity assays) were taken into account for analysis. Articles not investigating whole snake venoms (e.g., reviews, publications focusing only on single venom fraction analysis, single toxin studies), and/or not published in refereed, impacted journals were not considered.

The following information was recorded from each article: (i) publication year, (ii) taxonomy of the analysed species, (iii) country and biogeographic realm of origin of the analysed specimens, and (iv) topics covered.

Taxonomic information

In order to assess what the most studied and most represented snake taxa were, information about family, subfamily, genus, and species of the specimens analysed in each article was collected. Due to phylogenetic uncertainty within the family Elapidae (Lee et al., 2016; Williams et al., 2006; Zaher et al., 2019), we did not consider subfamilies for this group, but instead divided it into two main categories widely used in the literature, irrespective of concerns over monophyly (Scanlon et al., 2004; Slowinski et al., 1997, 2000): (i) Old World and American elapids and (ii) Australo-Papuan and marine elapids. The retrieved taxonomic information was updated mainly following the taxonomy reported by The Reptile Database (Uetz et al., 2021), based on information about species names and sampling localities of the specimens. When insufficient locality and taxonomic information did not allow the unambiguous identification of the analysed snake species, we kept the specific IDs as reported in the original articles.

Hazard categories

In order to test whether the harmful potential of a species' venom could influence eventual biases in terms on number of studies dedicated to it, we developed a hazard index based on the existing bibliography (e.g., Gutiérrez et al., 2017; Weinstein et al., 2011), WHO guidelines (e.g., WHO, 2010, 2016, 2020), and authors' opinion. We classified the snake species considered in the retrieved studies into four categories, based on the severity of the envenomation they can cause: (i) category 1—"critical clinical relevance": envenomations have a generally high chance to cause death or significant disability if professional medical care is not obtained; (ii) category 2—"high clinical relevance": envenomations usually cause significant illness, hospitalisation is required, death and/or disability are unlikely but possible if professional medical care is not obtained; (iii) category 3—"moderate clinical relevance":

envenomations are unpleasant but typically not life-threatening, significant disability is exceptional, typically treated symptomatically; (iv) category 4—“low clinical relevance”: envenomations likely cause only very mild symptoms (e.g., local swelling, itching, limited blistering), generally not interfering with normal activities and not being life-threatening, and professional medical care rarely necessary. Species we could not assign to any of the abovementioned categories were classified as “unknown” and not included in the analyses.

Origin of the specimens

Information about the country where each snake species that produced the analysed venom samples came from, and the corresponding biogeographic realm, was also gathered and used to assess possible geographical biases in snake venom studies. Country and biogeographic realm of origin of specimens for which information about the place of origin was ambiguous or unavailable (e.g., captive specimens, pooled venoms) were considered as “unknown” and not included in the analyses. Biogeographic realms were identified following the RESOLVE Ecoregions 2017 website (Dinerstein et al., 2017).

Topics covered

In order to identify the most investigated research topics in the retrieved articles, we gathered information about the research topics covered in the reviewed publications, and grouped them into eight categories: (i) “venom characterisation”: defining the composition of the venom of snake species through the application of one or more techniques, from basic venom fractionation to “omic” approaches (i.e., proteomics, transcriptomics, genomics); (ii) “antivenomics and neutralisation”: evaluating immunological mechanisms in model animals and/or efficacy of one or more antivenoms against the venom of the analysed snake species; (iii) “biological activity”: assessing the enzymatic, toxic, and/or lethal (i.e., LD_{50}) activity of the venom produced by the analysed snake species; (iv) “envenomation symptoms”: description of envenomation symptoms in humans resulting from snakebite accident; (v) “geographic venom variation”: comparing venom profiles, components, and/or biological activity between individuals belonging to the same snake species but coming from different populations and/or habitats across their natural range; (vi) “individual venom variation”: comparing venom profiles, components, and/or biological activity between individuals of the same snake species, with a focus on venom variation related to differences in age (i.e., ontogeny), sex, and/or diet; (vii) “interspecific venom variation”: comparing profiles, components, and/or activity of venoms produced by snakes belonging to different species; (viii) “prey specificity”: testing efficacy and/or efficiency of the venom of the analysed snake species against the preferred natural prey.

Chronological trends

Information about the publication year of each analysed article was gathered in order to define the total number of publications per year, and thus identify the most and least productive years in terms of published articles. Using this information, we built cumulative curves in order to identify trends in terms of studied families, subfamilies, and research topics varied across the retrieved articles along the considered timeframe. The data obtained this way allowed to assess patterns of chronological variation in the above-mentioned categories.

Statistical analyses

We performed chi-squared (χ^2) tests to assess the significance of the differences in terms of article coverage detected between snake taxa (i.e., family, subfamily, genus), countries, biogeographic realms, and topic categories. To investigate the presence of significant relationships between number of publications on snake venom and years from 1964 to 2021, we tested the following regression models: (i) 1st order polynomial, (ii) 2nd order polynomial, and (iii) 3rd order polynomial. We ranked the models on the basis of the corrected Akaike's Information Criterion (AICc) (Burnham and Anderson, 2002), ultimately applying the model with the lowest AICc score considered as the best-fitting one. We applied the same method to also choose the best model to test the presence of significant relationships between the number of years that passed from 1964 to 2021 and the number of yearly papers covering each of the eight topic categories defined. To investigate whether family, hazard category, and biogeographic realm of origin of the snake species retrieved from the analysed articles could be correlated with the number of articles dedicated to each one of them, we used Generalised Linear Models (GLM) assuming a Poisson distribution for the response variable. Country of origin and subfamily were excluded from the used predictors because the retrieved information relative to them was often fragmentary and ambiguous, and because they were nested in the predictors “biogeographic realm” and “family”, respectively. Collinearity between the three predictors considered (i.e., family, hazard category, biogeographic realm) was low (Variance Inflation Factors (VIF) always < 5.11), thus we included all of them in the regression models generated. We built the models using the number of articles dedicated to each species as response variable, and all possible combinations of the three predictors considered. The produced models were ranked on the basis of their AICc score, considering the model with the lowest AICc score as the best-fitting one. Polynomial regression models were generated using the software SPSS (version 13.0.; SPSS Inc., 2003). All other analyses were performed in R environment (version 4.1.1; R Core Team, 2021). We used the packages *vegan* (Oksanen, 2016) and *MuMIn* to build the full set of Generalised Linear Models (Bartoń, 2020).

Results

Taxonomic information

A total of 267 articles was considered for the current study (complete list provided in Table A1.1). From the analysis of these articles, we gathered information about a total of 298 snake species belonging to seven different families: Viperidae, Elapidae, Colubridae, Atractaspididae, Homalopsidae, Psammophiidae, Pseudoxyrhophiidae. Most of the retrieved species belonged to the families Viperidae and Elapidae.

The differences in article coverage of snake families and subfamilies/groups were significant (families: $\chi^2_{(6)} = 243.1$, $p < 0.0001$; subfamilies/groups: $\chi^2_{(12)} = 228.9$, $p < 0.0001$). The family Viperidae was the most studied one, followed by the families Elapidae and Colubridae. Most of the viperids belonged to the subfamily Crotalinae, which was the most studied snake subfamily. In terms of number of articles and studied species, the snake families Atractaspididae, Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae were both the least studied and the least represented. For further details about the number of species and articles retrieved for each family and subfamily/group, see Figure 3.1.

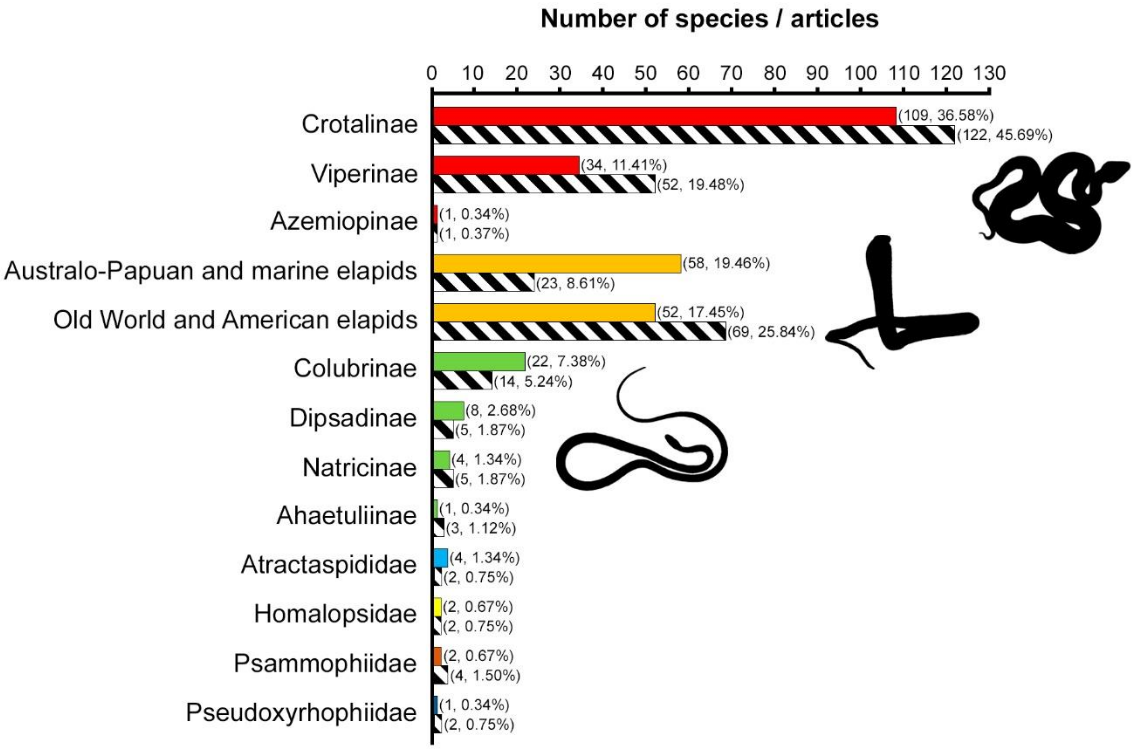

Figure 3.1 Number of species and articles for the snake families and subfamilies studied in the reviewed publications. Coloured bars refer to the number of species belonging to from the analysed publications; striped bars refer to the number of gathered articles studying members of each taxon. Exact numbers are reported in parentheses. The percentages refer to the total number of species and publications retrieved. Bars of the same colour correspond to subfamilies belonging to the same family (i.e., red = Viperidae, orange = Elapidae, green = Colubridae). Following Uetz et al. (2021), for the families Atractaspididae, Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae, no subfamilies are currently identified. Original elapid silhouette by Chris Hay, provided via www.phylopic.org, and modified and used under license CC BY-NC 3.0.

A total of 96 snake genera were retrieved from the literature analysis, mostly belonging to the families Elapidae (35 genera, 36.46%), Viperidae (30 genera, 31.25%), and Colubridae (25 genera, 26.04%). The differences in article coverage between snake genera were significant ($\chi^2_{(95)} = 196.7$, $p < 0.0001$). With 26 species studied in the considered publications, *Bothrops* was the most represented genus, followed by *Crotalus* (24 studied species) and *Micrurus* (19 studied species). *Bothrops* and *Crotalus* were also the two most studied genera (43 and 39 articles, respectively). The most studied species overall was the South American pit viper *Bothrops atrox* (20 publications, 7.49% of all retrieved articles; Figure 3.2). The complete list of all retrieved snake taxa is reported in Table A1.2.

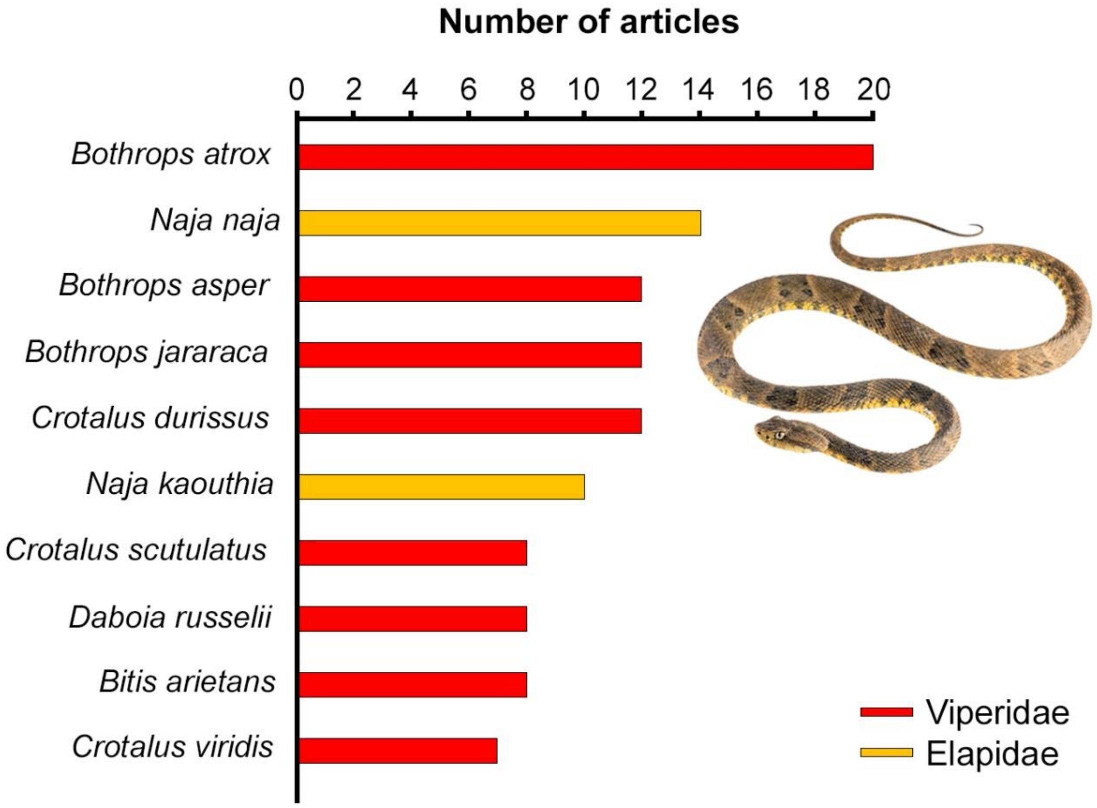

Figure 3.2 Information about the top ten most studied snake species. The graph shows the number of retrieved articles studying each species. Depicted in photo, *Bothrops atrox* (edited from Arteaga et al., 2020).

Hazard categories

Most of the 298 snake species retrieved from the analysed literature were assigned to the first two hazard categories. Specifically, most of viperids and elapids were considered of critical clinical relevance/category 1 or high clinical relevance/category 2. The species considered of moderate clinical relevance/category 3 and low clinical relevance/category 4 encompassed most of the Colubridae, and all of the Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae species retrieved. Because of the lack of data about envenomation caused by the elapid *Toxicocalamus longissimus*, this species was the only one we were unable to assign to any on the four hazard categories defined. For detailed information about the number of species included in each hazard category, and the hazard category assigned to each one of them, see Tables 3.1 and A1.2.

Table 3.1 Number of snake species assigned to each of the four hazard categories defined by family and subfamily/group. The percentages refer to the total number of species retrieved for the considered taxonomic category/group from the publications analysed.

		Hazard Category				
	N Species	**Cat. 1**	**Cat. 2**	**Cat. 3**	**Cat. 4**	**Unknown**
Viperidae	144	73 (50.69%)	65 (45.14%)	6 (4.17%)	0	0
Azemiopinae	1	0	1 (100%)	0	0	0
Crotalinae	109	55 (50.46%)	54 (49.54%)	0	0	0
Viperinae	34	18 (52.94%)	10 (29.41%)	6 (17.65)	0	0
Elapidae	110	55 (50%)	33 (30%)	15 (13.64%)	6 (5.45%)	1 (0.91%)
Australo-Papuan and marine elapids	58	25 (43.1%)	12 (20.69%)	14 (24.14%)	6 (10.35%)	1 (1.72%)
Old World and American elapids	52	30 (57.69%)	21 (40.39%)	1 (1.92%)	0	0
Colubridae	35	2 (5.71%)	2 (5.71%)	12 (34.39%)	19 (54.39%)	0
Ahaetuliinae	1	0	0	0	1 (100%)	0
Colubrinae	28	2 (9.1%)	0	8 (36.4%)	12 (54.5)	0
Dipsadinae	4	0	0	4 (50.0%)	4 (50.0%)	0
Natricinae	2	0	2 (50.0%)	0	2 (50.0%)	0
Atractaspididae	4	0	4 (100%)	0	0	0
Homalopsidae	2	0	0	0	2 (100%)	0
Psammophiidae	2	0	0	1 (50.0%)	1 (50.0%)	0
Pseudoxyrhophiidae	1	0	0	0	1 (100%)	0
Total	298	130 (43.62%)	104 (34.9%)	34 (11.41%)	29 (9.73%)	1 (0.34%)

Countries and biogeographic realms

The most represented country in terms of number of studied species was Australia (55 species), followed by Brazil (35 species), and the USA (31 species; Figure 3.3A). The country of origin of 42 specimens belonging to 34 different species was impossible to identify based on the information reported in the publications. Detailed information about the number of species retrieved for each country is reported in Table A1.3. Overall, the frequency of papers by country was significantly biased ($\chi^2_{(75)} = 217.6$, $p < 0.0001$), and Australia exceeded all other countries in terms of number of published studies. Since information about the country of origin of the retrieved species was generally more incomplete than the information about the biogeographic realms, we excluded it from further analysis.

The most represented biogeographic realm was the Neotropics (89 species), followed by the Australasia and the Indomalayan realms (60 species each; Figure 3.3B). The biogeographic realm of origin of six specimens belonging to five different species could not be identified (see Table A1.1). The differences in number of species studied for the various realms were statistically significant ($\chi^2_{(6)} = 66.1$, $p < 0.0001$).

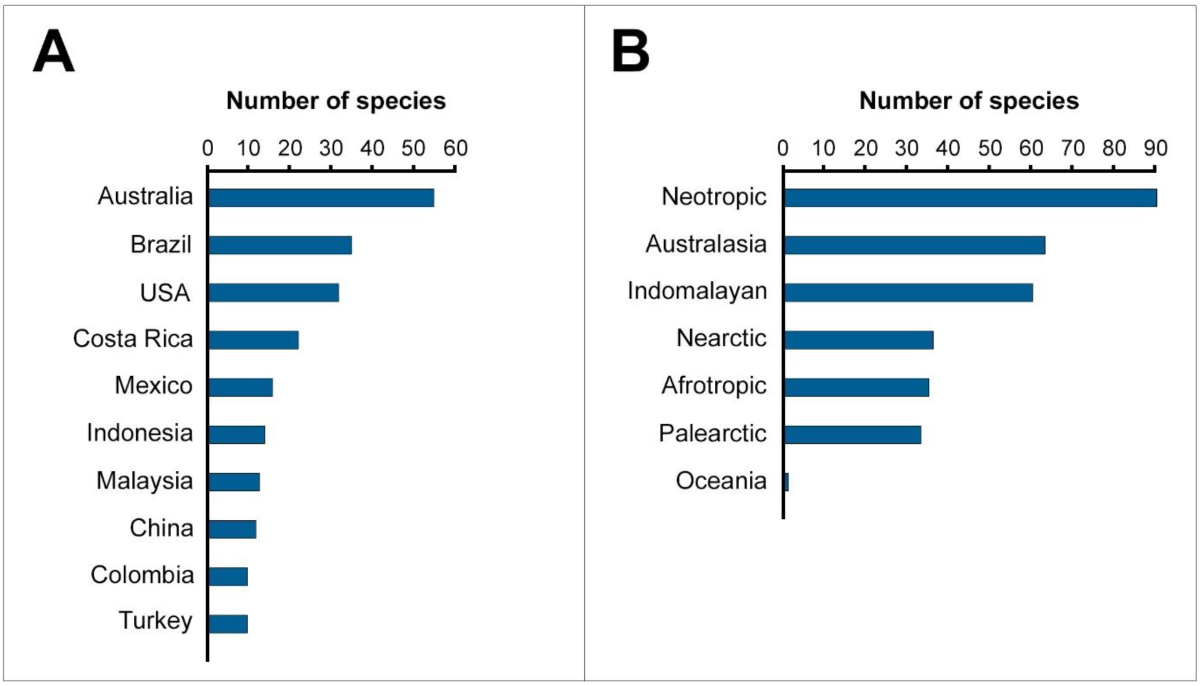

Figure 3.3 Information about the geographic origin of the species retrieved from the analysed publications. The graphs show the number of species recorded for the ten most represented countries (panel A) and biogeographic realms of origin (panel B).

Topics investigated

None of the articles covered all the eight defined topic categories. The highest number of topics covered by one article was five (eight articles, 3% of the total), whereas the lowest was one (23 articles, 8.61% of the total). Most of the articles (110 articles, 41.2% of the total) covered three topic categories. The most covered topic was “venom characterisation” (228 articles), whereas the least covered one was “envenomation symptoms”, studied in only five publications. The most studied combination of topics was “venom characterisation + interspecific venom variation” (Figure A1.1), found in 24 articles. The differences in number of articles covering each topic category were significant ($\chi^2_{(7)} = 225.9$, $p < 0.0001$).

Further information about the topics investigated in the analysed publications is reported in Figure 3.4.

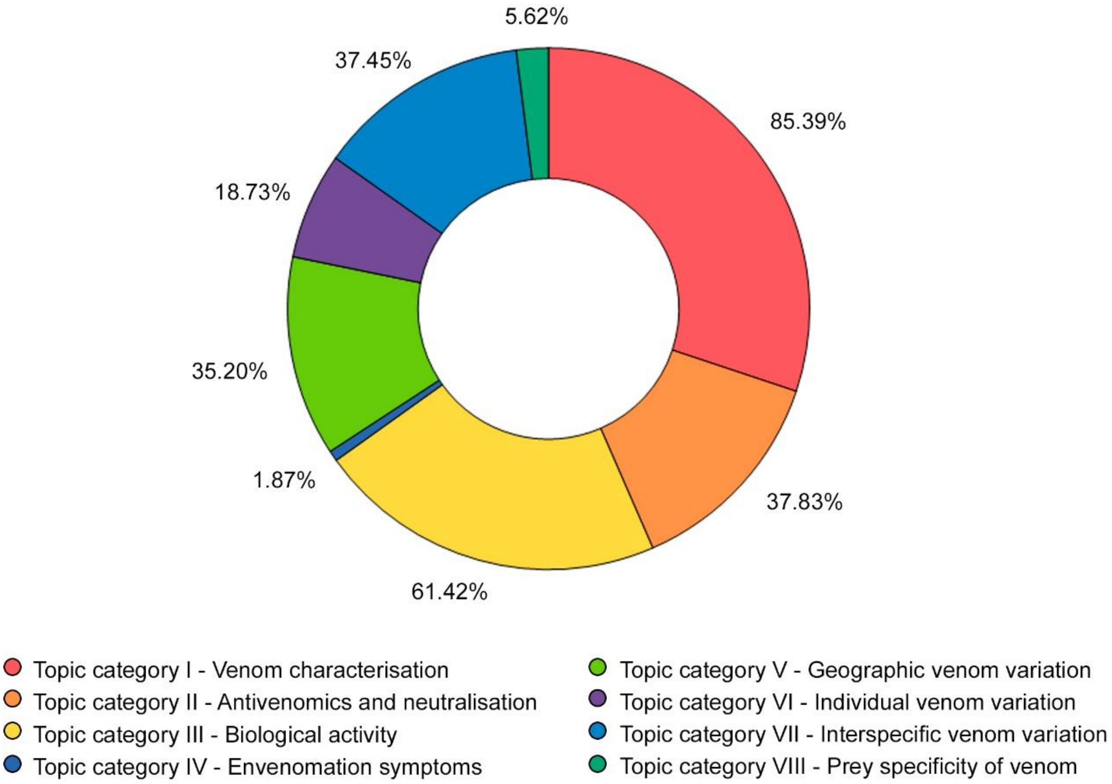

Figure 3.4 Information about the topics investigated in the reviewed articles. The graphs show the percentages of articles covering each of the eight topic categories defined. The results about topic cover are based on added up values and each topic has been counted separately; therefore, the overall sum of resulting percentages is greater than 100%.

Chronological trends

Our analysis performed on articles published between 1964 and 2021 showed that the number of publications on snake venom increased significantly and non-linearly over the years, with the best fitting model curve [y = yearly number of studies; x = years passed since the beginning of the survey (i.e., 1964)] being a 3rd-order polynomial fit (yearly number of articles = $0.003654x^3 - 21.72x^2 + 4.303 \times 10^4x - 2.842 \times 10^7$; AICc = 2199, $\chi^2 = 2190$, $r^2 = 0.9942$, $p < 0.000001$). A conspicuous increase in number of articles published each year was detected starting in the early 2000s, with most of the retrieved articles (240 articles, 89.9% of the total) being published after 1995. Considering the whole timeframe, between 4 and 5 articles were published on average every year. The number of gathered articles reached double digits for the first time in 2006 (11 articles, 4.12% of the total) and its peak in 2019 (29 articles, 10.9% of the total).

Notably, the number of articles dedicated to members of the families Viperidae and, to a lesser degree, Elapidae has been growing at a particularly fast pace, outdistancing the curves relative to other families already in the late 90s (see Figure 3.5). The beginning of the twenty-first century also marked an increase in the curve relative to the family Colubridae, which however remained relatively low. Along the considered timeframe, the families Atractaspididae, Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae were confirmed to be consistently less studied than the families Viperidae, Elapidae, and Colubridae, and did not experience any significant increase in number of articles (see Figure 3.5).

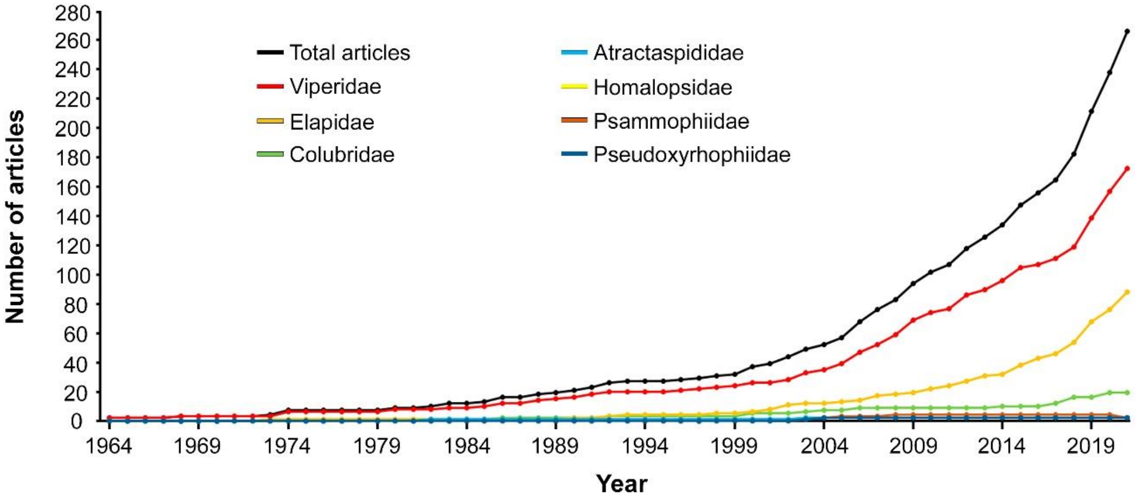

Figure 3.5 Chronological distribution of the analysed articles by snake families. The number of articles analysed per each year of the defined time frame is reported in Table A1.4. The black cumulative curve shows the overall positive trend of the analysed articles along the considered timeframe.

Overall, the number of articles focusing on elapid and viperid subfamilies increased since the second half of the first decade of the 2000s (see Figure A1.2). The number of articles focusing on Crotalinae was lower than the number of articles focusing on the other viperid subfamily Viperinae until the mid-1980s, but then increased to the point of largely outdistancing all the others. The curve corresponding to Old World and American elapids showed a very similar pattern (see Figure A1.2). Among colubrids, Colubrinae was the most studied subfamily, and underwent a slight increase in articles in the last three years (Figure A1.2). The subfamilies Azemiopinae, Ahaetuliinae, Dipsadinae, and Natricinae constantly were the least studied ones across the whole timeframe.

A general increase in publications can be detected from the beginning of the 2000s (see Figure 3.6). Concerning the topics investigated, the chronological trend of articles focusing on “biological activity” showed a moderate growth until the early 2000s, and then underwent a considerable rise. A similar trend was detected for the studies dealing with the topic “antivenomics and neutralisation”. The curves relative to the topics “geographic venom variation” and “interspecific venom variation” were almost overlapping throughout the considered time frame (Figure 3.6). A significant increase was evident in the number of yearly papers concerning the former topic category, and an almost exponential by-year increase in the number of papers dedicated to the latter was observed. We also detected a significant growth throughout the years in the number of published studies focusing on the topic “venom characterisation”, obtained exactly for the overall number of publications. The chronological trend concerning articles focusing on the topic “individual venom variation”, although significant, was less evident.

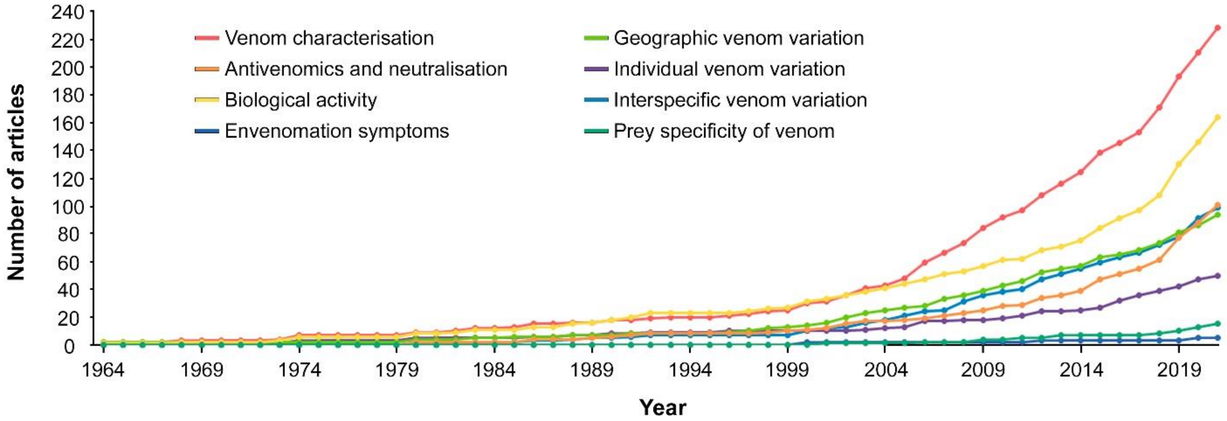

Figure 3.6 Chronological distribution of topic cover in the analysed articles. The cumulative curves show the trend of the analysed articles along the considered timeframe by topic category.

Although a certain degree of convergence between the positive trajectories followed by the curves relative to the abovementioned topic categories was evident, other subjects did not show such defined growths along the whole time frame considered. Specifically, because of the extremely small number of retrieved publications concerning “envenomation symptoms” and “prey specificity of venom”, we were unable to detect any marked chronological trend in terms of yearly number of articles focusing on these two topic categories.

Details of the statistical analyses performed are reported in Table A1.5.

Factors influencing the differences in number of articles between species

The model that best described the variation in number of articles dedicated to each snake species included the biogeographic realm and hazard category as independent variables (see Table 3.2). The effect of the hazard category assigned to each species was statistically significant ($\chi^2_{(3)} = 59.8$; $p < 0.001$), as well as the effect of the biogeographic realm of origin of each species ($\chi^2_{(5)} = 21.5$; $p < 0.001$).

Table 3.2 Final set of Generalised Linear Models (GLM) tested. The models relate the number of articles dedicated to each snake species retrieved in the analysed articles with the selected independent variables: family, biogeographic realm, and hazard category. The best-fitting model is reported in bold. The table reports the number of parameters in the model (K), the information score of the model (Akaike’s Information Criterion corrected for small sample sizes; AICc), the difference in AICc score between the best model and the model being compared (ΔAICc), and the AICc weight (i.e., the proportion of the total amount of predictive power provided by the full set of models contained in the model being assessed; *w*AICc).

Model	**K**	**AICc**	**ΔAICc**	***w*AICc**
Biogeographic realm and Hazard category	10	1058.710	0.000	0.991
Hazard category	4	1068.161	9.450	0.009
Biogeographic realm	7	1110.483	51.772	5.675×10^{-12}
Family	8	1115.132	56.421	5.552×10^{-13}
Null	1	1116.503	57.792	2.797×10^{-13}

Discussion

Viperids are the most studied snakes

From the analysis of all the considered publications, members of the family Viperidae were the most studied both in terms of number of species investigated and articles (Figure 3.1). Among the factors we tested to try to understand what could determine the prevalence of viperids, and more in general the disproportion in terms of number of articles between the studied snake taxa, the hazard categories we assigned to the species were statistically significant. Specifically, the results of our analysis showed that the number of articles focusing on species of critical clinical relevance/category 1 is significantly higher than the number of articles focusing on species with a lower hazard rating (see Table A1.6). Assuming that the hazard index we defined is able to accurately represent the danger a snake species can pose to humans because of its venom, our findings suggest that one of the main criteria used to select which snake venom to analyse might be its noxious potential. This is supported by the fact that snakes belonging to the three most studied snake families (i.e., Viperidae, Elapidae, Colubridae) are the ones most frequently and notoriously involved in snakebite accidents (Málaque and Gutiérrez, 2015; Mamede et al., 2020; WHO, 2020).

Viperids, widely distributed and highly diverse (Uetz et l., 2021), have indeed a major impact on human health in terms of snakebite, being responsible for a large number of bites and deaths in the three global snakebite hotspots (i.e., Africa, Asia, and Central and South America; Karunanayake et al., 2014; WHO, 2010, 2016). Within Viperidae, the subfamily Crotalinae (i.e., pit vipers, exclusive to America and Asia) was the most studied subfamily overall. In the American continent, pit vipers cause the great majority of snakebite accidents, which are usually characterised by higher morbidity and mortality than those caused by their Asian counterparts (Otero-Patiño, 2009; Warrell, 2017). In particular, species belonging to the genus *Bothrops*, the most studied genus across the analysed articles, account for 50–80% of all the snakebite accidents happening in most countries of Latin America (Málaque and Gutiérrez, 2015). In this scenario, it appears plausible that the prevalence of pit vipers throughout the considered publications might be related to their perceived harmfulness and relevance for human health.

Elapid snakes are generally accountable for fewer ophidic accidents than viperids in the American continent (e.g., Málaque and Gutiérrez, 2015), but are of extreme medical importance in Asia and Africa (e.g., WHO 2010, 2016, 2020). We hypothesise that the detected disproportion in terms of article coverage between elapids and viperids might be related to factors different from those we accounted for in our analysis. Specifically, we speculate that this disproportion to be due to socio-economic factors, namely research on snake venom being generally less developed in most Asian and African countries (Groneberg et al., 2016; Sofyantoro et al., 2022), resulting a lower number of studies focusing on species originating from these areas. Conversely, we suspect the underrepresentation of Atractaspididae, Colubridae, Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae in the analysed articles to be mainly caused by these families being typically considered of only minor medical relevance, and to the general lack of detailed information about the danger many of their members can pose to humans (Tilbury et al., 1989; Weinstein et al., 2011).

The Neotropics as a gold mine for snake venom studies

In line with the bias towards American pit vipers mentioned earlier, the most represented biogeographic realm was the Neotropics (Figure 3.3B). Encompassing Central and South America, it is home to about 900 snake species (Guedes et al., 2018; Uetz et al., 2021). As a consequence of this remarkable ophidian diversity, the Neotropics are a global hotspot of medically important snake species, for many of which no effective therapy is listed by the WHO (like the Congo Basin and southeast Asia (Longbottom et al., 2018), and which pose a serious threat to the large part of the local population, leading a markedly rural lifestyle (Gutiérrez, 2014; Harrison et al., 2009; Kasturiratne et al., 2008). In recent years, various research centres and laboratories located in Central and South America (e.g., Instituto Butantan in Brazil, Instituto Clodomiro Picado in Costa Rica) have made a remarkable contribution to snakebite studies (Groneberg et al., 2016; Sofyantoro et al., 2022), largely focusing on local medically relevant snake species. In light of this, we suspect that the prevalence of the Neotropics in terms of number of studied snake species might be determined not only by this realm's abundance of species relevant for snakebite and snake venom research, but also by the large number of studies developed by Central and South American institutions included in our analysis (see Table A1.1).

In spite of the evident prevalence of Neotropical snakes in the analysed publications, the effect of the Neotropics on the number of articles dedicated to each retrieved species was generally non-significant. In fact, compared to species originating from the Neotropics, only the Australasian species appear to be significantly underrepresented in terms of number of articles (B ± SE = - 0.386 ± 0.133; $p = 0.004$; Table A1.6). From this perspective, it is interesting to note that in our analysis, species originating from Palearctic, Nearctic, and Indomalayan realms appear to perform positively in terms of number of articles when compared to Neotropical species, although non-significantly (see Table A1.6). Although we found the biogeographic realm of a snake species to have an overall significant effect on the number of articles focusing on it, these results suggest that the success of Neotropical species in snake venom research is not strictly because of their realm of origin, thus supporting the role of the danger a snake species can pose to humans as one of the main factors determining a species' popularity in snake venom studies.

The neglect of the ecological context

The characterisation of the compounds present in snake venom is a crucial step for a wide spectrum of studies, from those focusing mainly on its biological and evolutionary significance to those focusing on snakebite management and antivenom testing (Calvete, 2009, 2011; Fox and Serrano, 2008). The same considerations can bemade for the analysis of the biological activity of snake venom, relevant in venom variation investigation (Chippaux, 1998) and comparative research (e.g., Ainsworth et al., 2018; Debono et al., 2017), and fundamental for the study of the pathophysiological effects of envenomations. The publications we collected and analysed encompass a considerable part of this spectrum, which could thus possibly explain the significant prevalence of the topic categories “venom characterisation” and “biological activity”, the two most studied topic categories overall (93.91% and 59.90% of all analysed publications, respectively; Figure 3.4).

Despite the very relevant and topical issue of snakebite and the antivenom crisis (Habib and Brown, 2018; Harrison et al., 2019; Schiermeier, 2019), the topic categories “antivenomics and neutralisation” and “envenomation symptoms” are underrepresented in our analyses (Figure 3.4). However, considering that the aim of this study was to analyse the general trends in snake venom research, we believe this potential underrepresentation to be due to our keywords not directly addressing antivenom studies and envenomation reports. Nevertheless, we were able to detect an increase in the curves relative to these categories starting from the first half of the 2010s (see Figure 3.6). This is concordant with several publications and awareness campaigns which, together with the very recent official recognition of snakebite as a neglected tropical disease by the World Health Organization (Chippaux, 2017), have recently been addressing the human health burden of snakebite and the antivenom crisis (Groneberg et al., 2016; Gutiérrez et al., 2006; Kasturiratne et al., 2008; Longbottom et al., 2018; Williams et al., 2011), renewing the interest in snake venom research in general and likely stimulating the study of these topics.

The topic category “prey specificity of venom” was, after “envenomation symptoms”, the least studied one (Figure 3.4), but the curve relative to it underwent a significant increase over the past few years. While acknowledging the possible presence of topic biases determined by our article search criteria, we believe that the very low number of articles covering this category might be due to the current neglect of this topic. Indeed, toxinological research has been slow to embrace the importance of focusing on the relationship between snake venom and prey to improve the understanding of the drivers behind snake venom evolution and variation (e.g., diet-related venom variation), and help the development of therapies against snakebite (Gutiérrez, 2020; Murray et al., 2020). In light of this, we suspect the recent rise we detected in the number of articles considering the topic category “prey specificity of venom” to be most likely linked to the general increase in snake venom studies rather than to the beginning of a change in trend.

The curves relative to the categories “interspecific venom variation”, “geographic venom variation”, and “individual venom variation”, all falling within the field of comparative venomics, follow very similar trends, presenting a considerable increase over the last two decades (Figure 3.6). Interestingly, the combination of the topic categories “interspecific venom variation” and “venom characterisation” is the combination most frequently encountered across the analysed articles (Figure A1.1), indicating that a consistent amount of them likely focused on the comparison of the venoms of different snake species. Taken together, these results suggest that most of the analysed studies likely opted for the application of a comparative approach, and that this might have become even more relevant in recent years.

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Chapter 4

Vipers of major clinical relevance in Europe

Introduction

Snakebites constitute a significant public health issue in developing and developed countries, with about 138,000 casualties registered worldwide on a yearly basis (Gutiérrez et al., 2017; Kasturiratne et al., 2008; Longbottom et al., 2018). When not lethal, snakebite outcomes often lead to the development of long-lasting disabilities, with more than 400,000 cases reported yearly worldwide. In May 2019, during the last World Health Assembly, the World Health Organization (WHO) stressed the importance of drastically reducing snakebite-related human deaths and disabilities by 2030 (The Lancet, 2019). Indeed, public health concern towards snakebite is relevant to both developing and developed countries, this primarily being an occupational hazard in the former, and an environmental hazard associated with outdoor activities in the latter (Alger et al., 2019; Kim et al., 2019).

European ophidian fauna is highly diverse, and includes several venomous snake species (Speybroeck et al., 2016; Uetz et al., 2022) of considerable medical relevance (WHO, 2020). Since the reporting of snakebites through Europe is not mandatory, the impact of ophidic accidents in the continent is likely underestimated (Gold et al., 2002). Furthermore, European snakebite victims do not always seek treatment, and physicians do not regularly consult poison-control centers (Gold et al., 2002). Indeed, most European physicians are not trained to identify snakebites, recognise their clinical manifestations and apply appropriate treatments.

To date, while the WHO and several authors have published general protocols to manage snakebites (e.g., Mohammad Alizadeh et al., 2016; Nelson et al., 2019; Pizon and Ruha, 2015; Walter et al., 1998; WHO, 2016), standardised protocols to investigate incidence, morbidity and mortality related to viper bites in Europe are lacking.

Aiming to constitute a tool to support physicians in recognising the most medically relevant European snake species and treat the envenomations they can cause, the present study provides (i) a key to distinguish the European snake species of highest medical relevance belonging to the genus *Vipera*, i.e., *Vipera ammodytes*, *Vipera aspis*, *Vipera berus*, *Vipera latastei*, *Vipera seoanei* and *Vipera ursinii* (based on Paolino et al., 2020), (ii) an overview of the general composition of their venoms, and (iii) a protocol to support clinicians for the management of *Vipera* envenomations.

Zoological framework

Morphological distinctions between vipers and other European snakes

An important first step in the management of snakebite accidents is the identification of the species involved. According to the recent taxonomic updates (e.g., Freitas et al., 2020; Speybroeck et al., 2020; Zaher et al., 2019), roughly 60 snake species belonging to six different families (i.e., Colubridae, Erycidae, Natricidae, Psammophiidae, Typhlopidae, Viperidae; see Figure 4.1) currently exist in Europe. Among these, members of the family Viperidae are typically considered medically important (WHO, 2020).

Figure 4.1 Heads of representative members of the six snake families present in Europe: Colubridae (A), Natricidae (B), Psammophiidae (C), Viperidae (D), Erycidae (E), Typhlopidae (F). The species portrayed in the pictures are: *Zamenis lineatus* (A), *Natrix maura* (B), *Malpolon insignitus* (C), *Vipera ursinii* (D), *Eryx jaculus* (E), *Indotyphlops braminus* (F). Photo credits: Matteo R. Di Nicola.

Vipers can be easily distinguished from other European snakes based on a series of morphological characteristics. Excluding members of the families Erycyidae and Typhlopidae, presenting unique morphological features (Figure 4.1), the remaining European non-viperid snakes potentially identifiable as viperids belong to the families Colubridae, Natricidae, and Psammophiidae.

The following key represents an useful tool to distinguish between viperid and non-viperid snakes of Europe (Figure 4.2):

- Vipers are proportionally shorter and stockier than non-viperid snakes (Figure 4.2A1 and 4.2B1), rarely reaching 100 cm in total length; several non-viperid snakes often abundantly exceed 100 cm in total length.

- Viperid eye pupil is vertical, and slit-like in full light (Figure 4.2A2); non-viperid eye pupil is generally round (Figure 4.2B2). A notable exception is the European cat snake *Telescopus fallax*, an opistoglyphous member of the family Colubridae present in N-E Italy, western portion of the Balkan Peninsula, and Greece.

- Vipers have at least one row of subocular scales separating the eye from the supralabial scales(Figure 4.2A2); in non-viperid snakes, the eye is generally in contact with the supralabial scales (Figure 4.2B2). Exceptions are two non-venomous colubrids of the genus *Hemorrhois*, namely the horseshoe whip snake *Hemorrhois hippocrepis* (present in the Iberian Peninsula, Mallorca, Ibiza, South Sardinia and Pantelleria) and the Algerian whip snake *Hemorrhois algirus* (in Europe exclusively present in Malta).

- The head of viperid snakes (Figure 4.2A3) is dorsally covered by small scales arranged irregulary, or by three larger shields arranged simmetrically, surrounded by smaller scales; the head of non-viperid snakes (Figure 4.2B3) is dorsally covered by about 10 large smooth shields symmetrically arranged.

- Vipers have invariably keeled dorsal scales (Figure 4.2A4); non-viperid snakes generally have smooth dorsal scales (Figure 4.2B4). Nonetheless, some non-viperid specie present keeled dorsal scales (e.g., the Montpellier snake *Malpolon monspessulanus*, a member of the family Psammophiidae).

- Vipers typically present a more or less triangular head shape; non-viperid snakes generally have a more sub-oval head shape. Nonetheless, non-viperid snakes can flatten their head in order to look bigger and/or mimic viperids as a defensive display, therefore identification based on head shape alone can be misleading.

Figure 4.2 Main morphological differences between European vipers (A) and colubrids (B). The species portrayed in the pictures are: *Vipera berus* (A1, A2, A3), *Vipera aspis* (A4), *Hierophis viridiflavus* (B1, B2, B3, B4 left), *Natrix helvetica* (B4 right). Photo credits: Matteo R. Di Nicola.

Although European non-viperid snakes are generally not considered medically relevant (see WHO, 2020), it should be mentioned that envenomations caused by some non-viperid European snakes can sometimes cause relevant clinical symptoms. This is for example the case of *Malpolon monspessulanus* (present in the Iberian Peninsula, Southern France and N-W Italy) and *Malpolon insignitus* (present along the Balkan coast, in Greece, Southern Bulgaria, Turkish Thrace, and in the Italian island of Lampedusa island) (Sindaco et al., 2013; Speybroeck et al., 2016). These two psammophiid snakes are opistoglyphous (i.e., present grooved, enlarged fangs in the rear part of the upper jaw through which they can inject venom), and their venom has been reported to cause symptoms going from local (e.g., pain, oedema) to systemic (e.g., ptosis, muscle weakness, dyspnea; Ottonello et al., 2011; Pommier and de Haro, 2007; Valenta, 2010). Currently, no antivenom is available to treat *Malpolon* envenomations (Valenta, 2010), and full recovery can be achieved through the application of symptomatic treatment (see Pommier and de Haro, 2007).

Identification of European *Vipera* species

In case of a snakebite, correct identification of the snake species is essential to apply the most appropriate treatment. Photographing the snake responsible for the bite is a practice recommended by the WHO (WHO, 2016), becoming more and more common (Bolon et al., 2020). Although the patient description of the biting snake can also be important for species identification, photographs are generally more reliable and can be rapidly shared with experts, allowing a faster, more accurate identification of the species (Bolon et al., 2020).

European vipers can be identified by morphological criteria, like pholidosis (i.e., the organisation of the body scales in number, shape, position and arrangement). Furthermore, viper species usually differ in ecological and distributional characteristics, with some inhabiting only specific areas and in specific conditions (Sindaco et al., 2013; Speybroeck et al., 2016). Therefore, a description of the geographical area, altitude and habitat type where the ophidic accident occurred could provide a basis for a tentative identification of the species involved.

Among European vipers (genus *Vipera*), the species considered of major medical relevance, based on their greater diffusion and the higher number of registered snake bites, are the following six: *V. ammodytes*, *V. aspis*, *V. berus*, *V. latastei*, *V. seoanei* and *V. ursinii* (Figure 4.3; see Paolino et al., 2020).

Figure 4.3 Heads of the main European vipers: *Vipera aspis* (A), *Vipera latastei* (B), *Vipera ammodytes* (C), *Vipera ursinii* (D), *Vipera seoanei* (E) and *Vipera berus* (F). Photo credits: Matteo R. Di Nicola (A, C, D, F); Matthieu Berroneau (B, E).

We hereby present a simplified key for the identification of the abovementioned six *Vipera* species, based on some morphological characteristics of the head and distribution in Europe.

Is it a European *Vipera*? → 1

1a. Tip of the snout upturned or with a scaly horn; top of the head usually covered only by small scales → 2

1b. Tip of the snout dorsally flat; top of the head usually with three main shields surrounded by smaller scales → 3

2a. Tip of the snout more or less upturned (without a horn covered by small scales); species present in N–E Spain, France (except Corsica), Italy (except Sardinia), Switzerland, extreme S–W Germany and extreme N–W Slovenia → *Vipera aspis* (Figure 4.3A)

2b. Tip of the snout with a more or less evident horn with three to nine apical scales; rostral scale extended onto the front of the horn; species present only in Portugal and Spain → *Vipera latastei* (Figure 4.3B)

2c. Tip of the snout with an evident horn covered by up to 20 small scales; rostral scale not extended onto the front of the horn; species present in N-E Italy, S Austria, Croatia (including some islands), Slovenia, Bosnia and Herzegovina, Montenegro, Albania, Greece (including many islands), Macedonia, Serbia, Bulgaria, S and W Romania, European Turkey → *Vipera ammodytes* (Figure 4.3C)

3a. Usually two apical scales, both in contact with the rostral scale → 4

3b. Usually one-two apical scales, in contact with the rostral scale; species present in limited areas of S–E France, E Austria, C Italy, Croatia, Bosnia & Herzegovina, Montenegro, Serbia, Macedonia, Hungary, Romania, Moldova and N Albania (of the same group: *Vipera graeca* from S Albania and Greece; *Vipera renardi* from E Ukraine and Crimea) → *Vipera ursinii* (Figure 4.3D)

4a. Species present only in N Spain, extreme N–E Portugal and extreme S–W France → *Vipera seoanei* (Figure 4.3E)

4b. Species present in Swiss, French, Italian and Austrian Alps, C and N France, Germany, Great Britain, Belgium, Netherlands, Denmark, Norway, Sweden, Finland, Poland, Czech Republic, Slovakia, Hungary, Slovenia, Croatia, Bosnia and Herzegovina, Romania, Bulgaria, Ukraine, Belarus, Lithuania, Latvia, Estonia, Russia, Montenegro, North Macedonia, Albania, Serbia, Moldova, and extreme N Greece (of the same group: *Vipera walser*, from N-E Piedmont, Italy) → *Vipera berus* (Figure 4.3F)

Venom composition of European *Vipera* species of major clinical relevance

Snake venom is a mixture of proteins and peptides, organic molecules and salts in an aqueous medium (Casewell et al., 2013; Chan et al., 2016). To date, snake venom has been found to consist of 50–200 different components, generally belonging to four main toxin families: phospholipases A_2 (PLA_2s), snake venom metalloproteinases (SVMPs), snake venom serine proteinases (SVSPs) and three-finger toxins (3FTx) (Slagboom et al., 2017; Tasoulis and Isbister, 2017). Interestingly, snake venom composition varies at both interspecific and intraspecific level, depending on factors like ontogeny (Alape-Girón et al., 2008), diet (Daltry et al., 1996), sex (Menezes et al., 2006; Zelanis et al., 2016), and local-scale adaptation to the physical environment (Zancolli et al., 2019). Vipers (family Viperidae) appear to be the snake family most frequently studied in compositional venom research, with most of the investigation efforts apparently focusing on the subfamily Crotalinae (Tasoulis and Ibsister 2017). Among the subfamily Viperinae, the genus *Vipera* is the most involved one in European snakebite accidents (Paolino et al., 2020; Zanetti et al., 2018), leading to mainly hemotoxic and cytotoxic envenomation symptoms (Al-Shekhadat et al., 2019; Komori et al., 1998; Maretić et al., 2013), although neurotoxic symptoms can sometimes also occur (Ferquel et al., 2007; Lukšić et al., 2006). In light of the high medical relevance of this genus, we hereby provide a comprehensive assessment of the venom components of the six *Vipera* species accountable for the highest number ophidic envenomations in Europe, namely *V. ammodytes*, *V. aspis*, *V. berus*, *V. latastei*, *V. seoanei*, and *V. ursinii*.

Vipera ammodytes (Linnaeus, 1758)

Officially listed in both Category 1 and 2 of medically important snake species of the WHO (WHO, 2020) and traditionally considered Europe's most dangerous venomous snake (Sket and Gubensek, 1976), the nose-horned viper *Vipera ammodytes* is capable of causing life-threatening envenomations, generally characterised by local and systemic haemorrhage, tissues damage, and neurotoxicity (Lukšić et al., 2006; Maretić et al., 2013; Radonic et al., 1997). In a recent study, Hempel et al. (2018) produced comprehensive proteomes of the venoms of the two *V. ammodytes* subspecies *V. a. transcaucasiana* and *V. a. montandoni* from Turkey. In the analysed venoms, the prevalent protein groups were phospholipases A_2 (PLA_2s), vascular endothelial growth factors (VEGFs), snake venom serine proteinases (SVSPs), snake venom metalloproteinases (SVMPs), L-amino-acid oxidases (LAAOs), cysteine-rich secretory proteins (CRISPs) and C-type lectins (CTLs). In both subspecies, PLA_2s resulted to be the most abundant protein group, highlighting the great similarity between their venoms. In a previous study by Georgieva et al. (2008), similarities were also found between the venoms of Bulgarian specimens belonging to the two subspecies *V. a. ammodytes* and *V. a. meridionalis*, with LAAOs, PLA_2s, SVMPs and SVSPs being the most abundant toxins overall. Despite this analogy, Vasilev et al. (2014) found the lethal potential of the venoms of these two subspecies to be different. The results of this study found *V. a. meridionalis* venom to present a higher lethality compared to that from *V. a. ammodytes* venom (LD_{50} = 0.431 μg/g and 3.681 μg/g, respectively), likely because of the presence, in the former, of a monomeric form of phospholipase A_2. Remarkably, in all four abovementioned subspecies the neurotoxic PLA_2 vipoxin was the most abundant PLA_2, highlighting the importance of this toxin in the general venom composition of *V. ammodytes* (Georgieva et al., 2008; Hempel et al., 2018). A very recent study focusing on *V. a. ammodytes* venom of

Croatian origin, and combining both proteomics and transcriptomics, found SVSPs, CTLs, PLA_2s, and SVMPs to account for the vast majority of the identified venom proteins (Leonardi et al., 2019). The analysis of *V. ammodytes* venom from Serbia performed by Gopcevic et al. (2021) resulted in the identification of 9 main toxin families, similarly to what reported in previous works (Georgieva et al., 2008; Hempel et al., 2018; Leonardi et al., 2019), thus partially confirming the general compositional pattern of this species' venom.

Vipera aspis **(Linnaeus, 1758)**

Early characterisations of the venom of the asp viper *V. aspis* showed the presence of proteolytic enzymes, LAAOs, phospholipases, hyaluronidases, hypotensive factors, haemorrhagic factors and coagulation inhibitors (Boquet, 1967; Komori and Sugihara, 1990; Komori et al., 1993). A recent work combining transcriptomic and proteomic analyses identified a total of 64 proteins in the venom of *V. a. aspis*, with various haemotoxins (e.g., P-III snake venom metalloproteinases, C-type lectins and disintegrins) detected in considerable abundances, and phospholipases A_2 being the prevalent component (Giribaldi et al., 2020). These findings are concordant with the mostly haemotoxic and cytotoxic properties of the species' venom. Komori et al. (1998) measured the LD_{50} values of the two subspecies *V. a. aspis* and *V. a. zinnikeri*, concluding that the venom of the latter had a higher lethal potency (LD_{50} = 0.35 µg/g, against LD_{50} = 0.55 µg/g of *V. a. aspis*). The same authors suggested this difference to be attributable to the presence, in *V. a. zinnikeri* venom, of the highly lethal phospholipase A_2 PLA_2-I, which they did not find in *V. a. aspis* venom. Interestingly, neurotoxic effects of *V. aspis* venom, causing neuromuscular paralysis through selective degeneration of peripheral motor nerve terminals (Zanetti et al., 2018), have also been reported from southern France and Italy (Ferquel et al., 2007; Lonati et al., 2014). French populations of *V. aspis* have been known to produce neurotoxic symptoms for many years (de Haro et al., 1994, 2002, 2009). Nevertheless, the neurotoxic component of *V. aspis* venom has been characterised only recently, with the description of two neurotoxins of the phospholipase A_2 type, ammodytoxin B (also present in the venom of *V. ammodytes*) and vaspin, and with the identification of genes encoding PLA_2 neurotoxins in the *V. aspis* genome (Ferquel et al., 2007; Jan et al., 2002). Intriguingly, the expression of these genes does not appear to be constant, but is instead thought to be determined by particular environmental and/or physiological stimuli. Hence the detection of different levels of PLA_2 neurotoxins in different *V. aspis* specimens, and the recommendation by some authors to consider the asp viper a “cryptoneurotoxic’’ species (Ferquel et al., 2007).

Vipera berus (Linnaeus, 1758)

The common adder *V. berus* is the most widely distributed viper in Europe (Sindaco et al., 2013), and is known to cause more snakebite accidents than any other species of the genus *Vipera* (Chippaux, 2012; Reading, 1996). Because of the wide distribution and the medical relevance of this species (WHO, 2020), both the composition and the effects of *V. berus* venom have been thoroughly investigated. The venom of this species appears to have predominantly proteolytic, haemolytic and cytotoxic properties (Hawley, 1990; Zajkowska et al., 2010). Recent studies have focused on the characterisation of the *V. berus* venom proteome, producing different results. Latinovic et al. (2016) analysed *V. berus* venoms of Russian origin, identifying 10 different protein families: serine proteinases (SVSPs), metalloproteinases (SVMPs), natriuretic peptides (NP), phospholipases A_2 (PLA_2s), aspartic proteinases (AspPs), cysteine-rich secretory proteins (CRISPs), C-type lectins (CTLs), L-amino-acid oxidases (LAAOs), disintegrins (DISIs), and Kunitz-type inhibitors (KUNs). The produced proteome allowed to determine the relatively simple composition of *V. berus* venom, and to identify SVSPs and SVMPs as the two most abundant venom protein groups (31% and 19% of all identified venom proteins, respectively). This result is concordant with the clinical picture of *V. berus* envenomation being characterised by marked haemotoxic activity. More recently, Al-Shekhadat et al. (2019) also analysed the venoms of Russian *V. berus* specimens, and identified 15 different groups of venom components, the major ones being phospholipases A_2 (PLA_2s), serine proteinases (SVSPs), metalloproteinases (SVMPs), bradykinin-potentiating peptides (BPPs), C-type natriuretic peptides (C-NAPs), cysteine-rich secretory proteins (CRISPs) and L-amino-acid oxidases (LAAOs) Although confirming the abundance of SVSPs and SVMPs in the venom of this species (16.2% and 17.2% of all identified venom proteins, respectively), this study identified PLA_2s as the prevalent group of venom components (25.3% of the venom proteome). Similarly, Bocian et al. (2016) analysed the venom of *V. berus* specimens collected from the Slovakian Republic and identified 11 different protein groups. From this analysis, the most abundant proteins resulted to be phospholipases (almost 60 % of all identified venom proteins) and serine proteinases (15% of all identified venom proteins). Other venom components were CTLs, CRISPs, LAAOs and angiotensin-like peptides. Interestingly, SVMPs were the least abundant protein group, accounting for less than 0.15% of all identified proteins, while in the studies from Latinovic et al. (2016) and Al-Shekhadat et al. (2019) they were the second most abundant class of venom components. Nevertheless, the results obtained by Bocian et al. (2016) are concordant with the substantially haemotoxic effects of *V. berus* envenomation. The discrepancies present between the results of the abovementioned studies might be due to the application of different protein identification techniques and/or to a certain degree of venom variability within *V. berus* (Malina et al., 2017;

Varga et al., 2018). Such variation has been demonstrated in the past at individual level (Malenev et al., 2007; Nedospasov and Rodina, 1992) and, more recently, also between geographically distant populations. Particularly, Malina et al. (2017) recorded varying proteinase and phospholipase activity among adders of different sex and age. Furthermore, the authors detected significant differences in lethal toxicity among individual adders. Specifically, the LD_{50} values of Hungarian specimens were lower than the values recorded for an Austrian specimen used as control, and varied between 0.41 and 0.72 μg/g. These values are partially concordant with the median LD_{50} traditionally reported for *V. berus* venom in mice, being 0.55 μg/g (Minton Jr., 1974), but not with the median LD_{50} reported by (Al-Shekhadat et al., 2019) for Russian adders, being 19.8 μg/mouse in 18–20 g mice. This discordance, however, could be attributable to the different venom injection modes applied in the considered studies (i.e., intraperitoneal in Al-Shekhadat et al., 2019; intravenous in Malina et al., 2017). Finally, Malina et al. (2017) reported for the first time predominantly neurotoxic neuromuscular activity in *V. berus* venom collected from Hungarian specimens, furtherly highlighting the presence of geographic venom variation in the species.

Vipera latastei (Boscá, 1878)

Despite the acknowledged medical importance of this species (WHO, 2020), to date a comprehensive assessment of *V. latastei* venom composition has yet to be produced. In a study aiming at characterising the toxic activity of *V. latastei* venom, Arez et al. (1993) considered venom samples collected from only two specimens, one male and one female, from northwest Portugal. The performed analyses showed a certain degree of intersexual variation, with the male's venom apparently presenting a more complex composition than the venom produced by the female. The venom profiles also seemed to differ from the ones produced by Saint-Girons and Detrait (1992), obtained from animals collected in Spain, suggesting the presence of geographic variation. In the same work from 1993, Arez et al. performed LD_{50} tests on 18–20 g mice, obtaining a LD_{50} of 14.43 g/mouse for the male specimen, and of 27.30 g/mouse for the female. These results are partially concordant with the LD_{50} values obtained by Detrait et al. (1983) for *V. latastei* (LD_{50} = 25 g/20 g mouse) and for the subspecies *V. latastei gaditana* (LD_{50} = 35.3 g/20 g mouse). Moreover, in the venoms of the two *V. latastei* specimens considered, the authors identified components determining haemorrhagic activity likely corresponding to haemorrhagic snake venom metalloproteinases (SVMPs). Interestingly, the antibodies present in ViperaTAb® antivenom, produced using *V. berus* venom, appear to very effectively recognise and neutralise the toxic components present in the venom of *V. latastei* (and of other European vipers; see Casewell et al., 2014). Although these findings could possibly suggest the presence of similarities between the venoms of *V. latastei* and *V. berus*, the lack of knowledge about *V. latastei* venom components does not allow any actual comparison.

Vipera seoanei **Lataste, 1879**

As already stated for *V. latastei*, currently no exhaustive information about the composition of *V. seoanei* venom is available, despite the recognised medical relevance of this species (WHO, 2020). Nonetheless, the toxicity of *V. seoanei* venom has been studied in the past. Detrait et al. (1990) performed LD_{50} tests on 20 g mice using venoms gathered from different *V. seoanei* populations from Spain. Interestingly, while the obtained proteinograms showed very limited levels of compositional divergence among the investigated populations, the toxicity appeared to vary geographically. Specifically, while venoms from populations from the Basque Country and the Cantabrian coastal areas showed very limited lethality (LD_{50} = 23.1–23.6 µg/mouse), the venoms gathered from the westernmost populations (i.e., Galicia and North of León) appeared to have a consistently higher toxicity (LD_{50} = 6.9–9.9 µg/mouse). Similar levels of toxicity have been reported for *V. seoanei* specimens from Portugal, showing an average LD_{50} of 9.7 µg per 18–20 g mouse (Archundia et al., 2011), potentially supporting the presence of a West-East toxicity gradient. However, the lack of detailed information about the components present in *V. seoanei* venom and their effects doesn't allow to go beyond mere speculation about what could cause these differences.

Vipera ursinii **(Bonaparte, 1835)**

V. ursinii is generally considered to be the least medically significant species of the genus *Vipera*, mainly because of the limited amount of venom it can inject and the typically very mild and local envenomation symptoms it can cause (Dely and Joger, 2005; Krecsák et al., 2011). The venom of this species has been reported to cause haemorrhagic effects in mice, but no myotoxicity (Mebs and Langelüddeke, 1992). Lang Balija et al. (2020) assessed the lethal toxicity of *V. ursinii* venoms collected from Croatian specimens by performing LD_{50} tests on both rats and crickets, Orthoptera composing almost the totality of the species' diet (Dely and Joger, 2005; Nilson and Andren, 2001). The results of these tests showed higher toxicity of *V. ursinii* venom in crickets (i.e., mass normalised LD_{50}s being 9.8 µg/g for crickets and 1.94 µg/g for mice, respectively), suggesting strong specificity of the venom for the insect prey. Interestingly, the injected mice and crickets showed similar modes of dying, presenting symptoms suggesting neurotoxicity, independently from the amount of venom injected (Lang Balija et al., 2020). Proteomic analyses of *V. ursinii* venom performed by the same authors allowed the identification of 25 different proteins belonging to seven main protein families: snake venom metalloproteinases (SVMPs), snake venom serine proteinases (SVSPs), phospholipases A_2 (PLA_2s), cysteine-rich secretory proteins (CRISPs), snake C-type lectin-like proteins (CTLs), Kunitz-type proteinase inhibitors (KUNs), and venom nerve growth factors (VNGFs). SVMPs resulted to be the most abundant toxin family in *V. ursinii* venom, representing 55% of all detected venom proteins (Lang Balija et al., 2020). The predominance of P-III SVMPs, known to have high haemorrhagic potential, very likely explains the haemorrhagic effects of this species' venom (Mebs and Langelüddeke, 1992). These effects might furtherly be exacerbated by the action of other proteins also detected in *V. ursinii* venom, the snake venom serine proteinases (SVSPs), which are known to affect haemostasis and cause coagulopathy (Sajevic et al., 2011).

Clinical management of viper envenomation

First aid in the field

The first aid procedure to support viper bite victims in the field is resumed in Figure 4.4.

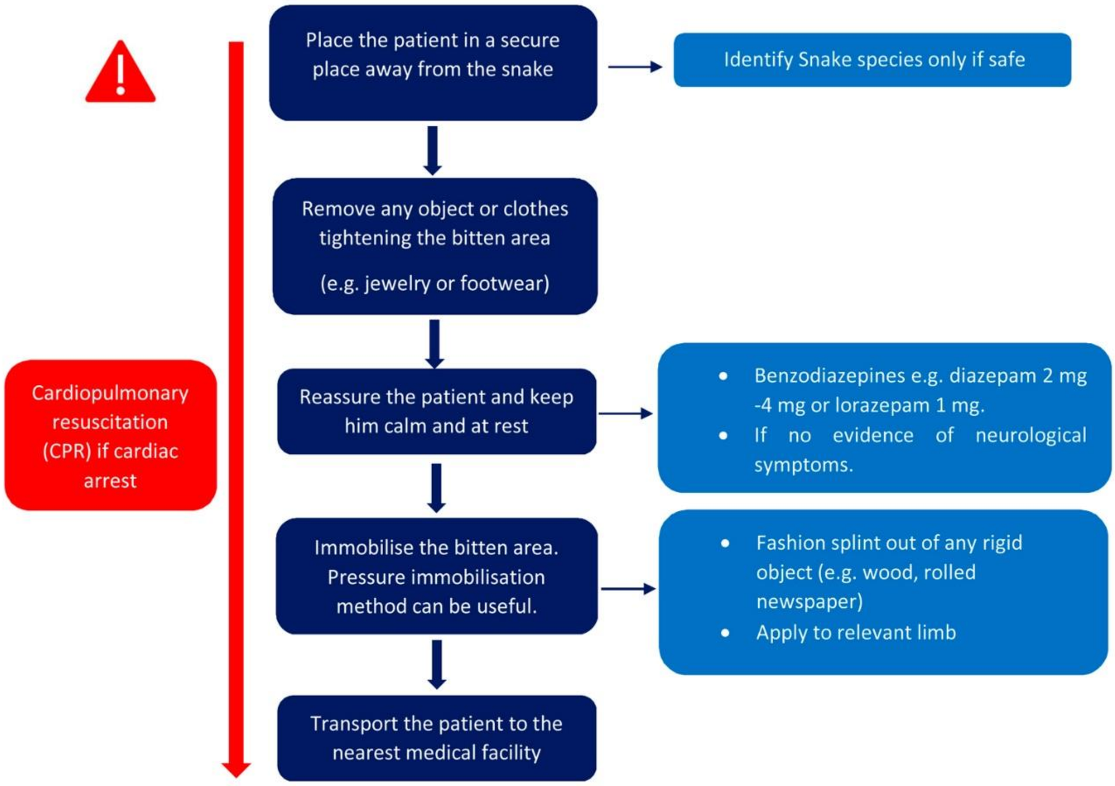

Figure 4.4 First aid in the field after viper envenomation.

In case of bites inflicted by a potentially venomous snake, an emergency number should immediately be called. Helping the bitten subject to remain calm is then particularly relevant. Agitation and movements, causing an increase in blood flow, might indeed lead to the accelerated circulation of toxins in the blood system and to a consequent worsening of the envenomation. Immobilisation of the bitten area is recommended, and should be applied by experienced personnel. For bites interesting lower limbs, it is possible to apply a bandage at least 10 cm wide while pulling and exerting a moderate compression. The bandage width should be extended as much as possible, preferably below the area of the bite, and rigid splint should be used to keep the limb as still as possible. If the bandage and the rigid splint have been placed correctly, the compression applied around the bitten area will not cause any discomfort to the patient. For bites interesting upper limbs, a compression bandage about 7 cm wide is also applicable. Bandaging should start from the fingertips and reach up to the elbow, and should not prevent arterial circulation (checking that the pulse is perceptible is recommended). For snake bites near or above the elbow, the entire arm should be bandaged up to the shoulder. As in the case of snakebites interesting lower limbs, immobilising the bitten area with a splint is advisable, but in this case the arm should be kept blocked against the trunk. In the rare cases of bites to the head and neck region, it is advisable to apply a rigid pad over the bitten area, keeping it compressed with an adhesive elastic patch. Immobilisation bandages and splints will be removed once the patient gets to the hospital.

Self-treatment is not recommended. Any commonly known techniques supposedly helping reduce envenomation severity, such as arterial compression, application of tourniquets, cutting and open the bite wound, sucking the venom out with the mouth or with extractors, stung guns, electric shock, etc., are ineffective and may only increase the risk of clinical complications (Dart and Gustafson, 1991; Panfoli et al., 2010). Although the use of pharmaceutical drugs without a proper prescription is not recommended, an analgesic therapy using paracetamol (adult dose maximum 3 g in 24 h; children 10–15 mg/kg/day maximum 100 mg/kg/day) can be performed in the case of pain following the bite. Anti-inflammatory drugs, such as acetyl salicylic acid, should not be used, in order to avoid raising blood pressure. In case of anxiety, and if there is no evidence of neurotoxic symptoms, common sedatives such as benzodiazepines (diazepam 2 mg–4 mg [10–20 drops]) or sleeping tablets (lorazepam 1 mg [10 drops]) might also be administered.

Transport to hospital should be facilitated by emergency services, especially in the case of snakebite accidents taking place in remote areas (e.g., mountains). During transport to hospital, the patient should make as little movements as possible, and should be constantly monitored and reassured. The neck should be supported in a neutral position and the patient should be seated, due to the risk of suffocation due to the possibility of regurgitation of material coming from the stomach.

Laboratory and clinical investigations

After a snake bite, the possible injection of a small amount of venom might cause only mild, localised signs. However, the development of more severe envenomation symptoms and complications can arise in a matter of hours, so clinicians should remain alert. The patient should remain under observation for at least one day (24 h). Once the patient has been hospitalised, the closest poison control center (PCC) should be contacted as soon as possible, in order to prepare for any worsening of symptoms and to access antivenom. For each patient, baseline laboratory investigations should be always performed, including coagulation tests (e.g., prothrombin time, thrombin time, partial thromboplastin time, fibrinogen, platelet count, international normalised ratio, whole blood clotting test), blood count, urinalysis, clinical chemistry for liver function (e.g., bilirubin, alanine Aminotransferase, aspartate aminotransferase, Gamma-glutamyl-transpeptidase, lactate dehydrogenase, creatine phosphokinase), glycaemia, renal function. All laboratory investigations should be performed at Time 0 and every 6 h for 24 h, together with digital oximetry and electrocardiogram (ECG). Glycaemic control should be considered, especially in critically ill patients. Based on the patient’s medical history, other analyses may also be conducted. If no clinical symptoms of envenomation occur within 24 h and laboratory investigations are satisfactory, the patient can be discharged.

Treatment of local symptoms

Local symptoms arising following viper bites can range from mild to severe. The bitten area is generaly characterised by the presence of two (sometimes one) fang marks, typically associated with a blood drip. However, fang marks may sometimes not be immediately visible, and could thus result in a diagnostic delay that may lead to severe consequences for the patient (Beer and Putorti, 1998). On the other hand, “dry bites” are also characterised by the presence of fang marks but are not associated with venom injection, and therefore do not lead to any envenomation symptoms (AAOS, 2016; Nelson et al., 2019). Nonetheless, patients who suffered a dry bite may experience symptoms often associated with fear of venomous bites (e.g., arrhythmia, dyspnea, anxiety, vaso-vagal shock, increase in blood pressure, sweating, tremor), which might mislead clinicians (WHO, 2010, 2016).

In case of envenomation, the bitten area generally becomes swollen and painful in a matter of minutes. In lower limbs, however, swelling can arise hours after (Nelson et al., 2019). Local oedema may then occur and extend to the whole limb. Ecchymosis, initially located around the fang marks but potentially extending to the whole limb, usually also occurs. Lymphangitis and lympho-adenopathy, indicative of venom spreading into the lymphatic system, may sometimes be present. Haemorrhagic vesicles and blisters may eventually arise in the bitten area, typically 12 h after envenomation. It is important to perform an accurate clinical evaluation of vesicles and blisters, since their extension can be symptom of an underlying necrosis, which arises in 5.5 % of envenomation cases attributable to European *Vipera* bites (Lukšić et al., 2006; Nelson et al., 2019).

For local treatment, objects in close proximity to the bitten area (e.g., jewellery, watches) should be removed, as these could hinder local disinfection and, in case of oedema, tear the skin apart thus accelerating the necrosis process. The bitten area should be examined with caution, any residual dirt should be removed, and irrigation with hydrogen peroxide or plain water can be performed. The interested area must be marked with a dermographic pen and monitored every hour, to record swelling, bruising and/or necrosis. Measurements are initially performed every 1–2 hours, but may be more frequent in case of rapid progression of local symptoms. In this case, the affected extremity may be slightly raised, taking care not to reduce arterial perfusion pressure in the swollen limb, which may potentially increase the risk of intra-compartmental ischaemia (Anz et al., 2010; WHO, 2010, 2016).

Although teeth and fangs of the viper can be pathogen carriers, the prophylactic administration of antibiotics is not generally advised. However, in the case of risk of secondary bacterial infections and acute infection, broad spectrum antibiotics (e.g., amoxicillin, cephalosporin, azithromycin, metronidazole) may be prescribed. Overall, prophylactic antibiotic treatment is recommended only in the presence of symptoms clearly sugegsting local infection (WHO, 2010, 2016). The tetanus immunisation status of the patient should always be assessed, and immunisation should be provided when appropriate. From historical data, it is noted that the percentage of ulceration and massive necrosis is extremely rare in cases of bites from European vipers compared to bites from other Viperidae (Lukšić et al., 2006; Nelson et al., 2019). A swab of the area affected by such complications, most often arising within 24–72 hours from the bite, is recommended for diagnostic purposes. The most common pathogens that have been isolated in patients after snakebites include *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Morganella morganii*, *Proteus* sp. and *Enterococcus faecalis* (Wagener et al., 2017). While ciprofloxacin and amikacin have proven to be the most effective systemic treatments against the first two pathogens, Enterobacteriaceae are mostly sensitive to ampicillin, amoxicillin/clavulanic acid, cefuroxime, ceftriaxone, ciprofloxacin, gentamicin and amikacin (Nagoba et al., 2011; Wagener et al., 2017). In addition to systemic treatments, local treatment, particularly under important localised cutaneous necrosis, involves local wash with a solution of undecyl-starch propyl betaine or a topical collagenase ointment together with chlortetracycline cream. Debridement and subsequent wound management play a pivotal role in these cases (Nagoba et al., 2011). Flaps and full-thickness skin graft should be considered only when soft tissue defect has been diagnosed (Bozkurt et al., 2008). Once the skin ulcer has healed, an annual dermatological follow-up should be performed in the patient to prevent possible scar-related cutaneous degeneration (Mercuri et al., 2018, 2020; WHO, 2010, 2016).

In some rare cases, compartment syndrome may arise. This is characterised by an excessive pressure inside an enclosed muscle space in the body, reducing blood flow to the tissues, and may induce a massive, rapid, life-threatening necrosis. In physiological conditions, pressure within the compartments is between 0 mmHg–8 mmHg (Torlincasi et al., 2020). An intra-compartmental pressure greater than 30 mmHg associated with clinical symptoms known as the Five “Ps”, i.e., Pain, Pulselessness, Paraesthesia, Paralysis and Pallor, indicates a compartment syndrome and a need for fasciotomy (Kim et al., 2019; Torlincasi et al., 2020). The intra-compartment pressure should be measured every 4 h for a minimum of 24 h (Kakagia, 2015; Wall et al., 2010). In children, compartment pressure cannot be easily measured, and fasciotomy should thus not be performed without adequate diagnosis of the compartment syndrome (Laohawiriyakamol et al., 2011). The main differential diagnosis for compartment syndromes includes deep vein thrombosis, cellulitis, gas gangrene, phlegmasia cerulea dolens, rhabdomyolysis and peripheral vascular injuries (Torlincasi et al., 2020). Fasciotomy should be performed ideally within six hours after the diagnosis of compartment syndrome, but it is not recommended after 36 h (Torlincasi et al., 2020).

Finger bites need to be treated separately, since pressure within the compartment of may rapidly exceed the vascular capacity and compromise the integrity of small vessels and nerves in the digits (Bozkurt et al., 2008). Existing literature reports that dermotomy and decompression of the entire finger must be performed as soon as possible, in order to provide sound functional and cosmetic results (Bozkurt et al., 2008; Watt Jr., 1985). Other supportive treatments include mannitol (e.g., 25 g intravenous bolus followed by 5–10 g intravenous/h), as it may reduce intra-compartmental pressure (Shah et al., 1996), or hyperbaric oxygen (Fitzpatrick et al., 1998; Watt Jr., 1985). Systemic steroids have also been shown to provide positive results (Watt Jr., 1985).

Finally, one of the most severe consequences of the bite is the amputation of a finger or of a limb, with a serious impact on the patient’s quality of life, as well as psychological implications. The amputation may only be required in the case of massive, non-responsive necrosis involving a bone, and/or based on a clinical and radiographic diagnosis.

Treatment of systemic symptoms

Once in the hospital, a general physical examination of the bitten subject is required after monitoring the local site of the bite. Blood pressure and heart rate should be checked, and electrocardiogram (ECG) and pulse oximetry should be performed. The skin and mucous membranes (i.e., mouth, anorectal and genital tract) should be assessed for any evidence of petechiae, purpura, discoid haemorrhages and ecchymoses. In addition, the conjunctive should be checked for eventual signs of haemorrhage, as well as gums and nose for any signs of bleeding and epistaxis. Abdominal tenderness may suggest gastrointestinal or retroperitoneal bleeding. Intra-cranial haemorrhage is suggested by lateralising neurological signs, asymmetrical pupils, convulsions, or impaired consciousness (WHO, 2010, 2016). Finally, the clinician should ask the patient for any known allergies in order to plan the most appropriate therapy. In fact, patients allergic to stings from Hymenoptera (e.g., bees, wasps) and other allergens might be at risk of anaphylactic reactions as consequences of European viper bites (Valenta, 2010). Treatment of systemic symptoms is discussed in detail in the following sections.

Severe envenomation cases

In severe envenomation cases resulting from European viper bites, patients may develop circulatory shock and angioedema a few minutes after the bite, most likely as a consequence of anaphylactic shock. It is important to highlight that anaphylactic or anaphylactoid reactions to the venom may appear both in subjects previously exposed to snake venom and in unexposed subjects (see Beer and Putorti, 1998). Airway patency, respiratory movements, arterial pulse and level of consciousness must be assessed immediately and monitored constantly (WHO, 2010, 2016). When needed, rapid primary clinical assessment and resuscitation can be performed based the ABCDE approach: Airway; Breathing (i.e., respiratory movements); Circulation (i.e., arterial pulse); Disability of the nervous system (i.e., level of consciousness); Exposure and environmental control (i.e., protect from heat, cold, etc.).

In case of anaphylactic reaction, epinephrine should be quickly administered intramuscularly (0.3–0.5 ml as 0.3–0.5 mg in adults, 1:1000 dilution or 0.01 mL/kg body weight in children). Repeated doses may be given every five minutes until symptoms improve. It is then important to improve the stabilisation of the airways, administer high flow oxygen, fluid bolus (500–1000 ml in adults and 20 mL kg^{-1} in children), chlorphenamine (adults and children ≥ 13 years: 10 mg intramuscular or intravenous injection; children between 6–12 years 5 mg; infant between 6 months and 6 years 2.5 mg; newborn ≤ 5 months 250 mcg kg^{-1}) and hydrocortisone (adults and children ≥ 13 years: 200 mg intramuscular or intravenous injection; children between 6–12 years 100 mg; infant between 6 months and 6 years 50 mg; newborn ≤ 5 months 25 mg). Pulse oximetry, blood pressure and electrocardiogram should always be performed (European Resuscitation Council, 2020). Finally, in the case of loss of consciousness due to neurological, cardiovascular or haematological causes, the rescue techniques and advanced life support methods should be applied according to the guidelines of the European Resuscitation Council (2020).

Anxiety and the use of benzodiazepines

Upon arrival at the hospital, the patient should remain calm, since a normal/low heartbeat helps reduce venom circulation in the blood stream. Considering that subjects bitten by snakes often experience great fear and anxiety, this is often difficult to achieve without the application of specific drugs. In the absence of neurotoxic clinical signs, it can thus be useful to administer low doses of benzodiazepines, such as diazepam 2 mg–4 mg (10–20 drops) or lorazepam 1 mg (10 drops). These compounds should be avoided and/or administered carefully, especially considering that neurotoxic symptoms can occur after envenomation from some *Vipera* species (e.g., Giribaldi et al., 2020; Malina et al., 2017). Any deep sedation is generally not desirable in the case of ophidic accidents (WHO, 2010, 2016). If deep sedation is necessary, the essential life functions of the patient must be monitored with care, and respiratory airways should be protected from aspiration of the stomach content.

Hypotension and hypertension

Patients suffering from hypotension, vasodilation and extravasation should be treated with catecholamines and plasma expansion. In case of severe hypotension, additional application of colloid infusions might be required (Valenta, 2010). Administration of fresh frozen plasma (at least 10 mL/kg of body weight) is useful in supporting plasma volume-expansion, as well as normalisation of potential disseminated intravascular coagulation disorders. However, if the blood pressure decreases considerably as a consequence of the envenomation, catecholamines (norepinephrine, 0.1 μg/kg/min achieved by diluting 4 mg in 50 mL of volume and applied at a rate of 5 mL per hour) must be taken into consideration. When envenomation symptoms are also associated with signs of myocardial toxicity and arrhythmias, the infusion of catecholamines with a β-mimetic effect (e.g., dobutamine with a mean dosage of 5 μg/kg/min) should be considered (Valenta, 2010). Neuromuscular blockade at bulbar level, neurotoxin venom–induced release of catecholamines, decreased parasympathetic stimulation, dysautonomia and renal injury appear to rarely cause high blood pressure following viper bites (Malina et al., 2008; Senthilkumaran et al., 2014). With regards to treatment, angiotensin-converting-enzyme (ACE) inhibitors have been proven to be quite useful in lowering blood pressure (Senthilkumaran et al., 2014).

Gastrointestinal symptoms

Gastrointestinal symptoms, including vomiting, nausea, abdominal pain and diarrhoea, are common early symptoms of systemic envenoming (Valenta, 2010; WHO, 2010, 2016). In healthy adults, these symptoms are generally mild, and do not represent a reason to administer antivenom. In children, however, they should be evaluated carefully because of the likely greater risks of complications, and can provide a sufficient basis to start antivenom treatment (Valenta, 2010). In case of gastrointestinal symptoms, adequate hydration should always be available, and electrolytes provided if needed.

Neurotoxicity

Signs of neurotoxicity may arise following viper bites. In these cases, oral intake of drugs is not recommended because of the risk of aspiration caused by the potential loss of the swallowing reflex. If respiratory failure occurs, intubation and mechanical ventilation should be considered. Neurotoxic symptoms have been reported following envenomation by some *Vipera* species (e.g., *V. ammodytes*, *V. aspis*, *V. berus*), and are generally attributable to presynaptically acting neurotoxic PLA_2 (Malina et al. 2017; Hempel et al., 2018; Zanetti et al., 2018; Valenta, 2010). Neurotoxicity often involves cranial nerves, inducing ptosis, ophthalmoplegia with double or fuzzy vision, dysphagia with increased salivation, dysarthria, and a variable degree of visible facial muscle paralysis, but is also associated to general muscular weakness. An important symptom of acute and severe neurotoxicity is the “broken neck sign”, for which the muscles flexing the neck are paralysed, as well as “paradoxical respiration” for which the abdomen expands rather than the chest on attempted inspiration (WHO, 2010, 2016). If untreated, these serious clinical conditions may lead to loss of consciousness, respiratory failure, and consequent death.

Symptomatic treatment of neurotoxic symptoms involves securing the patient’s respiratory airways, for example through tracheal intubation and mechanical ventilation. In the presence of neurotoxic signs and absence of antivenom, ventilation with air or oxygen is needed. When mechanical ventilation is not available, manual ventilation can be performed. In patients presenting neurotoxic symptoms, the Tensilon test should be performed in order to differentiate between symptoms potentially due to myasthenia gravis and symptoms caused by other conditions. The test involves intravenous injection of 2 mg edrophonium, and of aadditional 8 mg after 30 s. The patient is observed for 10–20 min, and is monitored for an improvement of ptosis and ventilation capacity. When edrophonium is not available, intravenous atropine sulphate (0.6 mg for adults and 50 µg/kg for children) followed by an intramuscular injection of neostigmine bromide or methyl-sulphate (0.02 mg/kg for adults and 0.04 mg/kg for children) are good alternatives. Under a positive Tensilon test, atropine and neostigmine can be administered to patients capable of swallowing (WHO, 2010, 2016). Patients who unable to swallow can receive intramuscular, intravenous, or subcutaneous injections of neostigmine methyl-sulphate together with atropine, in order to block muscarinic side effects (WHO, 2010, 2016). The Tensilon test should be performed by a neurologist, with particular care for individuals over 50 years old, and /or under corticosteroids or pro-cholinergic drugs (Pascuzzi, 2003). An alternative to the Tensilon test is the ice test. The ice test aims to check the presence of neurotoxic symptoms, and consists in applying an ice-filled plastic glove to one eye for 2 min to assess improvement of ptosis, possibly due to inhibition of anticholinesterase (WHO, 2010, 2016).

Symptomatic treatments may prove ineffective, particularly when envenomation is associated with neurotoxins combined with presynaptic toxins that may block the neuromuscular junction at the presynaptic level (Georgieva et al., 2008; Giribaldi et al., 2020; Pungercar et al., 1999). Accordingly, nerve ending damage can generally be prevented by immunologically unbinding through early administration of a relevant antivenom (Valenta, 2010). Overall, the symptomatic treatments reported above should not be considered an alternative to the use of viper antivenom, but as a complementary therapy (Valenta, 2010).

Cardiotoxicity and arrhythmias

Adverse Cardiovascular Events after a Venomous Snakebite (ACVE) are defined as the occurrence of at least one of the following conditions: i) myocardial injury (based on troponine I elevation within 48 h of presentation or ECG evidence of ischemic changes, such as ST elevation, ST depression, or T wave inversion), ii) shock (defined as hypotension requiring vasopressors), iii) ventricular dysrhythmias (ventricular tachycardia, ventricular fibrillation, torsades de pointes), and iv) cardiac arrest (see Kim et al., 2016, and Nayak et al., 1990). Elevation of the ST segment in II, III, AVF leads, transient horizontal ST depression in V5-V6, peaked T-waves, intermittent 2:1 s degree heart block and transitional junctional escape rhythm are the most common ECG alterations following *Vipera* bites (Frangides et al., 2006; Kurtović et al., 2016; Moore, 1988; Varga et al., 2018). Any myocardial and electrocardiographic changes must be analysed and treated specifically, in combination with antivenom administration.

Haematological alterations

Coagulopathy and haemorrhagic effects are common symptoms of envenomations caused by snakes of the family Viperidae (Gutiérrez et al., 2005a, 2005b, 2016). Minimal signs of coagulopathy can be detected only after laboratory investigations, while more severe haematological complications are detectable with the analysis of symptoms such as bleeding from mucous membrane tissues, nose, mouth and gums, as well as internal haemorrhages (e.g., gastro-intestinal tract, body cavities, brain). Pro-coagulative clinical complications may cause microembolisation or thrombo-embolism, leading to DIC-like disorders and, eventually, organ dysfunction syndrome. Prognosis for these clinical manifestations involve the presence of micro-thrombotisation and interstitial oedema when capillary integrity is damaged. Symptoms include different levels of respiratory distress syndrome, anuria, and alterations of blood chemistry (i.e., increase in bilirubin and hepatic enzymes), while clinical hypofibrinogenemia or defibrination may be observed and associated with blood levels decreasing next to null.

In case of systemic haematological alterations, the first choice of treatments remains antivenom administration, and symptomatic treatments should be performed only if antivenom administration is contraindicated or unavailable on a temporary/long-term basis. In the absence of bleeding, application of a fibrinogen concentrate is not recommended (Valenta, 2010). In contrast, when bleeding is observed, fibrinogen is replenished using fibrinogen concentrates or fresh-frozen plasma (10–20 ml/kg body weight). Administration of coagulation factor concentrates is indicated if a critical decrease in these factors has been noted. Heparin treatment (5000 units and additional 2500 units every 8 h) has been recommended to treat DIC-like disorders following the bite (Valenta, 2010). Nonetheless, it should be mentioned that WHO does not recommend the use of heparin in the case of snakebite, since it is ineffective against venom-induced thrombi and may cause bleeding because of its anti-coagulant properties (WHO, 2010, 2016). However, if DIC has been diagnosed, the patient stabilised and bleeding has stopped, minimal doses of non-fractionated heparin or more preferably low-molecular heparin are to be taken into account (Valenta, 2010). Anti-fibrinolytics, such as tranexamic acid, can be effective if the bleeding has been caused by an increase in plasminogen activation. However, caution is needed since antifibrinolytics inhibit the degradation of microembolisation; moreover, they may increase the risk of organ failure as part of the DIC-like disorder, and they should be avoided in the case of snake-bites (Valenta, 2010; WHO, 2010, 2016). In case of persistent bleeding, it is important to substitute platelets, in decline under 20,000–50,000/mm3. The same protocol should be followed in case of a decrease in erythrocyte concentrations, particularly below 25%–30% of the physiological values (Valenta, 2010). In the case of severe bleeding or need for urgent surgery, once antivenom has been given to neutralise venom pro-coagulants and other anti-haemostatic toxins, restoration of blood coagulation and platelet function can be accelerated through the adminstration of fresh frozen plasma, cryoprecipitate (fibrinogen, factor VIII), fresh whole blood, and/or platelet concentrates (WHO, 2010, 2016).

Myotoxicity

Myonecrosis or acute muscle damage is a very common outcome of snakebite envenomation. Viperid venom is known to induce local myonecrosis, particularly prominent in envenomations caused by members of the subfamily Crotalinae (Gutiérrez et al., 2008, 2009). The myotoxic effects of viper venom are mostly due to non-enzymatic toxins and enzymes of the PLA_2 type, which cause destruction of striated muscle cells (i.e., rhabdomyolysis), resulting in minor or even major myonecrosis (Lomonte and Gutiérrez, 2011; Valenta, 2010).

Rhabdomyolysis is characterised by the disruption of skeletal muscle integrity, leading to the direct release of intracellular muscle components, including myoglobin, creatine kinase (CK), aldolase and lactate dehydrogenase, as well as electrolytes, into the bloodstream and extracellular compartment (Lomonte and Gutiérrez, 2011; Torres et al., 2015). Rhabdomyolysis can range from asymptomatic illness with elevation in the CK levels to life-threatening condition associated with extreme elevations in CK, electrolyte imbalances, acute renal failure and DIC (Torres et al., 2015). The classic triad of symptoms of rhabdomyolysis consists of myalgia, weakness, and tea-coloured urine (Torres et al., 2015). Systemic manifestations may include tachycardia, general malaise, fever, nausea and vomiting. Clinical manifestations of DIC and multi-organ failure may subsequently appear (Torres et al., 2015). The main complications of rhabdomyolysis are acute kidney injury, compartment syndrome, hypovolemia, late hypercalcemia, hypocalcemia, hypophosphatemia, hyperkalaemia and DIC (Torres et al., 2015). The main treatment for snakebite-related rhabdomyolysis is antivenom therapy. Symptomatic treatment against rhabdomyolysis is limited to an adequate parenteral supply of liquids aimed to prevent a decrease in perfusion pressure in the glomeruli and facilitate production of a sufficient quantity of primary urine (Nelson et al., 2019).

Renal damage and failure

Actute renal failure can be induced by reduced blood pressure, a typical symptom of viper envenomation, and by the development of microthrombi in instances of DIC-like coagulation disorders (Valenta, 2010; WHO, 2010, 2016). To minimise the risk of renal damage from excessive excreted myoglobin (i.e., myoglobinuria) and/or haemoglobin (i.e., haemoglobinuria), it is important to correct hypovolemia, maintain saline diuresis, and correct severe acidosis with bicarbonate through a single infusion of mannitol (200 mL of 20% solution over 20 min).

Several nephrotoxic elements present in snake venom can directly produce renal damage (Nelson et al., 2019). To protect kidneys from such direct damage, adequate perfusion pressure and sufficient renal blood flow must be guaranteed. If systemic pressure cannot be sustained by increasing intravascular volume, vasopressor therapy is recommended. Additionally, catecholamines can be used to maintain sufficient renal blood flow, but not before intravascular volume is restored (Valenta, 2010).

As a rule of thumb, two litres of isotonic saline solution can be administered to an adult patient over one hour, bearing in mind that it should be suspended if the patient experiences pulmonary oedema. The stimulation of diuresis is often managed through a slow injection of 100 mg of furosemide (4–5 mg/minute); it is possible to administer a second dose of furosemide of 200 mg if the normal urine output of 40 mL/hour is still not restored. If after treatment the urine output is still below the required baseline, the patient should be transferred to a Renal Unit. Serum troponin, ECG, potassium, urea, creatinine, pH, bicarbonate, calcium and phosphate should be monitored frequently. The patient's diet should be bland, high in calories (1700 kcal/day) and low in proteins (less than 40 g/day) (WHO, 2010, 2016). In the case of a renal failure, treatment does not differ from that of other organs' failure from different etiologies, with the exception of antivenom administration (Valenta, 2010). If the renal insufficiency is too severe and characterised by clinical uraemia, fluid overload, changes in blood biochemistry (including one or more of the following: creatinine > 4 mg/dl [500 µmol/l]; urea > 130 mg/dl [27 mmol/l], potassium > 7 mmol/l [or hyperkalaemic ECG changes]) as well as symptomatic acidosis, alternative treatments such as hemofiltration or haemodialysis can be applied depending on the patient's status.

Hyperglycaemia

Stress hyperglycaemia is a clinical manifestation associated to inflammatory and/or stressful conditions due to acute injury or stress responses, and has been associated with increased morbidity and mortality in critically ill patients from intensive care settings (Viana et al., 2014). Snakebite envenomation, as well as envenomations caused by other organisms (e.g., scorpions), pain, acidosis, alteration in intravascular volume and hypoxia can potentially induce stress hyperglycaemia (Ali Abdelhamid et al., 2016). Hyperglycaemia is a potential risk factor for high-grade envenomation after European *Vipera* bites in children (Claudet et al., 2016). The presence of hyperglycaemia in association with other factors that may increase the progression of symptoms to high-grade envenomation, may require transferring paediatric patients to a tertiary level hospital for antivenom treatment (Claudet et al., 2012).

Although the role of hyperglycaemia as a risk factor for progression to high-grade envenomation is still unclear, it should be taken into account when treating snakebite victims.

Antivenom therapy

Specific immunotherapy for snakebites involves the administration of snake antivenom, which can be monovalent or polyvalent. The former, being species-specific, should be preferred when the species responsible for the bite can be reliably identified. As this is not always possible, the latter, effective against the venom of more than one species, tends to be used more frequently (Gutiérrez et al., 2005a, 2005b, 2014; Valenta, 2010).

Antivenom administration, although recommended when signs of systemic envenomation exist or in the case of locally advanced or progressive symptoms, must always be considered with caution because of the severe potential side-effects (e.g., anaphylactic shock) it can trigger (León et al., 2013). However, the possible onset of side effects should not delay or negate the administration of antivenom. Concerning *Vipera* antivenoms currently available in Europe, this point is of particular relevance, since a recent study concluded that adverse reactions attributable to them are rare and treatable with standard therapy (Lamb et al., 2017).

Snake antivenom is generally available from local, regional, or national poison control centers across Europe. In the rare evinience that antivenom is not available at all, therapeutic measures specifically aimed at treating the onsetting envenomation symptoms must be implemented.

When should antivenom be administered?

The timely administration of antivenom is essential. Decisions concerning its administration should be assessed rapidly, although always based on the entity of the envenomation symptoms. The clinical, laboratory and instrumental alterations that are commonly considered to require antivenom injection are resumed by the so-called "Stockholm criteria" (Persson and Karlson-Stiber, 1996).

The Stockholm criteria state that antivenom should be administered when the following symptoms arise: hypotension and circulatory shock, protracted severe gastrointestinal symptomatology, mucous membrane oedema with a risk of bronchial obstruction, rapid extension of oedema to an entire limb and/or to the torso, neurological symptomatology with depressed CNS and peripheral and central paresis. In rare cases of insufficient clinical signs, antivenom may be administered when any of the following conditions are fulfilled: leukocytosis exceeding 15–20 × 10^9/l, elevation of AST, ALT, CK or other enzymes, metabolic acidosis, hemolysis, ECG changes, coagulation disorders (Persson and Karlson-Stiber, 1996).

Although valid, the Stockholm criteria are less known and used than the grading of snake envenomation (G). According to Boels et al. (2012), there are 4 main grades of envenomation severity: G0, G1, G2 (divided into G2a and G2b), and G3. This graduation is based on the grading defined by Audebert's et al. (1994), and is resumed in Table 1. The application of antivenom is recommended from G2 stage onwards (Kang et al., 2016).

Table 4.1 Clinical gradation of viper envenomation (based on Boels et al., 2012).

Grade (G)	Envenomation	Clinical features
0	No envenomation	Fang marks No oedema No local reaction
1	Minimal	Local oedema around bite site No systemic symptoms
2	Moderate	2a: Regional oedema (most of the bitten limb) and/or haematoma 2b: Grade 2a + moderate general symptoms: mild hypotension, vomiting, diarrhoea, neurotoxic signs and/or biological criteria for severity:

		Platelets < 150 G/L Leukocytes > 15 G/L INR > 1.5 Fibrinogen < 2g/L
3	Severe	Extensive oedema spreading to the trunk and/or severe general symptoms (severe hypotension < 80 mmHg systolic, shock, bleeding)

Types of antivenom

To date, several antivenoms are available in Europe against *Vipera* envenomations (Lamb et al., 2017; WHO, 2020). Among them, it is worth mentioning the polyvalent ViperFAV (Sanofi-Pasteur), effective against *V. ammodytes*, *V. aspis* and *V. berus* venoms, and ViperaTAb (MicroPharm Ltd.) effective against *V. ammodytes*, *V. aspis*, *V. berus* and *V. latastei* venoms. Monovalent antivenoms, like Biomed’s Viper Venom Antitoxin and Bulbio’s Snake Venom Antiserum (effective against *V. berus* and *V. ammodytes* venoms, respectively) have also been developed. An updated list of the antivenoms currently available against venoms of snakes of the genus *Vipera* (and other genera) is provided by WHO’s Snakebite Information and Data Platform (WHO, 2020).

Administration modality and doses

Antivenoms are made of large molecules (Fab fragments, sometimes whole IgG) which, when injected intramuscularly, are absorbed slowly via the lymphatic system, and are associated with a poor bioavailability. Therefore, although intramuscular administration is recommended by some manufacturers, the intravenous route should be the preferred route of administration, since it allows a greater bioavailability of the antivenom. Indeed, 1.4–6% of the antivenom is estimated to reach the venom injection site in 2 h from its intramuscular or subcutaneous inoculation, while this amount raises up to 85 % when the antivenom is administered intravenously (WHO, 2010, 2016).

Intramuscular administration of antivenom should be taken into consideration when the distance between the location where the snakebite took place and the closest hospital is large and requires hours of travel, or in patients with no intravenous access (WHO, 2010, 2016). In these exceptional circumstances, the dose of antivenom should be divided between a number of sites in the upper anterolateral region of both thighs, followed by massaging to aid absorption. Antivenom should not be injected into the gluteal region, as absorption from this area is exceptionally slow and unreliable if the injection is performed by an unexperienced operator. However, it is important to point out that antiophidic serum must be injected primarily in hospitals and in the presence of experienced personnel, particularly because its administration outside hospitals is most often intramuscular or subcutaneous, thus less effective, and can expose the patient to the risks of severe adverse reactions (WHO, 2010, 2016).

While lyophilised antivenoms can be stored at room temperature, liquid antivenoms should ideally be stored at 2–8 °C (Thekaston et al., 2003; Valenta, 2010). The WHO guidance proposes two major methods of administration of the antivenom: I) reconstituted freeze-dried antivenom or neat liquid antivenom diluted in approximately 5–10 ml of isotonic fluid per kg of body weight, infused at a constant rate over a period of about one hour; II) reconstituted freeze-dried antivenom or neat liquid antivenom administered through slow (not more than 2 mL/minute) intravenous injection (WHO, 2010, 2016). It is important to highlight that since snakes inject the same amount of venom in both adults and children, the antivenom dosage is independent from the patient's age and usually ranges between 4 and 50 ml, based on the type of antivenom used (WHO, 2010, 2016). Although manufacturers always report the recommended amount of serum to be injected, a formal contact with a poison control center before antivenom inoculation is always recommended.

Currently, there is no standardised and harmonised protocol for antivenom administration across Europe, and variation across countries is wide. However, 1–2 ampoules of antivenom are most often administered (Kang et al., 2016; Lamb et al., 2017). After the initial dose, additional administration of antivenom may be needed, typically because of poor therapeutic efficiency of the antivenom or recurrence of clinical manifestations (see Figure 4.5). These include persistence of poor blood coagulation and/or bleeding, and an increase in the clinical symptoms of neurotoxicity or cardiovascular toxicity (Nelson et al., 2019; WHO, 2010, 2016).

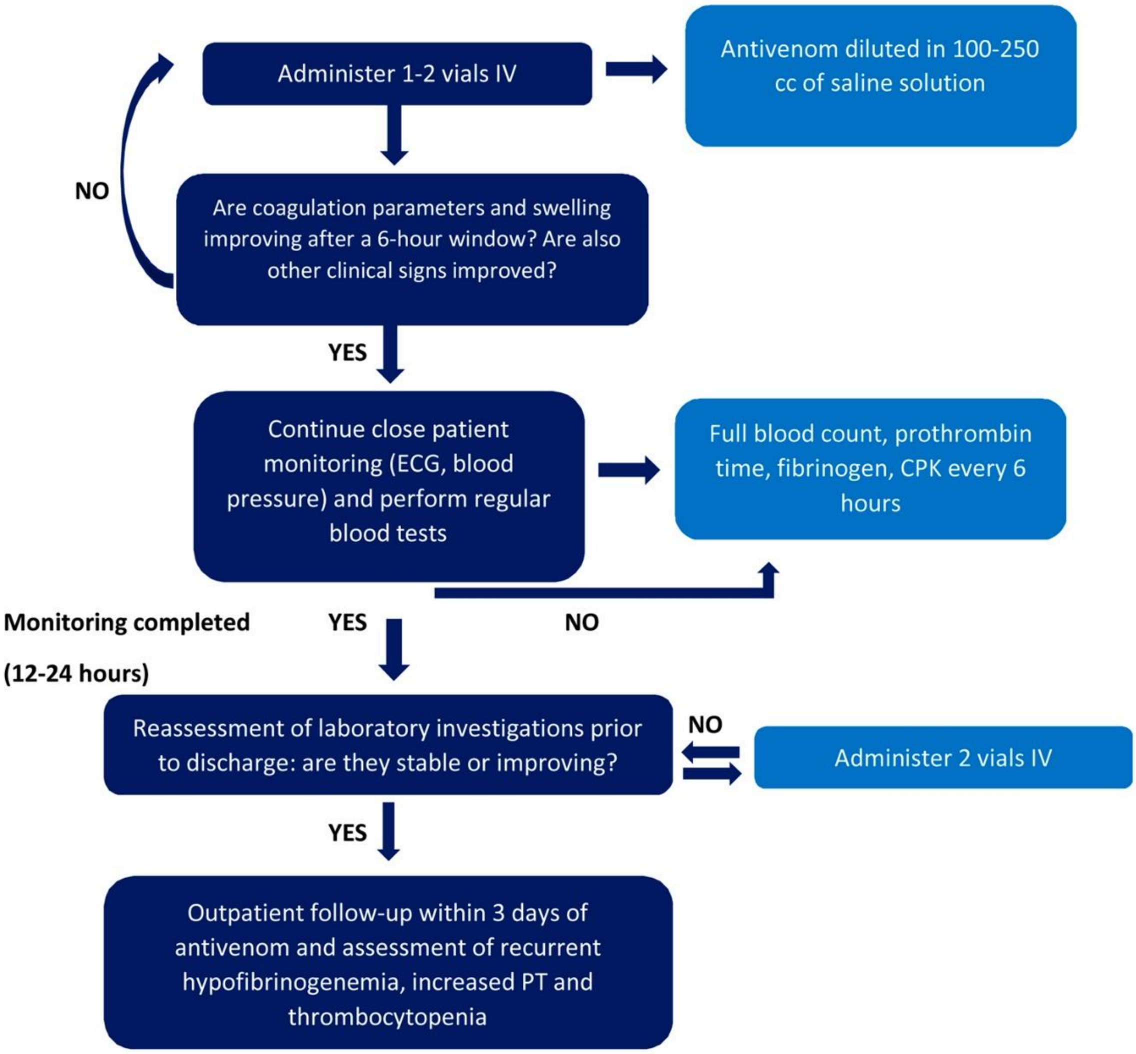

Figure 4.5 Steps of antivenom administration (based on Pizon and Ruha, 2015).

Envenomation caused by *Vipera* species may result in signs of systemic envenoming possibly recurring within 24–48 hours after snakebite in patients with an initial positive response to the antivenom, although cases of recurrence of symptoms 3–14 days after antivenom administration have also been reported (Valenta, 2010; WHO, 2010, 2016). The recurrence of envenomation symptoms has been more commonly associated with the injection of antivenoms containing antigens with a shorter elimination half-life, such as Fab fragments (Valenta, 2010).

Antivenom adverse reactions

According to a recent review, adverse reactions due to the administration of antivenom against *Vipera* venoms are rare (Lamb et al., 2017). Among some of the antivenoms most commonly used to treat *Vipera* envenomations, ViperaTAb showed the lowest incidence of adverse reactions, probably due to its reduced protein load and shorter elimination half-life (Lamb et al., 2017). Despite these results, clinicians should always monitor any possible adverse reactions case by case, since because of inter-individual differences in the toxicokinetics and toxicodynamics of the antivenoms they may occur unexpectedly. On a general basis, the risk of adverse reactions is dose-related, and they are common in many parts of the world where snakebite is prevalent (Gutiérrez et al., 2006; WHO, 2010, 2016).

In general, anaphylactic reactions may appear within 10–180 min after the administration of the antivenom. Patients that have developed reactions to equine or ovine serum in the past, and patients with a personal medical history indicating genetic tendency to develop allergic diseases are more likely to develop anaphylaxis. Anaphylactic reactions can be managed with the administration of subcutaneous epinephrine (dose of 0.25 mL/0.25 mg of epinephrine and dilution of 1:1000 [0.1%]) (Valenta, 2010). Hydrocortisone can also be administered (dose 2–4 mg/kg body weight), together with anti-H1 antihistamines (cimetidine or chlorphenamine) or anti-H2 antihistamines (cimetidine, cetirizine). If an acute anaphylactic reaction arises, antivenom administration must temporarily be suspended, and an appropriate therapy to treat it must be applied promptly. Pyrogenic reactions may also arise usually within 60–120 minutes after antivenom treatment, and are characterised by shaking, chills, fever, vasodilation, and a fall in blood pressure. In such cases, the patient’s body temperature must be lowered using antipyretics (e.g., paracetamol), and intravenous fluids should be given to treat eventual hypovolaemia.

Serum sickness syndrome may also occur as a delayed hypersensitivity reaction, triggered by the snake anti-venom, equine and rabbit anti-thymocyte globulin (Pascuzzi, 2003). Such syndrome may arise with a median time of 7 days after the administration of the antivenom (range between 1–12 days), and is mainly characterised by cutaneous rashes, itching, arthralgia, fever, lymphadenopathy, head and neck malaise, hypotension, splenomegaly, glomerulonephritis, proteinuria and haemoglobinuria. Treatment for serum sickness syndrome includes the administration of chlorphenamine as well as prednisolone (WHO, 2010, 2016).

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Chapter 5

Venomics of Lataste’s viper (*Vipera latastei*)

Introduction

Lataste's viper (*Vipera latastei*, Boscá 1878) is a medium-sized European viper (family Viperidae, subfamily Viperinae) endemic to the Iberian Peninsula (see (Martínez-Freiría et al., 2021), included within the subclade of the Western Mediterranean vipers (i.e., *Vipera* 1; Freitas et al., 2020; Martínez-Freiría et al., 2020). This species inhabits a wide variety of Mediterranean ecosystems and habitats, ranging from sea level to 2800 m a.s.l. (in Spain), and shows a general pattern of population isolation in mountain ranges (Martínez-Freiría et al., 2014). An ambush predator, *V. latastei* feeds on a wide variety of prey items, including mainly reptiles and small mammals and, more occasionally, arthropods, amphibians, and birds (Brito, 2004; Martínez-Freiría et al., 2010; Pleguezuelos et al., 2007a). Interestingly, Santos et al. (2008) found a certain degree of variation in diet composition across different environments, with small mammals being the vipers' main prey in colder, more humid areas, whereas the proportion of reptiles was higher in warmer, drier environments. Ontogenetic shift in diet has also been reported for *V. latastei*: juveniles feed mainly on ectothermic prey (i.e., invertebrates, reptiles, amphibians) and, to a lesser extent, on endotherms (e.g., shrews), whereas the diet of adult vipers is mainly composed of rodents (Martínez-Freiría et al., 2014, and references within).

Lataste's viper is recognised as a medically important snake species by the World Health Organization (WHO, 2020), and is one of the few native animal species of the Iberian Peninsula with the potential to cause severe illnesses to humans (Di Nicola et al., 2021; Valdoleiros et al., 2021). Although the venom produced by *V. latastei* is less toxic (intravenous LD_{50} = 15.1 µg/mouse, 18–20 g mice; Archudnia et al., 2011) than the venoms of other congeneric European vipers (e.g., *Vipera ammodytes ammodytes*, intravenous LD_{50} = 8.4 µg/mouse, 18–20 g mice; Archundia et al., 2011) this species is able to inject considerable amounts of it (Detrait et al. (1983) estimated that the subspecies *V. l. gaditana* can produce about 20 mg of dry venom per 100 g of body weight). Studies aiming at characterising the effects of *V. latastei* venom found it to possess coagulopathic and haemorrhagic activity (Arez et al., 1993; Detrait et al., 1983; Chowdury et al., 2021). Furthermore, comparative analyses of SDS-PAGE protein patterns of venoms collected from several species of the genus *Vipera* suggested the presence of a certain degree of geographic variation in the composition of the venom of Lataste's viper (Saint Girons & Detrait, 1992). Nevertheless, detailed venomic studies for this species are missing.

In the present work, we (i) provide the first proteomic characterisation of the venom of *V. latastei*, (ii) investigate the presence of ontogenetic change in the composition of the species' venom; (iii) assess the level of geographic venom variation between two environmentally different localities within the species' north-western distributional range in

Portugal. Considering the existence of an ontogenetic dietary shift in this species, we expect to detect a corresponding ontogenetic shift in venom composition. Furthermore, we hypothesise that the environmental differences between the two sampled localities (one located on the coast and under considerable anthropic disturbance, the other located in the mountains and less impacted by human activities) might influence factors affecting the vipers' feeding ecology (e.g., prey community), thus driving interpopulational venom variability.

Materials and Methods

Study areas

Vipers were collected in two environmentally different localities about 75 km from each other, situated in the north-western distributional range limit of the species (see Figure 5.1A).

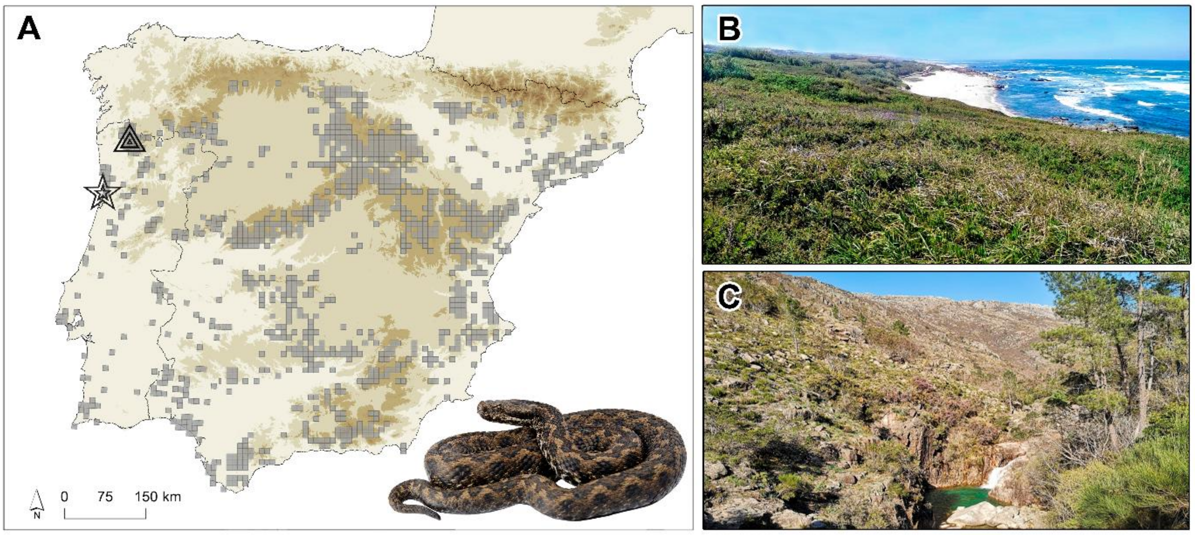

Figure 5.1 Sampling localities of the two studied *V. latastei* populations. In panel A, the star indicates the Vila Chã population, while the triangle indicates the Gerês population. The grey squares correspond to the current distribution range of *V. latastei* (adapted from Valdoleiros et al., 2021). Panels B and C show the habitats of the localities Vila Chã and Gerês, respectively.

The locality hereafter named “Vila Chã” is located on the northern Atlantic coast of Portugal (41.28 N, 8.72 W), close to the village of Vila Chã in the municipality of Vila do Conde, and within the Regional Protected Landscape of the Vila do Conde Coast. The climate in this area is temperate, with dry or mild summers (Csb climate type; AEmet, I.P.M.A., 2011). The average annual temperature is around 14 °C, with total annual rainfall ranging from 1600 to 2000 mm/year (I.P.M.A, 2021). The landscape is characterised by sandy beaches with granitic rock outcrops, surrounded by agricultural fields (mostly dedicated to maize farming) with stonewalls (Figure 5.1B). The natural vegetation is mainly herbaceous or scrubby (e.g., *Erica* sp., *Ulex* sp.), with the invasive ice plant (*Carpobrotus* sp.) being very abundant, especially in the areas closest to the coast. While an exhaustive description of the feeding ecology of

Lataste's vipers from Vila Chã is currently missing, an estimate based on the analysis of prey remains obtained from 23 adult specimens collected there suggests that adult vipers from this population mainly prey on small mammals (e.g., genus *Microtus*; authors, unpublished data).

The locality hereafter named “Gerês” is located in the Gerês /Xurés Mountains, within the Gerês-Xurés Transboundary Biosphere Reserve (Northern Portugal - North-western Spain), at an elevation ranging from 700 to 900 m a.s.l. (41.80 N, 8.13 W). The area is characterised by temperate climate, with a dry season and temperate summer (Cfb climate type; AEmet, I.P.M.A., 2011), with average annual temperature around 9 °C. Precipitation levels are generally high, with total annual rainfall ranging from 2800 to 3200 mm/year (I.P.M.A., 2021). The landscape consists of granite mountains, with abundant rock piles (Figure 5.1C), and vegetation generally composed of woodlands (dominated by *Quercus robur*) and scrublands (with *Erica* sp., *Genista* sp., *Rubus* sp., *Ulex* sp.). From the analysis of prey remains collected from 101 *V. latastei* specimens from the Gerês Mountains, Brito (2004) found evidence of ontogenetic dietary shift, with adults feeding almost exclusively on small mammals (i.e., mainly genus *Apodemus*, and, less abundantly, genera *Crocidura*, *Sorex* and *Microtus*), composing > 90% of their diet, and juveniles mainly feeding on ectotherms (e.g., genus *Podarcis*), composing > 60% of their diet.

Vipers from Vila Chã and Gerês share a very recent common ancestor, as demonstrated by the fact that they belong to the same mitochondrial lineage, and even the same haplotype (i.e., the West CNW lineage, haplotype CNW1 (Martínez-Freiría et al., 2020; Velo-Antón et al., 2012). Differences in venom composition may thus be due to different local selective regimes rather than neutral evolutionary divergence.

Viper sampling and venom collection

A total of 63 specimens of *V. latastei* were used in this study. Specifically, 38 specimens were collected in Vila Chã, and 25 specimens were collected in Gerês (Table A2.1). Variation in head scale fragmentation (analysed through the software APHIS v.1.0.0 (Moya et al., 2015), body scale counts, and dorsal colouration, were used as criteria to identify each specimen, and thus recognise potential recaptures.

Sampling was performed between 2018 and 2021, from spring to late summer/early autumn. Venom was obtained by letting each viper bite a parafilm-covered 1.5 ml tube (Eppendorf, Hamburg, Germany). After venom extraction, sex was determined, and the snout-vent length (SVL) of each sampled snake was measured. Vipers were then released exactly where they had been captured. All vipers and venom samples were collected with permission of Instituto da Conservação da Natureza e das Florestas (ICNF), Portugal (ref. 537/2018, 362/2019, and 295/2020), and Xunta de Galicia, Spain (ref. EB-017/2019).

We followed Pleguezuelos et al. (2007b) to assign each animal to an age class, i.e., all males with SVL > 240 mm and all females with SVL > 263 mm were considered adults, while vipers with SVLs smaller than these values were considered juveniles. In the light of this classification, our dataset ultimately consisted of 32 adult and 6 juvenile venom samples from Vila Chã, and 20 adult and 5 juvenile venom samples from Gerês (Table A2.1). Crude venoms were stored at −20 ◦C, and lyophilised in a Scanvac (Coolsafe, Lynge, Denmark) freeze dryer. After lyophilisation, the venoms were transported to the Evolutionary and Translational Venomics Laboratory of the Institute of Biomedicine of Valencia (Spain) for proteomic analyses.

Preliminary screening of the venoms

For a first assessment of similarities and differences among the collected venoms, all venom samples were screened through reversephase high-performance liquid chromatography (RP-HPLC). Specifically, 0.2 mg of each lyophilised venom were dissolved in 80 µl of 0.1% trifluoroacetic acid (TFA) and 5% acetonitrile (ACN). Insoluble material was spun down in an Eppendorf centrifuge at 13,000 g for 10 min at room temperature, and the proteins contained in 40 µl were fractionated by RP-HPLC using a Discovery Bio Wide C18 (150 × 2.1 mm, 3 µm particle size, 300 Å pore size) Supelco column and Agilent LC 1200 chromatograph equipped with DAD detector. The column was developed at 0.4 ml/min flow rate applying the following gradient of 0.1% TFA in water (solution A) and acetonitrile (solution B): the following gradient was used for elution: isocratically 5% B for 1 min, followed by 5–25% B for 5 min, 25–45% B for 30 min, and 45–70% B for 5 min. Venom samples were analysed individually. However, due to the very low amount (< 5 µl) of venom we were able to collect from some of the juveniles, we pooled them. Two pools were generated: one for the population of Vila Chã, comprising samples from five juveniles (i.e., 20VL001, 20VL003, 20VL038, 21VL011, 21VL019), and one for the population of Gerês, made of samples from four juveniles (i.e., 18VL260, 19VL034, 19VL456, 19VL458). These pools were analysed using the same chromatographic protocol mentioned above. Details about the pooled venom samples are reported in Table A2.1.

All the chromatographic profiles produced were then overlapped and compared visually, in order to identify the most representative ones in number and relative intensities of their toxin peaks, to be submitted to bottom-up venomics analysis (Calvete, 2014; Eichberg et al., 2015).

Venom fractionation by RP-HPLC

Pre-MS decomplexation of individual venoms was performed by reverse-phase chromatography (RP-HPLC), following the protocol described by Pla et al. (2019). As a first step, 1 mg of each lyophilised individual venom was dissolved in 200 µl of 0.1% trifluoroacetic acid

(TFA) and 5% acetonitrile (ACN). In the case of 19VL013, we could use only 0.3 mg of lyophilised venom, because of the low amount of venom we were able to collect from this specimen. Insoluble material was spun down in an Eppendorff centrifuge at 13,000 g for 10 min at room temperature, and the proteins contained in 40 µl were fractionated by RPHPLC using a Teknokroma Europa C18 (250 × 4 mm, 5 µm particle size, 300 Å pore size) column and Agilent LC 1100 High Pressure Gradient chromatography system equipped with DAD detector. The following gradient was used for elution: isocratically 5% solution B (0.1% TFA in ACN) for 5 min, followed by 5–25% B for 10 min, 25–45% B for 60 min, and 45–70% B for 10 min, at 1 ml/min flow rate. Peaks were collected manually and dried in a centrifugal vacuum evaporator (SpeedVac®, ThermoSavant).

Molecular mass determination

Molecular masses of the RP-HPLC-purified proteins were estimated by SDS-PAGE analysis or determined by electrospray ionization (ESI) mass spectrometry (MS). For SDS-PAGE analysis, dried aliquots of the RP-HPLC fractions were redissolved in sample buffer (0.25 M Tris-HCl pH 6.8, 8% SDS, 30% glycerol, 0.02% bromophenol blue, with or without 1% 2-mercaptoethanol) and heated at 100 °C for 15 min. SDSPAGE analysis was run under non-reducing and reducing conditions, and the gels were stained with Coomassie Brilliant Blue G-250. For ESIMS mass profiling, the proteins eluted in the different RP-HPLC fractions of individual venoms were separated by nano-Acquity UltraPerformance LC® (UPLC®) using BEH130 C18 (100 µm × 100 mm, 1.7 µm particle size) column in-line with a Waters SYNAPT G2 High Definition Mass Spectrometry System. The flow rate was set to 0.6 µl/min and the column was developed with a linear gradient of 0.1% formic acid in water (solution A) and 0.1% formic acid in ACN (solution B), isocratically 1% B for 1 min, followed by 1–12% B for 1 min, 12–40% B for 15 min, 40–85% B for 2 min. Monoisotopic and isotope-averaged molecular masses were calculated by manual deconvolution of the isotope-resolved multiplycharged MS1 mass spectra.

Characterisation of the toxin families present in the venoms

Protein bands were excised from Coomassie Brilliant Blue stained SDS-PAGE gels, and subjected to automated in-gel reduction (10 mM dithiothreitol, 30 min at 65 °C) and alkylation (50 mM iodacetamide, 2 hours in the dark at room temperature), followed by overnight digestion with sequencing grade trypsin (66 ng/µl in 25 mM ammonium bicarbonate, 10% ACN; 0.25 µg/sample). The procedure was performed on a ProGest Protein Digestion

Workstation (Genomics Solution). Tryptic digests were dried in a vacuum centrifuge (SpeedVac®, ThermoSavant), redissolved in 15 µl of water containing 0.1% formic acid, and submitted to LC-MS/MS. Tryptic peptides were separated by nano-Acquity Ultra Performance LC® (UPLC®) using a BEH130 C18 (100 µm × 100 mm, 1.7 µm particle size) column in-line with a Waters SYNAPT G2 High Definition Mass Spectrometry System. The flow rate was set to 0.6 µl/min and the column developed a linear gradient of 0.1% formic acid in MilliQ® water (solution A) and ACN (solution B) with the following conditions: isocratically 1% B for 1 min, followed by 1–12% B for 1 min, 12–40% B for 15 min, 40–85% B for 2 min. For peptide ion fragmentation by collision-induced dissociation tandem mass spectrometry (CID-MS/MS), the electrospray ionization (ESI) source was operated in positive ion mode, and both singly and multiply charged ions were selected for CID-MS/MS at sample cone voltage of 28 V and source temperature of 100 °C. The UPLC eluate was continuously scanned from 300 to 1990 m/z in 1 s and peptide ion MS/MS analysis was performed over the range m/z 50–2000 with scan time of 0.6 s. The parent proteins were identified by interpretation of fragmentation spectra: a) manually (*de novo* sequencing), b) searched against the NCBIprot/SwissProt non-redundant databases using the online form of the MASCOT Server (version 2.6) at http://www.matrixscience.com in an automated way, and c) processed in Waters Corporation's ProteinLynx Global SERVER 2013 version 2.5.2. (with Expression version 2.0) The search parameters were: taxonomy: bony vertebrates; enzyme: trypsin (two-missed cleavage allowed); MS/MS mass tolerance was set to ± 0.6 Da; carbamidomethyl cysteine and oxidation of methionine were selected as fixed and variable modifications, respectively. All matched MS/MS data were manually checked. For missing/incomplete identifications, the MS/MS spectra were interpreted manually (*de novo* sequencing), and amino acid sequence similarity searches were performed at https://blast.ncbi.nlm.nih.gov/Blast.cgi against the non-redundant protein sequences database, using the default parameters of the BLASTP program (Altschul et al., 1990). Fragmentation spectra of peptides that yielded daughter ions diagnostic of the endogenous peptides BPP (m/z 116.1, y1 = P, and m/z 213.1, y2 = PP) or tripeptide inhibitors of metalloproteinases (SVMPi) at m/z 205.1 (y1 = W), m/z 112.1 (b1 = pyroglutamate, Z) and m/z 240.1 (b2 = Z(K/Q) or m/z 226.1 (b2 = ZN) (Coutinho-Neto et al., 2013; Menin et al., 2008) were also sequenced manually.

Relative quantification of the venom proteomes

To compile the relative composition of toxin families in the venom proteomes, we applied the 3-step hierarchical venom proteome quantification protocol developed in the Evolutionary and Translational Venomics Laboratory of the Institute of Biomedicine of Valencia (Calvete, 2014; Eichberg et al., 2015). In the first step, the relative abundances of the reverse-phase chromatographic peaks were calculated by dividing peak areas by the total area of the chromatogram, using ChemStation B.01.01.069 (Agilent Technologies). Recording the eluate at the absorbance wavelength of the peptide bond [190–230 nm], and applying the Lambert-Beer law (A = εcl, where A = absorbance; ε is the molar absorption [extinction] coefficient, [M^{-1} cm^{-1}]; c = concentration [M]; and l = light path length [cm]), these percentages correspond to the "% of total peptide bond concentration in the peak". For chromatographic peaks containing single components (as judged by SDS-PAGE and/or MS), this figure is a good estimate of the % by weight (g/100 g) of the pure venom component (Calderón-Celis et al., 2017). When more than one venom protein was present in a reverse-phase fraction, their proportions (% of total protein bands area) were estimated by densitometry of Coomassie-stained SDS polyacrylamide gels using Image Studio Lite®, version 5.2 (LI-COR Biosciences) software. Conversely, the relative abundances of different proteins contained in the same SDS-PAGE band were estimated based on the relative ion intensities of the three most abundant peptide ions associated with each protein by MS/MS analysis. The relative abundances of the protein families present in the venoms were calculated as the ratio of the sum of the percentages of the individual proteins belonging to the same family to the total area of venom protein peaks in the reverse-phase chromatogram.

Assessment of interpopulational venom diversity

Considering the environmental differences present between the montane site of Gerês and the coastal site of Vila Chã, we sought to investigate the potential presence of variation among the *V. latastei* venoms collected in these two localities. To assess the levels of such variation, we followed the individual-based approach reported by Zancolli et al. (2017). Chromatograms recorded for the two juvenile venom pools, not providing individual-level information, were not taken into account. Briefly, we generated a presence-absence matrix of the peaks present in each individual RP-HPLC chromatogram we produced. Peaks with frequency equal to 1 (i.e., present in every chromatogram, and thus not informative) or difficult to identify were excluded from the dataset before performing the analyses. The final binary matrix was used to calculate individual venom richness (i.e., total number of peaks detected in each chromatogram), and to analyse patterns of venom variation using non-metric multidimensional scaling (NMDS) based on pairwise Bray-Curtis similarity distances among the chromatograms (Minchin, 1987). In NMDS analyses, the stress value provides an estimate of the goodness of fit of the analysis performed. An overall stress value above 0.2 generally indicates poor fit (Kruskal, 1964). In order to keep the stress value below the 0.2 threshold, we included an additional dimension to our NMDS analysis, thus opting for a three-dimensional NMDS analysis. The individual NMDS scores on the first two axes (i.e., NMDS1 and NMDS2) were then used to produce an ordination plot representing the associations between the RP-HPLC venom profiles.

We used simple linear regressions to investigate the relationship between the individual scores on the first NMDS axis (i.e., NMDS1, used as response variable) and snout-vent length (SVL), sex, date of collection of the venom samples (i.e., the ordinal day of the year), and population of origin (Gerês or Vila Chã). We scaled all continuous variables (i.e., mean = 0; SD = 1) for easier comparison of their effect size. Collinearity between explanatory variables was low [Variance Inflation Factors (VIF) always < 2], thus we included all of them in the models. We built models using all possible combinations of independent variables, and ranked them on the basis of the Akaike's Information Criterion corrected for small sample sizes (AICc) (Burnham & Anderson, 2002). The final set of candidate models was obtained by removing all models which had a simpler nested version with lower AICc (Richards et al., 2011).

We also tested whether the presence or absence of specific peaks identified in the venom chromatograms was significantly correlated with snout-vent length, sex, date of collection of the venom samples, and population of origin. Specifically, we used binomial Generalised Linear Models (GLMs), considering the presence/absence of each peak as binomial dependent variable, and the four above-mentioned variables as predictors. Also in this analysis, VIF values lower than 2 confirmed low collinearity between the explanatory variables, which were thus all included in the models. These were again built using all possible combinations of independent variables, and ranked on the basis of their AICc scores.

We used the packages *vegan* (Oksanen, 2016) to perform the NMDS analysis, *MuMIn* to build the full set of models (Bartoń, 2020), and *ggeffects* (Lüdecke, 2018) to plot model predictions. All analyses were performed in R environment (version 4.1.1; R Core Team, 2021).

Results and Discussion

Analysis of the chromatograms

A total of 56 chromatograms were recorded, namely 54 for individual venoms and two for the juvenile venom pools. By visually comparing the chromatographic profiles obtained through this approach, we detected differences in chromatographic peaks present within each of the two sampled populations. The most striking difference concerned the intensity of a peak appearing around minute 17, evident in some venoms (although with different intensity/height) and completely absent in others (Figure 5.2). This peak was absent in the profiles produced from the individual juvenile venoms (i.e., 19VL013 and 19VL026) and in the pool of juvenile venoms from Gerês, but it was evident in the pool of juvenile venoms from Vila Chã (Figure

A2.1). We also noted other differences among the analysed chromatograms, mainly involving different intensities in the initial reverse-phase chromatographic peaks (eluting between 7 and 10 min) and in late-eluting peaks (39–44 min; see Figure 5.2). Based on these differences, we selected the following six representative venoms to be used for the proteomic analyses: 19VL013 (juvenile), 18VL253 (adult), and 18VL011(adult) from the Vila Chã population; 19VL026 (juvenile), 18VL258 (adult), and 19VL029 (adult) from the Gerês population.

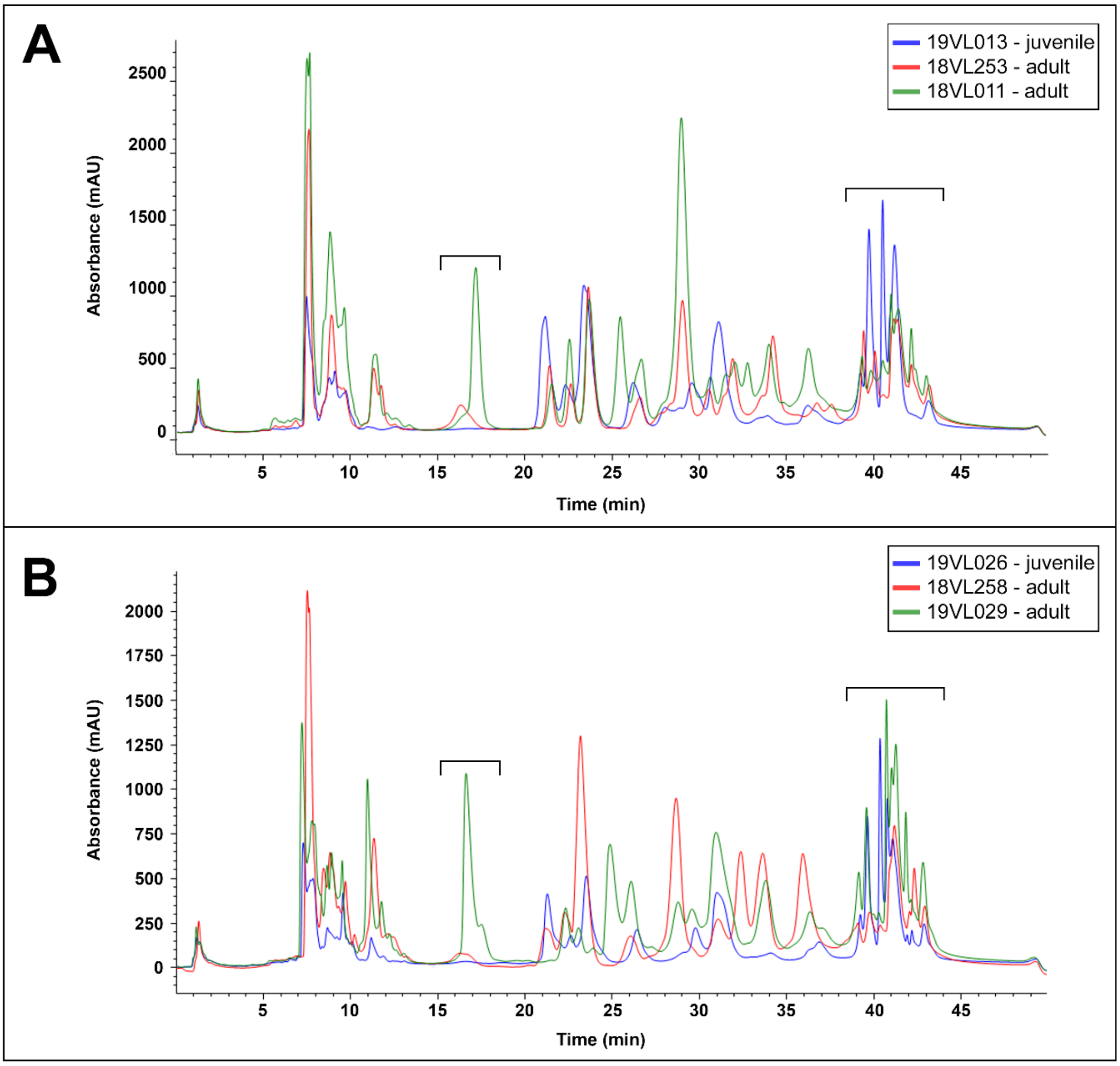

Figure 5.2 Overlapped chromatograms of the six venom samples analysed through bottom-up proteomics. Panels A and B display chromatographic traces of the venoms from Vila Chã and Gerês, respectively. Sample codes and corresponding colours are reported in the panel insets. Notice the differences in the intensities of the peaks, particularly the ones in the two time intervals highlighted by the brackets (i.e., minutes 16–18, and minutes 39–44).

Protein composition of *V. latastei* venom

The number of chromatographic peaks recovered from the six venoms selected for proteomic analyses varied between 43 (in the juvenile 19VL013, from Vila Chã) and 69 (in the adult 18VL253, from Vila Chã; see Figure A2.2). The number of toxin classes identified across the analysed venoms varied between 11 (19VL013) and 18 (18VL253, from Vila Chã). Table 5.1 and Figure 5.3 display the relative abundances of the components of the six venom proteomes produced.

Table 5.1 Relative abundances (in percentage of the total venom proteome) of the components identified in the six representative *V. latastei* venoms analysed by bottom-up proteomics. 5'NT, 5'-nucleotidase; AP, aminopeptidase; BIP, bradykinin-inhibitory peptide; BPP, bradykinin-potentiating peptide; CRISP, cysteine-rich secretory protein; CTL, C-type lectin-like; DISI, disintegrin; Hyal, hyaluronidase; KUN, Kunitz-type inhibitor; LAAO, L-amino-acid oxidase; D49/K49-PLA$_2$, D49/K49-phospholipase A$_2$; PLB, phospholipase B; PDE, phosphodiesterase; PI-/PIII-SVMP, snake venom metalloproteinase of class PI/PIII; DC, disintegrin-like/cysteine-rich domain; QC, glutaminyl cyclase; SVMP, metalloproteinases of unidentified class (PI/PII/PIII); SVMPi, endogenous tripeptide inhibitors of SVMP; SVSP, snake venom serine proteinase; VEGF, vascular endothelial growth factor; VNGF, venom nerve growth factor.

Venom components	**Vila Chã**			**Gerês**		
	19VL013	**18VL253**	**18VL011**	**19VL026**	**18VL258**	**19VL029**
5'NT	-	0.2	-	-	0.12	0.12
AP	-	0.09	0.15	0.07	0.05	0.03
BIP	-	-	0.14	-	-	-
BPP	4.85	2.81	8.89	1.4	4.38	1.83
CRISP	6.15	2.29	2.98	5.54	2.88	3.75
CTL	7.08	19.16	8.52	3.01	14.95	9.98
DC	-	1.93	0.62	0.54	-	2.98
DISI	-	-	0.12	1.56	6.94	4.38
Dimeric DISI	0.99	3.09	3.66	2.52	1.18	2.56
(K/R)TS-DISI	-	0.65	1.67	3.69	3.14	0.7
Medium-sized DISI	-	-	0.55	0.33	-	-
QC	-	0.001	-	-	-	-
Hyal	0.005	-	-	0.04	-	-
KUN	1.51	1.93	5.79	1.6	6.09	3.93
LAAO	1.9	5.13	6.48	2.68	8.26	3.39
PDE	-	0.12	-	0.06	0.06	0.05
D49-PLA$_2$	17.14	11.94	16.23	13.43	15.41	14.89
K49-PLA$_2$	-	-	0.02	-	-	-
PLB	-	0.05	0.003	0.31	-	0.01
PIII-SVMP	21.92	9.39	2.07	21.66	3.14	13.62
PI-SVMP	-	0.24	0.001	1.2	1.28	0.89
SVMP	20.06	3.05	3.23	19.67	2.18	9.6
SVMP fragment	0.15	0.23	0.23	3.55	0.001	0.93
SVMPi	5.87	15.42	7.99	8.94	11.36	9.77
SVSP	5.9	16.21	26.87	6.08	16.73	11.99
VEGF	-	3.29	0.69	-	1.65	-
VNGF	-	0.24	0.42	-	0.01	0.02
Unidentified	6.49	2.53	2.67	2.1	0.2	4.59

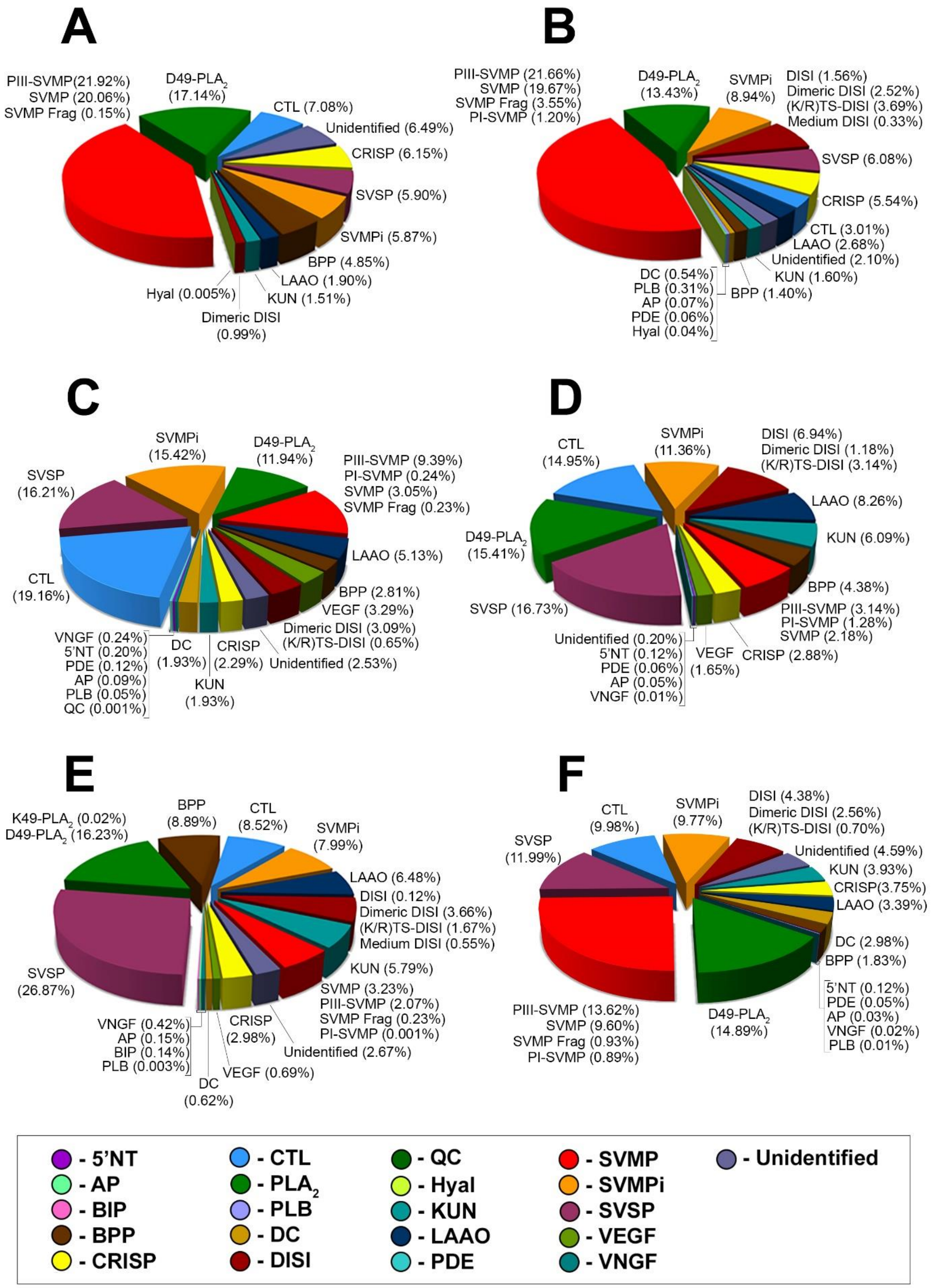

Figure 5.3 Pie chart representations displaying the relative abundances of the toxin families found in the six *V. latastei* venom proteomes sampled. A) 19VL013 (juvenile viper from Vila Chã); B) 19VL026 (juvenile viper from Gerês); C) 18VL253 (adult viper from Vila Chã); D) 18VL258 (adult viper from Gerês); E) 18VL011 (adult viper from Vila Chã); F) 19VL029 (adult viper from Gerês). For further details, please consult Table 5.1 and Tables A2.2-A2.7.

The most abundant protein families retrieved across the six venom proteomes, although unequally distributed, were: snake venom metalloproteinase (SVMP), particularly of class PIII (PIII-SVMP); snake venom serine proteinase (SVSP); D49-phospholipase A_2 (PLA_2); and C-type lectin-like (CTL; see Table 5.1 and Figure 5.3). These four toxin families are the predominant components of all the Old World viper (i.e., subfamily Viperinae) venoms characterised to date, accounting for 60–90% of their total venom proteomes (Damm et al., 2021). Whether acting alone or synergistically, they likely contribute to the coagulopathic and haemorrhagic effects induced by *V. latastei* venom (Arez et al., 1993; Detrait et al., 1983; Chowdury et al., 2021). Specifically, CTLs and SVSPs affect blood coagulation, fibrinolysis, and platelet aggregation (Kini, 2005; Matsui et al., 2000; Ogawa et al., 2005), PLA_2s can cause haemolysis and inhibition of the coagulation cascade (Xiao et al., 2017), and PIII-SVMPs are notorious for their mainly haemorrhagic effects (Fox and Gutiérrez, 2017; Gutiérrez et al., 2010; Ramos and Selistre-de-Araujo, 2006). The potent action of PIII-SVMPs, resulting in severe haemorrhage and tissue lesions (Moura-da-Silva et al., 2007), has typically been correlated to fast prey subjugation/killing (Daltry et al., 1996; Mackessy, 2021; Mebs, 1999). These toxins were particularly abundant in the venoms of juvenile Lataste's vipers (Table 5.1; Figure 5.3). Given the direct relationship existing between a snake's size and the venom volume it can produce (Mackessy, 1988), it is possible that high levels of PIII-SVMPs might aid young *V. latastei* specimens in subduing their prey despite the low amount of venom they can deploy. PIII-SVMPs might also be at play in aiding prey digestion, but evidence supporting this role is controversial (see McCue, 2007). In addition to these toxins, we found other haemotoxic components in all analysed *V. latastei* venoms, namely BPPs and KUNs, reported to induce vasodilation and to potentially act as antifibrinolytic agents, respectively (Ding et al., 2015; Morjen et al., 2014). The coagulopathic effects of *V. latastei* venom could also be amplified by VNGFs and VEGFs, which we only detected in the venoms of adult specimens. The former are known to cause inflammatory reactions and increase vascular permeability (Sunagar et al., 2013), while the latter are angiogenic and lymphangiogenic regulators (Ferreira et al., 2021).

A new RTS-disintegrin from the venom of *V. latastei*

A short RTS-disintegrin (monoisotopic ESI-MS of m/z 4432.9) structurally similar to KTS-disintegrins obtustatin [P83469] (Marcinkiewicz et al., 2003; Monleón et al., 2003), lebestatin [Q3BK14] (Kallech-Ziri et al., 2005), russelistatin (Sanz-Soler et al., 2012), and viperistain [P0C6E2] (Kisiel et al., 2004), was identified in five of the six venom proteomes produced (i.e., 18VL253, 18VL011, 19VL026, 18VL258, and 19VL029; see Tables A2.2-A2.7). This subfamily of non-canonical disintegrins, which selectively hit the collagen (I and IV)-binding α1β1 integrin (Calvete et al., 2008), form a distinct clade of short disintegrins that emerged by neofunctionalization of a copy of a RPTLN gene (Sanz-Soler et al., 2020). (K/R)TS-disintegrins had so far been found only in the venoms of a few Eurasian vipers of the genera *Macrovipera* and *Daboia* (i.e., *Daboia mauritanica*, *Daboia palaestinae*, *Daboia russelii*, *Macrovipera lebetina*) (Sanz-Soler et al., 2012; Saviola and Calvete, 2021). Our finding of another member of this subfamily of short disintegrins, for which we have coined the name "latastin", in the genus *Vipera*, indicates that the evolutionary origin of (K/R)TS-disintegrins predates the split of the genera *Daboia* and *Vipera* about 25 Mya, between Oligocene and Miocene (Freitas et al., 2020). This predicts the occurrence of this subfamily of toxins in the venoms of other species of *Vipera*.

Ontogenetic shift in the venom of *V. latastei*

The venomic data gathered from the six produced proteomes highlighted the presence of distinct compositional differences between juvenile and adult viper venoms, suggesting the occurrence of ontogenetic changes. Specifically, regardless of geographic origin, the venom proteomes exhibited similar patterns of relative toxin family abundances within the same age class, but distinct ones between different age classes (Table 5.1; Figure 5.3). For example, the two juvenile venom proteomes 19VL013 (Vila Chã) and 19VL026 (Gerês) were characterised by very high abundances of PIII-SVMPs (> 40% of the total venom proteomes), followed by D49-PLA$_2$s (13–17%), CRISPs (5.5–6%), SVSPs (6%), and CTLs (3–7%) (Table 5.1; Figure 5.3). Adult *V. latastei* venom proteomes 18VL253 (Vila Chã) and 18VL258 (Gerês) also shared some compositional features: similar abundances of CTLs (8.5–19%), SVSPs (16–26%), and D49-PLA$_2$s (12–16%), and low levels (5–12%) of SVMPs (Table 5.1; Figure 5.3). The peak eluting in adult venoms at 17 min, not detected in the two juvenile venoms, contained VEGF, VNGF, D49-PLA$_2$, and CRISP. The content of the peak in question for each of the four adult *V. latastei* venoms produced is reported in Tables A2.3 (Spot ID 31), S4 (Spot ID 25), S6 (Spot ID 21), and S7 (Spot ID 20). Interestingly, the proteome produced for venom 19VL029 from Gerês shares features with both juvenile (i.e., predominance of PIII-SVMPs, 23% of the venom proteome) and adult (i.e., high abundances of PLA$_2$s (14.9%), SVSPs (12%), and CTLs (10%)) venom proteomes (Table 5.1; Figure 5.3). The venom sample in question was obtained from an adult female with 280 mm of SVL (see Table A2.1). While according to Pleguezuelos et al. (2007b) this value is enough to consider the viper as sexually mature/adult, Brito and Rebelo (2003) reported that female Lataste's vipers from Gerês to reach sexual maturity at 350–400 mm of SVL. Geographic variation in growth rate has been reported for some European vipers (e.g., *Vipera berus*; Forsman, 1991), and also suggested for *V. latastei* (Santos et al., 2008). Furthermore, evidence suggests that ontogenetic changes in snake venom composition do not occur sharply during the snake's development (Durban et al., 2013). In light of the above considerations, it is reasonable to hypothesise that the intermediate venom phenotype observed for viper 19VL029 may indicate that the specimen was collected at a transitional stage between immaturity and maturity.

Snakes are typically considered gape-limited predators, with a positive correlation between the size of a snake and the size of the prey it can ingest (Mushinsky, 1987). The limited mouth gape of juvenile vipers likely is a morphological constraint, forcing them to essentially feed on ectotherms, with a generally smaller diameter than endotherm prey, until they reach a larger size (Brito, 2004; Forsman and Lindell, 1995). Juvenile Lataste's vipers from the two studied populations likely mainly feed on small-sized prey with ectothermic physiology (e.g., lizards of the genus *Podarcis*), very abundant in both Vila Chã (authors' personal observation) and Gerês (Brito, 2004). Conversely, the diet of adult *V. latastei* mainly comprises endotherms (i.e., small mammals), almost absent in the diet of juvenile Lataste's vipers (Brito, 2004; Martínez-Freiría et al., 2014). Further highlighting the influence that trophic ecology has on the evolution of snake venom, ontogenetic shifts in snake diet are often mirrored by changes in venom composition (Alape-Girón et al., 2008; Andrade and Abe, 1999; Calvete et al., 2021; Casewell et al., 2020; Saviola et al., 2015). In light of this, we suspect the different venom formulations secreted by juvenile and adult Lataste's vipers may represent adaptive solutions for the effective disruption of their prey's different physiologies.

Assessment of interpopulational venom diversity

The final binary matrix used to assess the interpopulational diversity in venom composition included 34 polymorphic peaks (i.e., not appearing in every chromatogram). Their number varied between 11 (19VL013) and 23 (19VL029 and 19VL454) across the analysed 54 individual chromatograms (see Table A2.8), and was on average significantly lower in venoms from Vila Chã (17.3) than in those from Gerês (19.3) (Student's t-test: $t = 3.37$; df = 48.49; $p = 0.001$). The difference in number of peaks between the two populations was statistically significant ($B \pm \mathrm{SE} = -2.06 \pm 0.64$; $t = -3.23$; $p < 0.001$). The three-dimensional NMDS analysis achieved an overall stress value of 0.16, indicating that the method could represent the differences between the venom profiles considered. The statistical analyses performed on the individual NMDS1 scores, representing each venom phenotype, found significant differences between Gerês and Vila Chã. This can be seen in the NMDS ordination plot we generated using the individual NMDS scores on the first two axes (i.e., NMDS1 and NMDS2), in which the two populations form two quite distinct groups, although with some level of overlap (Figure 5.4).

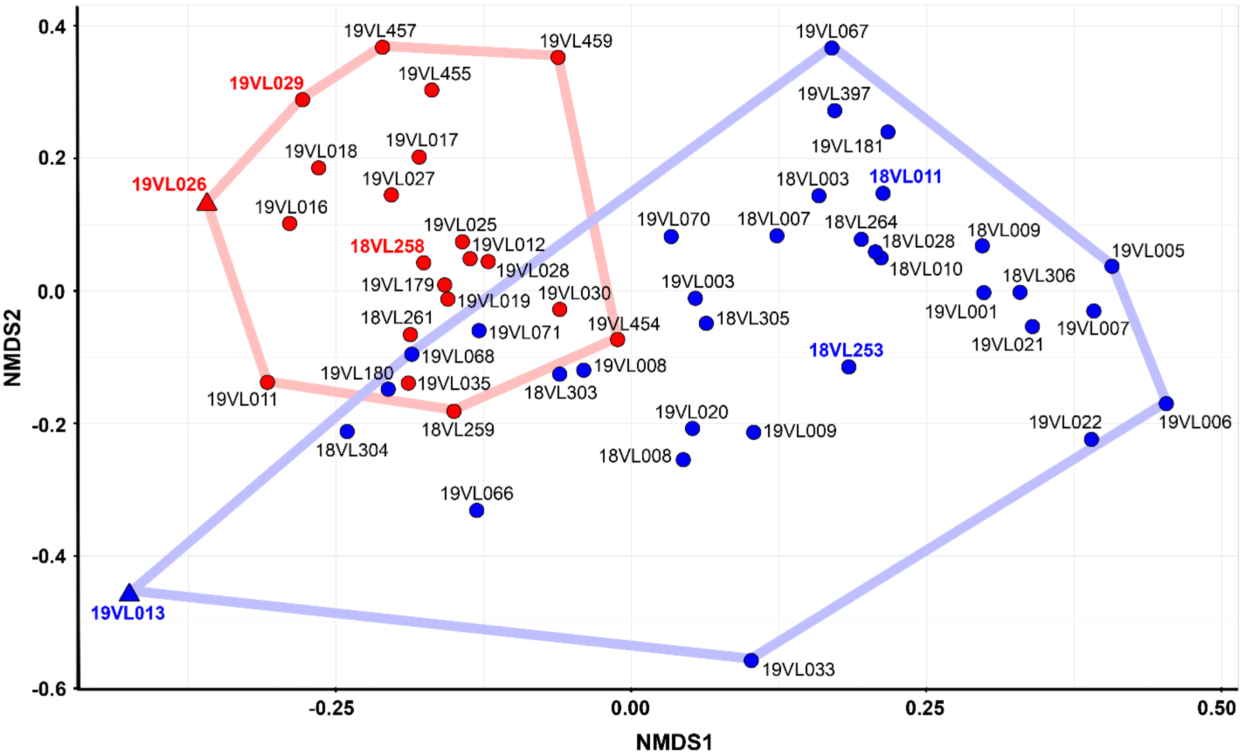

Figure 5.4 Non-metric multidimensional scaling (NMDS) ordination plot of the 54 *V. latastei* venom chromatographic profiles considered. Venom samples from Vila Chã and Gerês are identified, respectively, by blue and red filled circles (adult) and triangles (juveniles). Blue and red convex hulls delimit the venoms from the Vila Chã and Gerês populations, respectively. Venoms submitted to proteomics analysis are in bold, identified by their sample code (Table A2.1), and coloured according to their geographic origin (i.e., blue = Vila Chã, red = Gerês). The almost centred position of venom samples 18VL253 and 18VL258 in the two convex hulls implies that these venoms are among the least diverging ones of each population. This suggests that 18VL253 and 18VL258 might be considered "average" adult *V. latastei* venom profiles for Vila Chã and Gerês, respectively.

The model that best described the variation among venom phenotypes (i.e., individual NMDS1 scores) included population and date of collection of the venom samples as independent variables (Table 5.2).

Table 5.2 Final set of candidate simple linear regression models tested. The reported models relate the individual scores on the first NMDS axis (i.e., NMDS1) with the independent variables snout-vent length (SVL), date of collection of the venom samples (Day year), and population of origin (i.e., Gerês or Vila Chã). The best-fitting linear regression model is reported in bold. The table displays the number of parameters in the model (K), the information score of the model (Akaike's Information Criterion corrected for small sample sizes; AICc), the difference in AICc score between the best model and the model being compared (ΔAICc), and the AICc weight (i.e., the proportion of the total amount of predictive power provided by the full set of models contained in the model being assessed; *w*AICc).

Model	K	AICc	ΔAICc	*w*AICc
Population + Day year	**5**	**-40.92**	**0.00**	**0.50**
Population	3	-40.88	0.05	0.49
SVL	3	-19.42	21.50	1.08×10^{-5}
Null	2	-8.53	32.39	4.68×10^{-8}

Although venom phenotypes were found to vary significantly between the two studied populations (*B* ± SE = −0.31 ± 0.04; *t* = −7.07; *p* < 0.001), the effect of the date of collection of the venom sample was non-significant (*B* ± SE = 0.28 ± 0.14; *t* = 1.92; *p* = 0.08). Furthermore, the binomial Generalised Linear Models (GLMs) performed on the 34 peaks taken into account showed that the presence/absence of eleven peaks (i.e., 1, 6, 7, 16, 19, 20, 22, 23, 26, 31, 33) was significantly correlated to at least one of the four independent variables considered, indicating variation of peaks' presence in relation to body size, date of collection, sex, and population (Table A2.9). More precisely, peaks 16, 20, 22, and 26 were significantly more frequent in vipers from Vila Chã, while the opposite was observed in peaks 1, 6, 7, 23, 31, and 33 (Figure 5.5C; Table A2.10). Peaks 1 and 33 were significantly less detected in individuals collected between October and the end of March (Figure 5.5A; Table A2.10). The probability of detecting peak 6 increased with the size of the individual (Figure 5.5B), while the opposite trend was observed in peak 19 (Figure 5.5C; Table A2.10). Lastly, peak 23 was observed more frequently in females (Figure 5.5D).

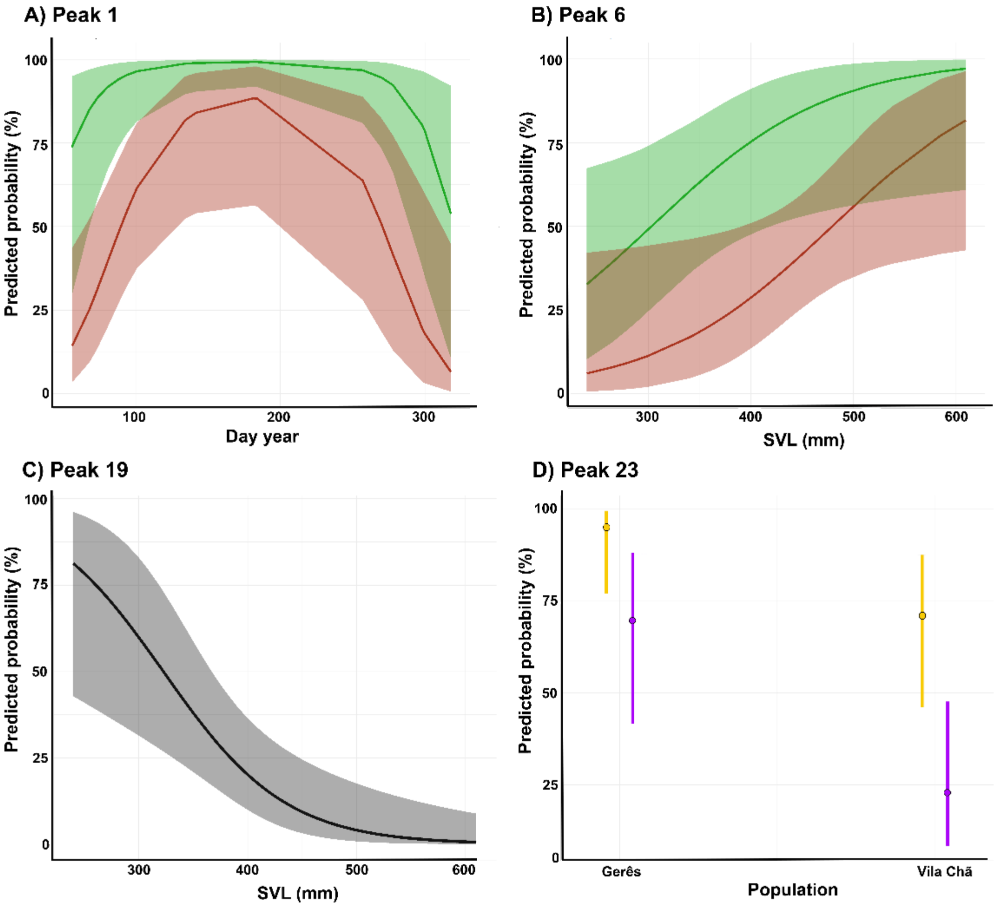

Figure 5.5 Best model predictions of occurrence of peaks 1, 6, 19, and 23 in individual chromatograms. The panels display the predicted probability of occurrence of A) peak 1 in relation to the day of the year and to population (green = Gerês; red = Vila Chã). The same relation was observed in peak 33; B) peak 6 in relation to SVL and to population (green = Gerês; red = Vila Chã); C) peak 19 in relation to SVL; and D) peak 23 in relation to sex and to population (yellow = females; purple = males).

A fast-evolving phenotype, snake venom has been found to vary in composition depending on factors of different nature, like phylogeny and prey availability (Furtado et al., 2006; Gibbs et al., 2013; Minton & Weinstein, 1986), and high levels of individual toxin variability have been observed in several species (e.g., Amazonas et al., 2019; da Costa Galizio et al., 2018; Daltry et al., 1996). In the light of such a highly dynamic scenario, and with the limited information gathered in this study, trying to understand what could determine the significant differences we detected in venom phenotypes between the two studied populations is difficult. The habitat of the Gerês site is quite pristine, and human activity in its surroundings is mostly limited to tourist season. On the contrary, human disturbance on the habitat of the Vila Chã sampling site, surrounded by cultivated fields and with people living in its immediate proximity, is very conspicuous all year round. High levels of disturbance are expected to negatively affect species diversity, thus depleting communities (Connell, 1978). In this context, the better-preserved habitat of Gerês likely hosts a higher number of species and more complex communities than Vila Chã. This could imply the presence in Gerês of more diverse prey items for the vipers to feed on, which might explain the significantly higher average number of peaks detected in their venom profiles. The lack of phylogeographic distinctness between the two populations indeed suggests that differences in venom composition are likely to be due to differences in local selection. In this perspective, it would be interesting for future studies to test whether differences between the *V. latastei* venom phenotypes of Gerês and Vila Chã might be due to differences in prey type or availability between these two populations, and thus to rapid venom adaptation.

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Chapter 6

Venomics of the Iberian adder (*Vipera seoanei*)

Introduction

The Iberian adder, *Vipera seoanei*, Lataste 1879, a venomous snake belonging to the family Viperidae (subfamily Viperinae), member of the clade of vipers with Euro-Siberian affinity (i.e., *Pelias*, Freitas et al., 2020). Endemic to the northern Iberian Peninsula and south-western France, this species mainly inhabits areas with an Atlantic climate, typically occupying humid ecotones between meadows and forests, and zones with abundant basal vegetation, from sea level to about 1900 m of altitude (i.e., Cantabrian Mountains; Martínez-Freiría and Brito, 2014). Sister species of the common adder *V. berus* (see Freitas et al., 2020), *V. seoanei* displays low intraspecific genetic variability, likely as result of a late Pleistocene expansion from north-western Iberian refugia (Martínez-Freiría et al., 2015). Despite its shallow genetic structure, *V. seoanei* shows considerable variation in biometric and pholidotic traits across its range (Lucchini et al., 2020; Martínez-Freiría and Brito, 2013). The species is notable for high levels of polymorphism in body colouration, with five colour phenotypes currently recognised (i.e., *bilineata*, *cantabrica*, *classic*, *melanistic*, *uniform*). These appear to be geographically structured and not concordant with mitochondrial DNA haplotypes (Martínez-Freiría et al., 2015, 2017).

The diet of *V. seoanei* mainly comprises small mammals, and less frequently reptiles, amphibians, arthropods, and birds (Braña et al., 1988; Espasandín et al., 2022; Galán, 1988). Like many other species of the genus *Vipera* (e.g., *V. aspis*, Luiselli and Agrimi, 1991; *V. latastei*, Brito, 2004), *V. seoanei* exhibits ontogenetic shift in diet composition, with ectotherms (e.g., reptiles, amphibians) constituting more than 70% of the diet of juvenile vipers, whereas small mammals (i.e., shrews and rodents) account for roughly 90% of the diet of the adults (Espasandín et al., 2022). Interestingly, significant correlations have been found between climatic and habitat conditions and differences in frequency of consumption of the prey items *V. seoanei* mainly feeds on (i.e., amphibians, reptiles and small-mammals; Espasandín et al., 2022). Such environment-related variation in diet composition, observed also in other *Vipera* species (e.g., *V. ammodytes*, Tomović et al., 2022; *V. latastei*, Santos et al., 2008), suggests the presence of dietary differences across the species range.

The Iberian adder is recognised as medically important by the World Health Organization (WHO, 2020), and is considered one of the venomous snake species of major clinical relevance in Europe (Di Nicola et al., 2021; Paolino et al., 2020). An early study by Detrait et al. (1990) aiming at investigating the toxicity of *V. seoanei* venom across its Spanish distribution suggested the presence of a West-East gradient, with venoms from the western populations presenting higher lethal potencies than those collected from eastern populations (e.g., Galicia: LD_{50} = 6.9–9.9 µg per 20 g mouse; Basque Country: LD_{50} = 23.1–23.6 µg per 20 g mouse). A more recent study by Archundia et al. (2011) reported for *V. seoanei* of

Portuguese origin toxicity values (i.e., LD_{50} = 9.7 µg per 18–20 g mouse) comparable to those previously obtained by Detrait et al. (1990) for individuals from Galicia and North of León, potentially supporting the higher toxicity of westernmost populations. Interestingly, although *V. seoanei* venoms collected from different localities across the species' Spanish distribution presented differences in LD_{50} values, the corresponding proteinograms appeared very similar among them, hinting low levels of interpopulational divergence in venom compositions (Detrait et al., 1990). In spite of the presence of this intriguing scenario, and of the recognised medical relevance of *V. seoanei*, no other studies regarding this species' venom have been conducted, and further information about it is currently unavailable.

In the present work, we (i) provide the first proteomic characterisation of the venom of *V. seoanei*; (ii) assess the level of venom variation across the viper's range in the Iberian Peninsula; (iii) test for associations between biological, geographic, genetic and eco-geographic factors and venom variation within this species across its ecologically and physiographically diverse range.

Materials and Methods

Sampling

Between 2018 and 2021, a total of 49 individuals of *V. seoanei* were collected from 20 localities distributed across the species' range in the Iberian Peninsula, with a maximum of five per locality (Figure 6.1; Table A3.1). Venom samples were collected from each individual following the same protocol reported in Chapter 5. After venom extraction, tissue samples (i.e., buccal swabs) to be used for genetic analyses (see Predictors section) were collected, and sex and snout-vent length (SVL) of each snake were recorded. All vipers had SVL > 325 mm, and were thus considered adults (see Braña, 1998; Lucchini et al., 2020).

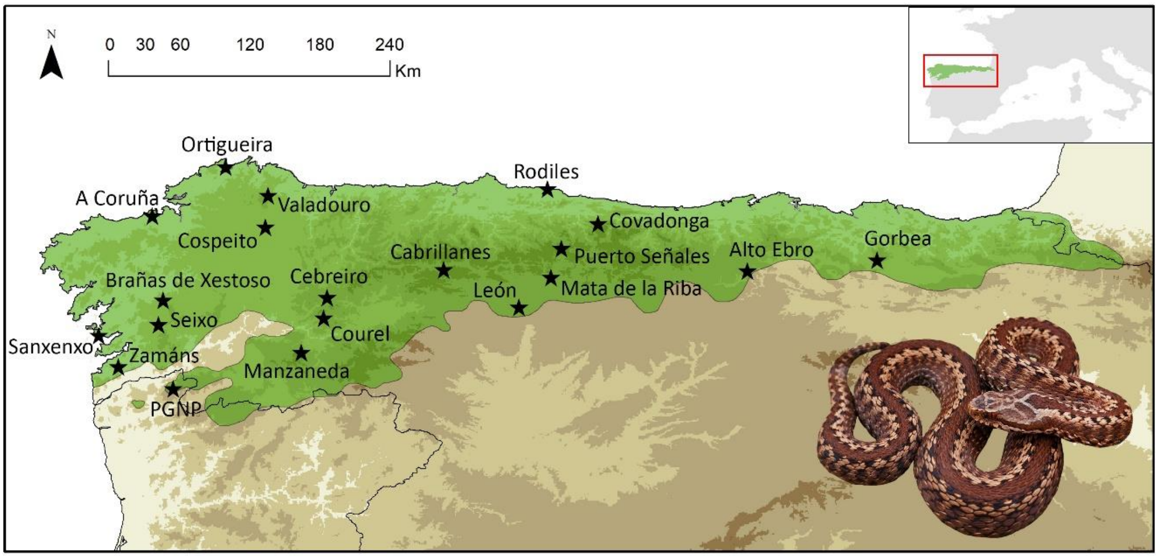

Figure 6.1 Map of the 20 localities (black stars) sampled across the Iberian distribution of *V. seoanei*. The area in green represents the species' full distributional range. Additional details about the sampling are reported in Table A3.1.

Information about the colour phenotypes displayed by the collected vipers was also recorded, and each individual was assigned to one of the five categories reported by Martínez-Freiría et al., 2017 (see Table A3.1 and Figure A3.1). Each viper was then released exactly where it had been captured. Venoms were lyophilised in a Scanvac (Coolsafe, Lynge, Denmark) freeze dryer, and stored at -20 °C until being transported to the Süssmuth Laboratory of the Institut für Chemie, Technische Universität Berlin (Germany) for proteomic analysis.

Vipers, venoms and tissue samples were collected with permission of Instituto da Conservação da Natureza e das Florestas, Portugal (ref. 537/2018, 362/2019, 295/2020 and 146/2021), Xunta de Galicia, Spain (ref. EB-017/2019, 018/2020 and 015/2021), Gobierno del Principado de Asturias, Spain (ref. 2019/003003, 2020/682020 and CO/09/017/2020), and Junta de Castilla y León, Spain (ref. EP/CyL/56/2018, 27/2019, 192/2020 and 54/2021).

Venom fractionation by RP-HPLC

Due to the low amount of venom we collected from each viper, we performed the proteomic analyses on a pool composed of equal amounts (i.e., 10 µL) of each of the 49 individual *V. seoanei* venoms. For reverse-phase chromatography (RP-HPLC), 1 mg of lyophilised venom from the pool was dissolved to a final concentration of 10 mg/mL in aqueous 5% (v/v) ACN with 1% (v/v) formic acid (HFo), and centrifuged for 5 min at 10,000 x g. The supernatant was then fractionated using a HPLC Agilent 1200 (Agilent Technologies, Waldbronn, Germany) chromatography system equipped with a reversed-phase Supelco Discovery BIO wide Pore C18-3 (4.6 × 150 mm, 3 µm particle size) column. The following gradient with ultrapure water with 0.1% (v/v) HFo (solvent A) and ACN with 0.1% (v/v) HFo (solvent B) was used at 1 mL/min, with a linear solvent change given at min (B%): 0 (5%), 5 (5%), 100 (40%), 120 (70%), 130 (70%), and 5 min re-equilibration to 5% B. For monitoring of the chromatography run a diode array detector (DAD) was used at λ = 214 nm detection wavelength. Samples were collected by time-based fractionation (1 fraction/min) and peak fractions were dried in a centrifugal vacuum evaporator.

SDS-PAGE profiling

The dried fractions were redissolved in 10 µL reducing 2× SDS sample buffer, heated for 10 min at 95 °C, and separated by 12% SDS-PAGE (SurePage Bis-Tris, Genscript, Piscataway, NJ, USA), run with MES buffer at 200 V for 21 min. PageRuler Unstained Protein Ladder (Thermo Scientific, Waltham, MA, USA) was used as protein standard. Gels were short-washed with water three times. Proteins were fixed three times for 10 min each with hot fixation buffer (aqueous, 40% (v/v) methanol, 10% (v/v) acetic acid), stained for 45 min in hot fast staining buffer (aqueous, 0.3% (v/v) HCl 37%, 100 mg/L Coomassie 250G) under constant mild shaking, and kept overnight at 4 °C in storage buffer (aqueous, 20% (v/v) methanol, 10% (v/v) acetic acid) for destaining. The produced gels were then scanned for documentation and quantification.

To produce profiles that could allow the assessment of similarities and differences among the 49 individual venoms, 20 µg of each lyophilised venom sample were loaded in 10 µL reducing 2× SDS sample buffer, and subjected to SDS-PAGE profiling following the same protocol applied for the venom pool. The resulting gels were scanned for documentation, and the obtained digital images were used for statistical analysis. SDS-PAGE profiling was performed once for each venom sample.

Tryptic digestion

Bands of interest of the SDS-PAGE venom pool profile were cut, dried with 500 µL ACN, and stored at -20 °C until tryptic digestion. Disulphide bridges were reduced with 30 µL freshly prepared dithiothreitol DTT (100 mM in 100 mM ammonium hydrogen carbonate (ABC) per gel band) for 30 min at 56 °C, and dried with 500 µL ACN for 10 min. Cysteines were alkylated with freshly prepared iodacetamid IAC (55 mM in 100 mM ABC) for 20 min at RT in the dark to protect the reduced thiols from oxidation, and washed with 500 µL ACN for 2 min. Samples were dried with 500 µL ACN for 15 min, followed by 30 min incubation on ice with 20-30 µL freshly activated trypsin (13.3 ng/µL, 10% (v/v) ACN in 10 mM ABC; Thermo, Rockfeld, IL, USA). When necessary, additional volumes of trypsin were added. Samples were incubated for 90 min on ice, then 20 µL ABC buffer (10 mM) was added to all of them, and incubated overnight at 37 °C. Peptides were extracted with 100 µL elution buffer (aqueous, 30% (v/v) ACN MS grade, 5% (v/v) HFo) pre-warmed at 37 °C for 30 min. The supernatant was transferred into a separate microtube and vacuum dried. Following a second HPLC purification of 1 mg crude venom, smaller dried fractions were submitted to LC-MS for direct peptide detection, without any SDS-PAGE separation or tryptic digestion.

Mass spectrometry

For the mass spectrometry (MS) analysis, the excised SDS-PAGE bands of interest were re-dissolved in 30 µL aqueous 3% (v/v) ACN with 1% (v/v) HFo, and 20 µL of each were injected into an Orbitrap XL mass spectrometer (Thermo, Bremen, Germany), via an Agilent 1260 HPLC system (Agilent Technologies, Waldbronn, Germany) using a reversed-phase Grace Vydac 218MS C18 (2.1 × 150 mm; particle size, 5 µm) column. The following gradient with ultrapure water with 0.1% (v/v) HFo (solvent A) and ACN with 0.1% (v/v) HFo (solvent B) was used at 0.3 mL/min, with a linear buffer change given at min (B%): 0 (5%), 1 (5%), 11 (40%), 12 (99%), 13 (99%), and 2 min re-equilibration to 5% B. The parameters in the ESI positive modus were as follows: 270 °C capillary temperature, 45 L/min sheath gas, 10 L/min auxiliary gas, 4.0 kV source voltage, 100.0 µA source current, 20 V capillary voltage, 130 V tube lens. FTMS measurements were performed with 1 µ scans and 1000 ms maximal fill time. AGC targets were set to 10^6 for full scans, and to 3×10^5 for MS2 scans. MS2 scans were performed with a mass resolution (R) of 60,000 (at m/z 400) for m/z 250-2000. MS2 spectra were obtained in data-dependent acquisition (DDA) mode as top2 with 35 V Normalized CID energy, and 500 as minimal signal required with an isolation width of 3.0. The default charge state was set to z = 2, and the activation time to 30 ms. Unassigned charge states and charge state 1 were rejected.

LC-MS/MS data RAW files were converted into the MASCOT generic file (MGF) format using the MSConvert (Version 3.0.22187) with peak picking (vendor msLevel=1−) (Chambers et al., 2012). For an automated database comparison, files were analysed using pFind Studio (Guangcan et al., 2021), with pFind (Version 3.1.5) and the integrated pBuild. The parameters used were: MS Data (Format: MGF; MS Instrument: CID-FTMS); Identification with Database search (Enzyme: Trypsin KR_C, full-specific up to 3 missed cleavages; precursor tolerance +20ppm; fragment tolerance +20ppm); open search setup with fixed carbamidomethyl [C] and Result Filter (show spectra with FDR ≤ 1%, peptide mass 500-10,000 Da, peptide length 5-100 and show proteins with number of peptides > 1 and FDR ≤ 1%).

The used database included UniProt ‘Serpentes’ (ID 8750, reviewed, canonical & isoform, 2674 entries, last accessed on 10 February 2022; available at: https://www.uniprot.org/) and the common Repository of Adventitious Proteins (215 entries, last accessed on 10 February 2022; available at: https://www.thegpm.org/crap/index.html). The results were batch exported as PSM Score of all peptides identified by pBuild, manually cleared from decoy entries, contaminations and artifacts. Finally, a list of unique peptide sequences per sample with the best Final Score was generated. For a second confirmation of identified sequences, all unique ones were analysed by BLAST search (Altschul et al., 2005), with blastp against the non-redundant protein sequences (nr) of the Uniprot database “Serpentes” (taxid: 8570). In case of non-automatically annotated bands, files were checked manually using Thermo Xcalibur Qual Browser (version 2.2 SP1.4), *de novo* annotated, and/or compared on MS1 and MS2 levels with other bands to confirm band and peptide identities. Deconvolution of isotopically resolved spectra was carried out by using the XTRACT algorithm of Thermo Xcalibur.

Relative quantification of the venom pool proteome

The quantification protocol is adapted from the three-step hierarchical venom proteome quantification protocol developed at the Evolutionary and Translational Venomics Laboratory of the Institute of Biomedicine of Valencia (Calderón-Celis et al., 2017; Calvete, 2014; Eichberg et al., 2015), based on a combination of separation and quantification of HPLC peaks, SDS-PAGE bands, and ion intensities. Briefly, it defines the normalised toxin abundances within a single SDS-PAGE band, with the normalised values of the RP-HPLC peak integral measured at 214 nm, the gel band intensity and, if necessary, the MS ion intensity of the most abundant peptides identified.

The gel band abundance measurement was performed by densitometry on the scanned gel images. Non-highly compressed PNG images of the SDS-PAGE gels were processed using the software Fiji (Schindelin et al., 2012). Colour depth was changed to 8 bit grayscale, and area and integrated density of each SDS-PAGE band were measured. The integrated relative densities were calculated using a representative background region as reference, and normalised considering the area of the correspondent chromatographic peaks. In case of multiple toxin families identified within a single band, normalised toxin abundances were estimated based on the difference between the sum of the relative ion intensities of the three most abundant peptide ions of a toxin family and the sum of the three most abundant peptide ions of any other comigrated toxins family.

Non-Metric Multidimensional Scaling

To assess presence and extent of variation among the 49 *V. seoanei* venoms collected, we applied the individual-based approach reported by Zancolli et al., 2017. We thus generated a presence-absence matrix of the bands present in the individual SDS-PAGE venom profiles, excluding bands with frequency = 1 (i.e., not informative) or difficult to identify. We preferred to analyse SDS-PAGE profiles rather than RP-HPLC profiles because, in the latter, reliable peak identification can often be difficult due to venom complexity and differences in protein elution times. Indeed, during different RP-HPLC runs, the same proteins can present different elution times for a number of reasons (e.g., fluctuations in room temperature), further complicating the analysis of the chromatograms (see Zancolli et al., 2017). The final binary matrix (Table S2) was used to analyse patterns of venom variation using Non-Metric Multidimensional Scaling (NMDS) based on pairwise Bray-Curtis similarity distances among profiles (see Minchin, 1987). In order to keep the stress value below the 0.2 threshold (i.e., poor fit; Kruskal, 1964), we opted for a three-dimensional NMDS analysis. We then used the individual NMDS scores on the first two axes (i.e., NMDS1 and NMDS2) to produce an ordination plot representing the dissimilarity between the individual SDS-PAGE profiles of the *V. seoanei* venoms analysed.

Predictors

To investigate which factors could potentially influence the occurrence of variation in the venoms of *V. seoanei*, we considered a total of 14 predictors: (i) three referring to biological traits of the vipers; (ii) one corresponding to the locality of origin of each viper (POPULATION);

(iii) eight describing the climatic and habitat conditions of the geographic position where each viper was collected; and (iv) two corresponding to the first two principal components (GEN1 and GEN2) of a Spatial Principal Component Analysis (SPCA) performed for the interpolated mtDNA genetic distances estimated within *V. seoanei*.

The predictors related to biological traits of the vipers were snout-vent length (SVL, in mm), sex (SEX), and colour phenotype (COLOUR) of each individual. The *uniform* colour phenotype, displayed by only one of the sampled individuals (i.e., 20VS165), was excluded from analyses involving the predictor COLOUR in order to avoid model performance hindering due to small sample size. The predictors related to bioclimatic and habitat conditions of the geographic position where each viper was collected comprised four bioclimatic variables (i.e., annual mean temperature, BIO1; maximum temperature of the warmest month, BIO5; annual precipitation, BIO12; precipitation of driest month, BIO14) and the percentage of ground cover for four habitat types (i.e., cultivated fields, AGRIC; forest, FOREST; moors, MOOR; pastures and grasslands, PASTURE). These eight predictors, used in previous works on the ecology of *V. seoanei* and other *Vipera* species (e.g., Martínez-Freiría et al., 2008; Chamorro et al., 2021), have been found to influence the distribution and abundance of *V. seoanei* prey such as amphibians, reptiles, and small mammals (e.g., Mira et al., 2008; Sillero et al., 2009), as well as their frequency in the species' diet (Espasandín et al., 2022). Values for bioclimatic predictors were extracted from raster layers at a resolution of 30 arc seconds (~1km) from WorldClim version 2.1 (Fick and Hijmans, 2017; available at ww.worldclim.org). Values for habitat types were extracted from Corine Land Cover version 2020_20u1 (available at https://land.copernicus.eu/pan-european/corine-land-cover/clc2018) after grouping land cover categories describing similar structural habitat types and upscaling the resulting rasters at 2 km^2 resolution (see Espasandín et al., 2022).

In order to obtain information on the genetic structure within *V. seoanei*, to be used as a predictor of venom variation in regression analyses, we estimated mtDNA genetic distances within this species. While *V. seoanei* sequences are available from previous works (see Martínez-Freiría et al., 2015), we aimed to obtain a better geographic coverage of the genetic diversity existing across the species' range, and thus decided to also consider genetic data obtained from the individuals we collected. To this end, total genomic DNA was extracted from buccal swabs from 20 vipers (1 specimen from each sampled locality; see Table S1), using a standard saline method. Two mitochondrial (mtDNA) gene fragments, NADH dehydrogenase subunit 4 (ND4; 630 bp) and cytochrome b (cyt b; 554 bp), were amplified by polymerase chain reaction (PCR) using primers VSnd4-F/VSnd4-R (Martínez-Freiría et al., 2015) and CB1/CB2 (Palumbi, 1996), respectively. Laboratory procedures for DNA amplification and sequencing followed protocols used in Martínez-Freiría et al. (2015). In order to produce a geographically comprehensive genetic distance matrix, we considered the sequences of 65 specimens, namely 20 retrieved from this study, 44 from GenBank, and one from a specimen included exclusively in the genetic analyses to enhance geographic coverage (specimen code 20VS008). Sequences were manually aligned and edited using Geneious v 4.8.5 (Kearse et al., 2012). Uncorrected p-distances between populations were estimated for the resulting alignment using MEGA X (Kumar et al., 2018). For information about the 65 specimens used to produce the genetic distance matrix and GenBank sequence accession numbers, see Table A3.3.

The genetic distances calculated this way were then spatially interpolated using the kriging method, and summarised by Spatial Principal Component Analysis (SPCA). The first two of the resulting principal components, hereafter named GEN1 and GEN2, explained 54% and 40% of the variance, respectively (see Figure A3.2). GEN1 and GEN2 were used as predictors in the subsequent regression analyses, as proxy of the genetic structure of *V. seoanei*. Values of GEN1 and GEN2 were obtained in ArcGIS version 10.5 by extracting information on the geographic position of each specimen from the original SPCA raster. Interpolations and SPCA were performed in ArcGIS version 10.5 (ESRI, 2016), following the same procedure applied by Martínez-Freiría et al. (2015). The genetic distance matrix was calculated using the *ape* package (Paradis et al., 2004) in R version 4.2.2 (R Core Team, 2022).

Regression analysis

We applied linear regression models to investigate the relationship between the predictors considered and the individual scores on the first two axes of the NMDS analysis performed on the polymorphic bands of the SDS-PAGE venom profiles. To this end, using NMDS1 and NMDS2 as response variables, we performed univariate linear regression models for each of the 14 predictors. In order to separate the effects of the different predictors tested, we then performed multiple regression models built using NMDS1 and NMDS2 as response variables and including all the predictors which resulted to be significant in univariate linear regression models.

We then tested whether the presence or absence of the polymorphic bands identified in the venom SDS-PAGE profiles was significantly correlated with the predictors considered. We thus performed single predictor binomial Generalised Linear Models (GLMs) for each predictor, considering the presence/absence of each band as a binomial dependent variable. Following the same approach described above, we then built multiple predictor GLMs including all the predictors which resulted to be significant in single predictor GLMs.

In all models, all continuous predictors were scaled (i.e., mean = 0; SD = 1). The presence of spatial autocorrelation for all variables included in the models with more than one predictor was tested by calculating Moran's I (Moran, 1950). Correlation between the predictors included in the multiple regression models was generally low (< 50%), but predictors POPULATION and COLOUR showed strong association (Cramér's V = 0.899; see Cramér, 1946). Since the number of levels of POPULATION (five times greater than COLOUR's; i.e., 20 vs 4) was more likely to hinder model performance (see Hastie et al., 2009), it was thus excluded from multiple regression models and multiple predictor GLMs including the predictor COLOUR.

We used the packages *vegan* (Oksanen, 2016) to perform the NMDS analysis, *car* to perform the regression models (Fox and Weisberg, 2018), and *ggeffects* (Lüdecke, 2018) to plot model predictions. All analyses were performed in R version 4.2.2 (R Core Team, 2022).

Results

Protein composition of *V. seoanei* venom

A total of 55 peaks were identified within the chromatographic profile of the *V. seoanei* venom pool (Figure 6.2A). The chromatogram shows several broad peaks with high abundance (e.g., peaks 6, 26, 32, 33, 36, 40, 54 and 55) and complex regions with smaller peaks, e.g., eluting between 35 and 50 min, as well as between 80 and 95 min. The subsequent reducing SDS-PAGE analysis revealed that the highest RP-HPLC peaks are often dominated by few, highly abundant protein bands (see Figure 6.2B).

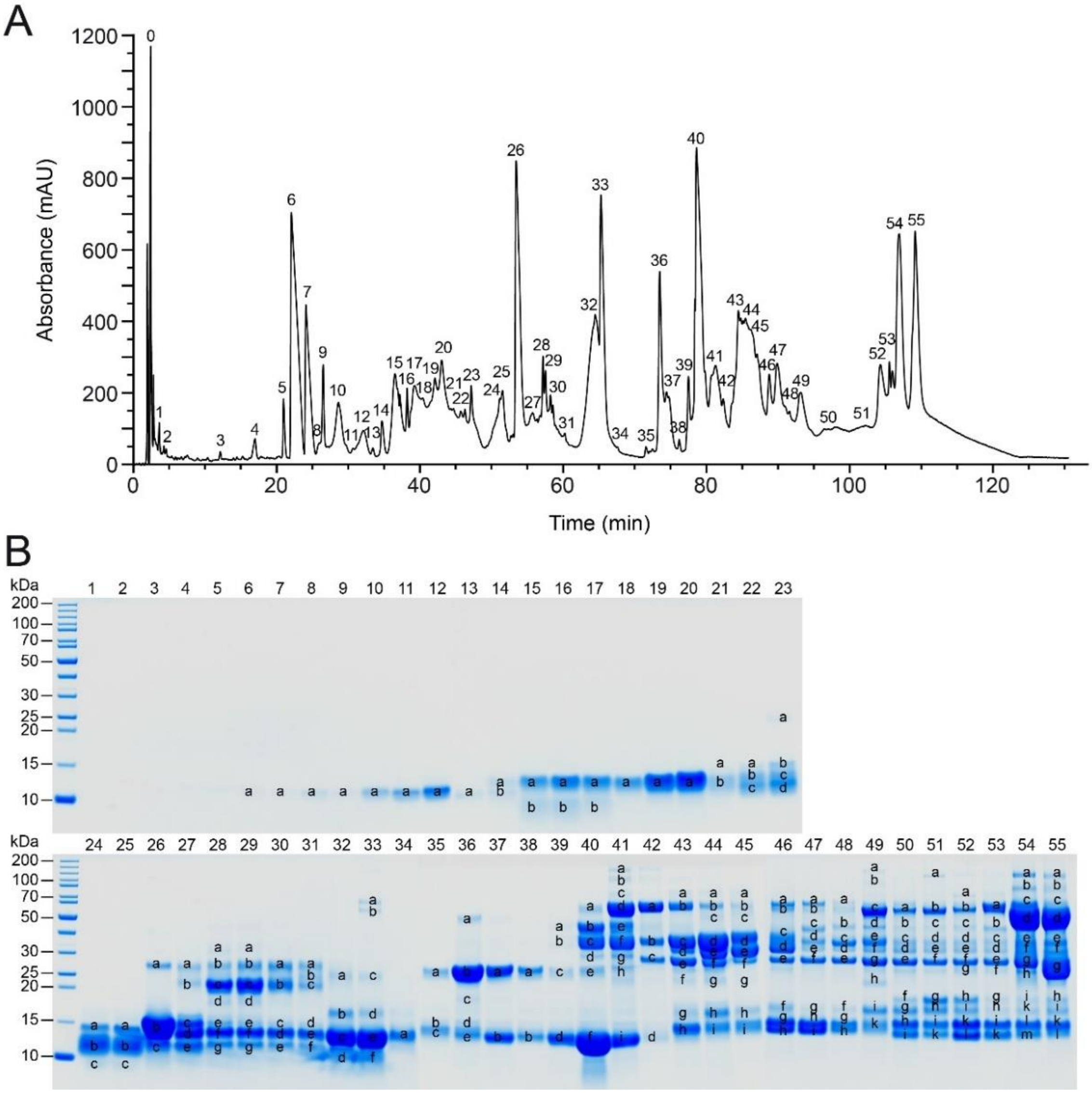

Figure 6.2 Fractionation of the *V. seoanei* venom pool. The figure shows RP-HPLC profile (A), with peak 0 corresponding to the injection peak, and SDS-PAGE, Coomassie stained profile (B) of the venom pool under reducing conditions. PAGE line nomenclature is based on RP-HPLC fractions. Labelled bands were cut, subjected to tryptic digestion, and analysed by LC-MS.

The venom proteome included as major toxin families phospholipases of type A_2 (PLA_2) and snake venom serine proteinases (SVSP), followed by the slightly less abundant disintegrins (DISI), C-type lectin-like proteins (CTL), and snake venom metalloproteinases (SVMP). Other toxin families like vascular endothelial growth factors (VEGF), cysteine-rich secretory proteins (CRISP), L-amino-acid oxidases (LAAO), Kunitz-type inhibitors (KUN) and venom nerve growth factors (VNGF) were also detected with relative abundances of 6% or less. The peptidic part, made of inhibitors of SVMP (SVMPi), natriuretic peptides (NP), and other peptides composed about 11% of the venom proteome. Non-annotated proteins (NA) accounted for less than 0.2% of the venom proteome. For further details, see Figure 6.3, and Table A3.4.

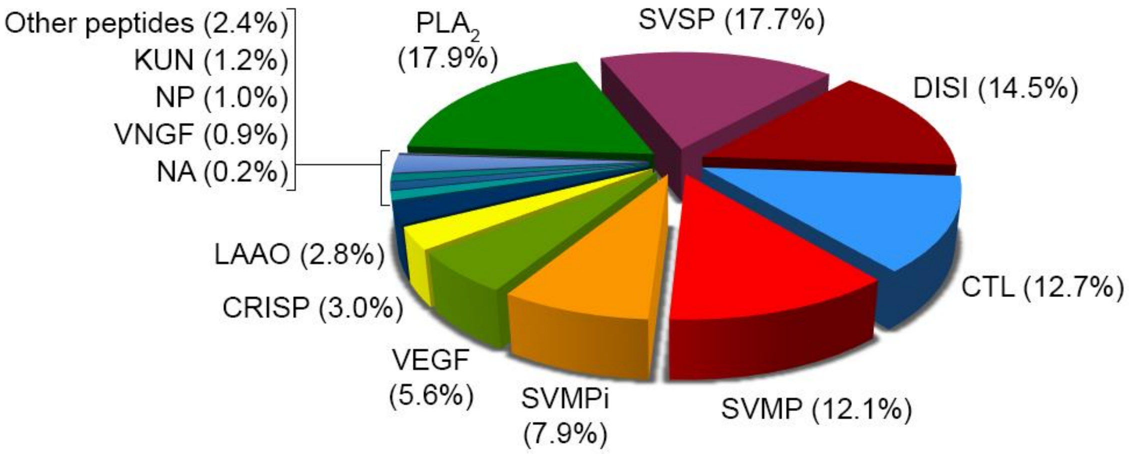

Figure 6.3 Reference composition of *V. seoanei* venom. The pie chart displays the relative abundances of the toxin families found in the proteome of the *V. seoanei* venom pool. PLA_2, phospholipases A_2; SVSP, snake venom serine proteinases; DISI, disintegrins; CTL, C-type lectin-like proteins; SVMP, snake venom metalloproteinases; VEGF, vascular endothelial growth factors; CRISP, cysteine-rich secretory proteins; LAAO, L-amino-acid oxidases; KUN, Kunitz-type inhibitors; VNGF, venom nerve growth factors; SVMPi, svMP inhibitors; NP, natriuretic peptides; NA, non-annotated proteins. The sum of the percentages does not match 100% because of rounding. Detailed percentages are reported in Table A3.4.

Among the PLA_2, we detected a variety of different proteoforms, some highly similar to the non-enzymatic PLA_2 homologue S49 ammodytin L(2) [Q6A394], and two enzymatic active D49 forms, namely ammodytin I1 and I2 [Q910A1;P34180]. Therefore, *V. seoanei* venom includes basic, neutral, as well as acidic PLA_2. The main SVSP we identified (6%, peak 44–45) shows high similarity with nikobin [E5AJX2] and a RVV-Vγ homolog [P18965] (4%, peak 43–45). Similarities were also found with other SVSPs, like SP-4/5/8 isoforms [A0A1I9KNR8; A0A1I9KNR5; A0A6B7FPJ0] of *Vipera ammodytes ammodytes*.

All SVMP fragments were annotated by MS as members of the PIII-SVMP subfamily, including ions from SDS bands with molecular weight of 30 kDa or less. This range of lower molecular SVMP masses usually originates from mature PI or processed PII fragments, but is uncommon for PIII. Sequence analysis showed that peaks 28–30 refer only to the DC-domain of a PIII-svMP, being a strong evidence for PIIIe, since no PII could be assigned. (Olaoba et al., 2020; Požek et al., 2022). The DISIs detected in the venom of *V. seoanei* are mostly composed of homologs of dimeric RGD-disintegrins, like VA6 [P0C6A5], lebein-1α [P83253] and VB7B [P0C6A7]. CTLs were constantly detected in two- or four-band patterns at late retention times of 85-110 min. These toxins are known to form multimeric structures with one, two (αβ) or four (αβγδ) subunits in different complexities, like (αβ)4 heterooctamers, and in combination with svMP P-IIIe (Eble, 2019; Olaoba et al., 2020). We identified several homologs to different CTL subunits isolated from *Vipera ammodytes ammodytes* and from the Eurasian viper genera *Daboia* and *Macrovipera*.

The less abundant toxins include two classes of growth factors, namely VNGF with two populations of 15 kDa and VEGF, almost exclusively identified as Vammin-1 homologs [APB93447]. A single band population of 25 kDa (peak 36–37) contains CRISP homologs of *V. berus* CRVP [B7FDI1]. The peptide part (11%) of the produced venom proteome is dominated by small tripeptidic SVMPis, as is the case for most peptidomes of Old World viper venoms (Damm et al., 2021). Also included in the peptidic part are natriuretic peptides and fragments of bradykinin-potentiating and C-type natriuretic peptides.

Analysis of the SDS-PAGE profiles

In total, 49 SDS-PAGE whole venom profiles were produced from the individual *V. seoanei* venoms collected (Figure A3.3). By visually comparing the obtained profiles, we did not detect stark differences in terms of presence/absence of bands, and instead noticed an overall considerable level of similarity between them. The least diverse profiles had 13 evident bands, whereas the most diverse had 18. Six bands turned out to be difficult to identify reliably. Nine bands were present in all venom profiles, and were thus excluded from further analyses as uninformative.

Band analysis and NMDS

The final binary matrix (Table A3.2) used to assess the diversity between the 49 SDS-PAGE whole venom profiles included 10 polymorphic (i.e., not appearing in every profile) bands. Their number varied between four (samples 19VS076, 19VS185, 21VS005, and 21VS006) and nine (samples 19VS450, 19VS451, and 21VS022) across the profiles (see Table A3.2).

The three-dimensional NMDS analysis achieved an overall stress value of 0.08, indicating that the method could suitably represent the differences between the venom profiles. The NMDS ordination plot generated using the individual NMDS scores on the first two axes (i.e., NMDS1 and NMDS2; Figure 6.4) showed low dispersion of the samples across the defined space and a considerable level of overlap.

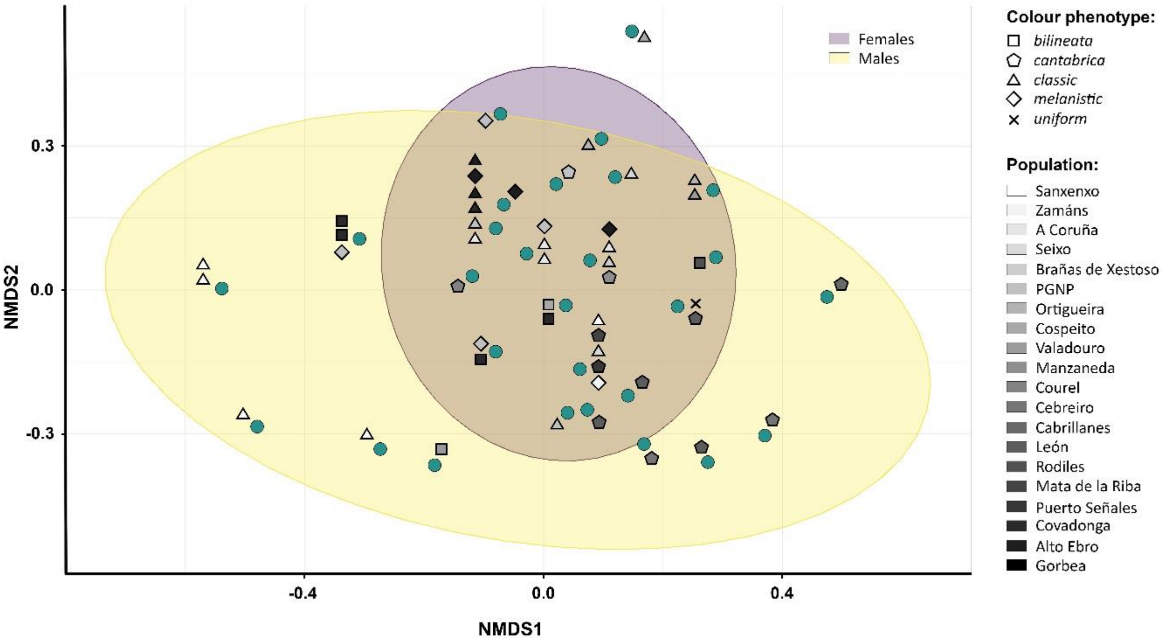

Figure 6.4 Non-metric multidimensional scaling (NMDS) ordination plot of the 49 *V. seoanei* venom SDS-PAGE profiles. Teal circles represent the venom profiles. Notice that some circles correspond to overlapping profiles (up to six).

Regression analysis

Of the 14 predictors tested using the NMDS1 scores as response variable, only four were significant in univariate linear regression analyses, namely SVL (p = 0.016), COLOUR (p = 0.028), POPULATION (p = 0.001) and FOREST (p = 0.035). In the univariate linear regression analyses testing the effect of each of the 14 predictors on the NMDS2 scores, only the three predictors SEX, COLOUR, and FOREST were significant (p = 0.022, p = 0.041, and p = 0.033, respectively). Details of the univariate linear regression models performed are reported in Table 6.1.

Table 6.1 Results of the univariate linear regression models performed on the individual NMDS1 and NMDS2 scores. For each predictor tested, sum of squares (Sum Sq), degrees of freedom (Df), F value (*F*) and associated p-value (*p*) are reported. Significant predictors and corresponding p-values are in bold.

	NMDS1				NMDS2			
Predictor	**Sum Sq**	**Df**	***F***	***p***	**Sum Sq**	**Df**	***F***	***p***
SVL	0.263	1	6.351	**0.016**	< 0.001	1	0.013	0.911
SEX	0.081	1	1.794	0.187	0.205	1	5.626	**0.022**
COLOUR	0.397	3	3.312	**0.028**	0.324	3	2.983	**0.041**
POPULATION	1.538	19	3.508	**0.001**	1.032	19	1.779	0.079
GEN1	0.029	1	0.635	0.429	< 0.001	1	< 0.001	0.997
GEN2	0.015	1	0.322	0.573	0.016	1	0.403	0.529
BIO1	0.061	1	1.334	0.254	0.001	1	0.031	0.861
BIO5	0.145	1	3.314	0.075	0.123	1	3.379	0.072
BIO12	0.133	1	3.019	0.089	< 0.001	1	0.009	0.925
BIO14	0.002	1	0.048	0.823	0.015	1	0.363	0.549
AGRIC	0.016	1	0.345	0.559	0.102	1	2.646	0.111
FOREST	0.201	1	4.702	**0.035**	0.178	1	4.793	**0.033**
MOOR	0.002	1	0.051	0.823	0.004	1	0.107	0.746
PASTURE	< 0.001	1	< 0.001	0.981	< 0.001	1	0.011	0.912

In the multiple regression model comprising individual NMDS1 scores as response variable, and SVL, COLOUR and FOREST as predictors, no significant effects were detected. In the multiple regression model built including individual NMDS2 scores as response variable, and the three predictors SEX, COLOUR and FOREST, only SEX had a significant effect (*p* = 0.045). The p-value relative to Moran's I calculated for all variables included in the two multiple regression models was > 0.1, indicating absence of statistically significant spatial autocorrelation. Details of the multiple regression models performed are reported in Table 6.2.

Table 6.2 Results of the multiple regression models performed. For each predictor included in the model, sum of squares (Sum Sq), degrees of freedom (Df), F value (*F*) and associated p-values (*p*) are reported. Residual sum of squares (Res. Sum Sq) and residual degrees of freedom (Res. Df) of the full models are also presented. Significant predictors and corresponding p-values are in bold.

Response	Predictor	Sum Sq	Df	*F*	*p*	Res. Sum Sq	Res. Df
NMDS1	SVL	0.084	1	2.142	0.151	1.641	42
	COLOUR	0.208	3	1.773	0.167		
	FOREST	0.021	1	0.536	0.468		
NMDS2	**SEX**	0.136	1	4.255	**0.045**	1.347	42
	COLOUR	0.223	3	2.317	0.089		
	FOREST	0.084	1	2.611	0.114		

Following the same approach, we performed single predictor Generalised Linear Models (GLMs) to test the effect of each of the 14 selected predictors on the presence/absence of each of the 10 polymorphic bands retrieved from the individual whole venom profiles. While no significant effects on presence/absence of bands 2, 5 and 6 were detected, at least one predictor was significantly correlated with presence/absence of the remaining seven polymorphic bands. The effect of only one predictor was significant for bands 1 (i.e., SVL, $p = 0.022$) and 3 (i.e., POPULATION, $p = 0.021$), thus we could not perform multiple predictor GLMs for these two bands. Similarly, we could not build a multiple predictor GLM for band 7, because single predictor GLMs performed for this band found significance only for the predictors COLOUR ($p = 0.002$) and POPULATION ($p = 0.026$), that could not be included in the same model because of the high level of association between them (Cramér's V = 0.899). Of all single predictor GLMs performed, some provided unreliable fit and low prediction power, and were thus not considered in subsequent analyses. Additional details of the single predictor binomial GLMs performed are reported in Table A3.5 and Figure A3.4.

Multiple predictor GLMs were built for bands 4, 8, 9, and 10, by including all the predictors that had a significant effect in the single predictor GLMs performed for these four bands. Significant effects were found for the predictors SEX ($p = 0.018$) and AGRIC ($p = 0.044$) on the presence/absence of band 4, and for the predictor COLOUR ($p < 0.001$) on the presence/absence of band 10 (Table 6.3). Specifically, band 4 was significantly less detected in females than in males (Figure 6.5A), and the probability of detecting it appeared inversely related to the percentage of agricultural areas (Figure 6.5B). Concerning the significant effect of the predictor COLOUR on the presence/absence of band 10, the four *V. seoanei* colour phenotypes considered (i.e., *bilineata*, *cantabrica*, *classic*, *melanistic*) were related differently to the response variable (Figure 6.5C).

The effect of predictors SEX and GEN2 on the presence/absence of band 9 was also significant, but the multiple predictor GLM performed for this band showed unreliable fit and low prediction power, and was therefore not considered. None of the predictors included in the model having the presence/absence of band 8 as response variable was significant.

The p-value relative to Moran's I calculated for all variables included in the four multiple predictor GLMs was > 0.1, meaning that there was no statistically significant spatial autocorrelation in the data.

Table 6.3 Results of the multiple predictor binomial GLMs performed. The models investigate the probability of occurrence of bands 4, 8, 9, and 10 in an SDS-PAGE venom profile. Likelihood Ratio Chi-square (LR χ^2), degrees of freedom (Df), and associated p-values (*p*) are reported. Significant predictors and corresponding p-values are in bold. The asterisks (*) indicate predictors that, although significant, were not considered because the corresponding models did not converge.

Response	Predictors	LR χ^2	Df	*P*
Band 4	**SEX**	5.544	1	**0.018**
	AGRIC	4.068	1	**0.044**
Band 8	SVL	0.529	1	0.467
	COLOUR	3.638	3	0.303
	BIO5	0.059	1	0.807
	BIO12	0.000	1	0.996
Band 9	**SEX***	20.679	1	**< 0.001**
	GEN2*	16.784	1	**< 0.001**
Band 10	**COLOUR**	16.612	3	**< 0.001**
	BIO5	2.387	1	0.122
	FOREST	3.765	1	0.052

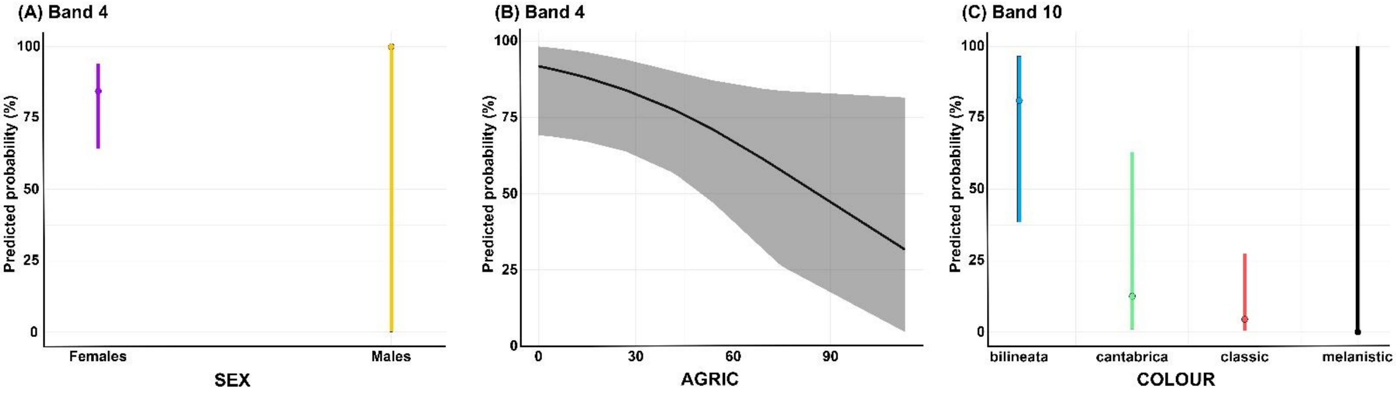

Figure 6.5 Multiple predictor GLM predictions of occurrence of bands 4 and 10 in individual SDS-PAGE venom profiles. The panels display the predicted probability of occurrence of band 4 in relation to the sex of the viper (A) and amount of cultivated fields (B), and of band 10 in relation to four different colour phenotypes displayed by *V. seoanei* (C). The high standard deviations are attributable to model limitations owed to small sample size.

Discussion

Protein composition of *V. seoanei* venom

Through the application of bottom-up venomics, we were able to provide the first characterisation of the protein components present in the venom of *V. seoanei*. As shown by the high number of peaks and bands retrieved from the RP-HPLC and SDS-PAGE profiles produced for the venom pool (see Figure 6.2), the Iberian adder's venom comprises at least 12 different toxin families. Five of these families, namely PLA_2, SVSP, DISI, CTL and SVMP, constitute about 75% of the full venom proteome (see Figure 6.3, and Table A3.4). Similar compositional patterns have been described for the venoms of *V. seoanei*'s sister species *V. berus* (Latinović et al., 2016) and the Iberian endemic *V. latastei* (Avella et al., 2022), in line with the general composition of Viperinae venoms, typically composed for 60–90% by the four toxin families PLA_2, SVSP, CTL and SVMP (Damm et al., 2021).

The effects generally elicited by the five major toxin families composing the venom of *V. seoanei* are concordant with the mainly haemorrhagic and cytotoxic symptoms typically reported for viper envenomation (Gutiérrez et al., 2017; Warrell, 2010). Specifically, DISI, CTL and SVSP can affect blood coagulation, fibrinolysis, angiogenesis, and platelet aggregation (Kini, 2005; Lazarovici et al., 2019; Marcinkiewicz, 2005), and SVMP (especially class PIII) are known to inhibit the coagulation cascade and platelet aggregation, and to cause severe haemorrhage (Gutiérrez et al., 2017; Ramos and Selistre-de-Araujo, 2006). Phospholipases of the PLA_2 type, the most abundant component of the analysed venom pool, constitute a very diverse toxin family (Jan et al., 2007) which can produce a plethora of different effects, including myotoxicity, cardiotoxicity, cytotoxicity, and coagulotoxicity (Rouault et al., 2006). Of the several different PLA_2 proteoforms we detected in the *V. seoanei* venom, some of them appear to correspond to ammodytin L and ammodytin I, suggesting myotoxic and haemolytic effects (see Jan et al., 2007).

Among the less abundant toxins we found in *V. seoanei* venom, KUN and LAAO have been reported to interfere with platelet aggregation, fibrinolysis, and angiogenesis (Du and Clemetson, 2002; Morjen et al., 2014; Mukherjee et al., 2014), with the latter being potentially disrupted also by CRISP and VEGF (Ferreira et al., 2021; Lecht et al., 2015). Finally, VNGF can increase vascular permeability in the envenomated organism, thus aiding the spread of other toxins (Sunagar et al., 2013), while NP can decrease myocardial contractility and cause hypotension, rapidly leading to loss of consciousness (Oliveira et al., 2022).

Low levels of geographic variation

In order to assess presence and extent of geographic venom variation within *V. seoanei*, we performed comparative analyses of the SDS-PAGE whole venom profiles obtained from the 49 individuals collected across the species' distribution in northern Iberia. By visually comparing the profiles in question (Figure A3.3), we noticed the lack of marked differences among them. Additionally, in the NMDS ordination plot generated using the individual NMDS scores on the first two axes (i.e., NMDS1 and NMDS2), most of the points were clustered in an almost central position, several of them were overlapping, and we did not detect a defined pattern of geographic venom variation (see Figure 6.4). Although the Shapiro-Wilk test performed for NMDS1 and NMDS2 values showed that only the latter did not depart significantly from normal distribution (W = 0.951, p = 0.041 and W = 0.966, p = 0.168, respectively), the statistical models supported the classification of NMDS1 and NMDS2 values as normally distributed (41% of probability, against 20% of probability of following a beta distribution). Taken together, these results suggest the presence of low levels of variation within the adult *V. seoanei* venoms considered.

Being an ecologically critical functional trait, snake venom is under strong selective pressures, shaping its composition and activity to facilitate the snake's survival (Casewell et al., 2013, 2020). The several reported cases of snake venom varying between different areas, likely in response to differences in ecological and environmental conditions (e.g., prey availability and susceptibility to venom), appear to provide consistent support to the adaptive value of snake venom variation (see Daltry et al., 1996; Holding et al., 2018). Nonetheless, cases of geographic snake venom variation being almost undetectable at intraspecific level are known. For example, Hofmann et al. (2018) and Rautsaw et al. (2019) did not detect a defined pattern of geographic variation in the venoms of *Crotalus cerastes* from Arizona and California, possibly due to stabilising selection favouring generalist venom phenotypes (Margres et al., 2019). Similarly, Margres et al. (2015) found no significant variation in the expression of toxins and toxin genes across individuals of *Micrurus fulvius* from Florida, perhaps as result of relaxed selective constraints or a recent range expansion. It would thus be interesting to investigate if the low variation we observed among the SDS-PAGE *V. seoanei* venom profiles analysed could be a consequence of factors potentially preventing local venom adaptation, such as the recent population expansion from north-western towards eastern Iberian Peninsula suggested for this species (Martínez-Freiría et al., 2015), or considerable levels of gene flow (see Rautsaw et al., 2019)

Additionally, in the light of the arms race between snakes and their prey, typically consisting in prey evolving resistance to venom and snake venom evolving to bypass it (Gibbs et al., 2020; Poran et al., 1987; van Thiel et al., 2022), it has been suggested that balancing selection might favour a diverse set of venom alleles over a single optimal venom genotype, in order to prevent fixed venom alleles from becoming ineffective due to evolved prey resistance (Schield et al., 2022). In this scenario, considering that adult Iberian adders are small mammal specialists (Espasandín et al., 2022), the low venom variation detected might align with balancing selection acting to allow the effective subjugation of their potentially coevolving preferred prey while also avoiding evolutionary dead ends.

Correlates of venom variation

We implemented in our regression models the same predictors Espasandín et al. (2022) used to study the effect of eco-geographic variables on the trophic ecology of *V. seoanei.* Considering the strong link between snake venom variation and diet, we aimed to test whether they could be at play in determining occurrence and extent of venom variation within this species. Although we detected overall low levels of venom variation, the univariate linear regression analyses performed showed significant effects of body size (i.e., SVL), colour phenotype, sex, and locality of origin of the vipers, and percentage of forested area on the NMDS1 and NMDS2 scores (see Table 6.1 for details). Nonetheless, in the multiple regression models performed, only the predictor SEX had a significant effect on the variation detected across the analysed venoms (see Table 6.2).

In gape-limited animals like snakes (Forsman, 1991), sexual dimorphism in body and/or head size can define the spectrum of prey items each sex can feed on (Shine, 1991). While no sexual dimorphism concerning head size has been detected in *V. seoanei*, significant intersexual variation in body size (i.e., SVL) has been reported for this species (Lucchini et al., 2020). Interestingly, significant differences in feeding frequencies have been found between male and female Iberian adders, with females feeding more often than males, and males reducing their feeding rates as they grow (Espasandín et al., 2022). Although these considerations might suggest a potential role of intersexual differences in feeding ecology on the low variation detected across the *V. seoanei* venoms analysed, we did not identify sex-specific venom protein bands. Additionally, despite the NMDS ordination plot indicating less divergence within female venoms than within male venoms (see Figure 6.4), male and female venom profiles did not differ significantly in their complexity (i.e., number of bands; Mann-Whitney $U = 284$, $p = 0.991$). The significance of sex and body size of the vipers could thus be related to factors not included in our analyses (e.g., seasonality, reproductive stage), which might be unravelled by studies developed at a finer scale.

Considering the strong correlation between the two predictors POPULATION and COLOUR, and that the five colour phenotypes currently recognised for *V. seoanei* are geographically structured, the significance of these two predictors in our analyses might refer to different local selective regimes acting on the analysed venoms. For instance, individuals presenting the four colour phenotypes included in our analyses, i.e., *bilineata*, *cantabrica*, *classic*, and *melanistic*, are known to differ in body proportions, likely due to them being subjected to different ecological pressures (e.g., climatic conditions, predatory pressure) in the habitats where they occur (Lucchini et al., 2020). Additionally, we suspect the significance of the predictor FOREST to be related to changes in the feeding ecology of *V. seoanei* associated with this habitat type (e.g., the consumption of amphibians by Iberian adders appears to increase in rainy and forested areas; Espasandín et al., 2022). Considering the lack of marked genetic distinctness within *V. seoanei*, these results could hint that the little venom variation we detected might be related to ecological factors determining differences in local selective pressures acting on distinct colour phenotypes, and/or local changes in prey availability.

The single predictor binomial Generalised Linear Models (GLMs) performed on the 10 polymorphic SDS-PAGE bands showed that the presence/absence of eight bands (i.e., 1, 2, 3, 4, 7, 8, 9, 10) was significantly correlated to at least one of the 14 predictors tested. Specifically, the models showed variation in band presence/absence in relation to body size (SVL), sex (SEX), colour phenotype (COLOUR), locality of origin (POPULATION), the PC2 of the SPCA of the interpolated genetic distances (GEN2), maximum temperature of the warmest month (BIO5), annual precipitation (BIO12), and the amount of cultivated fields (AGRIC) and forested area (FOREST) (see Figure A3.4 and Table A3.5). Multiple predictor GLMs performed for bands 4, 8, 9 and 10 supported the significance of predictors SEX and AGRIC for band 4, and of the predictor COLOUR for band 10, but did not provide significant or reliable results for bands 8 and 9 (see Table 6.3).

Based on the molecular weight of the corresponding bands in the SDS-PAGE profile of the venom pool (Figure 6.2), we suspect bands 1, 2, 3, 4 and 10 of the whole venom SDS-PAGE profiles to likely represent SVMPs. Based on the same criterion, the content of the remaining five bands is more difficult to identify, since they likely include different toxin families (e.g., CRISP, LAAO, SVSP). It is interesting to notice that, while the probability of occurrence of bands 2 and 10 increases with the amount of forested area (FOREST) and with the increase of maximum temperature of the warmest month (BIO5), respectively, the probability of occurrence of band 4 is negatively correlated with the amount of cultivated fields (AGRIC; see Figures 6.5 and A3.4). Snake venom metalloproteinases are thought to allow fast prey subjugation (Daltry et al. 1996; Gutiérrez et al., 2017; Ramos and Selistre-de-Araujo, 2006) and possibly aid prey digestion (controversial; see McCue, 2007). In a number of snake species undergoing an ontogenetic dietary shift from an ectotherm-based to an endotherm-based diet, smaller, younger individuals have been shown to produce more SVMPs than larger, older specimens (e.g., *V. latastei*, Avella et al., 2022; *Bothrops asper*, Saldarriaga et al., 2003; *Crotalus viridis*, Saviola et al., 2015). While the number of ectotherms consumed by *V. seoanei* decreases as the viper grows, adult Iberian adders were found to consume more reptiles and amphibians in warm habitats and forests, respectively, and to feed on small-mammals more frequently in agricultural lands (Espasandín et al., 2022). In this scenario, the results of the single predictor GLMs appear to at least partially support the importance of SVMPs in subduing amphibians and reptiles. Indeed, the probability of occurrence of SVMP-related bands 2 and 10 appears to be positively correlated with conditions that might favour an increase in the consumption of ectotherm prey (i.e., BIO5, FOREST). Conversely, the probability of detecting SVMP-related band 4 decreases with the increase of conditions that have been linked to an increase in the consumption of endotherm prey by *V. seoanei* (i.e., AGRIC). It could thus be interesting to investigate the toxins actually comprising these SDS-PAGE whole venom profile bands, and test whether their presence provides any functional advantages in the subjugation of one prey type rather than the other (e.g., Calvete et al., 2020; Modahl et al., 2018).

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Chapter 7

General Discussion and Future Perspectives

General Discussion

The general aim of this thesis was to contribute to the current knowledge of the venoms of European vipers (genus *Vipera*), with a focus on Lataste's viper (*V. latastei*) and the Iberian adder (*V. seoanei*). Three main goals were targeted: 1) define trends and biases currently present in snake venom studies in terms of topics and taxa considered; 2) provide a tool to facilitate physicians in recognising the *Vipera* species of major medical relevance, an overview of the general composition of their venoms, and a protocol for the management of the envenomations they can cause; 3) provide the first venomics-based investigation on composition and variation of *V. latastei* and *V. seoanei* venoms. This section presents a resume of the major achievements of this thesis concerning the abovementioned goals, and provides a series of concluding remarks and future research prospects.

7.1 Key findings

Virtues and flaws of snake venom research

Undeniably, the application in recent years of the high-throughput methodologies constituting snake venomics has provided the fields of toxinology, biology and, more in general, snake venom research with new enthusiasm, leading to the rapid production of a tremendous amount of information on different taxa. Indeed, from the analysis of published snake venom studies described in Chapter 3 we detected an overall positive trend, with a considerable increase in the number of articles published yearly since the early 2000s. This trend, even more apparent over the last decades, indicates a renewed interest in the investigation of snake venom, possibly linked to the recent recognition of snakebite as a neglected tropical disease by the World Health Organization (Chippaux, 2017), and several publications and campaigns addressing snakebite and the antivenom crisis (Groneberg et al., 2016; Kasturiratne et al., 2008; Longbottom et al., 2018).

Our study indicates that the higher the noxious potential of a venom, the more studies will focus on the snake species producing it. The predominance in snake venom studies of species belonging to the families Viperidae, Elapidae and Colubridae, known to be the ones most frequently involved in snakebite accidents and to cause severe envenomation symptoms (Calvete, 2013; Málaque and Gutiérrez, 2015; Mamede et al., 2020), appears to be in line with this result. More specifically, members of the viperid subfamily Crotalinae (i.e., pit vipers), especially of South American origin (e.g., genera *Bothrops* and *Crotalus*), are the most studied ones, contributing to the prevalence of Neotropical species detected in the analysed publications. Conversely, the underrepresentation of the families Atractaspididae, Homalopsidae, Psammophiidae, and Pseudoxyrhophiidae is likely related to them being generally considered of minor medical importance, as well as to the lack of information on the severity of the envenomations they can cause. While the major relevance of American pit vipers in terms of snakebite (Málaque and Gutiérrez, 2015; Otero-Patiño, 2009; Warrell, 2017) is surely at play in determining their prevalence over other snake taxa in snake venom studies, the role of other factors should also be taken into account. Considering socio-economic factors, for instance, snake venom studies are more often developed in middle- and high-income countries, mainly because these are more likely to possess the means for the technology needed to develop research in this field. In this scenario, the prevalence of species from the Neotropics could be explained with the large number of studies developed by Central and South American institutions, globally very knowledgeable in snake venom research (Groneberg et al., 2016; Sofyantoro et al., 2020), while the limitation that this field of study faces in low-income countries because of lack of resources might explain the apparently little focus on species from Asia and Africa.

The relatively recent advent of snake venomics has allowed the probing of a multitude of snake venoms, providing a comprehensive view of their compositions. This has led to the identification of compounds potentially relevant for drug development, and, together with the application of antivenomics, to obtaining a detailed insight into antivenom efficacy (Calvete, 2011; Gutiérrez et al., 2009; Lomonte and Calvete, 2017). In light of this, the prevalence of the topics “venom characterisation” and “biological activity” in the analysed studies is unsurprising, given their crucial importance for a wide spectrum of research fields (e.g., evolutionary biology, toxinology, medicine, etc.; Calvete, 2009, 2011; Chippaux, 1998). Conversely, the underrepresentation of the other topic categories, particularly those related to prey specificity and venom variation at different levels (e.g., interspecific, individual), reflects an apparently limited interest of toxinological research in considering snake venom from an ecological and evolutionary perspective, despite the potential relevance this approach might have for purposes like, for instance, the development of effective therapies against snakebite (Gutiérrez, 2020; Murray et al., 2020).

A tool for the management of *Vipera* snakebite in Europe

Snakes of the genus *Vipera* are the most frequently involved ones in snakebite accidents in Europe, as a likely consequence of their wide distribution across this continent (Chippaux, 2012; Paolino et al., 2020; Zanetti et al., 2018). Specifically, a recent analysis has found the six species *V. ammodytes*, *V. aspis*, *V. berus*, *V. latastei*, *V. seoanei* and *V. ursinii* to cause the vast majority of envenomations in Europe (Paolino et al., 2020). Nonetheless, the impact of ophidic accidents might be more severe than what is currently estimated, for three main reasons: (i) the reporting of snakebite accidents in Europe is non-mandatory; (ii) European snakebite victims do not always seek treatment; (iii) European physicians are generally not trained to identify snakebites, recognise their clinical manifestations, and apply appropriate treatment (Gold, 2002). In this scenario, European clinicians are in need of tools to help them with the management of European *Vipera* envenomations. In Chapter 4, we thus defined taxonomic keys for the identification of the abovementioned six *Vipera* species, reviewed and resumed the data currently available on the composition of their venoms and the clinical manifestations they can cause, and defined a standardised clinical protocol for *Vipera* snakebite treatment.

Correctly identifying the snake causing the envenomation is crucial for healthcare providers to support decision making when administering treatment, since it can allow to predict the ensuing clinical effects (Gutiérrez et al., 2017; Ralph et al., 2019; Warrell, 2017). The taxonomic key we present is meant to help healthcare providers to easily identify the European *Vipera* species involved in the snakebite accident. Specifically, we provide a key to distinguish between snakes of the genus *Vipera* and those belonging to other genera, and a key to help differentiate between the six *Vipera* species of major medical relevance in Europe. The keys are based on morphological characteristics and distribution of each species, and are most useful when in combination with photographs of the snake involved in the accident, more reliable than victim descriptions and easy to share between clinicians and snake experts, accelerating and improving the identification process (WHO, 2016).

We then aimed to provide a comprehensive assessment of the venom components of *V. ammodytes*, *V. aspis*, *V. berus*, *V. latastei*, *V. seoanei* and *V. ursinii*, developed by gathering the information available in existing literature. Notably, while we were able to retrieve several publications concerning the characterisation of the venoms of *V. ammodytes*, *V.aspis*, *V. berus* and *V. ursinii* (e.g., Georgieva et al., 2008; Giribaldi et al., 2020; Lang Balija et al., 2020; Latinović et al., 2016), we found that information regarding *V. latastei* and *V. seoanei* venoms was almost non-existent. Considering the venoms of the species for which we could gather information, we found their compositions to be quite similar, and to overall follow the typical compositional pattern of Viperinae venoms. Indeed, the venoms of *V. ammodytes*, *V.aspis*, *V. berus* and *V. ursinii* appear to be characterised by few major toxin families accounting for most of their compositions, namely SVMP, PLA_2, SVSP and CTL, and by a more or less considerable number of less abundant components (e.g., DISI, CRISP, VEGF, KUN, LAAO, etc.; see Damm et al., 2021 and references within).

In line with the retrieved information concerning the compositions of their venoms, the European *Vipera* species of major medical relevance mainly cause haemorrhagic and cytotoxic effects (typical of viper envenomation; Gutiérrez et al., 2017; Warrell, 2010), although in some cases neurotoxic symptoms can also occur (Ferquel et al., 2007; Lukšić et al., 2006). More specifically, the clinical manifestations caused by the *Vipera* species in question range from local and only requiring topical treatment (e.g., algesia, swelling) to systemic, potentially lethal, and requiring antivenom therapy (e.g., renal failure, haematological alterations;

Chippaux, 2012; Paolino et al., 2020). The list of the different clinical manifestations elicited by *Vipera* venoms we report is meant to constitute a tool for healthcare providers to quickly identify their onset, and to facilitate the decision making process concerning their treatment.

In light of the overview we presented on the symptoms caused by *Vipera* envenomations, we also provided a protocol for first aid on the field and a series of recommendations for the clinical management of *Vipera* snakebite. These address in detail the treatment of local and systemic symptoms and administration of antivenom, and revolve around the need for physicians to closely monitor snakebite patients, be wary of the possible progression from non-severe to severe clinical manifestations, and have a low threshold to escalate therapy as needed.

First look into the venoms of *Vipera latastei* and *Vipera seoanei*

The application of bottom-up proteomics proved to be a very powerful tool for providing a detailed picture of the diversity of the toxin families present in snake venom, together with reliable estimates of their relative abundances (e.g., Alape-Girón et al., 2008; Calvete et al., 2010; Mora-Obando et al., 2020). Indeed, sample decomplexation before mass spectrometry being arguably the best approach for obtaining deeper proteomic coverage (Fox et al., 2006), bottom-up proteomics protocols could likely be considered the cornerstone of venomic analysis (Calvete, 2011, 2013).

In the studies reported in Chapters 5 and 6, centred around the application of bottom-up proteomics, we provide, respectively, the first assessment of the protein composition of the venoms of *V. latastei* and *V. seoanei*. In line with the findings of previous research on the venom of other *Vipera* species (e.g., *V. ammodytes*, Gopcevic et al., 2021; *V. aspis*, Giribaldi et al., 2020; *V. berus*, Al-Shekhadat et al., 2019), we identified SVMPs, CTLs, PLA_2s and SVSPs as some of the most abundant toxins in the venoms of both species, which thus follow the general compositional pattern of Viperinae venoms (see Damm et al., 2021 and references within).

The obtained adult *V. latastei* and adult *V. seoanei* venom proteomes appear to be overall quite similar in terms of components, possibly as a result of the parallels between the feeding ecologies of the two species (Brito, 2004; Espasandín et al., 2022; Santos et al., 2007). Nonetheless, we found in the venom of *V. latastei* a short RTS-disintegrin (i.e., latastin) that we did not detect in the analysed *V. seoanei* venom. Intriguingly, (K/R)TS-disintegrins had so far been found exclusively in *Macrovipera* and *Daboia* venoms (Sanz-Soler et al., 2012; Saviola and Calvete, 2021). The discovery of latastin in *V. latastei* venom thus indicates that the evolutionary origin of (K/R)TS-disintegrins is prior to the split of the genera *Daboia* and *Vipera* (about 25 Mya; see Freitas et al., 2020).

Aiming to investigate the presence of venom variation in *V. latastei* and *V. seoanei*, we performed comparative analyses at different intraspecific levels. In the case of *V. latastei*, we compared the venoms of specimens belonging to different age classes (i.e., juveniles vs adults), and the venoms of adult specimens from environmentally different localities (i.e., Gerês, mountain vs Vila Chã, ocean coast). When comparing juvenile and adult *V. latastei* venoms, we found evidence of an ontogenetic shift in the composition of the venom of this species, likely mirroring the ontogenetic shift from ectotherm-based diet to a diet including mostly endotherm prey reported for Lataste's viper (Brito, 2004). Furthermore, when comparing the RP-HPLC profiles of adult *V. latastei* venoms from Gerês and Vila Chã, we showed the presence of a certain degree of variation, strongly supported by statistical analyses, possibly due to differences in local selective regimes. The obtained results also suggested that factors like sex and body size of the viper could play a role in shaping this species' venom composition. Although indirectly, these factors might reflect different diets through ontogeny and/or between sexes. Their significance in the statistical analyses performed might thus potentially provide further support to the relevance of diet in the occurrence of venom variation in *V. latastei*.

In the case of *V. seoanei*, we did not investigate the presence of venom variation between vipers of different age classes, but instead compared the SDS-PAGE profiles of 49 adult individuals from 20 localities across the species' Iberian range. Surprisingly, we found the analysed venom profiles to be remarkably similar, and hypothesised this to be the result of factors like balancing selection, stabilising selection, or the by-product of a recent population expansion. Similarly to what found for *V. latastei*, regression analyses retrieved significant effects of body size, colour phenotype, sex, and locality of origin of the Iberian adders, and percentage of forested area on the low levels of venom variation detected across the analysed *V. seoanei* venom profiles.

While the information gathered with this project partially filled the long-existing knowledge gap about the venoms of *V. latastei* and *V. seoanei*, it opened new questions as to the selective drivers that underlie venom evolution in these two species.

7.2 Concluding remarks and future prospects

The production of a study on trends and biases in snake venom research defined the starting point for this doctoral project, by identifying the main focus and aims of this research field, as well as its most glaring knowledge gaps. While we acknowledge that the exclusive use of Google Scholar for article search, in combination with the article selection criteria applied, might have led to the exclusion of relevant publications from our analysis, the results we obtained are in line with trends and biases already detected in other studies (Diz and

Calvete, 2016; Jackson et al., 2019; Sofyantoro et al., 2022), supporting their reliability. In light of our findings, we join the chorus of those who advocate the need for future snake venom studies to focus on the venoms produced by other venomous snake taxa than the typically more studied families (i.e., Viperidae, Elapidae, Colubridae), in order to increase the knowledge about snake venom evolution and composition, and help widen the spectrum of treatable snakebite envenomations. Additionally, more effort should be put into developing studies focusing on species originating from areas where snakebite incidence is high and the economical level low, such as the Indomalayan and the Afrotropic realms, which appear to be under-investigated. Finally, the analysis of snake venom performed taking into account ecological and functional contexts of the species producing it would likely provide a more detailed and comprehensive view of the driving forces behind its evolution and variation.

By reviewing the information available on the venom composition of the six *Vipera* species of major clinical relevance in Europe and the symptoms they can cause, and by defining protocols for their clinical management, we were able to provide an overview on current knowledge on these species' venom compositions and activities, and tool for the management of *Vipera* envenomations in Europe. During the development of this work, we noticed a severe lack of information on the venoms of several *Vipera* species and the envenomations they can cause. We thus support the need for European clinicians to start reporting snakebite cases in order to provide sound statistics of the frequency of viper bites and associated clinical features, ideally in a structured database. Furthermore, we advocate for the need to develop venomic studies focusing on a greater number of *Vipera* species, in order to improve our understanding of compositions and activities of *Vipera* venoms and the clinical management of *Vipera* bites.

The production of proteomes from representative *V. latastei* and *V. seoanei* venoms has not only enhanced current knowledge on the venom of the medically important genus *Vipera*, but also paved the way for new research opportunities. In the light of the dietary shift reported for *V. seoanei* (Espasandín et al., 2022) for instance, proteomic analyses of venoms from individuals of this species belonging to different age classes would likely reveal the presence of ontogenetic venom variation. Similarly, performing proteomic analyses on the venoms of *V. latastei* specimens from across this viper's whole distribution would certainly provide a more comprehensive insight into venom variation within this species.

In the light of the diversity of components detected within *V. latastei* and *V. seoanei* venoms, the investigation of their mode of action and biological roles would facilitate a better understanding of the clinical symptoms envenomations caused by these species can elicit, potentially helping to improve patient management. Indeed, whilst comparative proteomic data provides a useful tool to assess venom variation, experimental evidence of the functional activity of venom components remains essential to understand their physiological roles in envenoming. Considering the ontogenetic shift in SVMP abundance we detected in *V. latastei*, for instance, investigating the biological activities of venoms produced by *V. latastei* individuals belonging to different age classes, by performing biological assays on cell lines of different origin (see Luddecke et al., 2023), could elucidate the potentially selective value of the SVMP-rich venoms of juvenile Lataste's vipers, possibly facilitating their ectotherm-based diet (see Brito, 2004). Similarly, developing this kind of experiments on cell lines mimicking different natural prey items could help us understand whether the low levels of venom variation we detected within *V. seoanei* are due to selection acting to maintain a generalist venom phenotype or not.

Furthermore, the implementation of genomic and venom gland transcriptomic analyses could allow elucidating the mechanisms involved in the regulation of the expression of specific toxins in *V. latastei* and *V. seoanei* venoms, by providing the full landscape of the venom-encoding genes of these species (see Vonk et al., 2013) and allowing to investigate the presence of differences in venom modulation between conspecifics (e.g., Durban et al., 2013; Sunagar et al., 2014; Rautsaw et al., 2019). Considering *V. latastei*, it would for instance be interesting to investigate modes and times of the change in SVMP abundances between juveniles and adults we detected. In the case of *V. seoanei*, taking into account that the low venom variation we detected within this species might be explained as a result of factors such as balancing selection and recent population expansion, the application of genomics and venom gland transcriptomics may be revealing in testing these hypotheses. Moreover, the implementation of transcriptomic analyses could confirm the presence of specific toxins identified in the venom proteomes (e.g., the RTS-disintegrin latastin we found in the venom of *V. latastei*), facilitate the detection of new ones, and potentially lead to the discovery of molecules of pharmacological and/or biotechnological interest. Finally, the application of "-omic" technologies to the study of *Vipera* venoms might help elucidate the mechanisms behind the origin and occurrence of different toxins within this genus. In particular, it might help understand the distribution of neurotoxins across the venoms of some *Vipera* species (e.g., *V. ammodytes*, Logonder et al., 2008; *V. aspis*, Zanetti et al., 2018; *V. berus*, Malina et al., 2017), not following any clear phylogenetic pattern and constituting one of the unresolved conundrums of snake venomics.

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Appendix A

Supplementary Information

Supplementary Information for Chapter 3

Analysis of general trends and biases in snake venom research

List of Supplementary Tables and Figures

Table A1.1 Complete dataset of the articles analysed. For each article, DOI/link, publication year, taxonomic information of the snake species considered and topic categories covered are reported. Additional details are available at: https://www.mdpi.com/2072-6651/14/12/884.

Table A1.2 Complete list of all retrieved snake species. For each species, family, subfamily/group, and assigned hazard category are reported.

Table A1.3 Country of origin of the retrieved snake species. The overall species number is higher than the number of species actually retrieved from the analysed publications because some species were assigned to more than one country.

Table A1.4 Number of publications considered per each year of the defined time frame. Years for which no articles were considered are not reported.

Table A1.5 Polynomial regression models applied to test the relationship between topic categories and number of yearly papers covering each one of them. For each model, predicted outcome value (y), information score (Akaike's Information Criterion corrected for small sample sizes; AICc), observed-versus-expected chi-squared value (χ^2), coefficient of determination (r^2), and p-value (*p*) are reported.

Table A1.6 Summary of the Generalised Linear Model (GLM) applied to test the relationship between number of articles retrieved for each snake species and hazard category (HAZARD) and biogeographic realm (REALM). The levels "Critical" and "Neotropic" have been used as reference for the predictors HAZARD and REALM, respectively. For each predictor level, coefficients (*B*), standard error (*SE*), and p-value (*p*) are reported. Significant p-values are displayed in bold.

Figure A1.1 Information about the combinations of topic categories retrieved in the analysed articles. The graph shows the eight most represented combinations in terms of number of articles.

Figure A1.2 Chronological trends of the analysed publications, by snake subfamily/group considered. Notice the prevalence of Crotalinae, Viperinae, and Old World and American elapids over the other subfamilies/groups.

Table A1.1 Complete dataset of the articles analysed. For each article, DOI/link, publication year, taxonomic information of the snake species considered and topic categories covered are reported. Additional details are available at: https://www.mdpi.com/2072-6651/14/12/884.

#	DOI/LINK	YEAR	FAMILY	SUBFAMILY/GROUP	SPECIES	COUNTRY	REALM	TOPIC CATEGORIES
1	https://doi.org/10.1016/j.toxicon.2021.03.014	2021	Elapidae	Old World and American elapids	*Naja haje*	Nigeria	Afrotropic	I, VII
			Elapidae	Old World and American elapids	*Naja katiensis*	Nigeria	Afrotropic	
			Elapidae	Old World and American elapids	*Naja nigricollis*	Nigeria	Afrotropic	
2	https://doi.org/10.1016/j.toxicon.2007.03.012	2007	Viperidae	Crotalinae	*Crotalus durissus*	Venezuela	Neotropic	I, V, III
3	https://doi.org/10.1016/j.jprot.2017.08.016	2018	Elapidae	Old World and American elapids	*Dendroaspis angusticeps*	Tanzania	Afrotropic	I, VII, III, II
			Elapidae	Old World and American elapids	*Dendroaspis jamesoni*	Cameroon	Afrotropic	
			Elapidae	Old World and American elapids	*Dendroaspis jamesoni*	Uganda	Afrotropic	
			Elapidae	Old World and American elapids	*Dendroaspis polylepis*	Tanzania	Afrotropic	
			Elapidae	Old World and American elapids	*Dendroaspis viridis*	Togo	Afrotropic	
4	https://doi.org/10.1016/0041-0101(85)90394-0	1985	Viperidae	Crotalinae	*Crotalus concolor*	USA	Nearctic	I, VII, V
			Viperidae	Crotalinae	*Crotalus lutosus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	
5	https://doi.org/10.1186/1471-2164-14-790	2013	Viperidae	Crotalinae	*Ovophis okinavensis*	Japan	Indomalayan	I, VII
			Viperidae	Crotalinae	*Protobothrops flavoviridis*	Japan	Indomalayan	
6	https://doi.org/10.1186/s12864-015-1832-6	2015	Viperidae	Crotalinae	*Protobothrops elegans*	Japan	Indomalayan	I, VII, VI
			Viperidae	Crotalinae	*Protobothrops flavoviridis*	Japan	Indomalayan	
7	https://doi.org/10.3390/toxins11020090	2019	Viperidae	Viperinae	*Vipera berus*	Russia	Palearctic	I, III, II
8	https://doi.org/10.1021/pr800332p	2008	Viperidae	Crotalinae	*Bothrops asper*	Costa Rica	Neotropic	I, VI, V
9	https://doi.org/10.1016/j.jprot.2013.05.015	2013	Elapidae	Old World and American elapids	*Bungarus sindanus*	Pakistan	Indomalayan	I, VII, III, II
			Elapidae	Old World and American elapids	*Naja naja*	Pakistan	Indomalayan	
10	https://doi.org/10.3390/toxins11050294	2019	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, VI
11	https://doi.org/10.1016/j.jprot.2018.03.032	2018	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, VI, V
12	https://doi.org/10.1021/acs.jproteome.0c00737	2021	Viperidae	Crotalinae	*Bothrops alcatraz*	Brazil	Neotropic	I
13	https://doi.org/10.11646/zootaxa.1038.1.1	2005	Viperidae	Viperinae	*Macrovipera lebetina*	Cyprus	Palearctic	I, VII, V
			Viperidae	Viperinae	*Macrovipera lebetina*	Turkey	Palearctic	
			Psammophiidae	NA	*Malpolon insignitus*	Turkey	Palearctic	
			Viperidae	Viperinae	*Montivipera wagneri*	Turkey	Palearctic	
			Viperidae	Viperinae	*Montivipera xanthina*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera transcaucasiana*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera barani*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera eriwanensis*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera kaznakovi*	Turkey	Palearctic	
14	https://biozoojournals.ro/nwjz/content/v4.1/03.nwjz.04.01.Arikan.et.al..pdf	2008	Viperidae	Viperinae	*Macrovipera lebetina*	Turkey	Palearctic	I, VII
			Psammophiidae	NA	*Malpolon insignitus*	Turkey	Palearctic	
			Viperidae	Viperinae	*Montivipera wagneri*	Turkey	Palearctic	
			Viperidae	Viperinae	*Montivipera xanthina*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera transcaucasiana*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera barani*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera eriwanensis*	Turkey	Palearctic	
			Viperidae	Viperinae	*Vipera kaznakovi*	Turkey	Palearctic	
			Elapidae	Old World and American elapids	*Walterinnesia morgani*	Turkey	Palearctic	
15	https://doi.org/10.1016/j.toxicon.2021.01.014	2021	Viperidae	Crotalinae	*Crotalus catalinensis*	USA	Nearctic	I, VI
16	https://doi.org/10.1080/02772248.2019.1619743	2019	Elapidae	Old World and American elapids	*Naja naja*	Pakistan	Indomalayan	I
17	https://doi.org/10.1016/0041-0101(92)90539-H	1992	Colubridae	Dipsadinae	*Philodryas olfersii*	Brazil	Neotropic	I, III, II
18	https://doi.org/10.1016/j.cca.2005.02.008	2005	Viperidae	Viperinae	*Vipera ammodytes*	Croatia	Palearctic	I, V, III, II
19	https://doi.org/10.3390/toxins12030187	2020	Viperidae	Viperinae	*Vipera ursinii*	Croatia	Palearctic	I, III, VIII
20	https://doi.org/10.1098/rspb.2009.0048	2009	Viperidae	Viperinae	*Echis carinatus*	Pakistan	Indomalayan	I, VII, III, VIII
			Viperidae	Viperinae	*Echis coloratus*	Saudi Arabia	Palearctic	
			Viperidae	Viperinae	*Echis romani*	Nigeria	Afrotropic	
			Viperidae	Viperinae	*Echis pyramidum*	Kenya	Afrotropic	
21	https://doi.org/10.1002/pmic.200402024	2005	Viperidae	Viperinae	*Cerastes cerastes*	Tunisia	Palearctic	I, VII
			Viperidae	Viperinae	*Cerastes vipera*	Tunisia	Palearctic	
			Viperidae	Viperinae	*Daboia mauritanica*	Tunisia	Palearctic	
22	https://doi.org/10.1016/j.jprot.2020.103863	2020	Elapidae	Old World and American elapids	*Micrurus browni*	Mexico	Neotropic	I, II, III, VIII
23	https://doi.org/10.1016/j.biochi.2021.01.003	2021	Elapidae	Old World and American elapids	*Micruroides euryxanthus*	Mexico	Neotropic	I, II, III
24	https://doi.org/10.1016/j.toxcx.2020.100048	2020	Viperidae	Viperinae	*Echis carinatus*	India	Indomalayan	I, V

25	https://doi.org/10.1074/mcp.M500270-MCP200	2006	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja textilis*	Australia	Australasia	I, V
26	https://doi.org/10.1016/j.jprot.2010.06.001	2010	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, V, II
27	https://doi.org/10.1016/j.toxicon.2020.05.028	2020	Viperidae	Crotalinae	*Bothrops leucurus*	Brazil	Neotropic	I, II, VI
28	https://doi.org/10.1016/j.jprot.2020.103882	2020	Colubridae	Colubrinae	*Rhinobothryum bovalli*	Costa Rica	Neotropic	I, VI, VIII
29	https://doi.org/10.1021/pr0701714	2007	Viperidae	Viperinae	*Bitis caudalis*	UNKNOWN	Afrotropic	I, VII
			Viperidae	Viperinae	*Bitis nasicornis*	UNKNOWN	Afrotropic	
			Viperidae	Viperinae	*Bitis rhinoceros*	UNKNOWN	Afrotropic	
30	https://doi.org/10.1016/j.jprot.2009.01.005	2009	Viperidae	Crotalinae	*Bothrops asper*	Costa Rica	Neotropic	I, VII, V, II
			Viperidae	Crotalinae	*Bothrops atrox*	Peru	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Venezuela	Neotropic	
31	https://doi.org/10.1021/pr900249q	2009	Viperidae	Crotalinae	*Crotalus atrox*	USA	Nearctic	I
32	https://doi.org/10.1021/acs.jproteome.1c00608	2021	Elapidae	Old World and American elapids	*Walterinnesia aegyptia*	Egypt	Palearctic	I, III, VII
			Elapidae	Old World and American elapids	*Walterinnesia aegyptia*	Saudi Arabia	Palearctic	
			Elapidae	Old World and American elapids	*Walterinnesia morgani*	Turkey	Palearctic	
33	https://doi.org/10.1016/j.jprot.2011.01.003	2011	Viperidae	Crotalinae	*Bothrops atrox*	Venezuela	Neotropic	I, VI, V
			Viperidae	Crotalinae	*Bothrops asper*	Colombia	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	
34	https://doi.org/10.1016/j.jprot.2012.05.026	2012	Elapidae	Australo-Papuan and marine elapids	*Hydrophis cyanocinctus*	Iran	Palearctic	I, VII
			Elapidae	Australo-Papuan and marine elapids	*Toxicocalamus longissimus*	Papua New Guinea	Australasia	
35	https://doi.org/10.1038/s41598-018-29791-y	2018	Viperidae	Crotalinae	*Agkistrodon contortrix*	USA	Nearctic	I, VI, III
36	https://doi.org/10.1186/1471-2164-10-564	2009	Viperidae	Viperinae	*Echis carinatus*	UAE	Palearctic	I, VII
			Viperidae	Viperinae	*Echis coloratus*	Egypt	Palearctic	
			Viperidae	Viperinae	*Echis pyramidum*	Kenya	Afrotropic	
37	https://doi.org/10.1080/14789450.2019.1559735	2019	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, V, III, II
38	https://doi.org/10.1016/j.ijbiomac.2020.05.106	2020	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, II
39	https://doi.org/10.1016/j.jprot.2013.06.012	2013	Elapidae	Old World and American elapids	*Ophiophagus hannah*	Indonesia	Indomalayan	I, V, III, VIII
			Elapidae	Old World and American elapids	*Ophiophagus hannah*	Malaysia	Indomalayan	
			Elapidae	Old World and American elapids	*Ophiophagus hannah*	China	Indomalayan	
			Elapidae	Old World and American elapids	*Ophiophagus hannah*	Thailand	Indomalayan	
40	https://doi.org/10.5897/JCAB.9000027	2009	Elapidae	Old World and American elapids	*Bungarus candidus*	Thailand	Indomalayan	I, V, III
41	https://doi.org/10.3390/toxins10090373	2018	Elapidae	Old World and American elapids	*Bungarus flaviceps*	Indonesia	Indomalayan	I
42	https://doi.org/10.1016/j.actatropica.2018.09.017	2019	Viperidae	Crotalinae	*Deinagkistrodon acutus*	Taiwan	Indomalayan	I, II
43	https://doi.org/10.1016/j.febslet.2006.07.010	2006	Colubridae	Dipsadinae	*Philodryas olfersii*	UNKNOWN	Neotropic	I
44	https://doi.org/10.3390/toxins11020104	2019	Elapidae	Old World and American elapids	*Naja sumatrana*	Malaysia	Indomalayan	I
45	https://doi.org/10.1016/j.toxicon.2006.07.008	2006	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I
46	https://doi.org/10.1016/j.cbpc.2017.04.007	2017	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja affinis*	Australia	Australasia	VII, VI, V, III
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja aspidorhyncha*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja guttata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja inframacula*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja ingrami*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja mengdeni*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja modesta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja nuchalis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja textilis*	Australia	Australasia	
47	https://doi.org/10.1016/j.cbpc.2018.05.003	2018	Viperidae	Viperinae	*Causus lichtensteinii*	UNKNOWN	Afrotropic	I, VII, III
48	https://doi.org/10.1007/s00239-002-2403-4	2003	Viperidae	Crotalinae	*Trimeresurus stejnegeri*	Taiwan	Indomalayan	I, V
49	https://doi.org/10.1016/j.toxicon.2009.12.009	2010	Viperidae	Viperinae	*Bitis arietans*	Ghana	Afrotropic	I, V, III, II
			Viperidae	Viperinae	*Bitis arietans*	Nigeria	Afrotropic	
50	https://doi.org/10.1016/j.toxicon.2020.07.030	2020	Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	I, II, III, VII
51	https://doi.org/10.1590/1678-9199-JVATITD-2020-0016	2020	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, II, III, V
52	https://doi.org/10.1016/S1532-0456(00)00215-5	2001	Elapidae	Old World and American elapids	*Micrurus albicinctus*	Brazil	Neotropic	VII, V, III, VIII
			Elapidae	Old World and American elapids	*Micrurus baliocoryphus*	Argentina	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus altirostris*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus altirostris*	Argentina	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus brasiliensis*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus hemprichii*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus ibiboboca*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus lemniscatus*	Colombia	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus lemniscatus*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus pyrrhocryptus*	Argentina	Neotropic	

			Elapidae	Old World and American elapids	*Micrurus spixii*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus spixii*	Colombia	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus surinamensis*	Colombia	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus surinamensis*	Brazil	Neotropic	
53	https://doi.org/10.1016/0041-0101(95)00122-0	1996	Viperidae	Crotalinae	*Calloselasma rhodostoma*	Thailand	Indomalayan	I, VI, V
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Vietnam	Indomalayan	
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Indonesia	Indomalayan	
54	https://doi.org/10.1007/s00239-018-9864-6	2018	Colubridae	Colubrinae	*Boiga cynodon*	Indonesia	Indomalayan	I, VII, V
			Colubridae	Colubrinae	*Boiga dendrophila*	Indonesia	Indomalayan	
			Colubridae	Colubrinae	*Boiga irregularis*	Indonesia	Indomalayan	
			Colubridae	Colubrinae	*Boiga irregularis*	Australia	Australasia	
			Colubridae	Colubrinae	*Boiga nigriceps*	Indonesia	Indomalayan	
			Colubridae	Colubrinae	*Boiga trigonata*	Pakistan	Indomalayan	
			Colubridae	Colubrinae	*Toxicodryas vexator*	Tanzania	Afrotropic	
55	https://doi.org/10.3390/toxins13020124	2021	Elapidae	Old World and American elapids	*Calliophis bivirgatus*	Malaysia	Indomalayan	I
56	https://doi.org/10.1016/j.toxicon.2021.01.006	2021	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, III, VI
57	https://doi.org/10.1016/j.jprot.2018.02.020	2019	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, III
58	https://doi.org/10.1016/j.cbpc.2019.108625	2020	Colubridae	Colubrinae	*Dispholidus typus*	South Africa	Afrotropic	I, VII
			Colubridae	Colubrinae	*Thelotornis mossambicanus*	Mozambique	Afrotropic	
59	https://doi.org/10.3390/toxins9050171	2017	Colubridae	Colubrinae	*Dispholidus typus*	South Africa	Afrotropic	I, VII, III, II
			Colubridae	Colubrinae	*Thelotornis mossambicanus*	Mozambique	Afrotropic	
60	https://doi.org/10.1016/j.jprot.2019.103463	2019	Elapidae	Old World and American elapids	*Naja kaouthia*	India	Indomalayan	I, II, III
61	https://doi.org/10.1016/0041-0101(68)90092-5	1968	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, III
62	https://doi.org/10.1016/j.bbrep.2021.101164	2021	Viperidae	Viperinae	*Bitis arietans*	Nigeria	Afrotropic	I
			Viperidae	Viperinae	*Echis ocellatus*	Nigeria	Afrotropic	
63	https://doi.org/10.1016/j.toxicon.2005.06.008	2005	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, VI, III
64	https://doi.org/10.1021/acs.jproteome.7b00414	2017	Viperidae	Crotalinae	*Crotalus mictlantecuhtli*	Mexico	Neotropic	I, VI
			Viperidae	Crotalinae	*Crotalus tzabcan*	Mexico	Neotropic	
			Viperidae	Crotalinae	*Crotalus culminatus*	Mexico	Neotropic	
65	https://doi.org/10.1016/j.toxicon.2018.08.016	2018	Elapidae	Australo-Papuan and marine elapids	*Hydrophis platurus*	Costa Rica	Neotropic	I, VI
66	https://doi.org/10.1016/j.jprot.2016.12.018	2017	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, III
67	https://doi.org/10.1016/j.jprot.2012.02.021	2012	Viperidae	Viperinae	*Cerastes cerastes*	Morocco	Palearctic	I, VII, V, II
			Viperidae	Viperinae	*Cerastes cerastes*	Tunisia	Palearctic	
			Viperidae	Viperinae	*Cerastes cerastes*	Egypt	Palearctic	
			Viperidae	Viperinae	*Cerastes vipera*	Tunisia	Palearctic	
68	https://doi.org/10.1016/j.jprot.2009.12.006	2010	Viperidae	Viperinae	*Bitis arietans*	UNKNOWN	UNKNOWN	I
69	https://doi.org/10.1016/0041-0101(83)90137-X	1983	Colubridae	Natricinae	*Rhabdophis subminiatus*	UNKNOWN	Indomalayan	I, III
70	https://doi.org/10.1016/j.toxicon.2015.08.016	2015	Elapidae	Old World and American elapids	*Micrurus alleni*	Costa Rica	Neotropic	I, VII, III, II
			Elapidae	Old World and American elapids	*Micrurus mosquitensis*	Costa Rica	Neotropic	
71	https://doi.org/10.1371/journal.pone.0001194	2007	Viperidae	Viperinae	*Vipera ammodytes*	Bulgaria	Palearctic	I, V
			Viperidae	Viperinae	*Vipera aspis*	France	Palearctic	
			Viperidae	Viperinae	*Vipera aspis*	Italy	Palearctic	
			Viperidae	Viperinae	*Vipera latastei*	Spain	Palearctic	
			Viperidae	Viperinae	*Vipera ursinii*	France	Palearctic	
72	https://doi.org/10.2307/1565397	1997	Viperidae	Crotalinae	*Crotalus lepidus*	USA	Nearctic	I, V, III
73	https://doi.org/10.1016/S0742-8413(00)00129-8	2000	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, V, III
74	https://doi.org/10.3390/toxins12120791	2020	Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	I, III, VII
75	https://doi.org/10.1016/j.toxicon.2004.08.008	2004	Viperidae	Crotalinae	*Crotalus helleri*	USA	Nearctic	I, VII, V, III
			Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	
76	https://doi.org/10.1006/taap.2001.9233	2001	Elapidae	Australo-Papuan and marine elapids	*Acanthophis antarticus*	Australia	Australasia	I, VII, V, III, II
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis hawkei*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis laevis*	Indonesia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis praelongus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis pyrrhus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis rugosus*	Indonesia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis wellsi*	Australia	Australasia	
77	https://doi.org/10.1002/rcm.613	2002	Elapidae	Australo-Papuan and marine elapids	*Acanthophis antarticus*	Australia	Australasia	I, VII, V
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis hawkei*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis hawkei*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis laevis*	Indonesia	Australasia	

			Elapidae	Australo-Papuan and marine elapids	*Acanthophis praelongus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis pyrrhus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis rugosus*	Indonesia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis rugosus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis wellsi*	Australia	Australasia	
78	https://doi.org/10.1002/rcm.1148	2003	Colubridae	Ahaetuliinae	*Ahaetulla prasina*	Singapore	Indomalayan	I, VII
			Colubridae	Colubrinae	*Boiga cynodon*	Singapore	Indomalayan	
			Colubridae	Colubrinae	*Boiga dendrophila*	Bali	Indomalayan	
			Colubridae	Colubrinae	*Boiga dendrophila*	Sulawesi	Australasia	
			Colubridae	Colubrinae	*Boiga drapiezii*	Bali	Indomalayan	
			Colubridae	Colubrinae	*Boiga irregularis*	Papua New Guinea	Australasia	
			Colubridae	Colubrinae	*Boiga nigriceps*	Java	Indomalayan	
			Colubridae	Colubrinae	*Boiga trigonata*	Pakistan	Indomalayan	
			Colubridae	Colubrinae	*Coelognathus radiatus*	Java	Indomalayan	
			Colubridae	Colubrinae	*Dispholidus typus*	Uganda	Afrotropic	
			Colubridae	Colubrinae	*Gonyosoma oxycephalum*	Singapore	Indomalayan	
			Colubridae	Colubrinae	*Platyceps rhodorachis*	Egypt	Palearctic	
			Colubridae	Colubrinae	*Ptyas carinata*	Singapore	Indomalayan	
			Colubridae	Colubrinae	*Telescopus dhara*	Egypt	Palearctic	
			Colubridae	Colubrinae	*Trimorphodon lambda*	USA	Nearctic	
			Colubridae	Natricinae	*Rhabdophis tigrinus*	China	Indomalayan	
			Colubridae	Dipsadinae	*Heterodon nasicus*	USA	Nearctic	
			Colubridae	Dipsadinae	*Philodryas patagoniensis*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Aspidelaps lubricus*	UNKNOWN	Afrotropic	
			Elapidae	Old World and American elapids	*Dendroaspis polylepis*	Tanzania	Afrotropic	
			Elapidae	Australo-Papuan and marine elapids	*Aipysurus duboisii*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Aipysurus foliosquama*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Aipysurus fuscus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Cryptophis nigrescens*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Demansia papuensis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Echiopsis curta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Furina tristis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hydrophis schistosus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hydrophis platurus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Micropechis ikaheca*	Papua New Guinea	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta suta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Laticauda schistorhyncha*	Niue	Australasia	
			Homalopsidae	NA	*Cerberus rynchops*	Singapore	Indomalayan	
			Homalopsidae	NA	*Myrrophis chinensis*	China	Indomalayan	
			Atractaspididae	NA	*Atractaspis fallax*	Kenya	Afrotropic	
			Psammophiidae	NA	*Psammophis mossambicus*	Tanzania	Afrotropic	
			Pseudoxyrhophiidae	NA	*Leioheterodon madagascariensis*	Madagascar	Afrotropic	
			Viperidae	Azemiopinae	*Azemiops feae*	China	Indomalayan	
			Viperidae	Crotalinae	*Tropidolaemus subannulatus*	Sulawesi	Australasia	
			Viperidae	Viperinae	*Causus rhombeatus*	Tanzania	Afrotropic	
			Viperidae	Viperinae	*Proatheris superciliaris*	Tanzania	Afrotropic	
79	https://doi.org/10.1016/j.toxicon.2006.06.005	2006	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, VI, III
80	https://doi.org/10.1016/j.jprot.2014.01.019	2014	Viperidae	Crotalinae	*Gloydius brevicaudus*	China	Palearctic	I, VI, III, II
81	https://doi.org/10.1016/j.toxicon.2020.06.023	2021	Viperidae	Crotalinae	*Metlapilcoatlus nummifer*	Mexico	Neotropic	I, II, III, VII
82	https://doi.org/10.1016/0041-0101(89)90096-2	1989	Viperidae	Crotalinae	*Atropoides picadoi*	Costa Rica	Neotropic	VII, III, II
			Viperidae	Crotalinae	*Bothriechis lateralis*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Bothriechis schlegelii*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Bothrops asper*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Cerrophidion sasai*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Crotalus simus*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Lachesis stenophrys*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Metlapilcoatlus mexicanus*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Porthidium nasutum*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Porthidium ophryomegas*	Costa Rica	Neotropic	
83	https://doi.org/10.1021/acs.jproteome.0c00687	2021	Viperidae	Viperinae	*Echis carinatus*	Iran	Palearctic	I, III, V

84	https://doi.org/10.1007/s00239-011-9437-4	2011	Viperidae	Crotalinae	*Sistrurus catenatus*	USA	Nearctic	I, V
			Viperidae	Crotalinae	*Sistrurus catenatus*	Canada	Nearctic	
85	https://doi.org/10.1016/j.toxicon.2009.01.034	2009	Viperidae	Crotalinae	*Sistrurus catenatus*	USA	Nearctic	I, VII, III, VIII
			Viperidae	Crotalinae	*Sistrurus tergeminus*	USA	Nearctic	
			Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	
86	https://doi.org/10.1007/s00239-008-9186-1	2009	Viperidae	Crotalinae	*Sistrurus catenatus*	USA	Nearctic	I, VII
			Viperidae	Crotalinae	*Sistrurus catenatus*	Canada	Nearctic	
			Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	
87	https://doi.org/10.1016/j.jprot.2011.06.013	2011	Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	I, VI, VIII
88	https://doi.org/10.1371/journal.pone.0067220	2013	Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	I, V, VIII
89	https://doi.org/10.1016/j.jprot.2020.103707	2020	Viperidae	Viperinae	*Vipera aspis*	France	Palearctic	I, VII
90	https://doi.org/10.1016/0041-0101(83)90055-7	1983	Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	I, V, III
			Viperidae	Crotalinae	*Crotalus scutulatus*	Mexico	Neotropic	
91	https://doi.org/10.1016/j.toxicon.2021.09.006	2021	Viperidae	Crotalinae	*Crotalus simus*	Costa Rica	Neotropic	I, II, III, V
92	https://doi.org/10.1016/j.jprot.2015.04.029	2016	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, VI, V, III, II
93	https://doi.org/10.1016/j.toxicon.2019.09.011	2019	Viperidae	Crotalinae	*Crotalus pricei*	USA	Nearctic	I, III, V, VIII
94	https://doi.org/10.1016/j.cbd.2019.01.012	2019	Viperidae	Crotalinae	*Bothrops brazili*	Brazil	Neotropic	I, VII
			Viperidae	Crotalinae	*Bothrops cotiara*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops insularis*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops leucurus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops moojeni*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops neuwiedi*	Brazil	Neotropic	
95	https://doi.org/10.1016/0041-0101(74)90241-4	1974	Viperidae	Viperinae	*Vipera ammodytes*	Slovenia	Palearctic	I, VI, III
96	https://doi.org/10.1186/1477-5956-4-11	2006	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, VI
97	https://doi.org/10.1016/j.toxicon.2010.08.011	1980	Viperidae	Crotalinae	*Bothrops asper*	Costa Rica	Neotropic	I, VI, V, III, II
98	https://doi.org/10.1016/0041-0101(90)90080-Q	1990	Viperidae	Crotalinae	*Lachesis stenophrys*	Costa Rica	Neotropic	I, VI, III, II
99	https://doi.org/10.1021/pr8003826	2008	Viperidae	Crotalinae	*Bothrops caribbaeus*	Saint Lucia	Neotropic	I, VII, III, II
			Viperidae	Crotalinae	*Bothrops lanceolatus*	Martinique	Neotropic	
100	https://doi.org/10.1016/S0041-0101(02)00360-4	2003	Viperidae	Crotalinae	*Bothrops asper*	Belize	Neotropic	I, VII, V, II
			Viperidae	Crotalinae	*Bothrops asper*	Ecuador	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Suriname	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Ecuador	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Venezuela	Neotropic	
101	https://doi.org/10.1007/BF02023786	1980	Viperidae	Viperinae	*Cerastes cerastes*	Egypt	Palearctic	I, VI, V, III, II
			Viperidae	Viperinae	*Cerastes vipera*	Egypt	Palearctic	
102	https://doi.org/10.1590/1678-9199-JVATITD-2020-0018	2020	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, II, III, VI
103	https://doi.org/10.3390/toxins10010023	2018	Viperidae	Viperinae	*Vipera transcaucasiana*	Turkey	Palearctic	I, V, III
104	https://doi.org/10.1021/acs.jproteome.9b00869	2020	Viperidae	Viperinae	*Vipera anatolica*	Turkey	Palearctic	I, VII
105	https://doi.org/10.1016/j.jprot.2012.01.006	2012	Elapidae	Australo-Papuan and marine elapids	*Oxyuranus scutellatus*	Papua New Guinea	Australasia	I, V, III, II
106	https://doi.org/10.1016/S0041-0101(00)00091-X	2000	Colubridae	Natricinae	*Amphiesma stolatum*	UNKNOWN	Indomalayan	I, VII, III, IV
			Colubridae	Colubrinae	*Boiga cyanea*	UNKNOWN	Indomalayan	
			Colubridae	Colubrinae	*Boiga dendrophila*	UNKNOWN	Indomalayan	
			Colubridae	Colubrinae	*Boiga irregularis*	UNKNOWN	UNKNOWN	
			Colubridae	Dipsadinae	*Diadophis punctatus*	USA	Nearctic	
			Colubridae	Dipsadinae	*Heterodon kennerlyi*	USA	Nearctic	
			Colubridae	Dipsadinae	*Heterodon nasicus*	USA	Nearctic	
			Colubridae	Dipsadinae	*Hydrodynastes gigas*	UNKNOWN	Neotropic	
			Colubridae	Dipsadinae	*Hypsiglena jani*	USA	Neotropic	
			Colubridae	Colubrinae	*Salvadora grahamiae*	USA	Nearctic	
			Colubridae	Colubrinae	*Tantilla nigriceps*	USA	Nearctic	
			Colubridae	Natricinae	*Thamnophis elegans*	UNKNOWN	Neartic	
			Colubridae	Colubrinae	*Trimorphodon lambda*	UNKNOWN	Neartic	
107	https://doi.org/10.1016/j.jprot.2015.07.015	2015	Elapidae	Old World and American elapids	*Naja atra*	Taiwan	Indomalayan	I, V, III, II
108	https://doi.org/10.3390/molecules23030609	2018	Elapidae	Old World and American elapids	*Naja ashei*	Kenya	Afrotropic	I
109	https://doi.org/10.1080/00034983.1986.11812026	1986	Colubridae	Natricinae	*Rhabdophis subminiatus*	Hong Kong	Indomalayan	III, II
			Colubridae	Natricinae	*Rhabdophis subminiatus*	UNKNOWN	Indomalayan	
110	https://doi.org/10.3390/toxins5122621	2013	Elapidae	Australo-Papuan and marine elapids	*Acanthophis wellsi*	Australia	Australasia	I, VII

			Elapidae	Australo-Papuan and marine elapids	*Brachyurophis roperi*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Cacophis squamulosus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Denisonia devisi*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Echiopsis curta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Furina ornata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hemiaspis signata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus bungaroides*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja modesta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta fasciata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Vermicella annulata*	Australia	Australasia	
111	https://doi.org/10.3390/toxins8110309	2016	Elapidae	Australo-Papuan and marine elapids	*Acanthophis antarticus*	Australia	Australasia	I, VII, VI, III
			Elapidae	Australo-Papuan and marine elapids	*Antaioserpens warro*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Aspidomorphus muelleri*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Cacophis squamulosus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Cryptophis boschmai*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Cryptophis nigrescens*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Demansia papuensis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Demansia psammophis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Demansia rimicola*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Denisonia devisi*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Furina ornata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hemiaspis damelii*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hemiaspis signata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus bitorquatus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus bungaroides*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus stephensii*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Loveridgelaps elapoides*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Oxyuranus microlepidotus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Oxyuranus scutellatus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja affinis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Pseudonaja textilis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Simoselaps bertholdi*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta dwyeri*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta fasciata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta punctata*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta spectabilis*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Suta suta*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Vermicella annulata*	Australia	Australasia	
112	https://doi.org/10.1016/S0014-5793(02)03205-2	2002	Viperidae	Viperinae	*Vipera aspis*	France	Palearctic	I, V
113	https://doi.org/10.1016/0041-0101(88)90216-4	1988	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, V, III
114	https://doi.org/10.1186/1471-2164-12-1	2011	Elapidae	Old World and American elapids	*Bungarus multicinctus*	China	Indomalayan	I, VII
			Elapidae	Old World and American elapids	*Naja atra*	China	Indomalayan	
115	https://doi.org/10.1016/j.jprot.2014.11.016	2015	Viperidae	Crotalinae	*Porthidium lansbergii*	Colombia	Neotropic	I, V, III
116	https://doi.org/10.1016/0041-0101(64)90021-2	1964	Viperidae	Crotalinae	*Metlapilcoatlus mexicanus*	Costa Rica	Neotropic	I, VI, V
117	https://doi.org/10.1016/0041-0101(64)90017-0	1964	Viperidae	Crotalinae	*Bothrops asper*	Costa Rica	Neotropic	I, V, III
118	https://doi.org/10.1021/acs.jproteome.9b00077	2019	Viperidae	Crotalinae	*Protobothrops flavoviridis*	Japan	Indomalayan	I, II, III, VII
			Viperidae	Crotalinae	*Trimeresurus borneensis*	Borneo	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus gramineus*	India	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus insularis*	Indonesia	Australasia	
			Viperidae	Crotalinae	*Trimeresurus puniceus*	Java	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus purpureomaculatus*	Thailand	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus stejnegeri*	Taiwan	Indomalayan	
119	https://doi.org/10.1016/j.jprot.2014.11.011	2015	Viperidae	Crotalinae	*Bothrops erythromelas*	Brazil	Neotropic	I, V, II
120	https://doi.org/10.1007/s00239-005-0268-z	2006	Viperidae	Viperinae	*Bitis arietans*	Ghana	Afrotropic	I
121	https://doi.org/10.1534/genetics.106.056515	2006	Viperidae	Crotalinae	*Lachesis muta*	Brazil	Neotropic	I, VII
122	https://doi.org/10.1093/molbev/msu337	2015	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I
123	https://doi.org/10.1021/acs.jproteome.8b00291	2018	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, V, III, II
124	https://doi.org/10.1016/S0041-0101(00)00089-1	2000	Colubridae	Colubrinae	*Dispholidus typus*	South Africa	Afrotropic	I, VII
125	https://doi.org/10.3390/toxins12080520	2020	Elapidae	Old World and American elapids	*Naja mossambica*	Namibia	Afrotropic	I, VII
			Elapidae	Old World and American elapids	*Naja nigricincta*	Namibia	Afrotropic	

126	https://doi.org/10.1016/0041-0101(82)90052-6	1982	Atractaspididae	NA	*Atractaspis engaddensis*	Israel	Palearctic	I, VII, III
			Atractaspididae	NA	*Atractaspis bibronii*	South Africa	Afrotropic	
			Atractaspididae	NA	*Atractaspis microlepidota*	UNKNOWN	Afrotropic	
127	https://doi.org/10.1016/j.jprot.2012.01.020	2012	Viperidae	Crotalinae	*Bothrops atrox*	Peru	Neotropic	I, VII, V, III, II
			Viperidae	Crotalinae	*Bothrops barnetti*	Peru	Neotropic	
			Viperidae	Crotalinae	*Bothrops pictus*	Peru	Neotropic	
128	https://doi.org/10.1016/j.toxicon.2007.01.019	2007	Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	I, II
129	https://doi.org/10.3390/toxins12010054	2020	Viperidae	Crotalinae	*Trimeresurus hageni*	Thailand	Indomalayan	I, III, VII
			Viperidae	Crotalinae	*Trimeresurus macrops*	Thailand	Indomalayan	
130	https://doi.org/10.3390/toxins10110434	2018	Elapidae	Old World and American elapids	*Ophiophagus hannah*	Malaysia	Indomalayan	I, VII
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Malaysia	Indomalayan	
131	https://doi.org/10.1016/j.toxicon.2010.01.015	2010	Viperidae	Crotalinae	*Bothrops alternatus*	Argentina	Neotropic	I, V, III
132	https://doi.org/10.1016/j.jprot.2015.02.002	2015	Elapidae	Old World and American elapids	*Dendroaspis polylepis*	Kenya	Afrotropic	I, III, II
133	https://doi.org/10.1016/j.cbd.2021.100875	2021	Viperidae	Crotalinae	*Trimeresurus puniceus*	Indonesia	Indomalayan	I, II, VII
			Viperidae	Crotalinae	*Trimeresurus wiroti*	Malaysia	Indomalayan	
134	https://doi.org/10.1021/acs.jproteome.9b00120	2019	Viperidae	Viperinae	*Vipera ammodytes*	Croatia	Palearctic	I
135	https://doi.org/10.1007/s00239-004-0138-0	2005	Elapidae	Australo-Papuan and marine elapids	*Aipysurus mosaicus*	Australia	Australasia	I, VII, III
136	https://doi.org/10.1016/j.jprot.2019.01.007	2019	Elapidae	Old World and American elapids	*Micrurus ruatanus*	Honduras	Neotropic	I, III, II
137	https://doi.org/10.1016/j.jprot.2020.104084	2021	Viperidae	Crotalinae	*Protobothrops mucrosquamatus*	Taiwan	Indomalayan	I, II, III
138	https://doi.org/10.1016/j.jprot.2011.12.016	2012	Viperidae	Crotalinae	*Cerrophidion sasai*	Costa Rica	Neotropic	I, VII, III
			Viperidae	Crotalinae	*Porthidium nasutum*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Porthidium ophryomegas*	Costa Rica	Neotropic	
139	https://doi.org/10.1016/j.jprot.2013.10.036	2014	Viperidae	Crotalinae	*Agkistrodon bilineatus*	Mexico	Neotropic	I, VII, III
			Viperidae	Crotalinae	*Agkistrodon conanti*	USA	Nearctic	
			Viperidae	Crotalinae	*Agkistrodon contortrix*	USA	Nearctic	
			Viperidae	Crotalinae	*Agkistrodon howardgloydi*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Agkistrodon laticinctus*	USA	Nearctic	
			Viperidae	Crotalinae	*Agkistrodon piscivorus*	USA	Nearctic	
			Viperidae	Crotalinae	*Agkistrodon taylori*	Mexico	Neotropic	
140	https://doi.org/10.3390/toxins8050138	2016	Elapidae	Old World and American elapids	*Micrurus clarki*	Costa Rica	Neotropic	I, III, II
141	https://doi.org/10.1016/j.toxicon.2004.03.012	2004	Colubridae	Ahaetuliinae	*Ahaetulla prasina*	Singapore	Indomalayan	VII, III
			Colubridae	Colubrinae	*Boiga cynodon*	Singapore	Indomalayan	
			Colubridae	Colubrinae	*Boiga dendrophila*	Bali	Indomalayan	
			Colubridae	Colubrinae	*Boiga dendrophila*	Sulawesi	Indomalayan	
			Colubridae	Colubrinae	*Boiga drapiezii*	Bali	Indomalayan	
			Colubridae	Colubrinae	*Boiga irregularis*	West Papua	Australasia	
			Colubridae	Colubrinae	*Boiga nigriceps*	Indonesia	Indomalayan	
			Pseudoxyrhophiidae	NA	*Leioheterodon madagascariensis*	Madagascar	Afrotropic	
			Homalopsidae	NA	*Myrrophis chinensis*	China	Indomalayan	
			Psammophiidae	NA	*Psammophis mossambicus*	Tanzania	Afrotropic	
			Colubridae	Natricinae	*Rhabdophis tigrinus*	China	Indomalayan	
			Colubridae	Colubrinae	*Telescopus dhara*	Egypt	Palearctic	
			Colubridae	Colubrinae	*Trimorphodon lambda*	USA	Nearctic	
142	https://doi.org/10.2307/1445927	1988	Viperidae	Crotalinae	*Crotalus helleri*	USA	Nearctic	VII, VI, III
143	https://doi.org/10.1016/j.toxicon.2010.02.028	2010	Viperidae	Crotalinae	*Crotalus cerberus*	USA	Nearctic	I, VII, V, III
			Viperidae	Crotalinae	*Crotalus concolor*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus helleri*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus lutosus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	
144	https://doi.org/10.1016/j.jprot.2020.103778	2020	Colubridae	Colubrinae	*Trimorphodon quadruplex*	Costa Rica	Neotropic	I, III
145	https://doi.org/10.1016/j.toxicon.2006.01.007	2006	Colubridae	Colubrinae	*Boiga irregularis*	Guam	Oceania	I, VI, III, VIII
			Colubridae	Colubrinae	*Boiga irregularis*	Indonesia	Australasia	
146	https://doi.org/10.1016/j.jprot.2012.09.003	2012	Viperidae	Crotalinae	*Lachesis acrochorda*	Colombia	Neotropic	I, VII, VI, V
			Viperidae	Crotalinae	*Lachesis melanocephala*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Lachesis muta*	Bolivia	Neotropic	
			Viperidae	Crotalinae	*Lachesis stenophrys*	Costa Rica	Neotropic	
147	https://doi.org/10.1016/j.jprot.2012.02.022	2012	Viperidae	Viperinae	*Daboia mauritanica*	Morocco	Palearctic	I, VII, V, II
148	https://doi.org/10.1016/j.toxicon.2017.06.004	2017	Viperidae	Viperinae	*Vipera berus*	Hungary	Palearctic	I, VI, V, III
			Viperidae	Viperinae	*Vipera berus*	Austria	Palearctic	
			Viperidae	Viperinae	*Vipera nikolskii*	Ukraine	Palearctic	

149	https://doi.org/10.3390/toxins12110669	2020	Elapidae	Old World and American elapids	*Naja naja*	Pakistan	Indomalayan	I, VII
			Elapidae	Old World and American elapids	*Naja oxiana*	Pakistan	Indomalayan	
150	https://doi.org/10.1016/j.jprot.2013.11.001	2014	Viperidae	Crotalinae	*Crotalus adamanteus*	USA	Nearctic	I
151	https://doi.org/10.1534/genetics.114.172437	2015	Elapidae	Old World and American elapids	*Micrurus fulvius*	USA	Nearctic	I, VII, V
			Viperidae	Crotalinae	*Crotalus adamanteus*	USA	Nearctic	
152	https://doi.org/10.1016/0041-0101(74)90196-2	1974	Viperidae	Viperinae	*Bitis nasicornis*	UNKNOWN	Afrotropic	I, VI, III
153	https://doi.org/10.1111/j.1365-2141.1974.tb00474.x	1974	Viperidae	Viperinae	*Bitis gabonica*	Uganda	Afrotropic	I, III
154	https://doi.org/10.1016/j.toxicon.2013.05.006	2013	Viperidae	Crotalinae	*Crotalus lepidus*	Mexico	Nearctic	I, V, III
			Viperidae	Crotalinae	*Crotalus morulus*	Mexico	Nearctic	
155	https://doi.org/10.1016/j.jprot.2012.02.035	2012	Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	I, V, III, IV
156	https://doi.org/10.1186/1471-2164-15-1061	2014	Colubridae	Colubrinae	*Boiga irregularis*	Indonesia	Indomalayan	I, VII
157	https://doi.org/10.1016/0041-0101(86)90164-9	1986	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, VI, III
158	https://doi.org/10.1016/j.actatropica.2019.02.030	2019	Viperidae	Crotalinae	*Porthidium porrasi*	Costa Rica	Nearctic	I, III, VII
159	https://doi.org/10.1016/j.toxicon.2005.11.007	2006	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, VI, III
160	https://doi.org/10.1016/0041-0101(86)90167-4	1986	Viperidae	Crotalinae	*Crotalus atrox*	USA	Nearctic	I, VII, II
161	https://doi.org/10.1016/j.toxicon.2009.10.018	2010	Elapidae	Old World and American elapids	*Naja naja*	UNKNOWN	Indomalayan	I, VI
162	https://doi.org/10.1016/j.toxicon.2016.04.049	2016	Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	I, VI, III
163	https://doi.org/10.1098/rspb.2018.1003	2018	Colubridae	Colubrinae	*Spilotes sulphureus*	Suriname	Neotropic	I, VII, VIII
164	https://doi.org/10.1016/j.jprot.2018.08.004	2018	Colubridae	Ahaetuliinae	*Ahaetulla prasina*	Indonesia	Indomalayan	I, VII, III
			Colubridae	Dipsadinae	*Borikenophis portoricensis*	British Virgin Islands	Neotropic	
			Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	
165	https://doi.org/10.1016/j.jprot.2013.11.005	2014	Viperidae	Crotalinae	*Bothrops asper*	Colombia	Neotropic	I, VII, III, II
166	https://doi.org/10.1016/j.jprot.2020.103945	2020	Viperidae	Crotalinae	*Bothrops asper*	Colombia	Neotropic	I, V, VI
			Viperidae	Crotalinae	*Bothrops asper*	Ecuador	Neotropic	
167	https://doi.org/10.1371/journal.pntd.0008299	2020	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, IV, V
168	https://doi.org/10.1016/S1095-6433(97)00475-3	1998	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, V, III, II
169	https://doi.org/10.1016/S1096-4959(01)00473-0	2002	Elapidae	Old World and American elapids	*Naja kaouthia*	India	Indomalayan	I, III, II
			Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	
170	https://doi.org/10.1016/S0041-0101(99)00125-7	2000	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, III, IV
171	https://doi.org/10.3390/toxins6030850	2014	Elapidae	Old World and American elapids	*Naja mossambica*	UNKNOWN	Afrotropic	I, VII
			Elapidae	Australo-Papuan and marine elapids	*Notechis scutatus*	Australia	Australasia	
172	https://doi.org/10.1016/0041-0101(92)90530-I	1992	Viperidae	Viperinae	*Vipera berus*	Russia	Palearctic	VI, III
173	https://doi.org/10.1016/j.toxicon.2009.01.006	2009	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I
174	https://doi.org/10.1016/j.jprot.2018.09.002	2019	Viperidae	Crotalinae	*Ophryacus smaragdinus*	Mexico	Neotropic	I, III, II
			Viperidae	Crotalinae	*Ophryacus sphenophrys*	Mexico	Neotropic	
			Viperidae	Crotalinae	*Ophryacus undulatus*	Mexico	Neotropic	
175	https://doi.org/10.1016/j.jprot.2009.07.013	2009	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, V, II
			Viperidae	Crotalinae	*Bothrops atrox*	Colombia	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Ecuador	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Peru	Neotropic	
176	https://doi.org/10.1016/j.jprot.2018.10.016	2019	Elapidae	Old World and American elapids	*Bungarus sindanus*	Pakistan	Indomalayan	I, III, II
177	https://doi.org/10.1016/S0041-0101(98)00089-0	1998	Viperidae	Crotalinae	*Lachesis muta*	Brazil	Neotropic	I, V, III
			Viperidae	Crotalinae	*Lachesis acrochorda*	Colombia	Neotropic	
			Viperidae	Crotalinae	*Lachesis stenophrys*	Costa Rica	Neotropic	
178	http://dx.doi.org/10.1590/S1678-91992012000400009	2012	Viperidae	Viperinae	*Bitis arietans*	Morocco	Palearctic	I, VII, III, II
			Viperidae	Viperinae	*Cerastes cerastes*	Morocco	Palearctic	
			Viperidae	Viperinae	*Daboia mauritanica*	Morocco	Palearctic	
			Elapidae	Old World and American elapids	*Naja haje*	Morocco	Palearctic	
179	https://doi.org/10.1016/j.cbpc.2019.02.013	2019	Viperidae	Viperinae	*Cerastes cerastes*	Egypt	Palearctic	I, III, VII
			Viperidae	Crotalinae	*Trimeresurus purpureomaculatus*	Thailand	Indomalayan	
180	https://doi.org/10.1186/1471-2199-8-115	2007	Viperidae	Crotalinae	*Sistrurus tergeminus*	USA	Nearctic	I
181	https://doi.org/10.1371/journal.pntd.0003419	2015	Viperidae	Viperinae	*Bitis arietans*	UNKNOWN	Afrotropic	I, VII, III, II
			Viperidae	Viperinae	*Bitis nasicornis*	UNKNOWN	Afrotropic	
			Viperidae	Viperinae	*Bitis rhinoceros*	UNKNOWN	Afrotropic	
182	https://doi.org/10.3389/fphar.2021.727756	2020	Elapidae	Old World and American elapids	*Naja samarensis*	Philippines	Indomalayan	I, II, III, VII
183	https://doi.org/10.1080/14789450.2019.1609945	2019	Elapidae	Old World and American elapids	*Bungarus caeruleus*	India	Indomalayan	I, II, III
184	https://doi.org/10.1021/acs.jproteome.0c00054	2020	Viperidae	Viperinae	*Echis carinatus*	Sri Lanka	Indomalayan	I, II, III
185	https://doi.org/10.1016/j.jprot.2020.103758	2020	Viperidae	Crotalinae	*Bothrocophias myersi*	Colombia	Neotropic	I, II, III, IV
			Viperidae	Crotalinae	*Bothrops asper*	Colombia	Neotropic	

186	https://doi.org/10.1002/elps.1150140171	1993	Elapidae	Old World and American elapids	*Dendroaspis polylepis*	UNKNOWN	Afrotropic	I
187	https://doi.org/10.1016/j.jprot.2019.02.004	2019	Viperidae	Viperinae	*Vipera kaznakovi*	Turkey	Palearctic	I, VI, V, III
188	https://doi.org/10.3390/toxins13050299	2021	Viperidae	Viperinae	*Bitis parviocula*	Ethiopia	Afrotropic	I, III
189	https://doi.org/10.1016/j.jprot.2016.09.007	2017	Elapidae	Australo-Papuan and marine elapids	*Pseudechis papuanus*	Papua New Guinea	Australasia	I, III, II
190	https://doi.org/10.1016/j.bbagen.2017.01.020	2017	Colubridae	Colubrinae	*Dispholidus typus*	South Africa	Afrotropic	I, II
191	https://doi.org/10.1016/j.jprot.2016.10.006	2017	Viperidae	Crotalinae	*Bothriechis aurifer*	Guatemala	Neotropic	I, VII, VI
			Viperidae	Crotalinae	*Bothriechis bicolor*	Guatemala	Neotropic	
			Viperidae	Crotalinae	*Bothriechis lateralis*	Guatemala	Neotropic	
			Viperidae	Crotalinae	*Bothriechis marchi*	Honduras	Neotropic	
			Viperidae	Crotalinae	*Bothriechis schlegelii*	Costa Rica	Neotropic	
			Viperidae	Crotalinae	*Bothriechis thalassinus*	Guatemala	Neotropic	
192	https://doi.org/10.1016/S0304-4165(99)00053-7	1999	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, V, III, II
193	https://doi.org/10.1016/j.toxicon.2008.10.002	2008	Viperidae	Crotalinae	*Bothrocophias hyoprora*	Brazil	Neotropic	I, VII, III, II
			Viperidae	Crotalinae	*Bothrops alternatus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops bilineatus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops brazili*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops cotiara*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops erythromelas*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops fonsecai*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops insularis*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops leucurus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops marajoensis*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops moojeni*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops neuwiedi*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops pirajai*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops taeniatus*	Brazil	Neotropic	
194	https://doi.org/10.1016/j.jprot.2021.104256	2021	Elapidae	Old World and American elapids	*Naja kaouthia*	India	Indomalayan	I, II, III, V
195	https://doi.org/10.1016/j.toxicon.2019.03.027	2019	Viperidae	Crotalinae	*Crotalus atrox*	USA	Nearctic	I, III, VI
196	https://doi.org/10.1111/jeb.13907	2021	Viperidae	Crotalinae	*Crotalus helleri*	USA	Nearctic	I, V, VI, VIII
			Viperidae	Crotalinae	*Crotalus ruber*	USA	Nearctic	
197	https://doi.org/10.1016/j.toxicon.2020.05.016	2020	Viperidae	Crotalinae	*Bothrops brazili*	Peru	Neotropic	I, II, III, VII
			Viperidae	Crotalinae	*Bothrops atrox*	Peru	Neotropic	
198	https://doi.org/10.1371/journal.pone.0227122	2019	Elapidae	Old World and American elapids	*Bungarus candidus*	Indonesia	Indomalayan	I, II, III, V
			Elapidae	Old World and American elapids	*Bungarus candidus*	Malaysia	Indomalayan	
			Elapidae	Old World and American elapids	*Bungarus candidus*	Thailand	Indomalayan	
199	https://doi.org/10.1016/j.jprot.2011.09.003	2011	Elapidae	Old World and American elapids	*Micrurus mipartitus*	Colombia	Neotropic	I, VII, V, III, II
			Elapidae	Old World and American elapids	*Micrurus mipartitus*	Costa Rica	Neotropic	
200	https://doi.org/10.1016/j.jprot.2009.01.006	2009	Viperidae	Viperinae	*Daboia siamensis*	Myanmar	Indomalayan	I, III
201	https://doi.org/10.1080/15287394.2012.697839	2012	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, VI, III
202	https://doi.org/10.1016/j.thromres.2006.07.004	2007	Viperidae	Crotalinae	*Bothrops atrox*	Venezuela	Neotropic	I, V, III
203	https://doi.org/10.1016/S0041-0101(03)00171-5	2003	Viperidae	Crotalinae	*Bothrops asper*	Colombia	Neotropic	I, VII, VI, III, II
			Viperidae	Crotalinae	*Bothrops atrox*	Colombia	Neotropic	
204	https://doi.org/10.22092/ari.2020.128766.1428	2021	Elapidae	Old World and American elapids	*Naja oxiana*	Iran	Palearctic	I, III
205	https://doi.org/10.1016/j.jprot.2021.104196	2021	Elapidae	Old World and American elapids	*Hemachatus haemachatus*	South Africa	Afrotropic	I, II, III, VII
			Elapidae	Old World and American elapids	*Naja annulifera*	Mozambique	Afrotropic	
			Elapidae	Old World and American elapids	*Naja mossambica*	South Africa	Afrotropic	
			Elapidae	Old World and American elapids	*Naja nigricollis*	UNKNOWN	Afrotropic	
206	https://doi.org/10.1016/0041-0101(92)90505-Y	1992	Viperidae	Crotalinae	*Bothrops alternatus*	Brazil	Neotropic	VII, III
			Viperidae	Crotalinae	*Bothrops alternatus*	Argentina	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops atrox*	Peru	Neotropic	
			Viperidae	Crotalinae	*Bothrops diporus*	Argentina	Neotropic	
			Viperidae	Crotalinae	*Bothrops erythromelas*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops leucurus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops matogrossensis*	Bolivia	Neotropic	

			Viperidae	Crotalinae	*Bothrops moojeni*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops neuwiedi*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops taeniatus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Crotalus durissus*	Bolivia	Neotropic	
			Viperidae	Crotalinae	*Crotalus durissus*	Argentina	Neotropic	
			Viperidae	Crotalinae	*Lachesis muta*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Lachesis muta*	Peru	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus frontalis*	Brazil	Neotropic	
207	https://doi.org/10.1016/j.jprot.2018.04.007	2018	Elapidae	Old World and American elapids	*Hemachatus haemachatus*	South Africa	Afrotropic	I, III
208	https://doi.org/10.1016/j.toxicon.2018.04.027	2018	Colubridae	Colubrinae	*Leptophis ahaetulla*	Argentina	Neotropic	I, III, II
209	https://doi.org/10.1021/pr0602500	2006	Viperidae	Crotalinae	*Sistrurus catenatus*	USA	Nearctic	I, VII
			Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	
			Viperidae	Crotalinae	*Sistrurus tergeminus*	USA	Nearctic	
210	https://doi.org/10.1016/j.jprot.2008.05.003	2008	Viperidae	Viperinae	*Macrovipera lebetina*	Armenia	Palearctic	I, VII, V
			Viperidae	Viperinae	*Montivipera raddei*	Armenia	Palearctic	
211	https://doi.org/10.1016/j.jprot.2007.10.004	2008	Viperidae	Crotalinae	*Lachesis muta*	Bolivia	Neotropic	I, VII, V
			Viperidae	Crotalinae	*Lachesis muta*	Peru	Neotropic	
			Viperidae	Crotalinae	*Lachesis muta*	UNKNOWN	Neotropic	
			Viperidae	Crotalinae	*Lachesis stenophrys*	Costa Rica	Neotropic	
212	https://doi.org/10.3390/tropicalmed3020066	2018	Viperidae	Viperinae	*Daboia siamensis*	Taiwan	Indomalayan	I, III, II
213	https://revistas.ucr.ac.cr/index.php/rbt/article/view/16293/15773	2002	Viperidae	Crotalinae	*Crotalus durissus*	Venezuela	Neotropic	I, V, III, II
			Viperidae	Crotalinae	*Crotalus simus*	Guatemala	Neotropic	
			Viperidae	Crotalinae	*Crotalus simus*	Costa Rica	Neotropic	
214	https://doi.org/10.1016/j.jprot.2015.03.015	2015	Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	I, VI, III, II
215	https://doi.org/10.1016/S0041-0101(09)80007-X	1990	Elapidae	Old World and American elapids	*Dendroaspis polylepis*	UNKNOWN	Afrotropic	I, III
216	https://doi.org/10.1371/journal.pntd.0007899	2019	Elapidae	Old World and American elapids	*Bungarus caeruleus*	India	Indomalayan	I, II, III, V, VII
			Elapidae	Old World and American elapids	*Bungarus fasciatus*	India	Indomalayan	
			Elapidae	Old World and American elapids	*Bungarus sindanus*	India	Indomalayan	
			Elapidae	Old World and American elapids	*Naja kaouthia*	India	Indomalayan	
			Elapidae	Old World and American elapids	*Naja kaouthia*	West Bengal	Indomalayan	
			Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	
			Viperidae	Viperinae	*Echis carinatus*	India	Indomalayan	
217	https://doi.org/10.1371/journal.pntd.0009150	2021	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, II, III, V
218	https://doi.org/10.1371/journal.pntd.0009247	2021	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, II, III, V
219	https://doi.org/10.1016/j.jprot.2016.02.028	2016	Elapidae	Old World and American elapids	*Bungarus multicinctus*	China	Indomalayan	I, VII, III, II
			Elapidae	Old World and American elapids	*Naja atra*	China	Palearctic	
220	https://doi.org/10.3109/15569543.2013.855789	2014	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, V, III, II
221	https://doi.org/10.1016/j.toxicon.2015.06.027	2015	Viperidae	Viperinae	*Daboia russelii*	India	Indomalayan	I, V, III
222	https://doi.org/10.1016/j.intimp.2006.08.014	2007	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	V, III, II
223	https://doi.org/10.1023/A:1017972511272	2002	Elapidae	Old World and American elapids	*Naja naja*	India	Indomalayan	I, V, III, II
224	https://doi.org/10.1111/j.1432-1033.1973.tb03202.x	1973	Elapidae	Old World and American elapids	*Dendroaspis viridis*	Guinea	Afrotropic	I, III
225	https://doi.org/10.1186/1471-2199-11-24	2010	Elapidae	Old World and American elapids	*Bungarus flaviceps*	Malaysia	Indomalayan	I
226	https://doi.org/10.1371/journal.pntd.0007017	2019	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, III, II
			Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	
			Elapidae	Old World and American elapids	*Naja annulifera*	South Africa	Afrotropic	
227	https://doi.org/10.1371/journal.pone.0260496	2021	Viperidae	Crotalinae	*Ovophis monticola*	Thailand	Indomalayan	I, II
228	https://doi.org/10.1016/j.toxicon.2016.08.001	2019	Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	I, VII, VI, III
229	https://doi.org/10.3390/toxins13110814	2021	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, III, V, VIII
230	https://doi.org/10.1371/journal.pntd.0002442	2013	Viperidae	Crotalinae	*Bothrops alternatus*	Brazil	Neotropic	I, VII, II
			Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops cotiara*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops diporus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops jararacussu*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops marmoratus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops matogrossensis*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops neuwiedi*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Bothrops pauloensis*	Brazil	Neotropic	
231	https://doi.org/10.1016/j.jprot.2017.03.003	2017	Viperidae	Crotalinae	*Bothrops atrox*	Brazil	Neotropic	I, V, III, II

232	https://doi.org/10.1016/j.jprot.2014.01.013	2014	Viperidae	Crotalinae	*Crotalus helleri*	USA	Nearctic	I, V
233	https://doi.org/10.3390/toxins13090613	2021	Viperidae	Crotalinae	*Agkistrodon piscivorus*	USA	Nearctic	I, III, VII
			Viperidae	Crotalinae	*Crotalus adamanteus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus atrox*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus horridus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	
234	https://doi.org/10.3390/toxins13020127	2021	Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	Malaysia	Indomalayan	I
235	https://doi.org/10.3390/toxins13080514	2021	Viperidae	Crotalinae	*Ovophis convictus*	Malaysia	Indomalayan	I, II, III, V, VII
			Viperidae	Crotalinae	*Ovophis okinavensis*	Japan	Indomalayan	
			Viperidae	Crotalinae	*Ovophis tonkinensis*	China	Indomalayan	
			Viperidae	Crotalinae	*Ovophis tonkinensis*	Vietnam	Indomalayan	
236	https://doi.org/10.1016/0742-8413(91)90233-J	1991	Viperidae	Crotalinae	*Crotalus adamanteus*	USA	Nearctic	VII, III
			Viperidae	Crotalinae	*Crotalus atrox*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus basiliscus*	Mexico	Nearctic	
			Viperidae	Crotalinae	*Crotalus cerastes*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus cerberus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	
			Viperidae	Crotalinae	*Crotalus totonacus*	Mexico	Nearctic	
			Viperidae	Crotalinae	*Crotalus horridus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus molossus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus oreganus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus ruber*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	
			Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	
			Viperidae	Crotalinae	*Sistrurus miliarius*	USA	Nearctic	
			Viperidae	Crotalinae	*Sistrurus tergeminus*	USA	Nearctic	
237	https://doi.org/10.1016/j.jprot.2015.05.035	2015	Elapidae	Australo-Papuan and marine elapids	*Hydrophis schistosus*	Malaysia	Indomalayan	I, III, II
238	https://doi.org/10.1016/j.jprot.2015.02.012	2015	Elapidae	Old World and American elapids	*Naja kaouthia*	Malaysia	Indomalayan	I, V, III, II
			Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	
			Elapidae	Old World and American elapids	*Naja kaouthia*	Vietnam	Indomalayan	
239	https://doi.org/10.1016/j.toxicon.2014.11.231	2015	Viperidae	Crotalinae	*Hypnale hypnale*	Sri Lanka	Indomalayan	I
240	https://doi.org/10.1016/j.cbpc.2016.03.005	2016	Elapidae	Old World and American elapids	*Naja kaouthia*	Malaysia	Indomalayan	V, III, II
			Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	
			Elapidae	Old World and American elapids	*Naja kaouthia*	Vietnam	Indomalayan	
241	https://doi.org/10.3390/toxins11010003	2018	Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	Malaysia	Indomalayan	I, III, II
242	https://doi.org/10.1016/j.jprot.2018.09.006	2019	Elapidae	Old World and American elapids	*Calliophis intestinalis*	Malaysia	Indomalayan	I, III, II
			Elapidae	Old World and American elapids	*Calliophis bivirgatus*	Malaysia	Indomalayan	
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Thailand	Indomalayan	
			Elapidae	Australo-Papuan and marine elapids	*Hydrophis schistosus*	Malaysia	Indomalayan	
			Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	
243	https://doi.org/10.3390/toxins11020095	2019	Elapidae	Old World and American elapids	*Naja kaouthia*	Thailand	Indomalayan	I, III, II
			Viperidae	Crotalinae	*Trimeresurus albolabris*	Thailand	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus nebularis*	Malaysia	Indomalayan	
244	https://doi.org/10.1016/j.toxicon.2019.08.004	2019	Viperidae	Crotalinae	*Calloselasma rhodostoma*	Indonesia	Indomalayan	I, II, III, V
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Malaysia	Indomalayan	
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Thailand	Indomalayan	
			Viperidae	Crotalinae	*Calloselasma rhodostoma*	Vietnam	Indomalayan	
245	https://doi.org/10.1371/journal.pntd.0000622	2010	Elapidae	Old World and American elapids	*Micrurus altirostris*	UNKNOWN	Neotropic	I, VII, III, II
			Elapidae	Old World and American elapids	*Micrurus corallinus*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus frontalis*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus fulvius*	UNKNOWN	Neartic	
			Elapidae	Old World and American elapids	*Micrurus hemprichii*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus ibiboboca*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus lemniscatus*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus spixii*	UNKNOWN	Neotropic	
			Elapidae	Old World and American elapids	*Micrurus surinamensis*	UNKNOWN	Neotropic	
246	https://doi.org/10.1016/j.jprot.2008.07.007	2008	Viperidae	Crotalinae	*Bothrops cotiara*	Brazil	Neotropic	I, VII
			Viperidae	Crotalinae	*Bothrops fonsecai*	Brazil	Neotropic	
247	https://doi.org/10.1016/j.toxicon.2020.07.001	2020	Viperidae	Crotalinae	*Crotalus durissus*	Brazil	Neotropic	I, II, III
248	https://doi.org/10.3390/toxins12080485	2020	Elapidae	Australo-Papuan and marine elapids	*Oxyuranus microlepidotus*	Australia	Australasia	I, III, V, VI, VII

			Elapidae	Australo-Papuan and marine elapids	*Oxyuranus scutellatus*	Australia	Australasia	
249	https://doi.org/10.1016/S0003-9861(02)00747-6	2003	Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	I, V, III
250	https://doi.org/10.1042/bj20030818	2004	Viperidae	Crotalinae	*Trimeresurus stejnegeri*	Taiwan	Indomalayan	I, VI, V, III
			Viperidae	Crotalinae	*Trimeresurus stejnegeri*	China	Indomalayan	
			Viperidae	Crotalinae	*Trimeresurus albolabris*	UNKNOWN	UNKNOWN	
			Viperidae	Crotalinae	*Trimeresurus popeiorum*	UNKNOWN	Indomalayan	
			Viperidae	Crotalinae	*Tropidolaemus wagleri*	Indonesia	Indomalayan	
251	https://doi.org/10.1111/j.1742-4658.2006.05598.x	2007	Elapidae	Old World and American elapids	*Bungarus fasciatus*	India	Indomalayan	I, V, III
252	https://doi.org/10.1016/S0041-0101(00)00101-X	2000	Elapidae	Australo-Papuan and marine elapids	*Acanthophis antarticus*	Australia	Australasia	I, VII, III, II
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis praelongus*	Australia	Australasia	
			Elapidae	Australo-Papuan and marine elapids	*Acanthophis pyrrhus*	Australia	Australasia	
253	https://doi.org/10.1073/pnas.1314702110	2013	Elapidae	Old World and American elapids	*Ophiophagus hannah*	Indonesia	Indomalayan	I
254	https://doi.org/10.1371/journal.pmed.0030184	2006	Viperidae	Viperinae	*Bitis arietans*	Ghana	Afrotropic	I, VII, II
			Viperidae	Viperinae	*Bitis rhinoceros*	Ghana	Afrotropic	
			Viperidae	Viperinae	*Cerastes cerastes*	Egypt	Palearctic	
			Viperidae	Viperinae	*Echis romani*	Nigeria	Afrotropic	
255	https://doi.org/10.1016/j.jprot.2008.10.003	2009	Viperidae	Viperinae	*Echis romani*	Nigeria	Afrotropic	I
256	https://doi.org/10.1016/j.jprot.2020.103680	2020	Viperidae	Viperinae	*Bitis arietans*	UNKNOWN	UNKNOWN	I, III, VII
			Elapidae	Australo-Papuan and marine elapids	*Pseudechis colletti*	Australia	Australasia	
257	https://doi.org/10.1016/j.toxicon.2020.08.012	2020	Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	China	Indomalayan	I, III, V, VII
			Elapidae	Australo-Papuan and marine elapids	*Hydrophis cyanocinctus*	China	Indomalayan	
			Elapidae	Old World and American elapids	*Bungarus multicinctus*	China	UNKNOWN	
			Elapidae	Old World and American elapids	*Naja atra*	China	UNKNOWN	
			Viperidae	Crotalinae	*Gloydius halys*	China	Palearctic	
258	https://doi.org/10.1016/j.jprot.2018.09.019	2019	Elapidae	Old World and American elapids	*Aspidelaps lubricus*	UNKNOWN	Afrotropic	I, II, III, VII
			Elapidae	Old World and American elapids	*Aspidelaps scutatus*	UNKNOWN	Afrotropic	
259	https://www.jstor.org/stable/3892815	1991	Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	V, III, II
260	https://doi.org/10.1016/j.jprot.2017.12.012	2018	Elapidae	Old World and American elapids	*Naja naja*	Pakistan	Indomalayan	I, V, III, II
261	https://doi.org/10.3390/toxins13010060	2021	Elapidae	Old World and American elapids	*Naja senegalensis*	UNKNOWN	Afrotropic	I, II, III
262	https://doi.org/10.1007/s10930-019-09852-5	2019	Elapidae	Old World and American elapids	*Ophiophagus hannah*	Thailand	Indomalayan	I, III, V
263	https://doi.org/10.3390/toxins8060188	2016	Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	I, VII, VI
			Viperidae	Crotalinae	*Crotalus viridis*	USA	Nearctic	
264	https://doi.org/10.1098/rspb.2018.2735	2019	Viperidae	Crotalinae	*Crotalus scutulatus*	USA	Nearctic	I, V, VIII
265	https://doi.org/10.1371/journal.pntd.0001554	2012	Viperidae	Crotalinae	*Bothrops jararaca*	Brazil	Neotropic	I, VI
266	https://doi.org/10.3390/toxins13080548	2021	Elapidae	Australo-Papuan and marine elapids	*Hydrophis cyanocinctus*	China	Indomalayan	I, III, VII
267	https://doi.org/10.1186/s12864-021-07824-7	2021	Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	China	Indomalayan	I, II

Table A1.2 Complete list of all retrieved snake species. For each species, family, subfamily/group, and assigned hazard category are reported.

#	Family	Subfamily/group	Species	Hazard category
1	Elapidae	Australo-Papuan and marine elapids	*Acanthophis antarticus*	Category 1 - Critical clinical relevance
2	Elapidae	Australo-Papuan and marine elapids	*Acanthophis hawkei*	Category 1 - Critical clinical relevance
3	Elapidae	Australo-Papuan and marine elapids	*Acanthophis laevis*	Category 1 - Critical clinical relevance
4	Elapidae	Australo-Papuan and marine elapids	*Acanthophis praelongus*	Category 1 - Critical clinical relevance
5	Elapidae	Australo-Papuan and marine elapids	*Acanthophis pyrrhus*	Category 1 - Critical clinical relevance
6	Elapidae	Australo-Papuan and marine elapids	*Acanthophis rugosus*	Category 1 - Critical clinical relevance
7	Elapidae	Australo-Papuan and marine elapids	*Acanthophis wellsi*	Category 1 - Critical clinical relevance
8	Viperidae	Crotalinae	*Agkistrodon bilineatus*	Category 2 - High clinical relevance
9	Viperidae	Crotalinae	*Agkistrodon conanti*	Category 2 - High clinical relevance
10	Viperidae	Crotalinae	*Agkistrodon contortrix*	Category 2 - High clinical relevance
11	Viperidae	Crotalinae	*Agkistrodon howardgloydi*	Category 2 - High clinical relevance
12	Viperidae	Crotalinae	*Agkistrodon laticinctus*	Category 2 - High clinical relevance
13	Viperidae	Crotalinae	*Agkistrodon piscivorus*	Category 2 - High clinical relevance
14	Viperidae	Crotalinae	*Agkistrodon taylori*	Category 2 - High clinical relevance
15	Colubridae	Ahaetuliinae	*Ahaetulla prasina*	Category 4 - Low clinical relevance
16	Elapidae	Australo-Papuan and marine elapids	*Aipysurus duboisii*	Category 2 - High clinical relevance
17	Elapidae	Australo-Papuan and marine elapids	*Aipysurus foliosquama*	Category 2 - High clinical relevance
18	Elapidae	Australo-Papuan and marine elapids	*Aipysurus fuscus*	Category 2 - High clinical relevance
19	Elapidae	Australo-Papuan and marine elapids	*Aipysurus mosaicus*	Category 3 - Moderate clinical relevance
20	Colubridae	Natricinae	*Amphiesma stolatum*	Category 4 - Low clinical relevance
21	Elapidae	Australo-Papuan and marine elapids	*Antaioserpens warro*	Category 4 - Low clinical relevance
22	Elapidae	Old World and American elapids	*Aspidelaps lubricus*	Category 2 - High clinical relevance
23	Elapidae	Old World and American elapids	*Aspidelaps scutatus*	Category 2 - High clinical relevance
24	Elapidae	Australo-Papuan and marine elapids	*Aspidomorphus muelleri*	Category 3 - Moderate clinical relevance
25	Atractaspididae	NA	*Atractaspis bibronii*	Category 2 - High clinical relevance
26	Atractaspididae	NA	*Atractaspis engaddensis*	Category 2 - High clinical relevance
27	Atractaspididae	NA	*Atractaspis fallax*	Category 2 - High clinical relevance
28	Atractaspididae	NA	*Atractaspis microlepidota*	Category 2 - High clinical relevance
29	Viperidae	Crotalinae	*Atropoides picadoi*	Category 1 - Critical clinical relevance
30	Viperidae	Azemiopinae	*Azemiops feae*	Category 2 - High clinical relevance
31	Viperidae	Viperinae	*Bitis arietans*	Category 1 - Critical clinical relevance
32	Viperidae	Viperinae	*Bitis caudalis*	Category 2 - High clinical relevance
33	Viperidae	Viperinae	*Bitis gabonica*	Category 1 - Critical clinical relevance
34	Viperidae	Viperinae	*Bitis nasicornis*	Category 1 - Critical clinical relevance
35	Viperidae	Viperinae	*Bitis parviocula*	Category 1 - Critical clinical relevance

36	Viperidae	Viperinae	*Bitis rhinoceros*	Category 1 - Critical clinical relevance
37	Colubridae	Colubrinae	*Boiga cyanea*	Category 3 - Moderate clinical relevance
38	Colubridae	Colubrinae	*Boiga cynodon*	Category 3 - Moderate clinical relevance
39	Colubridae	Colubrinae	*Boiga dendrophila*	Category 3 - Moderate clinical relevance
40	Colubridae	Colubrinae	*Boiga drapiezii*	Category 3 - Moderate clinical relevance
41	Colubridae	Colubrinae	*Boiga irregularis*	Category 3 - Moderate clinical relevance
42	Colubridae	Colubrinae	*Boiga nigriceps*	Category 3 - Moderate clinical relevance
43	Colubridae	Colubrinae	*Boiga trigonata*	Category 3 - Moderate clinical relevance
44	Colubridae	Dipsadinae	*Borikenophis portoricensis*	Category 3 - Moderate clinical relevance
45	Viperidae	Crotalinae	*Bothriechis aurifer*	Category 2 - High clinical relevance
46	Viperidae	Crotalinae	*Bothriechis bicolor*	Category 2 - High clinical relevance
47	Viperidae	Crotalinae	*Bothriechis lateralis*	Category 2 - High clinical relevance
48	Viperidae	Crotalinae	*Bothriechis marchi*	Category 2 - High clinical relevance
49	Viperidae	Crotalinae	*Bothriechis schlegelii*	Category 2 - High clinical relevance
50	Viperidae	Crotalinae	*Bothriechis thalassinus*	Category 2 - High clinical relevance
51	Viperidae	Crotalinae	*Bothrocophias hyoprora*	Category 2 - High clinical relevance
52	Viperidae	Crotalinae	*Bothrocophias myersi*	Category 2 - High clinical relevance
53	Viperidae	Crotalinae	*Bothrops alcatraz*	Category 1 - Critical clinical relevance
54	Viperidae	Crotalinae	*Bothrops alternatus*	Category 1 - Critical clinical relevance
55	Viperidae	Crotalinae	*Bothrops asper*	Category 1 - Critical clinical relevance
56	Viperidae	Crotalinae	*Bothrops atrox*	Category 1 - Critical clinical relevance
57	Viperidae	Crotalinae	*Bothrops barnetti*	Category 1 - Critical clinical relevance
58	Viperidae	Crotalinae	*Bothrops bilineatus*	Category 1 - Critical clinical relevance
59	Viperidae	Crotalinae	*Bothrops brazili*	Category 1 - Critical clinical relevance
60	Viperidae	Crotalinae	*Bothrops caribbaeus*	Category 1 - Critical clinical relevance
61	Viperidae	Crotalinae	*Bothrops cotiara*	Category 1 - Critical clinical relevance
62	Viperidae	Crotalinae	*Bothrops diporus*	Category 1 - Critical clinical relevance
63	Viperidae	Crotalinae	*Bothrops erythromelas*	Category 1 - Critical clinical relevance
64	Viperidae	Crotalinae	*Bothrops fonsecai*	Category 1 - Critical clinical relevance
65	Viperidae	Crotalinae	*Bothrops insularis*	Category 1 - Critical clinical relevance
66	Viperidae	Crotalinae	*Bothrops jararaca*	Category 1 - Critical clinical relevance
67	Viperidae	Crotalinae	*Bothrops jararacussu*	Category 1 - Critical clinical relevance
68	Viperidae	Crotalinae	*Bothrops lanceolatus*	Category 1 - Critical clinical relevance
69	Viperidae	Crotalinae	*Bothrops leucurus*	Category 1 - Critical clinical relevance
70	Viperidae	Crotalinae	*Bothrops marajoensis*	Category 1 - Critical clinical relevance
71	Viperidae	Crotalinae	*Bothrops marmoratus*	Category 1 - Critical clinical relevance
72	Viperidae	Crotalinae	*Bothrops matogrossensis*	Category 1 - Critical clinical relevance
73	Viperidae	Crotalinae	*Bothrops moojeni*	Category 1 - Critical clinical relevance
74	Viperidae	Crotalinae	*Bothrops neuwiedi*	Category 1 - Critical clinical relevance

75	Viperidae	Crotalinae	*Bothrops pauloensis*	Category 1 - Critical clinical relevance
76	Viperidae	Crotalinae	*Bothrops pictus*	Category 1 - Critical clinical relevance
77	Viperidae	Crotalinae	*Bothrops pirajai*	Category 1 - Critical clinical relevance
78	Viperidae	Crotalinae	*Bothrops taeniatus*	Category 1 - Critical clinical relevance
79	Elapidae	Australo-Papuan and marine elapids	*Brachyurophis roperi*	Category 4 - Low clinical relevance
80	Elapidae	Old World and American elapids	*Bungarus candidus*	Category 1 - Critical clinical relevance
81	Elapidae	Old World and American elapids	*Bungarus caeruleus*	Category 1 - Critical clinical relevance
82	Elapidae	Old World and American elapids	*Bungarus fasciatus*	Category 1 - Critical clinical relevance
83	Elapidae	Old World and American elapids	*Bungarus flaviceps*	Category 1 - Critical clinical relevance
84	Elapidae	Old World and American elapids	*Bungarus multicinctus*	Category 1 - Critical clinical relevance
85	Elapidae	Old World and American elapids	*Bungarus sindanus*	Category 1 - Critical clinical relevance
86	Elapidae	Australo-Papuan and marine elapids	*Cacophis squamulosus*	Category 3 - Moderate clinical relevance
87	Elapidae	Old World and American elapids	*Calliophis bivirgatus*	Category 1 - Critical clinical relevance
88	Elapidae	Old World and American elapids	*Calliophis intestinalis*	Category 2 - High clinical relevance
89	Viperidae	Crotalinae	*Calloselasma rhodostoma*	Category 1 - Critical clinical relevance
90	Viperidae	Viperinae	*Causus lichtensteinii*	Category 3 - Moderate clinical relevance
91	Viperidae	Viperinae	*Causus rhombeatus*	Category 3 - Moderate clinical relevance
92	Viperidae	Viperinae	*Cerastes cerastes*	Category 2 - High clinical relevance
93	Viperidae	Viperinae	*Cerastes vipera*	Category 3 - Moderate clinical relevance
94	Homalopsidae	NA	*Cerberus rynchops*	Category 4 - Low clinical relevance
95	Viperidae	Crotalinae	*Cerrophidion sasai*	Category 2 - High clinical relevance
96	Colubridae	Colubrinae	*Coelognathus radiatus*	Category 4 - Low clinical relevance
97	Viperidae	Crotalinae	*Crotalus adamanteus*	Category 1 - Critical clinical relevance
98	Viperidae	Crotalinae	*Crotalus atrox*	Category 1 - Critical clinical relevance
99	Viperidae	Crotalinae	*Crotalus basiliscus*	Category 1 - Critical clinical relevance
100	Viperidae	Crotalinae	*Crotalus catalinensis*	Category 1 - Critical clinical relevance
101	Viperidae	Crotalinae	*Crotalus cerastes*	Category 2 - High clinical relevance
102	Viperidae	Crotalinae	*Crotalus cerberus*	Category 2 - High clinical relevance
103	Viperidae	Crotalinae	*Crotalus concolor*	Category 2 - High clinical relevance
104	Viperidae	Crotalinae	*Crotalus culminatus*	Category 1 - Critical clinical relevance
105	Viperidae	Crotalinae	*Crotalus durissus*	Category 1 - Critical clinical relevance
106	Viperidae	Crotalinae	*Crotalus helleri*	Category 1 - Critical clinical relevance
107	Viperidae	Crotalinae	*Crotalus horridus*	Category 1 - Critical clinical relevance
108	Viperidae	Crotalinae	*Crotalus lepidus*	Category 2 - High clinical relevance
109	Viperidae	Crotalinae	*Crotalus lutosus*	Category 1 - Critical clinical relevance
110	Viperidae	Crotalinae	*Crotalus mictlantecuhtli*	Category 1 - Critical clinical relevance
111	Viperidae	Crotalinae	*Crotalus molossus*	Category 1 - Critical clinical relevance
112	Viperidae	Crotalinae	*Crotalus morulus*	Category 2 - High clinical relevance
113	Viperidae	Crotalinae	*Crotalus oreganus*	Category 1 - Critical clinical relevance

114	Viperidae	Crotalinae	*Crotalus pricei*	Category 2 - High clinical relevance
115	Viperidae	Crotalinae	*Crotalus ruber*	Category 1 - Critical clinical relevance
116	Viperidae	Crotalinae	*Crotalus scutulatus*	Category 1 - Critical clinical relevance
117	Viperidae	Crotalinae	*Crotalus simus*	Category 1 - Critical clinical relevance
118	Viperidae	Crotalinae	*Crotalus totonacus*	Category 1 - Critical clinical relevance
119	Viperidae	Crotalinae	*Crotalus tzabcan*	Category 1 - Critical clinical relevance
120	Viperidae	Crotalinae	*Crotalus viridis*	Category 1 - Critical clinical relevance
121	Elapidae	Australo-Papuan and marine elapids	*Cryptophis boschmai*	Category 2 - High clinical relevance
122	Elapidae	Australo-Papuan and marine elapids	*Cryptophis nigrescens*	Category 2 - High clinical relevance
123	Viperidae	Viperinae	*Daboia mauritanica*	Category 1 - Critical clinical relevance
124	Viperidae	Viperinae	*Daboia russelii*	Category 1 - Critical clinical relevance
125	Viperidae	Viperinae	*Daboia siamensis*	Category 1 - Critical clinical relevance
126	Viperidae	Crotalinae	*Deinagkistrodon acutus*	Category 1 - Critical clinical relevance
127	Elapidae	Australo-Papuan and marine elapids	*Demansia papuensis*	Category 2 - High clinical relevance
128	Elapidae	Australo-Papuan and marine elapids	*Demansia psammophis*	Category 3 - Moderate clinical relevance
129	Elapidae	Australo-Papuan and marine elapids	*Demansia rimicola*	Category 3 - Moderate clinical relevance
130	Elapidae	Old World and American elapids	*Dendroaspis angusticeps*	Category 1 - Critical clinical relevance
131	Elapidae	Old World and American elapids	*Dendroaspis jamesoni*	Category 1 - Critical clinical relevance
132	Elapidae	Old World and American elapids	*Dendroaspis polylepis*	Category 1 - Critical clinical relevance
133	Elapidae	Old World and American elapids	*Dendroaspis viridis*	Category 1 - Critical clinical relevance
134	Elapidae	Australo-Papuan and marine elapids	*Denisonia devisi*	Category 3 - Moderate clinical relevance
135	Colubridae	Dipsadinae	*Diadophis punctatus*	Category 4 - Low clinical relevance
136	Colubridae	Colubrinae	*Dispholidus typus*	Category 1 - Critical clinical relevance
137	Elapidae	Australo-Papuan and marine elapids	*Echiopsis curta*	Category 3 - Moderate clinical relevance
138	Viperidae	Viperinae	*Echis carinatus*	Category 1 - Critical clinical relevance
139	Viperidae	Viperinae	*Echis coloratus*	Category 1 - Critical clinical relevance
140	Viperidae	Viperinae	*Echis ocellatus*	Category 1 - Critical clinical relevance
141	Viperidae	Viperinae	*Echis pyramidum*	Category 1 - Critical clinical relevance
142	Viperidae	Viperinae	*Echis romani*	Category 1 - Critical clinical relevance
143	Elapidae	Australo-Papuan and marine elapids	*Furina ornata*	Category 4 - Low clinical relevance
144	Elapidae	Australo-Papuan and marine elapids	*Furina tristis*	Category 3 - Moderate clinical relevance
145	Viperidae	Crotalinae	*Gloydius brevicaudus*	Category 2 - High clinical relevance
146	Viperidae	Crotalinae	*Gloydius halys*	Category 2 - High clinical relevance
147	Colubridae	Colubrinae	*Gonyosoma oxycephalum*	Category 4 - Low clinical relevance
148	Elapidae	Old World and American elapids	*Hemachatus haemachatus*	Category 2 - High clinical relevance
149	Elapidae	Australo-Papuan and marine elapids	*Hemiaspis damelii*	Category 3 - Moderate clinical relevance
150	Elapidae	Australo-Papuan and marine elapids	*Hemiaspis signata*	Category 3 - Moderate clinical relevance
151	Colubridae	Dipsadinae	*Heterodon kennerlyi*	Category 4 - Low clinical relevance
152	Colubridae	Dipsadinae	*Heterodon nasicus*	Category 4 - Low clinical relevance

153	Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus bitorquatus*	Category 2 - High clinical relevance
154	Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus bungaroides*	Category 2 - High clinical relevance
155	Elapidae	Australo-Papuan and marine elapids	*Hoplocephalus stephensii*	Category 2 - High clinical relevance
156	Colubridae	Dipsadinae	*Hydrodynastes gigas*	Category 3 - Moderate clinical relevance
157	Elapidae	Australo-Papuan and marine elapids	*Hydrophis curtus*	Category 1 - Critical clinical relevance
158	Elapidae	Australo-Papuan and marine elapids	*Hydrophis cyanocinctus*	Category 1 - Critical clinical relevance
159	Elapidae	Australo-Papuan and marine elapids	*Hydrophis platurus*	Category 2 - High clinical relevance
160	Elapidae	Australo-Papuan and marine elapids	*Hydrophis schistosus*	Category 1 - Critical clinical relevance
161	Viperidae	Crotalinae	*Hypnale hypnale*	Category 1 - Critical clinical relevance
162	Colubridae	Dipsadinae	*Hypsiglena jani*	Category 4 - Low clinical relevance
163	Viperidae	Crotalinae	*Lachesis acrochorda*	Category 1 - Critical clinical relevance
164	Viperidae	Crotalinae	*Lachesis melanocephala*	Category 1 - Critical clinical relevance
165	Viperidae	Crotalinae	*Lachesis muta*	Category 1 - Critical clinical relevance
166	Viperidae	Crotalinae	*Lachesis stenophrys*	Category 1 - Critical clinical relevance
167	Elapidae	Australo-Papuan and marine elapids	*Laticauda schistorhyncha*	Category 1 - Critical clinical relevance
168	Pseudoxyrhophiidae	NA	*Leioheterodon madagascariensis*	Category 4 - Low clinical relevance
169	Colubridae	Colubrinae	*Leptophis ahaetulla*	Category 4 - Low clinical relevance
170	Elapidae	Australo-Papuan and marine elapids	*Loveridgelaps elapoides*	Category 2 - High clinical relevance
171	Viperidae	Viperinae	*Macrovipera lebetina*	Category 1 - Critical clinical relevance
172	Psammophiidae	NA	*Malpolon insignitus*	Category 3 - Moderate clinical relevance
173	Viperidae	Crotalinae	*Metlapilcoatlus mexicanus*	Category 2 - High clinical relevance
174	Viperidae	Crotalinae	*Metlapilcoatlus nummifer*	Category 2 - High clinical relevance
175	Elapidae	Australo-Papuan and marine elapids	*Micropechis ikaheca*	Category 1 - Critical clinical relevance
176	Elapidae	Old World and American elapids	*Micruroides euryxanthus*	Category 2 - High clinical relevance
177	Elapidae	Old World and American elapids	*Micrurus albicinctus*	Category 2 - High clinical relevance
178	Elapidae	Old World and American elapids	*Micrurus alleni*	Category 2 - High clinical relevance
179	Elapidae	Old World and American elapids	*Micrurus altirostris*	Category 2 - High clinical relevance
180	Elapidae	Old World and American elapids	*Micrurus baliocoryphus*	Category 2 - High clinical relevance
181	Elapidae	Old World and American elapids	*Micrurus brasiliensis*	Category 2 - High clinical relevance
182	Elapidae	Old World and American elapids	*Micrurus browni*	Category 2 - High clinical relevance
183	Elapidae	Old World and American elapids	*Micrurus clarki*	Category 2 - High clinical relevance
184	Elapidae	Old World and American elapids	*Micrurus corallinus*	Category 2 - High clinical relevance
185	Elapidae	Old World and American elapids	*Micrurus frontalis*	Category 2 - High clinical relevance
186	Elapidae	Old World and American elapids	*Micrurus fulvius*	Category 1 - Critical clinical relevance
187	Elapidae	Old World and American elapids	*Micrurus hemprichii*	Category 3 - Moderate clinical relevance
188	Elapidae	Old World and American elapids	*Micrurus ibiboboca*	Category 2 - High clinical relevance
189	Elapidae	Old World and American elapids	*Micrurus lemniscatus*	Category 1 - Critical clinical relevance
190	Elapidae	Old World and American elapids	*Micrurus mipartitus*	Category 1 - Critical clinical relevance
191	Elapidae	Old World and American elapids	*Micrurus mosquitensis*	Category 2 - High clinical relevance

192	Elapidae	Old World and American elapids	*Micrurus pyrrhocryptus*	Category 2 - High clinical relevance
193	Elapidae	Old World and American elapids	*Micrurus ruatanus*	Category 2 - High clinical relevance
194	Elapidae	Old World and American elapids	*Micrurus spixii*	Category 2 - High clinical relevance
195	Elapidae	Old World and American elapids	*Micrurus surinamensis*	Category 1 - Critical clinical relevance
196	Viperidae	Viperinae	*Montivipera raddei*	Category 1 - Critical clinical relevance
197	Viperidae	Viperinae	*Montivipera wagneri*	Category 1 - Critical clinical relevance
198	Viperidae	Viperinae	*Montivipera xanthina*	Category 1 - Critical clinical relevance
199	Homalopsidae	NA	*Myrrophis chinensis*	Category 4 - Low clinical relevance
200	Elapidae	Old World and American elapids	*Naja annulifera*	Category 1 - Critical clinical relevance
201	Elapidae	Old World and American elapids	*Naja ashei*	Category 1 - Critical clinical relevance
202	Elapidae	Old World and American elapids	*Naja atra*	Category 1 - Critical clinical relevance
203	Elapidae	Old World and American elapids	*Naja haje*	Category 1 - Critical clinical relevance
204	Elapidae	Old World and American elapids	*Naja kaouthia*	Category 1 - Critical clinical relevance
205	Elapidae	Old World and American elapids	*Naja katiensis*	Category 1 - Critical clinical relevance
206	Elapidae	Old World and American elapids	*Naja mossambica*	Category 1 - Critical clinical relevance
207	Elapidae	Old World and American elapids	*Naja naja*	Category 1 - Critical clinical relevance
208	Elapidae	Old World and American elapids	*Naja nigricincta*	Category 1 - Critical clinical relevance
209	Elapidae	Old World and American elapids	*Naja nigricollis*	Category 1 - Critical clinical relevance
210	Elapidae	Old World and American elapids	*Naja oxiana*	Category 1 - Critical clinical relevance
211	Elapidae	Old World and American elapids	*Naja samarensis*	Category 1 - Critical clinical relevance
212	Elapidae	Old World and American elapids	*Naja senegalensis*	Category 1 - Critical clinical relevance
213	Elapidae	Old World and American elapids	*Naja sumatrana*	Category 1 - Critical clinical relevance
214	Elapidae	Australo-Papuan and marine elapids	*Notechis scutatus*	Category 1 - Critical clinical relevance
215	Elapidae	Old World and American elapids	*Ophiophagus hannah*	Category 1 - Critical clinical relevance
216	Viperidae	Crotalinae	*Ophryacus smaragdinus*	Category 2 - High clinical relevance
217	Viperidae	Crotalinae	*Ophryacus sphenophrys*	Category 2 - High clinical relevance
218	Viperidae	Crotalinae	*Ophryacus undulatus*	Category 2 - High clinical relevance
219	Viperidae	Crotalinae	*Ovophis convictus*	Category 2 - High clinical relevance
220	Viperidae	Crotalinae	*Ovophis monticola*	Category 2 - High clinical relevance
221	Viperidae	Crotalinae	*Ovophis okinavensis*	Category 2 - High clinical relevance
222	Viperidae	Crotalinae	*Ovophis tonkinensis*	Category 2 - High clinical relevance
223	Elapidae	Australo-Papuan and marine elapids	*Oxyuranus microlepidotus*	Category 1 - Critical clinical relevance
224	Elapidae	Australo-Papuan and marine elapids	*Oxyuranus scutellatus*	Category 1 - Critical clinical relevance
225	Colubridae	Dipsadinae	*Philodryas olfersii*	Category 3 - Moderate clinical relevance
226	Colubridae	Dipsadinae	*Philodryas patagoniensis*	Category 3 - Moderate clinical relevance
227	Colubridae	Colubrinae	*Platyceps rhodorachis*	Category 4 - Low clinical relevance
228	Viperidae	Crotalinae	*Porthidium lansbergii*	Category 2 - High clinical relevance
229	Viperidae	Crotalinae	*Porthidium nasutum*	Category 2 - High clinical relevance
230	Viperidae	Crotalinae	*Porthidium ophryomegas*	Category 2 - High clinical relevance

231	Viperidae	Crotalinae	*Porthidium porrasi*	Category 2 - High clinical relevance
232	Viperidae	Viperinae	*Proatheris superciliaris*	Category 1 - Critical clinical relevance
233	Viperidae	Crotalinae	*Protobothrops elegans*	Category 1 - Critical clinical relevance
234	Viperidae	Crotalinae	*Protobothrops flavoviridis*	Category 1 - Critical clinical relevance
235	Viperidae	Crotalinae	*Protobothrops mucrosquamatus*	Category 1 - Critical clinical relevance
236	Psammophiidae	NA	*Psammophis mossambicus*	Category 4 - Low clinical relevance
237	Elapidae	Australo-Papuan and marine elapids	*Pseudechis colletti*	Category 1 - Critical clinical relevance
238	Elapidae	Australo-Papuan and marine elapids	*Pseudechis papuanus*	Category 1 - Critical clinical relevance
239	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja affinis*	Category 1 - Critical clinical relevance
240	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja aspidorhyncha*	Category 1 - Critical clinical relevance
241	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja guttata*	Category 1 - Critical clinical relevance
242	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja inframacula*	Category 1 - Critical clinical relevance
243	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja ingrami*	Category 1 - Critical clinical relevance
244	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja mengdeni*	Category 1 - Critical clinical relevance
245	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja modesta*	Category 3 - Moderate clinical relevance
246	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja nuchalis*	Category 1 - Critical clinical relevance
247	Elapidae	Australo-Papuan and marine elapids	*Pseudonaja textilis*	Category 1 - Critical clinical relevance
248	Colubridae	Colubrinae	*Ptyas carinata*	Category 4 - Low clinical relevance
249	Colubridae	Natricinae	*Rhabdophis subminiatus*	Category 2 - High clinical relevance
250	Colubridae	Natricinae	*Rhabdophis tigrinus*	Category 2 - High clinical relevance
251	Colubridae	Colubrinae	*Rhinobothryum bovalli*	Category 4 - Low clinical relevance
252	Colubridae	Colubrinae	*Salvadora grahamiae*	Category 4 - Low clinical relevance
253	Elapidae	Australo-Papuan and marine elapids	*Simoselaps bertholdi*	Category 4 - Low clinical relevance
254	Viperidae	Crotalinae	*Sistrurus catenatus*	Category 2 - High clinical relevance
255	Viperidae	Crotalinae	*Sistrurus miliarius*	Category 2 - High clinical relevance
256	Viperidae	Crotalinae	*Sistrurus tergeminus*	Category 2 - High clinical relevance
257	Colubridae	Colubrinae	*Spilotes sulphureus*	Category 4 - Low clinical relevance
258	Elapidae	Australo-Papuan and marine elapids	*Suta dwyeri*	Category 4 - Low clinical relevance
259	Elapidae	Australo-Papuan and marine elapids	*Suta fasciata*	Category 3 - Moderate clinical relevance
260	Elapidae	Australo-Papuan and marine elapids	*Suta punctata*	Category 3 - Moderate clinical relevance
261	Elapidae	Australo-Papuan and marine elapids	*Suta spectabilis*	Category 3 - Moderate clinical relevance
262	Elapidae	Australo-Papuan and marine elapids	*Suta suta*	Category 2 - High clinical relevance
263	Colubridae	Colubrinae	*Tantilla nigriceps*	Category 4 - Low clinical relevance
264	Colubridae	Colubrinae	*Telescopus dhara*	Category 4 - Low clinical relevance
265	Colubridae	Natricinae	*Thamnophis elegans*	Category 4 - Low clinical relevance
266	Colubridae	Colubrinae	*Thelotornis mossambicanus*	Category 1 - Critical clinical relevance
267	Elapidae	Australo-Papuan and marine elapids	*Toxicocalamus longissimus*	Unknown
268	Colubridae	Colubrinae	*Toxicodryas vexator*	Category 3 - Moderate clinical relevance
269	Viperidae	Crotalinae	*Trimeresurus albolabris*	Category 2 - High clinical relevance

270	Viperidae	Crotalinae	*Trimeresurus borneensis*	Category 2 - High clinical relevance
271	Viperidae	Crotalinae	*Trimeresurus gramineus*	Category 2 - High clinical relevance
272	Viperidae	Crotalinae	*Trimeresurus hageni*	Category 2 - High clinical relevance
273	Viperidae	Crotalinae	*Trimeresurus insularis*	Category 2 - High clinical relevance
274	Viperidae	Crotalinae	*Trimeresurus macrops*	Category 2 - High clinical relevance
275	Viperidae	Crotalinae	*Trimeresurus nebularis*	Category 2 - High clinical relevance
276	Viperidae	Crotalinae	*Trimeresurus popeiorum*	Category 2 - High clinical relevance
277	Viperidae	Crotalinae	*Trimeresurus puniceus*	Category 2 - High clinical relevance
278	Viperidae	Crotalinae	*Trimeresurus purpureomaculatus*	Category 2 - High clinical relevance
279	Viperidae	Crotalinae	*Trimeresurus stejnegeri*	Category 2 - High clinical relevance
280	Viperidae	Crotalinae	*Trimeresurus wiroti*	Category 2 - High clinical relevance
281	Colubridae	Colubrinae	*Trimorphodon lambda*	Category 4 - Low clinical relevance
282	Colubridae	Colubrinae	*Trimorphodon quadruplex*	Category 4 - Low clinical relevance
283	Viperidae	Crotalinae	*Tropidolaemus subannulatus*	Category 2 - High clinical relevance
284	Viperidae	Crotalinae	*Tropidolaemus wagleri*	Category 2 - High clinical relevance
285	Elapidae	Australo-Papuan and marine elapids	*Vermicella annulata*	Category 4 - Low clinical relevance
286	Viperidae	Viperinae	*Vipera ammodytes*	Category 3 - Moderate clinical relevance
287	Viperidae	Viperinae	*Vipera anatolica*	Category 2 - High clinical relevance
288	Viperidae	Viperinae	*Vipera aspis*	Category 2 - High clinical relevance
289	Viperidae	Viperinae	*Vipera barani*	Category 2 - High clinical relevance
290	Viperidae	Viperinae	*Vipera berus*	Category 2 - High clinical relevance
291	Viperidae	Viperinae	*Vipera eriwanensis*	Category 3 - Moderate clinical relevance
292	Viperidae	Viperinae	*Vipera kaznakovi*	Category 2 - High clinical relevance
293	Viperidae	Viperinae	*Vipera latastei*	Category 2 - High clinical relevance
294	Viperidae	Viperinae	*Vipera nikolskii*	Category 2 - High clinical relevance
295	Viperidae	Viperinae	*Vipera transcaucasiana*	Category 2 - High clinical relevance
296	Viperidae	Viperinae	*Vipera ursinii*	Category 3 - Moderate clinical relevance
297	Elapidae	Old World and American elapids	*Walterinnesia aegyptia*	Category 2 - High clinical relevance
298	Elapidae	Old World and American elapids	*Walterinnesia morgani*	Category 2 - High clinical relevance

Table A1.3 Country of origin of the retrieved snake species. The overall species number is higher than the number of species actually retrieved from the analysed publications because some species were assigned to more than one country.

Country	Species	Country	Species
Australia	55	Honduras	2
Brazil	35	Mozambique	2
USA	31	Namibia	2
Costa Rica	22	Saudi Arabia	2
Mexico	16	Sri Lanka	2
Indonesia	14	Sulawesi	2
Malaysia	13	Suriname	2
China	12	Venezuela	2
Colombia	10	Austria	1
Turkey	10	Belize	1
Thailand	9	Borneo	1
India	8	British Virgin Islands	1
Argentina	7	Bulgaria	1
Egypt	6	Cameroon	1
Nigeria	6	Canada	1
Tanzania	6	Cyprus	1
Guatemala	5	Ethiopia	1
Pakistan	5	Guam	1
Papua New Guinea	5	Guinea	1
Peru	5	Hong Kong	1
Singapore	5	Hungary	1
South Africa	5	Israel	1
Taiwan	5	Italy	1
Kenya	4	Kenya	1
Morocco	4	Madagascar	1
Bolivia	3	Martinique	1
Iran	3	Myanmar	1
Japan	3	Niue	1
Java	3	Philippines	1
Tunisia	3	Russia	1
Uganda	3	Saint Lucia	1
Vietnam	3	Slovenia	1
Armenia	2	Spain	1
Bali	2	Togo	1
Croatia	2	UAE	1
Ecuador	2	Ukraine	1
France	2	West Bengal	1
Ghana	2	West Papua	1

Table A1.4 Number of publications considered per each year of the defined time frame. Years for which no articles were considered are not reported.

Year	Number of publications
1964	2
1968	1
1973	1
1974	3
1980	2
1982	1
1983	2
1985	1
1986	3
1988	2
1989	1
1990	2
1991	2
1992	3
1993	1
1996	1
1997	1
1998	2
1999	1
2000	5
2001	2
2002	5
2003	5
2004	3
2005	5
2006	11
2007	8
2008	7
2009	11
2010	8
2011	5
2012	11
2013	8
2014	8
2015	14
2016	8
2017	9
2018	18
2019	29
2020	27
2021	28

Table A1.5 Polynomial regression models applied to test the relationship between topic categories and number of yearly papers covering each one of them. For each model, predicted outcome value (y), information score (Akaike's Information Criterion corrected for small sample sizes; AICc), observed-versus-expected chi-squared value (χ^2), coefficient of determination (r^2), and p-value (*p*) are reported.

Topic category	**Best-fitting model**	**y**	**AICc**	**χ^2**	**r^2**	***p***
"Biological activity"	3rd order polynomial	$0.0004007x^3-2.387x^2+4738x-3.136e6$	237.230	228.480	0.795	< 0.001
"Antivenomics and neutralisation"	3rd order polynomial	$0.0003516x^3-2.094x^2+4159x-2.753e6$	171.190	162.440	0.778	< 0.001
"Venom characterisation"	3rd order polynomial	$0.0034x^3-20.21x^2+4.004e4x-2.644e7$	872.180	863.430	0.996	< 0.001
"Geographic venom variation"	2nd order polynomial	$0.003282x^2-12.98x+1.284e4$	68.705	62.261	0.751	< 0.001
"Individual venom variation"	3rd order polynomial	$7.901e-5x^3-0.47x^2+931.9x-6.159e5$	50.732	41.977	0.592	< 0.001
"Interspecific venom variation"	3rd order polynomial	$0.0004634x^3-2.756x^2+5466x-3.613e6$	413.990	405.230	0.848	< 0.001
"Envenomation symptoms"	1st order polynomial	$0.005506x-10.88$	12.294	8.076	0.058	0.069
"Prey specificity of venom"	3rd order polynomial	$3.877e-5x^3-0.2307x^2+457.7x-3.026e5$	22.080	13.326	0.470	< 0.001

Table A1.6 Summary of the Generalised Linear Model (GLM) applied to test the relationship between number of articles retrieved for each snake species and hazard category (HAZARD) and biogeographic realm (REALM). The levels "Critical" and "Neotropic" have been used as reference for the predictors HAZARD and REALM, respectively. For each predictor level, coefficients (B), standard error (SE), and p-value (*p*) are reported. Significant p-values are displayed in bold.

	B	**SE**	***p***
(Intercept)	1.101	0.0792	< 2e-16
HAZARD_High	-0.6407	0.0953	**1.73e-11**
HAZARD_Moderate	-0.344	0.139	**0.0137**
HAZARD_Low	-0.765	0.168	**5.29e-06**
REALM_Afrotropic	-0.274	0.142	0.0535
REALM_Australasia	-0.386	0.133	**0.00372**
REALM_Indomalayan	0.124	0.1097	0.258
REALM_Nearctic	0.126	0.132	0.341
REALM_Palearctic	0.0566	0.149	0.7052

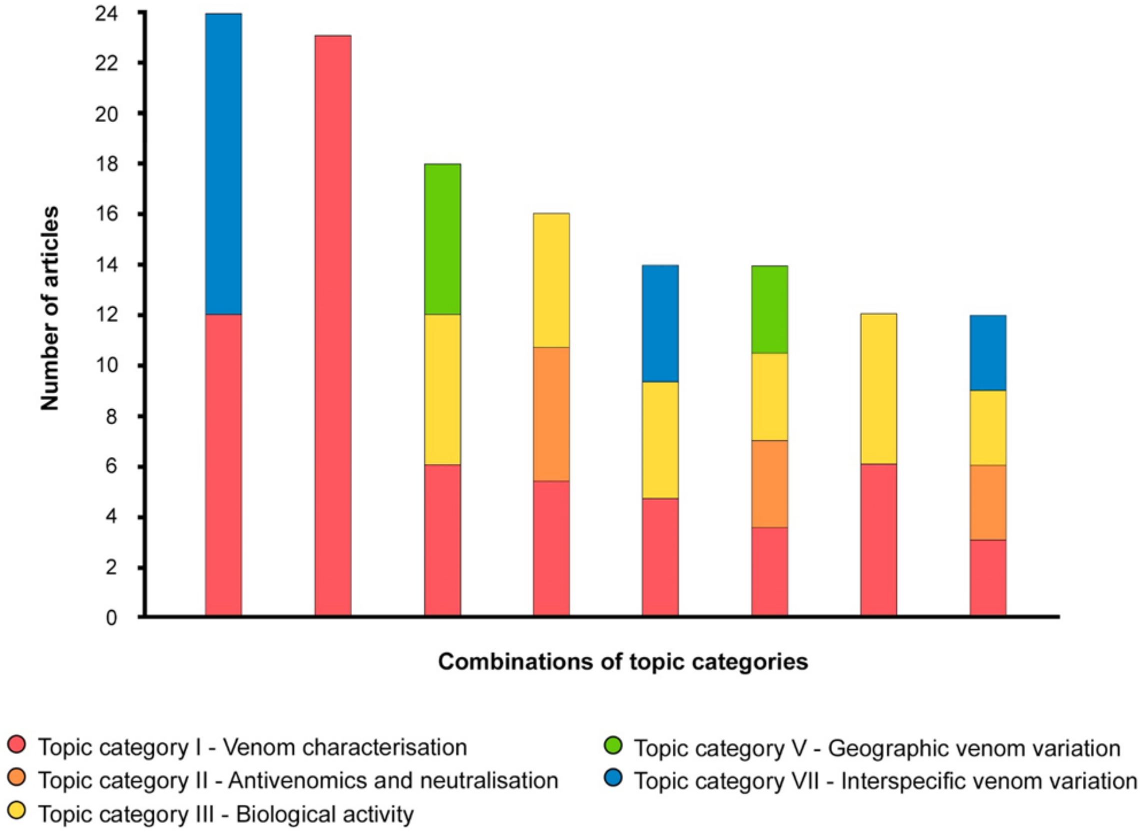


Figure A1.1 Information about the combinations of topic categories retrieved in the analysed articles. The graph shows the eight most represented combinations in terms of number of articles.

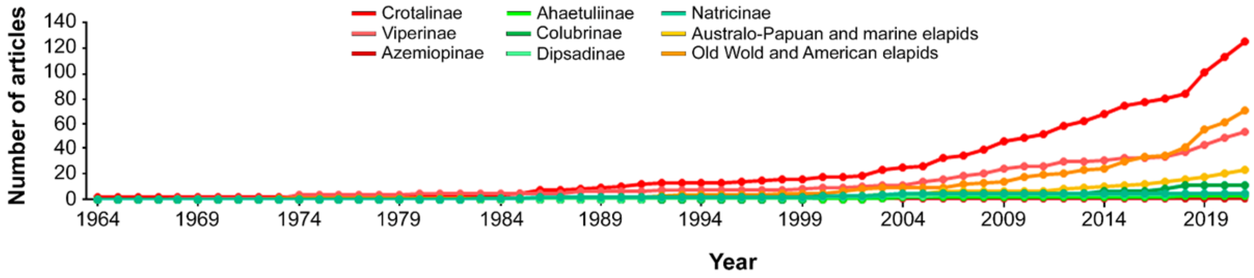


Figure A1.2 Chronological trends of the analysed publications, by snake subfamily/group considered. Notice the prevalence of Crotalinae, Viperinae, and Old World and American elapids over the other subfamilies/groups.

Supplementary Information for Chapter 5

Venomics of Lataste's viper (*Vipera latastei*)

List of Supplementary Tables and Figures

Table A2.1 List of the *V. latastei* specimens considered in the present work. Codes relative to the six venoms used to produce the six proteomes are reported in bold.

Table A2.2 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of juvenile *V. latastei* 19VL013 from Vila Chã. ■ = non-reduced; ▼= reduced.

Table A2.3 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL253 from Vila Chã. ■ = non-reduced; ▼= reduced.

Table A2.4 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL011 from Vila Chã. ■ = non-reduced; ▼= reduced.

Table A2.5 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of juvenile *V. latastei* 19VL026 from Gerês. ■ = non-reduced; ▼= reduced.

Table A2.6 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL258 from Gerês. ■ = non-reduced; ▼= reduced.

Table A2.7 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 19VL029 from Gerês. ■ = non-reduced; ▼= reduced.

Table A2.8 Final binary matrix of the 34 peaks considered for statistical testing. The elution time (min) of every peak is reported above each peak column. The total number of peaks of each chromaographic profile considered for analysis is reported in the column "Total peaks".

Table A2.9 List of binomial GLMs testing the probability of occurrence of eleven specific chromatographic peaks. The models relate the occurrence of peaks 1, 6, 7, 16, 19, 20, 22, 23, 26, 31, and 33 in each chromatogram with the selected independent variables: snout-vent length (SVL), sex (Sex), day of the year in which the venom sample was collected (in its quadratic term; Day year^2), and population of origin (i.e. Gerês or Vila Chã). The best-fitting model is reported in bold. The table reports the number of parameters in the model (K), the information score of the model (Akaike's Information Criterion corrected for small sample sizes; AICc), the difference in AICc score between the best model and the model being compared (ΔAICc), and the AICc weight (i.e. proportion of the total amount of predictive power provided by the full set of models contained in the model being assessed; wAICc).

Table A2.10 Best binomial GLMs explaining the probability of occurrence of peaks 1, 6, 7, 16, 19, 20, 22, 23, 26, 31, and 33 in a chromatogram. The table shows each peak as response variable (Response), related explanatory variables, coefficient estimate (β), Standard Error (SE), Z value (Z), and associated p-values. Significant p-values are in bold.

Figure A2.1 Comparison between the chromatographic profiles of venoms from single juvenile individuals and juvenile venom pools. In panel A, the overlapped chromatograms correspond to the venom of specimens from the Vila Chã population, namely 19VL013 (red profile) and the pooled venoms of specimens 20VL001, 20VL003, 20VL038, 21VL011, and 21VL019 (blue profile). In panel B, the overlapped chromatograms correspond to the venom of specimens from the Gerês population, namely 19VL026 (red profile) and the pooled venoms of specimens 18VL260, 19VL034, 19VL456, and 19VL458 (blue profile).

Figure A2.2 RP-HPLC profiles of the six *V. latastei* venoms used to produce the six venom proteomes by bottom-up venomics. Above each chromatogram, code, age class, and population of origin (i.e., Vila Chã or Gerês) of the corresponding viper are reported. The numbers linked to the peaks correspond to the numbers of the Spot IDs in Tables A2.2-A2.7.

Table A2.1 List of the *V. latastei* specimens considered in the present work. Codes relative to the six venoms used to produce the six proteomes are reported in bold.

Specimen code	Population	Sex	Age	SVL (mm)	Sample type	Collection date
19VL013	Vila Chã	NA	Juvenile	180	Individual	14/03/2019
18VL007	Vila Chã	Female	Adult	465	Individual	05/04/2018
18VL008	Vila Chã	Male	Adult	390	Individual	05/04/2018
18VL253	Vila Chã	Female	Adult	430	Individual	27/09/2018
18VL264	Vila Chã	Male	Adult	480	Individual	25/10/2018
18VL303	Vila Chã	Female	Adult	425	Individual	14/11/2018
18VL304	Vila Chã	Male	Adult	465	Individual	14/11/2018
18VL305	Vila Chã	Female	Adult	480	Individual	14/11/2018
19VL003	Vila Chã	Female	Adult	465	Individual	25/02/2019
19VL008	Vila Chã	Male	Adult	430	Individual	26/02/2019
19VL009	Vila Chã	Male	Adult	585	Individual	26/02/2019
19VL020	Vila Chã	Male	Adult	610	Individual	21/03/2019
19VL033	Vila Chã	Female	Adult	480	Individual	03/04/2019
19VL066	Vila Chã	Male	Adult	380	Individual	16/05/2019
19VL068	Vila Chã	Female	Adult	380	Individual	22/05/2019
19VL071	Vila Chã	Female	Adult	490	Individual	22/05/2019
19VL180	Vila Chã	Female	Adult	445	Individual	03/07/2019
18VL003	Vila Chã	Male	Adult	490	Individual	14/03/2019
18VL009	Vila Chã	Male	Adult	435	Individual	05/04/2018
18VL010	Vila Chã	Female	Adult	445	Individual	05/04/2018
18VL011	Vila Chã	Male	Adult	415	Individual	21/03/2019
18VL028	Vila Chã	Female	Adult	515	Individual	14/05/2018
18VL306	Vila Chã	Male	Adult	415	Individual	14/11/2018
19VL001	Vila Chã	Female	Adult	485	Individual	25/02/2019
19VL005	Vila Chã	Male	Adult	540	Individual	26/02/2019
19VL006	Vila Chã	Female	Adult	450	Individual	26/02/2019
19VL007	Vila Chã	Male	Adult	465	Individual	26/02/2019
19VL021	Vila Chã	Male	Adult	405	Individual	21/03/2019
19VL022	Vila Chã	Male	Adult	420	Individual	21/03/2019
19VL067	Vila Chã	Female	Adult	490	Individual	16/05/2019
19VL070	Vila Chã	Male	Adult	375	Individual	22/05/2019
19VL181	Vila Chã	Female	Adult	450	Individual	03/07/2019
19VL397	Vila Chã	Female	Adult	435	Individual	14/09/2019
20VL001	Vila Chã	Female	Juvenile	156	Pooled	13/02/2020
20VL003	Vila Chã	Male	Juvenile	190	Pooled	13/02/2020
20VL038	Vila Chã	NA	Juvenile	< 240	Pooled	01/07/2020
21VL011	Vila Chã	Female	Juvenile	198	Pooled	24/03/2021
21VL019	Vila Chã	NA	Juvenile	205	Pooled	05/04/2021
19VL026	Gerês	NA	Juvenile	185	Individual	22/03/2019
18VL258	Gerês	Female	Adult	440	Individual	27/10/2018
18VL259	Gerês	Male	Adult	280	Individual	27/10/2018
18VL261	Gerês	Male	Adult	300	Individual	27/10/2018
19VL011	Gerês	Male	Adult	240	Individual	09/03/2019
19VL012	Gerês	Male	Adult	365	Individual	09/03/2019
19VL016	Gerês	Female	Adult	345	Individual	15/03/2019
19VL017	Gerês	Male	Adult	390	Individual	15/03/2019
19VL018	Gerês	Male	Adult	300	Individual	15/03/2019
19VL019	Gerês	Male	Adult	385	Individual	15/03/2019
19VL025	Gerês	Female	Adult	540	Individual	22/03/2019
19VL027	Gerês	Male	Adult	290	Individual	29/03/2019
19VL028	Gerês	Female	Adult	265	Individual	29/03/2019
19VL030	Gerês	Male	Adult	360	Individual	29/03/2019
19VL035	Gerês	Male	Adult	520	Individual	11/04/2019
19VL179	Gerês	Female	Adult	340	Individual	30/06/2019
19VL454	Gerês	Male	Adult	390	Individual	05/10/2019
19VL455	Gerês	Female	Adult	530	Individual	05/10/2019
19VL457	Gerês	Male	Adult	345	Individual	05/10/2019

19VL029	Gerês	Female	Adult	280	Individual	29/03/2019
19VL459	Gerês	Female	Adult	> 263	Individual	11/10/2019
18VL260	Gerês	NA	Juvenile	160	Pooled	27/10/2018
19VL034	Gerês	NA	Juvenile	190	Pooled	11/04/2019
19VL456	Gerês	Male	Juvenile	182	Pooled	05/10/2019
19VL458	Gerês	Male	Juvenile	< 240	Pooled	11/10/2019

Table A2.2 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of juvenile *V. latastei* 19VL013 from Vila Chã. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
1	0.144			430.2	1	ZNW	*de novo*		SVMPi
2	5.721			444.2	1	ZKW	*de novo*	~*B. blomhoffii* P01021	SVMPi
3	0.676			481.3	2	PRVGPEXPP	*de novo*	~*Bothrops jararaca* P85169	BPP
				536.8	2	ZDPXDPPNPP	*de novo*		BPP
	0.001			649.3	1	PPEIPP	*de novo*	~*Vipera ammodytes ammodytes* APB93441	SVMPi
4	0.263			536.8	2	ZDPXDPPNPP	*de novo*		BPP
5	1.229			536.8	2	ZDPXDPPNPP	*de novo*		BPP
7	2.236			572.8	2	ZRWPGPKVPP	*de novo*	~*Vipera ammodytes ammodytes* AMB36335	BPP
8	0.448			572.8	2	ZRWPGPKVPP	*de novo*	~*Vipera ammodytes ammodytes* AMB36335	BPP
9	0.663	$14^{\blacksquare}$	13963.7						Unidentified (Dimeric disintegrin)
10	1.508	$14^{\blacksquare}$	14086.7/ 14029.7/ 13972.7/ 13915.6/ 13874.6	547.7	2	FYYDSASNK	39	*Bitis gabonica* Q6T269	KTSPi
12	0.351	$17^{\blacksquare}$	13986.8	598.2	3	LGEHCVSGPCCDNCK	130	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
				1009.4	2	GDWNDDYCTGISSDCPR			
				583.3	2	FLNAGTICNR	62	*Macrovipera lebetina* P83253	Dimeric disintegrin
				587.9	3	NSGNPCCDPVTCKPR	61	*Vipera berus berus* P0C6A7	Dimeric disintegrin
13	0.636	$17^{\blacksquare}$	13938.8	587.9	3	NSGNPCCDPVTCKPR	49	*Vipera berus berus* P0C6A7	Dimeric disintegrin
18a	6.273	$16^{\blacktriangledown}$	13580.8/ 13523.8	717.3	2	GDIVCGGDDPCLR	68	*Vipera aspis aspis* CAE47133	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				806.8	2	NYPSSHCTETEQC	67	*Vipera ammodytes ammodytes* P34180	D49-PLA2
				631.3	2	IVCGGDDPCLR	57	*Vipera aspis aspis* CAE47133	D49-PLA2
18b	2.012	$7^{\blacktriangledown}$		767.3	2	CCFVHDCCYGR	59	*Vipera aspis zinnikeri* CAE47307	D49-PLA2
19a	1.914	$29^{\blacktriangledown}$		485.2	2	CILSHSPR	238	*Vipera berus nikolskii* B7FDI0	CRISP
				581.3	2	SVNPTASNMLK			
				777.3	2	MoxEWYPEAAANAER			
				640.3	3	KPEIQNEIIDLHNSLR			
				569.8	2	SVDFDSESPR	176	*Crotalus horridus* ACE73560	CRISP
				703.8	2	EWYPEAAANAER	149	*Protobothrops mucrosquamatus* XP_015678374	CRISP
19b	0.263	$23^{\blacktriangledown}$		589.3	2	SVNPTASNMoxLK	41	*Protobothrops mucrosquamatus* XP_015678374	CRISP
				581.3	2	SVNPTASNMLK	35	*Protobothrops mucrosquamatus* XP_015678374	CRISP
19c	1.059	$16^{\blacktriangledown}$	13522.7	717.3	2	GDIVCGGDDPCLR	69	*Vipera aspis aspis* CAE47133	D49-PLA2
				1039.4	2	SALFSYSDYGCYCGWGGK	43	*Vipera ammodytes montandoni* CAE47243	D49-PLA2
				631.3	2	IVCGGDDPCLR	40	*Vipera aspis aspis* CAE47133	D49-PLA2
20a	1.928	$29^{\blacktriangledown}$		777.3	2	MoxEWYPEAAANAER	229	*Vipera berus* B7FDI1	CRISP
				545.9	3	WTAIIHEWHGEEK			
				960.0	2	KPEIQNEIIDLHNSLR			
				524.2	2	CIYDHSPR	228	*Vipera anatolica senliki* QHR82745	CRISP
				569.8	2	SVDFDSESPR	142	*Crotalus horridus* ACE73560	CRISP
20b	0.209	$23^{\blacktriangledown}$	24773.4	569.8	2	SVDFDSESPR	198	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
				777.3	2	MoxEWYPEAAANAER			
				524.2	2	CIYDHSPR	142	*Vipera anatolica senliki* QHR82745	CRISP
20c	0.695	$15^{\blacktriangledown}$	13695.8	511.9	3	CCFVHDCCYGR	38	*Vipera aspis zinnikeri* CAE47307	D49-PLA2
21a	1.605	$29^{\blacktriangledown}$		589.3	2	SVNPTASNMoxLK	431	*Vipera berus* B7FDI1	CRISP
				445.2	3	RSVNPTASNMoxLK			
				759.3	2	CGENIYMSTSPMK			
				769.3	2	MEWYPEAAANAER			
				818.4	2	WTAIIHEWHGEEK			
				640.3	3	KPEIQNEIIDLHNSLR			
				1162.8	3	SGCAAAYCPSSEYNYFYVCQYCPAGNIEGK	388	*Vipera ammodytes ammodytes* AMB36337	CRISP
				569.8	2	SVDFDSESPR	216	*Crotalus horridus* ACE73560	CRISP
				524.2	2	CIYDHSPR	215	*Vipera anatolica senliki* QHR82745	CRISP
21b	0.225	$23^{\blacktriangledown}$	24675.4/ 24732.3	589.3	2	SVNPTASNMoxLK	186	*Vipera berus* B7FDI1	CRISP
				769.3	2	MEWYPEAAANAER			
				640.3	3	KPEIQNEIIDLHNSLR			
				569.8	2	SVDFDSESPR	168	*Crotalus horridus* ACE73560	CRISP
				524.2	2	CIYDHSPR	149	*Vipera anatolica senliki* QHR82745	CRISP
21c	0.276	$15^{\blacktriangledown}$							Unidentified
22a	7.102	$15^{\blacktriangledown}$	13694.7/ 13752.8	670.3	2	YMLYSLFDCK	149	*Macrovipera lebetina* C3W4R6	D49-PLA2
				874.9	2	VAAICFGENMoxNTYDK			

22b	1.504	6▼							Unidentified
24a	3.873	40▼		433.8	2	IILGVHSK	372	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				444.7	2	FFCLSSK			
				573.3	2	EKFFCLSSK			
				603.3	2	WDKDIMoxLIR			
				612.8	2	IMoxGWGTITTTK			
				796.9	2	TLCAGILQGGIDSCK			
				892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
				616.3	4	VIGGDECNINEHPFLVALHTAR	245	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				696.4	3	FHCAGTLLNKEWVLTAAR	158	*Bitis gabonica* Q6T6S7	SVSP
				979.5	2	HAWCEALYPWVPADSR	101	*Macrovipera lebetina* Q9PT41	SVSP
				766.4	2	FPNGLDKDIMLIR	101	*Daboia siamensis* P18964	SVSP
				629.8	2	NIQNEDEQIR	92	*Protobothrops mucrosquamatus* XP_015671564	SVSP
				530.3	3	KDDVLDKDIMoxLIR	37	*Bothrops jararaca* P81824	SVSP
24b	0.526	29▼	24773.4/ 24675.2	653.3	3	HAWCEALYPWVPADSR	81	*Macrovipera lebetina* Q9PT41	SVSP
				629.8	2	NIQNEDEQIR	71	*Protobothrops mucrosquamatus* XP_015671564	SVSP
				696.4	3	FHCAGTLLNKEWVLTAAR	66	*Bitis gabonica* Q6T6S7	SVSP
				452.3	2	TLCAGILR	38	*Echis ocellatus* ADE45140	SVSP
25a	1.653	66▼		878.9	2	TDIVSPPVCGNDLLEK	63	*Echis ocellatus* ADW54336	PIII-SVMP
				885.9	2	TDIVSPPVCGNELLEK	51	*Echis ocellatus* ADW54351	PIII-SVMP
				777.9	2	IVSPPVCGNELLEK	43	*Echis ocellatus* ADW54351	PIII-SVMP
				742.3	3	LHSWVECESGECCEQCR	37	*Protobothrops mucrosquamatus* XP_015683679	PIII-SVMP
25b	0.635	32▼		878.9	2	TDIVSPPVCGNDLLEK	53	*Echis ocellatus* ADW54336	PIII-SVMP
				885.9	2	TDIVSPPVCGNELLEK	44	*Echis ocellatus* ADW54351	PIII-SVMP
27a	0.691	60▼		885.9	2	TDIVSPPVCGNELLEK	34	*Echis ocellatus* ADW54351	PIII-SVMP
27b	0.456	41▼		455.8	2	IELGVHDK	130	*Vipera berus nikolskii* E5AJX2	SVSP
				587.8	2	VVCAGIWQGGK			
				552.8	2	VLNEDEETR	91	*Vipera ammodytes ammodytes* AMB36344	SVSP
				559.8	2	AAYPWLLER			
				604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
				892.9	2	VIGGDECNINEHPFLA	34	*Daboia russelii* P86530	SVSP
				596.8	2	IMGWGTTTPTK	32	*Crotalus scutulatus* AUS82544	SVSP
27c	0.337	34▼		452.3	2	TLCAGILR	217	*Vipera ammodytes ammodytes* AMB36344	SVSP
				552.8	2	VLNEDEETR			
				563.6	3	VLNEDEETREPTEK			
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
				587.8	2	VVCAGIWQGGK	50	*Vipera anatolica senliki* QHR82809	SVSP
27d	0.243	31▼							Unidentified
28a	1.563	66▼		447.6	3	LVIVVDHSMVTK	81	*Echis coloratus* ADI47606	SVMP (PIII)
				702.9	2	LVIVVYHSMoxVTK			
	0.795	66▼		885.9	2	TDIVSPPVCGNELLEK	101	*Echis ocellatus* CAJ01687	PIII-SVMP
				747.0	3	LHSWVECEIGECCDQCR	73	*Echis carinatus sochureki* ADI47585	PIII-SVMP
28b	0.442	41▼		469.0	3	(389.3) (XYX)VVDHGXFTK	*de novo*	~*Crotalus scutulatus* QIV64912	SVMP (PIII)
28c	0.290	36▼		559.8	2	AAYPWLLER	111	*Vipera ammodytes ammodytes* AMB36344	SVSP
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.198	36▼		694.9	2	LVIVVFHSMoxVTK	28	*Echis coloratus* ADI47634	SVMP (PIII)
28d	0.792	32▼		885.9	2	TDIVSPPVCGNELLEK	34	*Echis ocellatus* ADW54351	PIII-SVMP
				953.7	3	RSECDIAESCTGQSDDCPTDDFHR	34	*Crotalus atrox* QIV64940	PIII-SVMP
28e	0.183	22▼							Unidentified
29a	0.199	57■		849.9	2	TDIVSPPVCGNGLLEK	27	*Echis coloratus* ADI47619	PIII-SVMP
29b	0.382	15▼		494.3	2	DHAQLLYK	164	*Vipera ammodytes ammodytes* APB93444	CTL
				517.3	2	TTDNQWLR			
				521.8	2	ADLVWIGLR			
				712.3	2	AWSDEPNCFVAK	96	*Macrovipera lebetina* B4XT06	CTL
				714.3	2	TWEDAENFCQK	72	*Vipera ammodytes ammodytes* AMB36338	CTL
31a	3.686	60▼		706.3	2	LFCEIVKNTCK	66	*Echis ocellatus* CAJ01680	PIII-SVMP
				849.9	2	TDIVSPPVCGNGLLEK	59	*Echis coloratus* ADI47619	PIII-SVMP
				733.0	3	LHSWAECESGECCQQCR	31	*Echis pyramidum leakeyi* ADI47676	PIII-SVMP
	1.196	60▼		471.3	3	LVIVVDHSMoxVRK	32	*Echis carinatus* Q9PRP9	SVMP (PIII)
31b	0.724	50▼		706.3	2	LFCEIVKNTCK	75	*Echis ocellatus* CAJ01680	PIII-SVMP
				862.9	2	KENDVPIPCAPEDIK	73	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
				849.9	2	TDIVSPPVCGNGLLEK	59	*Echis coloratus* ADI47619	PIII-SVMP
				856.9	2	TDIVSPPVCGNALLEK	36	Echis carinatus sochureki ADI47590	PIII-SVMP

	0.048	50▼	684.9	2	LVIVVDHSMVEK	79	*Echis carinatus* Q9PRP9	SVMP (PIII)
31c	0.636	41▼	456.9	3	LVIVVDHSMVEK	78	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
	0.423	41▼	474.7	2	NAYGGLPEK	38	*Vipera ammodytes ammodytes* QBF53414	SVSP
			509.6	3	IIGGDECNINEHR	37	*Bothrops fonsecai* P0DMH6	SVSP
	0.106	41▼	856.9	2	TDIVSPPVCGNALLEK	34	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			575.6	3	KENDVPIPCAPEDIK	32	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
31d	1.053	36▼	849.9	2	TDIVSPPVCGNGLLEK	72	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			733.0	3	LHSWVECESGECCEQCK	37	*Crotalus atrox* QIV64940	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	34	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.608	36▼	456.9	3	LVIVVDHSMVEK	51	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
			684.9	2	LVIVVDHSMVEK	46	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
31e	1.284	30▼	692.9	2	LVIVVDHSMoxVEK	117	*Echis carinatus* Q9PRP9	SVMP (PI)
			471.3	3	LVIVVDHSMoxVRK			
	0.252	30▼	849.9	2	TDIVSPPVCGNGLLEK	56	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	34	*Echis carinatus sochureki* ADI47590	PIII-SVMP
31f	0.574	26▼	684.9	2	LVIVVDHSMVEK	81	*Echis carinatus* Q9PRP9	SVMP (PI)
			471.3	3	LVIVVDHSMoxVRK			
	0.096	26▼	856.9	2	TDIVSPPVCGNALLEK	32	*Echis carinatus sochureki* ADI47590	SVMP fragment
31g	0.569	23▼	456.9	3	LVIVVDHSMVEK	38	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
			462.3	3	LVIVVDHSMoxVEK	25	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
31h	0.303	21▼	692.9	2	LVIVVDHSMoxVEK	67	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
			456.9	3	LVIVVDHSMVEK	50	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
			462.3	3	LVIVVDHSMoxVEK	50	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
32	1.165							Unidentified
34a	1.692	60▼	438.7	2	STTDLPSR	501	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			431.9	3	IKFEPPLPPKK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			555.8	2	FDEIVGGMDK	374	*Gloydius halys* Q6STF1	LAAO
			567.3	2	YPVKPSEEGK			
			641.8	2	RFDEIVGGMoxDK			
			626.8	2	SAGQLYEESLR	361	*Bothrops pictus* X2L4E2	LAAO
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			564.3	2	AHGWIDSTIK	103	*Calloselasma rhodostoma* P81382	LAAO
34b	0.196	45▼	438.7	2	STTDLPSR	252	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			555.8	2	FDEIVGGMDK	231	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
35a	0.430	57■	513.2	2	GSYYGYCR	132	*Macrovipera lebetina* Q7T046	PIII-SVMP
			521.3	2	IPCAPQDIK			
			534.3	2	QCISLFGSR			
35b	0.162	26▼	630.8	2	CGDDYPFVCK	76	*Vipera ammodytes ammodytes* QBF53411	CTL
35c	0.103	14▼						Unidentified
36a	1.022	97■	619.8	2	EEMoxNWADAEK	136	*Macrovipera lebetina* AJO70723	CTL
			798.9	2	VFKEEMNWADAEK			
			854.9	2	TSADYVWIGLWNQR	117	*Vipera ammodytes ammodytes* QBF53411	CTL
			547.3	3	VFKERMoxNWADAEK	30	*Echis carinatus* Q7T247	CTL
	0.038	97■	647.8	2	LIGVEFWCDR	138	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
			800.3	2	DCQNPCCDAATCK			
36b	0.417	64■	578.3	2	WTDGSSVIYK	141	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			619.8	2	EEMoxNWADAEK	39	*Daboia siamensis* Q4PRD0	CTL
36c	0.420	22▼	578.3	2	WTDGSSVIYK	140	*Vipera ammodytes ammodytes* QBF53411	CTL

			630.8	2	CGDDYPFVCK			
36d	0.484	20▼	578.3	2	WTDGSSVIYK	190	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
36e	0.576	14▼	633.3	2	ERMoxNWADAEK	39	*Echis carinatus* Q7T247	CTL
			619.8	2	EEMoxNWADAEK	36	*Daboia siamensis* Q4PRD0	CTL
37a	3.365	60▼	507.8	2	CILNEPLR	447	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
			513.2	2	GSYYGYCR			
			571.8	2	CILNEPLRK			
			585.3	2	KIPCAPQDIK			
			647.8	2	LIGVEFWCDR			
			800.3	2	DCQNPCCDAATCK			
			806.9	2	ATVAEDSCFEENLK			
			716.3	3	DECDVPEHCTGQSAECPR			
	1.232	60▼	534.3	2	QCISLFGSR	206	*Macrovipera lebetina* Q7T046	PIII-SVMP
			813.9	2	ATVAEDSCFQENQK			
			591.3	2	NQCISLFGSR	179	*Daboia russelii* Q7LZ61	PIII-SVMP
	0.014	60▼	750.8	2	EDDYEEFLEIAK	34	*Daboia russelii* G8XQX1	LAAO
	0.005	60▼	622.3	2	NDQLLWLWR	92	*Echis ocellatus* A3QVN2	Hyaluronidase
37b	0.703	41▼	507.8	2	CILNEPLR	340	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
			585.3	2	KIPCAPQDIK			
			640.3	2	LYCLNNSPGNK			
			647.8	2	LIGVEFWCDR			
			800.3	2	DCQNPCCDAATCK			
			806.9	2	ATVAEDSCFEENLK			
	0.176	41▼	534.3	2	QCISLFGSR	197	*Macrovipera lebetina* Q7T046	PIII-SVMP
37c	1.952	22▼	430.6	3	FITHFWIGLR	53	*Macrovipera lebetina* Q696W1	CTL
			645.4	2	FITHFWIGLR	47	*Macrovipera lebetina* Q696W1	CTL
	0.090	22▼	647.8	2	LIGVEFWCDR	68	*Vipera ammodytes ammodytes* QBF53415	SVMP (PI)
	0.055	22▼	534.3	2	QCISLFGSR	43	*Echis coloratus* ADI47635	SVMP fragment
37d	1.663	20▼	645.4	2	FITHFWIGLR	47	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
			578.3	2	WTDGSSVIYK	40	*Macrovipera lebetina* AJO70726	CTL
39a	4.623	66▼	677.3	2	NPKCILNKPLR	44	*Echis pyramidum leakeyi* ADI47744	SVMP (PIII)
			734.4	2	DLPQCILNKPLR	35	*Cerberus rynchops* D8VNS0	SVMP (PIII)
	0.402	66▼	885.9	2	TDIVSPPVCGNELLEK	60	*Echis ocellatus* ADW54351	PIII-SVMP
39b	0.656	50▼	677.3	2	NPQCIINKPLR	84	*Echis coloratus* ADI47654	SVMP (PIII)
	0.314	50▼	529.3	2	IPCAPKDEK	151	*Daboia russelii* B8K1W0	PIII-SVMP
			593.3	2	KIPCAPKDEK			
			666.8	2	LHSWVECESGK			
			893.0	2	TDIVSPPVCGNDLLER	34	*Echis carinatus sochureki* ADI47604	PIII-SVMP
39c	1.876	33▼						Unidentified
40a	0.376	66▼	529.3	2	IPCAPKDEK	69	*Echis coloratus* ADI47654	PIII-SVMP
			677.4	2	NPQCIINKPLR			
			593.3	2	KIPCAPKDEK	26	*Echis ocellatus* Q2UXQ5	PIII-SVMP
40b	1.670	33▼	676.9	2	NPQCILNKPLR	112	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
41a	0.586	>116▼	1007.9	2	LTPGSQCADGECCDQCR	26	*Echis carinatus sochureki* ADI47586	PIII-SVMP
41b	3.311	66▼	535.2	2	QCVDVNTAY	119	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			1007.9	2	LTPGSQCADGECCDQCR	34	*Echis carinatus sochureki* ADI47586	PIII-SVMP
41c	3.307	55▼	535.2	2	QCVDVNTAY	195	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			798.4	2	SAESVTLDLFGDWR			
			800.3	3	CFNNNLQGTENFHCGMENGR			
41d	1.045	41▼	798.4	2	SAESVTLDLFGDWR	68	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
41e	0.448	33▼	798.4	2	SAESVTLDLFGDWR	32	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
41f	0.472	32▼						Unidentified
43	1.199	>116■	430.7	2	ETDLLNR	607	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			442.3	2	INVLPEAK			
			446.8	2	VTLDLFGK			
			514.3	2	IPCAPQDVK			
			566.2	2	LGNEYGYCR			
			578.3	2	KIPCAPQDVK			

656.3	2	NPCQIYYTPR
718.3	2	LYCFDNLPEHK
799.8	2	DCQNPCCNAATCK
993.4	2	LTPGSQCADGECCDQCK

Table A2.3 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL253 from Vila Chã. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
12	8.726			444.2	1	ZKW	*de novo*	~*Vipera ammodytes ammodytes* APB93441	SVMPi
				649.3	1	PPEIPP	*de novo*	~*Vipera ammodytes ammodytes* APB93441	SVMPi
	1.589			536.8	2	ZDPXDPPNPP	*de novo*	~*Bothrops jararacussu* AAP83421	BPP
14	0.841			536.8	2	ZDPXDPPNPP	*de novo*	~*Bothrops jararacussu* AAP83421	BPP
15	0.381			536.8	2	ZDPXDPPNPP	*de novo*	~*Bothrops jararacussu* AAP83421	BPP
	0.027			649.3	1	PPEIPP	*de novo*	~*Vipera ammodytes ammodytes* APB93441	SVMPi
16	0.653	5▼	4435.9	418.9	3	TSXTSHYCTGK	*de novo*	~*Macrovipera lebetina obtusa* P83469	(K/R)TS disintegrin
17	3.129		7715.9	551.8	1.0	PEIPP	*de novo*	~*Vipera ammodytes ammodytes* APB93441	SVMPi
18	1.371	4▼		553.3	3	IGSVSGLGCNKFKPGH	29	*Vipera ammodytes ammodytes* AMB36336	SVMPi
19a	0.191	6▼	7085.2/ 7028.1/ 6980.1	547.7	2	FYYDSASNK	50	*Bitis gabonica* Q6T269	KTSPi
19b	0.966	4▼		553.3	3	IGSVSGLGCNKFKPGH	30	*Vipera ammodytes ammodytes* AMB36336	SVMPi
20a	1.739	6▼	12399.1/ 12346.5/ 12299.2/ 12246.8/ 12199.5	959.4	2	CLAYMPSFYYDSASNK	92	*Vipera ammodytes ammodytes* P00992	KTSPi
				736.0	3	CLAYMPSFYYDSASNKCK			
				547.7	2	FYYDSASNK	50	*Bitis gabonica* Q6T269	KTSPi
				1027.8	3	FCYLPAEPGECNAYMPSFYYDSASNK	32	*Vipera berus nikolskii* E5AJX3	KTSPi
	0.046	6▼		418.9	3	TSLTSHYCTGK	42	*Macrovipera lebetina obtusa* P83469	Dimeric disintegrin
20b	1.205	4▼		553.3	3	IGSVSGLGCNKFKPGH	30	*Vipera ammodytes ammodytes* AMB36336	SVMPi
24	0.222		13938.7						Unidentified
25	0.326		14452.1						Unidentified
26	2.741	8▼	14435.8/ 14306.1/ 14191.9/ 14062.1	525.3	2	FLNPGTICK	257	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				402.6	3	FLNPGTICKR			
				1080.9	2	AMoxLDGLNDYCTGISSDCPR			
	0.191	8▼		598.2	3	LGEHCVSGPCCDNCK	128	*Vipera ammodytes ammodytes* AMB36349	DC-domain
				1009.4	2	GDWNDDYCTGISSDCPR			
27	1.738	22▼	19735.9	533.2	2	HCVDVTTAY	309	*Vipera ammodytes ammodytes* QBF53416	DC-domain
				475.9	3	LFCELIKNTCK			
				798.9	2	ENDVPIPCAPEDIK			
				575.6	3	KENDVPIPCAPEDIK			
				657.3	3	ENDVPIPCAPEDIKCGR			
				700.0	3	KENDVPIPCAPEDIKCGR			
	0.063	22▼		743.8	2	ETDYEEFLEIAK	49	*Bothrops leucurus* P0DI89	LAAO
29	0.307	8▼	13107.3/ 13080.1	525.3	2	FLNPGTICK	197	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				402.6	3	FLNPGTICKR			
				1080.9	2	AMoxLDGLNDYCTGISSDCPR			
				1009.4	2	GDWNDDYCTGISSDCPR	81	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
				1088.0	2	AMoxLDGLNDYCTGISTDCPR	43	*Echis carinatus* P81631	Dimeric disintegrin
31a	0.221	17▼	24309.7/ 24291.7/ 23898.1	647.3	2	IDTACVCVISR	414	*Vipera ursinii* AEH59582	VNGF
				690.3	2	ALTMoxEGNQASWR			
				462.6	3	CKNPNPVPSGCR			
				570.6	3	FIRIDTACVCVISR			
				596.6	3	HWNSYCTTTDTFVR			
				758.0	3	GIDAKHWNSYCTTTDTFVR			
31b	3.118	10▼		556.8	2	HTVDLQIMR	295	*Vipera aspis aspis* P83942	VEGF
				658.7	2	CSGCCTDESLK			
				1050.5	3	ETLVSILQEYPDEISDIFRPSCVAVLR			
				956.5	4	SACQARETLVSILQEYPDEISDIFRPSCVAVLR			
31c	0.169	8▼		564.8	2	HTVDLQIMoxR	154	*Vipera aspis aspis* P83942	VEGF
				658.7	2	CSGCCTDESLK			
				1050.5	3	ETLVSILQEYPDEISDIFRPSCVAVLR			
34	3.157	14▼	13579.7/ 13522.7	767.3	2	CCFVHDCCYGR	301	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2

				1039.4	2	SALFSYSDYGCYCGWGGK			
				736.0	3	KSALFSYSDYGCYCGWGGK			
				626.3	4	GKPQDATDRCCFVHDCCYGR			
				1315.0	2	MoxGTYSYSFENGDIVCGGDDPCLR	203	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				717.3	2	GDIVCGGDDPCLR	157	*Vipera aspis aspis* CAE47133	D49-PLA2
				774.3	2	TGKIVCGGDDPCLR	87	*Daboia siamensis* Q7T3T5	D49-PLA2
35a	1.638	27▼	24500.3	569.8	2	SVDFDSESPR	207	*Daboia russelii* ACE73568	CRISP
				769.3	2	MEWYPEAAANAER			
				705.3	3	MoxEWYPEAAANAERWAFR			
	0.018	27▼		717.3	2	GDIVCGGDDPCLR	47	*Vipera aspis aspis* CAE47133	D49-PLA2
35b	0.298	14▼		511.9	3	CCFVHDCCYGR	76	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				631.3	2	IVCGGDDPCLR	40	*Vipera aspis aspis* CAE47133	D49-PLA2
37a	0.651	28▼	24773.4/24500.4/ 13692.8/ 13676.8	581.3	2	SVNPTASNMLK	235	*Vipera berus* B7FDI1	CRISP
				769.3	2	MEWYPEAAANAER			
				545.9	3	WTAIIHEWHGEEK			
				640.3	3	KPEIQNEIIDLHNSLR			
				569.8	2	SVDFDSESPR	203	*Crotalus horridus* ACE73560	CRISP
				524.2	2	CIYDHSPR	185	*Vipera anatolica senliki* QHR82745	CRISP
37b	0.540	13▼		717.3	2	GDIVCGGDDPCLR	210	*Vipera aspis aspis* CAE47133	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				874.9	2	VAAICFGENMoxNTYDK			
				938.9	2	VAAICFGENMoxNTYDKK			
				631.3	2	IVCGGDDPCLR	66	*Daboia siamensis* Q7T3T5	D49-PLA2
38a	7.429	13▼	13734.9/ 13677.8	455.2	2	AVCECDR	605	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				486.8	2	GKPLDATDR			
				678.3	2	YMoxLYSLFDCK			
				767.3	2	CCFVHDCCYGR			
				866.9	2	VAAICFGENMNTYDK			
				930.9	2	VAAICFGENMNTYDKK			
				1059.4	2	YMoxLYSLFDCKEESEQC			
				861.1	3	KTGIFGIMSYIYYGCYCGWGGK			
				1307.0	2	MGTYSYSFENGDIVCGGDDPCLR			
				717.3	2	GDIVCGGDDPCLR	447	*Vipera aspis aspis* CAE47133	D49-PLA2
				625.6	3	VAAICFAENMNTYDKK	418	*Vipera renardi* F8QN52	D49-PLA2
				631.3	2	IVCGGDDPCLR	174	*Daboia siamensis* Q7T3T5	D49-PLA2
				773.8	2	CCFVHDCCYAR			
38b	0.500	6▼		511.9	3	CCFVHDCCYGR	176	*Vipera ammodytes ruffoi* Q910A1	D49-PLA2
				874.9	2	VAAICFGENMoxNTYDK			
				930.9	2	VAAICFGENMNTYDKK			
				1307.0	2	MGTYSYSFQNGDIVCGGDDPCLR			
				717.3	2	GDIVCGGDDPCLR	172	*Vipera aspis aspis* CAE47133	D49-PLA2
39	0.602	45▼		437.7	2	ASYALPPR	488	*Vipera ammodytes ammodytes* AMB36343	SVSP
				457.8	2	KLCAGIPR			
				475.7	2	NGAPSIYTK			
				545.3	2	KDNDIMLIK			
				466.6	3	TCGKNGAPSIYTK			
				1061.5	2	GDSGGPLICNGEIQGIVSYGK			
				759.7	3	GDSGGPLICNGEIQGIVSYGKR			
				981.5	3	VYDYTDWIQSIIAGNTAATCPPLLYP			
				756.8	2	VIGGDECNINEHR	106	*Lachesis muta rhombeata* C0HLA1	SVSP
40	1.690	36▼		433.8	2	IILGVHSK	225	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				612.8	2	IMoxGWGTITTTK			
				796.9	2	TLCAGILQGGIDSCK			
				892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
				821.4	3	VIGGDECNINEHPFLVALHTAR	215	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				979.5	2	HAWCEALYPWVPADSR	123	*Macrovipera lebetina* Q9PT41	SVSP
				757.4	2	VTYPDVPHCANIK	111	*Echis coloratus* ADI47559	SVSP
				1044.0	2	FHCAGTLLNKEWVLTAAR	108	*Bitis gabonica* Q6T6S7	SVSP
				511.3	3	FPNGLDKDIMLIR	89	*Daboia siamensis* P18964	SVSP
				803.9	2	TLCAGILQGGIDTCK	62	*Vipera ammodytes ammodytes* AMB36345	SVSP
				629.8	2	NIQNEDEQIR	54	*Protobothrops mucrosquamatus* XP_015671564	SVSP
42	0.703								Unidentified
44a	0.462	66▼		552.8	2	VLNEDEETR	267	*Vipera ammodytes ammodytes* AMB36344	SVSP

			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			444.7	2	FFCLSSK	200	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			504.9	3	VIGGDECNINEHR	83	*Gloydius shedaoensis* Q6T5L0	SVSP
			604.8	2	IMoxGWGTTTPTK	45	*Crotalus scutulatus* AUS82544	SVSP
			892.9	2	VIGGDECNINEHPFLA	31	*Daboia russelii* P86530	SVSP
44b	7.415	36▼	587.8	2	VVCAGIWQGGK	312	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.7	3	CAGTLINQEWVLTAAHCNGK			
			559.8	2	AAYPWLLER	219	*Vipera ammodytes ammodytes* AMB36344	SVSP
			844.9	2	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			504.9	3	VIGGDECNINEHR	124	*Gloydius shedaoensis* Q6T5L0	SVSP
			634.8	2	AENPWLPAQSR	68	*Vipera ammodytes ammodytes* AMB36345	SVSP
			813.4	2	SYTLWDKDIMLIK	66	*Echis pyramidum leakeyi* ADI47546	SVSP
			604.8	2	IMoxGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			892.9	2	VIGGDECNINEHPFLA	38	*Daboia russelii* P86530	SVSP
44c	1.051	31▼	552.8	2	VLNEDEETR	292	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			844.9	2	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			820.4	2	PLSLPSSPPSVGSVCR	115	*Ovophis okinavensis* BAN82126	SVSP
			455.8	2	IELGVHDK	100	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
44d	0.415	29▼	559.8	2	AAYPWLLER	94	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
44e	0.447	26▼	559.8	2	AAYPWLLER	182	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			444.7	2	FFCLSSK	158	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			892.9	2	VIGGDECNINEHPFLA	43	*Daboia russelii* P86530	SVSP
45a	0.129	37▼	559.8	2	AAYPWLLER	136	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	81	*Vipera berus nikolskii* E5AJX2	SVSP
			604.8	2	IMoxGWGTTTPTK	38	*Crotalus scutulatus* AUS82544	SVSP
45b	0.325	33▼	559.8	2	AAYPWLLER	166	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	166	*Vipera ammodytes ammodytes* QBF53412	SVSP
			651.8	2	SIIAGNTTATCPP			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			604.8	2	IMoxGWGTTTPTK	31	*Crotalus scutulatus* AUS82544	SVSP
46a	0.482	200▼	584.3	2	HLATIEWLGK	359	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			781.2	4	ANFVAELVTLTKPETHVWIGLRVEDQR			
			517.3	2	TTDNQWLR	317	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			768.3	2	CNSSQYFVCQSR			
			590.9	3	TWEDAEKFCTEQAR			
			633.6	3	KTWEDAEKFCTEQAR			

			712.3	2	AWSDEPNCFVAK	210	*Macrovipera lebetina* B4XT06	CTL
			1081.4	2	DQDCLPGWSFYEGHCYK	126	*Macrovipera lebetina* B4XSY8	CTL
	0.001	200▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	50	*Macrovipera lebetina* E0Y420	SVSP
46b	0.033	56▼	849.9	2	TDIVSPPVCGNGLLEK	58	*Echis coloratus* ADI47619	PIII-SVMP
			706.3	2	LFCEIVKNTCK	44	*Echis ocellatus* ADW54348	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	39	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			575.6	3	KENDVPIPCAPEDIK	35	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
	0.021	56▼	714.3	2	TWEDAENFCQK	184	*Vipera ammodytes ammodytes* AMB36338	CTL
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			517.3	2	TTDNQWLR	96	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	83	*Macrovipera lebetina* B4XT06	CTL
46c	0.092	37▼	552.8	2	VLNEDEETR	244	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	64	*Vipera anatolica senliki* QHR82809	SVSP
			538.2	2	IYDYSVCR	43	*Vipera ammodytes ammodytes* QBF53414	SVSP
	0.001	37▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	42	*Vipera ammodytes ammodytes* AMB36338	CTL
46d	0.062	33▼	559.8	2	AAYPWLLER	243	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.033	33▼	494.3	2	DHAQLLYK	128	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	75	*Macrovipera lebetina* B4XT06	CTL
			624.3	4	ANFVAELVTLTKPETHVWIGLR	37	*Vipera ammodytes ammodytes* AMB36338	CTL
46e	0.039	31▼	714.3	2	TWEDAENFCQK	161	*Vipera ammodytes ammodytes* AMB36338	CTL
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			494.3	2	DHAQLLYK	155	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	96	*Macrovipera lebetina* B4XT06	CTL
			721.3	3	DQDCLPGWSFYEGHCYK	45	*Macrovipera lebetina* B4XSZ1	CTL
	0.003	31▼	514.3	2	IPCAPQDVK	35	*Protobothrops mucrosquamatus* XP_015683679	PIII-SVMP
	0.002	31▼	559.8	2	AAYPWLLER	33	*Vipera ammodytes ammodytes* AMB36344	SVSP
46f	0.099	18▼	494.3	2	DHAQLLYK	173	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	98	*Macrovipera lebetina* B4XT06	CTL
46g	1.309	14▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	261	*Vipera ammodytes ammodytes* AMB36338	CTL
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			481.2	2	DCHMGWR	231	*Vipera ammodytes ammodytes* APB93444	CTL
			494.3	2	DHAQLLYK			
			517.3	2	TTDNQWLR			
			768.3	2	CNSSQYFVCQSR			
			633.6	3	KTWEDAEKFCTEQAR			
			721.3	2	TWEDAEKFCQK	111	*Macrovipera lebetina* B4XSY8	CTL
			1081.4	2	DQDCLPGWSFYEGHCYK			
47a	1.467	56▼	713.3	2	LFCELIKNTCK	112	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
			862.9	2	KENDVPIPCAPEDIK			
			849.9	2	TDIVSPPVCGNGLLEK	61	*Echis coloratus* ADI47619	PIII-SVMP
			705.8	2	LFCEIVKNTCK	45	*Echis ocellatus* ADW54348	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	30	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.110	56▼	731.7	3	IYEIANIINEMYIPLNIR	36	*Echis coloratus* ADI47609	SVMP (PIII)
47b	0.147	38▼	533.2	2	HCVDVTTAY	76	*Echis carinatus sochureki* ADI47585	PIII-SVMP
			706.3	2	LFCEIVKNTCK			
47c	0.213	35▼	827.4	2	SYTLWDKDIMLIR	280	*Vipera ammodytes ammodytes* QBF53414	SVSP
			833.9	2	HPCAQPHLPAFYTK			
			1258.6	2	VFDYTDWIQSIIAGNTFATCPP			
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR	276	*Vipera ammodytes ammodytes* AMB36344	SVSP

			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			756.8	2	VIGGDECNINEHR	163	*Gloydius shedaoensis* Q6T5L0	SVSP
			841.4	2	NYTLWDKDIMLIR			
			455.8	2	IELGVHDK	106	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			611.0	3	VILPDVPHCANIEIIK			
			929.5	2	IAPFSLPSSPPSVGSVCR	95	*Crotalus atrox* AUS82483	SVSP
			999.5	3	MNRPVTYSTHVAPLSLPSSPPSVGSVCR	38	*Macrovipera lebetina* E0Y419	SVSP
	0.039	35▼	798.9	2	ENDVPIPCAPEDIK	71	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
			575.6	3	KENDVPIPCAPEDIK			
			706.3	2	LFCEIVKNTCK	61	*Echis ocellatus* ADW54348	PIII-SVMP
			849.9	2	TDIVSPPVCGNGLLEK	58	*Echis coloratus* ADI47619	PIII-SVMP
47d	0.261	14▼	412.8	2	GGHLISLK	305	*Vipera ammodytes ammodytes* APB93444	CTL
			494.3	2	DHAQLLYK			
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			595.3	2	TTDNQWLRR			
			768.3	2	CNSSQYFVCQSR			
			549.6	3	ADLVWIGLRDFWR			
			590.9	3	TWEDAEKFCTEQAR			
			712.3	2	AWSDEPNCFVAK	164	*Macrovipera lebetina* B4XT06	CTL
			584.3	2	HLATIEWLGK	116	*Macrovipera lebetina* B4XSY8	CTL
			721.3	3	DQDCLPGWSFYEGHCYK			
			714.3	2	TWEDAENFCQK	99	*Vipera ammodytes ammodytes* AMB36338	CTL
			584.8	2	YDIVWMoxGLR	71	*Vipera ammodytes ammodytes* AMB36341	CTL
			699.3	2	AWSDEPNCYGAK			
			1069.9	2	DQDCLPGWSFYEGNCYK	33	*Daboia palestinae* P0DJL4	CTL
48a	0.560	56▼	533.2	2	HCVDVTTAY	177	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
			798.9	2	ENDVPIPCAPEDIK			
			862.9	2	KENDVPIPCAPEDIK			
			706.3	2	LFCEIVKNTCK	106	*Echis carinatus sochureki* ADI47585	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	68	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			849.9	2	TDIVSPPVCGNGLLEK	53	*Echis coloratus* ADI47619	PIII-SVMP
	0.027	56▼	731.7	3	IYEIANIINEMYIPLNIR	71	*Echis coloratus* ADI47609	SVMP (PIII)
	0.004	56▼	552.0	3	SYTLWDKDIMLIR	46	*Vipera ammodytes ammodytes* QBF53414	SVMP (PIII)
48b	0.237	38▼	533.2	2	HCVDVTTAY	165	*Vipera ammodytes ammodytes* QBF53416	PIII-SVMP
			798.9	2	ENDVPIPCAPEDIK			
			575.6	3	KENDVPIPCAPEDIK			
			657.3	3	ENDVPIPCAPEDIKCGR			
			706.3	2	LFCEIVKNTCK	109	*Echis carinatus sochureki* ADI47585	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	64	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			849.9	2	TDIVSPPVCGNGLLEK	59	*Echis coloratus* ADI47619	PIII-SVMP
	0.021	38▼	504.9	3	VIGGDECNINEHR	84	*Lachesis muta rhombeata* C0HLA1	SVSP
	0.013	38▼	576.8	2	YDIVWMGLR	52	*Vipera ammodytes ammodytes* AMB36341	CTL
			512.8	2	HLASIEGLGK	33	*Daboia palestinae* P0DJL4	CTL
48c	1.015	33▼	474.7	2	NAYGGLPEK	512	*Vipera ammodytes ammodytes* QBF53414	SVSP
			538.2	2	IYDYSVCR			
			827.4	2	SYTLWDKDIMLIR			
			833.9	2	HPCAQPHLPAFYTK			
			839.4	3	VFDYTDWIQSIIAGNTFATCPP			
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR			
			452.3	2	TLCAGILR	184	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			756.8	2	VIGGDECNINEHR	147	*Gloydius shedaoensis* Q6T5L0	SVSP
			841.4	2	NYTLWDKDIMLIR			
			929.5	2	IAPFSLPSSPPSVGSVCR	108	*Crotalus atrox* AUS82483	SVSP

			509.6	3	IIGGDECNINEHR	83	*Gloydius halys* I4CHP3	SVSP
			587.8	2	VVCAGIWQGGK	51	*Vipera berus nikolskii* E5AJX2	SVSP
48d	2.429	14▼	584.8	2	YDIVWMoxGLR	304	*Daboia palestinae* P0DJL5	CTL
			704.3	2	DCPWKWSDDAK			
			892.9	2	NWEDAEKFCTEEVK			
			753.7	3	DQDCLPGWSYFEKYCYK			
			707.6	4	DGHLISLHSNEEVEFMTSLAFPILK			
			512.8	2	HLASIEGLGK	267	*Daboia palestinae* P0DJL4	CTL
			674.4	2	EPQIHVWIGLR			
			699.3	2	SWVDAEKFCQK			
			1069.9	2	DQDCLPGWSFYEGNCYK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR	144	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	85	*Macrovipera lebetina* B4XT06	CTL
			985.4	2	QQCSSHWTDGSAVSYEK	69	*Macrovipera lebetina* C0HKZ6	CTL
	0.002	14▼	504.9	3	IVGGDECNINEHR	59	*Lachesis muta rhombeata* C0HLA2	SVSP
50a	0.538	18▼	413.7	2	SVSFVCK	111	*Macrovipera lebetina* AJO70725	CTL
			958.0	2	GSHLASIHSSEEEAFVSK			
			707.6	4	DGHLISLHSNEEVEFMTSLAFPILK	51	*Daboia palestinae* P0DJL5	CTL
			468.3	2	IIYVNWK	38	*Daboisa siamensis* ADK22831	CTL
	0.019	18▼	647.3	2	IDTACVCVISR	34	*Protobothrops flavoviridis* BAP39981	VNGF
50b	0.512	14▼	584.3	2	HLATIEWLGK	138	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			624.3	4	ANFVAELVTLTKPETHVWIGLR			
			521.8	2	ADLVWIGLR	66	*Sistrurus catenatus edwardsi* B0VXV0	CTL
			699.3	2	AWSDEPNCYGAK	53	*Vipera ammodytes ammodytes* AMB36341	CTL
			512.8	2	HLASIEGLGK	47	*Daboia palestinae* P0DJL4	CTL
			468.3	2	IIYVNWK	38	*Daboisa siamensis* ADK22831	CTL
	0.075	14▼	1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR	65	*Vipera ammodytes ammodytes* QBF53414	SVSP
			559.8	2	AAYPWLLER	51	*Vipera ammodytes ammodytes* AMB36344	SVSP
50c	0.729	12▼	521.8	2	ADLVWIGLR	66	*Sistrurus catenatus edwardsi* B0VXV0	CTL
			639.8	2	ESEIVWMGLSK	49	*Echis carinatus* Q9PSM8	CTL
			647.8	2	ESEIVWMoxGLSK	39	*Echis carinatus* Q9PSM8	CTL
			468.3	2	IIYVNWK	38	*Daboisa siamensis* ADK22831	CTL
			576.8	2	YDIVWMGLR	38	*Vipera ammodytes ammodytes* AMB36341	CTL
			853.9	2	VWNQCDWGWSNGAK	30	*Macrovipera lebetina* B4XT02	CTL
51a	0.364	200▼	714.3	2	TWEDAENFCQK	37	*Vipera ammodytes ammodytes* AMB36338	CTL
			517.3	2	TTDNQWLR	29	*Daboia russelii russelii* ADK22822	CTL
51b	2.336	14▼	494.3	2	DHAQLLYK	171	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			768.3	2	CNSSQYFVCQSR			
			714.3	2	TWEDAENFCQK	160	*Vipera ammodytes ammodytes* AMB36338	CTL
			624.3	4	ANFVAELVTLTKPETHVWIGLR			
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			576.8	2	YDIVWMGLR	102	*Daboia palestinae* P0DJL5	CTL
			822.8	2	DQDCLPGWSYFEK			
			699.3	2	AWSDEPNCYGAK	99	*Vipera ammodytes ammodytes* AMB36341	CTL
			512.8	2	HLASIEGLGK	47	*Daboia palestinae* P0DJL4	CTL
			468.3	2	IIYVNWK	37	*Daboisa siamensis* ADK22831	CTL
51c	2.340	12▼	853.9	2	VWNQCDWGWSNGAK	72	*Macrovipera lebetina* B4XT02	CTL
			609.6	3	AWAEESYCVYFSSTK			
			639.8	2	ESEIVWMGLSK	66	*Echis carinatus* Q9PSM8	CTL
53e	0.072	61▼	438.7	2	STTDLPSR.F	244	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			567.3	2	YPVKPSEEGK	182	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			448.2	2	IFLTCNK	155	*Protobothrops elegans* BAP39915	LAAO
			563.8	2	FDEIVGGMoxDK	138	*Bothrops pictus* X2L4E2	LAAO
53a	1.038	55▼	462.8	2	FEPPLPPK	1158	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			583.4	2	IKFEPPLPPK			

			637.8	2	TFCYPSMIQK			
			826.4	2	NVEEGWYANLGPMoxR			
			1052.0	2	NVEEGWYANLGPMRIPEK			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			756.1	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			816.7	3	FGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1673.8	2	EANLSPGAVDMIGDLLNEDSGYYVSFIESLK			
			1221.9	3	WSLDKYAMGAITTFTPYQFQHFSEALTAPEGR			
			1117.0	4	EANLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEK			
			563.8	2	FDEIVGGMoxDK	285	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			633.8	2	RFDEIVGGMDK			
			690.9	2	SAGQLYEESLRK			
			694.8	2	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	268	*Gloydius halys* Q6STF1	LAAO
			605.1	4	RFDEIVGGMDQLPTSMoxYEAIK	267	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR			
			1053.2	3	ETKVTYQTSANEMoxSSVTADYVIVCTTSR	135	*Crotalus durissus terrificus* C0HJE7	LAAO
53b	0.042	19▼	502.3	2	VTVLEASER	392	*Vipera ammodytes ammodytes* QBF53419	LAAO
			818.4	2	NVEEGWYANLGPMR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			816.7	3	FGLQLNEFVQETDNGWYFIK			
			1116.2	3	EANLSPGAVDMIGDLLNEDSGYYVSFIESLK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	85	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.024	19▼	578.3	2	WTDGSSVIYK	140	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			639.0	3	GSHLASIHSSEEEAFVSK	31	*Macrovipera lebetina* AJO70725	CTL
53c	0.092	14▼	584.8	2	YDIVWMoxGLR	120	*Daboia palestinae* P0DJL5	CTL
			822.9	2	DQDCLPGWSYFEK			
			517.3	2	TTDNQWLR	119	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	105	*Macrovipera lebetina* B4XT06	CTL
			699.3	2	AWSDEPNCYGAK	99	*Vipera ammodytes ammodytes* AMB36341	CTL
			714.3	2	TWEDAENFCQK	52	*Vipera ammodytes ammodytes* AMB36338	CTL
	0.028	14▼	502.3	2	VTVLEASER	195	*Vipera ammodytes ammodytes* QBF53419	LAAO
			818.4	2	NVEEGWYANLGPMR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	69	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
53d	0.113	12▼	517.3	2	TTDNQWLR	56	*Daboia russelii russelii* ADK22822	CTL
			714.3	2	TWEDAENFCQK	45	*Vipera ammodytes ammodytes* AMB36338	CTL
55a	0.145	60▼	423.3	2	LTTLGVNK	796	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			437.7	2	VFPAVEGR			
			476.3	2	VGIIGYTTK			
			513.8	2	ASGNPILLNK			
			566.8	2	VVSLNVLCTK			
			661.3	2	VPTYVPLEMoxEK			
			762.4	2	HGQGTGELLQVSGIK			
			792.4	2	IQLQNYYSQEIGK			
			795.4	2	IIALGHSGFFEDQR			
			859.9	2	ETPVLSNPGPYLEFR			
			736.0	3	GDSSNHNSGDLDISIVGDYIK			
			812.4	3	FHECNLGNLICDAVIYNNLR			
			604.0	3	GSFELTILHTNDVHAR	488	*Naja atra* A0A2I4HXH5	5'-nucleotidase
			526.6	3	HANFPILSANIRPK	456	*Gloydius brevicaudus* B6EWW8	5'-nucleotidase
			863.1	3	YDAMALGNHEFDNGLAGLLDPLLK	411	*Crotalus adamanteus* F8S0Z7	5'-nucleotidase
			653.4	3	YLGYLNVVFDDKGNVIK	224	*Vipera anatolica senliki* QHR82712	5'-nucleotidase
	0.030	60▼	438.7	2	STTDLPSR	257	*Vipera ammodytes ammodytes* QBF53419	LAAO
			420.9	3	FWEDDGIHGGK			

			750.8	2	EDDYEEFLEIAK			
			818.4	2	NVEEGWYANLGPMR			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			567.3	2	YPVKPSEEGK	145	*Protobothrops flavoviridis* BAN82013	LAAO
			461.2	3	SAGQLYEESLRK			
			555.8	2	FDEIVGGMDK	135	*Macrovipera lebetina* P81375	LAAO
55b	1.213	55▼	502.3	2	VTVLEASER	1165	*Vipera ammodytes ammodytes* QBF53419	LAAO
			583.4	2	IKFEPPLPPK			
			630.8	2	FWEDDGIHGGK			
			637.8	2	TFCYPSMIQK			
			431.9	3	HDDIFAYEKR			
			818.4	2	NVEEGWYANLGPMR			
			701.7	3	NVEEGWYANLGPMRIPEK			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			859.4	3	KFGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			916.7	4	WSLDKYAMGAITTFTPYQFQHFSEALTAPEGR			
			463.6	3	KFWEDDGIHGGK	286	*Crotalus adamanteus* O93364	LAAO
			609.1	4	RFDEIVGGMoxDQLPTSMoxYEAIK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR			
			563.8	2	FDEIVGGMoxDK	284	*Bothrops atrox* P0CC17	LAAO
			626.8	2	SAGQLYEESLR	274	*Bothrops pictus* X2L4E2	LAAO
			690.9	2	SAGQLYEESLRK			
			428.3	3	VGEVKKDPGLLK	216	*Daboia russelii* G8XQX1	LAAO
			762.4	2	HGQGTGELLQVSGIK			
			812.4	3	FHECNLGNLICDAVIYNNLR			
			744.6	4	ADDKNPLEECFREDDYEEFLEIAK	176	*Macrovipera lebetina* P81375	LAAO
	0.051	55▼	476.3	2	VGIIGYTTK	184	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			863.1	3	YDAMALGNHEFDNGLAGLLDPLLK	114	*Crotalus adamanteus* F8S0Z7	5'-nucleotidase
			653.4	3	YLGYLNVVFDDKGNVIK	91	*Vipera anatolica senliki* QHR82712	5'-nucleotidase
55c	0.096	19▼	578.3	2	WTDGSSVIYK	238	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
	0.061	19▼	438.7	2	STTDLPSR	350	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			818.4	2	NVEEGWYANLGPMR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	105	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			747.7	3	VFFAGEYTAQAHGWIDSTIK	72	*Ovophis okinavensis* BAN82140	LAAO
55d	0.080	14▼	517.3	2	TTDNQWLR	108	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	91	*Macrovipera lebetina* B4XT06	CTL
			714.3	2	TWEDAENFCQK	80	*Vipera ammodytes ammodytes* AMB36338	CTL
	0.025	14▼	502.3	2	VTVLEASER	194	*Vipera ammodytes ammodytes* QBF53419	LAAO
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
55e	0.182	12▼	619.8	2	EEMoxNWADAEK	70	*Macrovipera lebetina* AJO70723	CTL
			538.2	3	VFKEEMoxNWADAEK			
			647.8	2	ESEIVWMoxGLSK	49	*Echis carinatus* Q9PSM8	CTL
56a	0.124	97▼	554.8	2	TLGMoxLMEGLK	428	*Macrovipera lebetina* W8E7D1	PDE
			567.8	2	NPFYNPSPAK			
			583.8	2	QPLPETLQLK			
			678.3	2	AATYFWPGSEVK			
			724.8	2	DFYTFDSEGIVR			
			785.9	2	SPPTSVPPSASDCLR			
			811.4	2	VNLMoxVDQQWMoxAVR			
			934.0	2	FGPVSGEIIMoxALQMoxADR			
			580.5	4	AERPDFVTLYIEEPDTTGHK			
	0.025	97▼	578.3	2	WTDGSSVIYK	90	*Vipera ammodytes ammodytes* QBF53411	CTL

			630.8	2	CGDDYPFVCK			
			714.3	2	TWEDAENFCQK	45	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	33	*Macrovipera lebetina* B4XT06	CTL
	0.008	97▼	502.3	2	VTVLEASER	64	*Cerastes cerastes* P0DQH9	LAAO
			460.9	3	SAGQLYEESLRK			
56b	0.166	55▼	438.7	2	STTDLPSR	536	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			502.3	2	VTVLEASER			
			583.4	2	IKFEPPLPPK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			817.2	4	HIVVVGAGMoxSGLSAAYVLAGAGHKVTVLEASER			
			567.3	2	YPVKPSEEGK	305	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			563.8	2	FDEIVGGMoxDK	285	*Bothrops atrox* P0CC17	LAAO
56c	0.276	19▼	578.3	2	WTDGSSVIYK	218	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			517.3	2	TTDNQWLR	109	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			430.6	3	FITHFWIGLR	42	*Macrovipera lebetina* Q696W1	CTL
			468.3	2	IIYVNWK	38	*Daboia siamensis* ADK22831	CTL
56d	0.489	17▼	578.3	2	WTDGSSVIYK	399	*Vipera ammodytes ammodytes* QBF53411	CTL
			628.3	2	FIKNCFGLEK			
			630.8	2	CGDDYPFVCK			
			500.3	3	QTNYRTWFNLR			
			854.9	2	TSADYVWIGLWNQR			
			613.0	3	TSADYVWIGLWNQRK			
			468.3	2	IIYVNWK	38	*Daboia siamensis* ADK22831	CTL
56e	0.392	11▼	798.9	2	VFKEEMNWADAEK	295	*Macrovipera lebetina* AJO70723	CTL
			646.0	3	GSHLVSLHNIAEADFVVK			
			688.7	3	GSHLVSLHNIAEADFVVKK			
			947.1	3	DGVIWMoxGLNDVWNECNWGWTDGAK			
			630.8	2	CGDDYPFVCK	129	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			521.8	2	ADIVWIGLR	35	*Echis ocellatus* B5U6Y7	CTL
			647.8	2	ESEIVWMoxGLSK	34	*Echis carinatus* Q9PSM8	CTL
			853.9	2	VWNQCDWGWSNGAK	30	*Macrovipera lebetina* B4XT02	CTL
57a	0.134	55▼	438.7	2	STTDLPSR	269	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			583.3	2	IKFEPPLPPK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			567.3	2	YPVKPSEEGK	212	*Vipera ammodytes ammodytes* P0DI84	LAAO
			626.8	2	SAGQLYEESLR	200	*Cerastes cerastes* P0DQH9	LAAO
			460.9	3	SAGQLYEESLRK			
			563.8	2	FDEIVGGMoxDK	182	*Gloydius halys* Q6STF1	LAAO
	0.017	55▼	587.8	2	VVCAGIWQGGK	61	*Vipera berus nikolskii* E5AJX2	SVSP
57b	0.361	19▼	578.3	2	WTDGSSVIYK	208	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			521.8	2	ADIVWIGLR	48	*Echis ocellatus* B5U6Y7	CTL
			645.4	2	FITHFWIGLR	47	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	39	*Macrovipera lebetina* Q696W1	CTL
57c	0.960	17▼	435.7	2	AQYCISK	116	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			860.9	2	SSPDYVWIGLWNQR	39	*Bitis arietans* AMK37409	CTL
			468.3	2	IIYVNWK	38	*Daboia siamensis* ADK22831	CTL
			430.6	3	FITHFWIGLR	34	*Macrovipera lebetina* Q696W1	CTL

57d	0.743	11▼	611.8	2	EEMNWADAEK	294	*Macrovipera lebetina* AJO70723	CTL
			798.9	2	VFKEEMNWADAEK			
			646.0	3	GSHLVSLHNIAEADFVVK			
			941.7	3	DGVIWMGLNDVWNECNWGWTDGAK			
			630.8	2	CGDDYPFVCK	121	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			633.3	2	ERMoxNWADAEK	105	*Echis carinatus* Q7T247	CTL
			547.3	3	VFKERMoxNWADAEK			
58a	0.171	55▼	438.7	2	STTDLPSR	772	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			431.9	3	HDDIFAYEKR			
			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			563.8	2	FDEIVGGMoxDK	452	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			633.8	2	RFDEIVGGMDK			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	409	*Gloydius halys* Q6STF1	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	303	*Macrovipera lebetina* P81375	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	302	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.016	55▼	534.3	2	QCISLFGSR	186	*Macrovipera lebetina* Q7T046	PIII-SVMP
			813.9	2	ATVAEDSCFQENQK			
			833.4	2	LTPGAECGNGLCCEK			
			507.8	2	CILNEPLR	166	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			806.9	2	ATVAEDSCFEENLK			
	0.002	55▼	504.9	3	VIGGDECNINEHR	67	*Lachesis muta rhombeata* C0HLA1	SVSP
58b	0.077	36▼	559.8	2	AAYPWLLER	210	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			455.8	2	IELGVHDK	98	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			538.2	2	IYDYSVCR	98	*Vipera ammodytes ammodytes* QBF53414	SVSP
			552.0	3	SYTLWDKDIMLIR			
			504.9	3	IVGGDECNINEHR	48	*Lachesis muta rhombeata* C0HLA2	SVSP
			604.8	2	IMoxGWGTTTPTK	45	*Crotalus scutulatus* AUS82544	SVSP
	0.001	36▼	627.8	2	WSPSDSLYGSR	110	*Crotalus atrox* P0CV92	Glutaminyl cyclase
			721.9	2	LIFFDGEEAFVR			
58c	0.068	31▼	452.3	2	TLCAGILR	411	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			820.4	2	PLSLPSSPPSVGSVCR	69	*Ovophis okinavensis* BAN82126	SVSP
58d	0.211	19▼	630.8	2	CGDDYPFVCK	148	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			712.3	2	AWSDEPNCFVAK	91	*Macrovipera lebetina* B4XT06	CTL
			645.4	2	FITHFWIGLR	50	*Macrovipera lebetina* Q696W1	CTL
			468.3	2	IIYVNWK	34	*Daboisa siamensis* ADK22831	CTL
58e	0.278	17▼	578.3	2	WTDGSSVIYK	254	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
58f	0.252	14▼	584.3	2	HLATIEWLGK	288	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			517.3	2	TTDNQWLR	193	*Vipera ammodytes ammodytes* APB93444	CTL

			521.8	2	ADLVWIGLR			
			768.3	2	CNSSQYFVCQSR			
			578.3	2	WTDGSSVIYK	183	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			721.3	3	DQDCLPGWSFYEGHCYK	126	*Macrovipera lebetina* B4XSY8	CTL
58g	0.245	11▼	806.9	2	VFKEEMoxNWADAEK	266	*Macrovipera lebetina* AJO70723	CTL
			688.7	3	GSHLVSLHNIAEADFVVKK			
			947.1	3	DGVIWMoxGLNDVWNECNWGWTDGAK			
			630.8	2	CGDDYPFVCK	85	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			647.8	2	ESEIVWMoxGLSK	64	*Echis carinatus* Q9PSM8	CTL
			521.8	2	ADIVWIGLR	52	*Echis ocellatus* B5U6Y7	CTL
59a	0.940	61▼	670.9	2	LVIVVDHSMVTK	502	*Vipera ammodytes ammodytes* AMB36352	PIII-SVMP
			747.9	2	VALVYLEMWTNR			
			799.4	2	IYEMVNTLNVVFR			
			559.9	3	ETIGLAHISSMoxCQSK			
			885.9	2	TDIVSPPVCGNELLEK			
			619.0	3	TRIYEMVNTLNVVFR			
			818.6	4	HDNAQLLTAIDFDRETIGLAHISSMCQSK			
			737.9	3	LHSWVECESGECCDQCR	153	*Echis ocellatus* CAJ01687	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	42	*Echis carinatus sochureki* ADI47595	PIII-SVMP
	0.271	61▼	461.9	3	LVIVVDHSMoxVKK	103	*Echis carinatus* Q9PRP9	SVMP (PIII)
59b	0.167	54▼	438.7	2	STTDLPSR	878	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			859.4	3	KFGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			916.7	4	WSLDKYAMGAITTFTPYQFQHFSEALTAPEGR			
			567.3	2	YPVKPSEEGK	258	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
			448.2	2	IFLTCNK	227	*Protobothrops elegans* BAP39915	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	207	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	200	*Macrovipera lebetina* P81375	LAAO
			564.3	2	AHGWIDSTIK	84	*Demansia vestigiata* A6MFL0	LAAO
	0.044	54▼	447.6	3	LVIVVDHSMVTK	379	*Vipera ammodytes ammodytes* AMB36352	SVMP (PIII)
			747.9	2	VALVYLEMWTNR			
			799.4	2	IYEMVNTLNVVFR			
			814.9	2	HDNAQLLTAIDFDR			
			586.3	3	KHDNAQLLTAIDFDR			
	0.019	54▼	737.9	3	LHSWVECESGECCDQCR	98	*Echis carinatus sochureki* ADI47596	PIII-SVMP
			833.4	2	LTPGAECGNGLCCEK	80	*Macrovipera lebetina* Q7T046	PIII-SVMP
			581.3	2	KGTDDFYCR	74	*Echis pyramidum leakeyi* ADI47673	PIII-SVMP
			535.7	2	QCVDVDTAY	44	*Protobothrops mucrosquamatus* XP_029142320	PIII-SVMP
59c	0.120	36▼	452.3	2	TLCAGILR	274	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			844.9	2	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			474.7	2	NAYGGLPEK	115	*Vipera ammodytes ammodytes* QBF53414	SVSP
			538.2	2	IYDYSVCR			
			556.3	3	HPCAQPHLPAFYTK			
			455.8	2	IELGVHDK	90	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			634.8	2	AENPWLPAQSR	41	*Vipera ammodytes ammodytes* AMB36345	SVSP

			504.9	3	VIGGNECNINEHR	37	*Crotalus atrox* Q9PRW2	SVSP
	0.007	36▼	447.6	3	LVIVVDHSMVTK	223	*Vipera ammodytes ammodytes* AMB36352	SVMP (PIII)
			747.9	2	VALVYLEMWTNR			
			799.4	2	IYEMVNTLNVVFR			
59d	0.113	31▼	452.3	2	TLCAGILR	331	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			820.4	2	PLSLPSSPPSVGSVCR	100	*Ovophis okinavensis* BAN82126	SVSP
	0.001	31▼	799.4	2	IYEMVNTLNVVFR	74	*Vipera ammodytes ammodytes* AMB36352	SVMP fragment
59e	0.361	14▼	494.3	2	DHAQLLYK	223	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			768.3	2	CNSSQYFVCQSR			
			584.3	2	HLATIEWLGK	147	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			624.3	4	ANFVAELVTLTKPETHVWIGLR			
			576.8	2	YDIVWMGLR	99	*Vipera ammodytes ammodytes* AMB36341	CTL
			699.3	2	AWSDEPNCYGAK			
			712.3	2	AWSDEPNCFVAK	94	*Macrovipera lebetina* B4XT06	CTL
	0.001	14▼	799.4	2	IYEMVNTLNVVFR	44	*Vipera ammodytes ammodytes* AMB36352	SVMP fragment
59f	0.276	11▼	538.2	3	VFKEEMoxNWADAEK	86	*Macrovipera lebetina* AJO70723	CTL
			947.1	3	DGVIWMoxGLNDVWNECNWGWTDGAK			
			712.3	2	AWSDEPNCFVAK	40	*Macrovipera lebetina* B4XT06	CTL
			853.9	2	VWNQCDWGWSNGAK	31	*Macrovipera lebetina* B4XT02	CTL
60a	0.082	66▼	411.2	2	LVESFAR	910	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			483.2	2	YWIQAER			
			483.7	2	QLEEEYR			
			502.3	2	VVSLVPYAR			
			553.3	2	VLMoxGNIDLSK			
			586.3	2	LPPPTNTIYR			
			676.3	2	QMDCNWELQK			
			472.2	3	TIHWGEPTAFQK			
			772.3	2	LADDFMoxGSTWQEK			
			945.9	2	EALQMLTAGCPESPCVK			
			1039.0	2	GDDIPYTPVFYAYTLLTK			
			1058.0	2	LSWMoxTGFSGSEGTGVITLQK			
			1081.1	2	NLINESLLSRDQIQYINK			
			731.3	3	GMoxFTSIEPGYYHDGEFGIR			
			1110.5	2	EIPQENLLEDDFSPVMoxLSK			
			1124.6	2	LSAYIVPNTDAHLSEYVAER			
			577.3	2	LEDVALVVPAK	534	*Pantherophis guttatus* XP_034279908	Aminopeptidase
			864.9	2	TKYPVNEEPYLTFK	525	*Notechis scutatus* XP_026530513	Aminopeptidase
			1036.1	2	TLNMPEVNLVDLVWGSER			
			520.3	2	QVIGPELQR	188	*Pseudonaja textilis* XP_026580739	Aminopeptidase
	0.010	66▼	438.7	2	STTDLPSR	155	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			818.4	2	NVEEGWYANLGPMR			
			567.3	2	YPVKPSEEGK	153	*Vipera ammodytes ammodytes* P0DI84	LAAO
	0.004	66▼	559.8	2	AAYPWLLER	115	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.001	66▼	860.0	2	SLEDGTLYIIEQIPK	40	*Ovophis okinavensis* BAN82155	PLB
60b	0.131	61▼	447.6	3	LVIVVDHSMVTK	325	*Vipera ammodytes ammodytes* AMB36352	PIII-SVMP
			755.9	2	VALVYLEMoxWTNR			
			799.4	2	IYEMVNTLNVVFR			
			885.9	2	TDIVSPPVCGNELLEK			
			517.2	2	GTDDFYCR	114	*Echis pyramidum leakeyi* ADI47673	PIII-SVMP
			581.3	2	KGTDDFYCR			
	0.037	61▼	438.7	2	STTDLPSR	200	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			

			750.8	2	EDDYEEFLEIAK			
			460.9	3	SAGQLYEESLRK	142	*Protobothrops flavoviridis* BAN82013	LAAO
	0.011	61$^{\blacktriangledown}$	577.3	2	LEDVALVVPAK	79	*Pantherophis guttatus* XP_034279908	Aminopeptidase
			1039.0	2	GDDIPYTPVFYAYTLLTK			
	0.005	61$^{\blacktriangledown}$	461.9	3	LVIVVDHSMoxVKK	103	*Echis carinatus* Q9PRP9	SVMP (PIII)
60c	0.257	54$^{\blacktriangledown}$	438.7	2	STTDLPSR	928	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			431.9	3	HDDIFAYEKR			
			818.4	2	NVEEGWYANLGPMR			
			1060.0	2	NVEEGWYANLGPMoxRIPEK			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			920.7	4	WSLDKYAMoxGAITTFTPYQFQHFSEALTAPEGR			
			563.8	2	FDEIVGGMoxDK	409	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			690.9	2	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	398	*Protobothrops flavoviridis* BAN82013	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	316	*Macrovipera lebetina* P81375	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	309	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			448.2	2	IFLTCNK	302	*Protobothrops elegans* BAP39915	LAAO
			472.0	4	KDPGLLQYPVKPSEEGK	210	*Bothriechis schlegelii* A0A024BTN9	LAAO
	0.006	54$^{\blacktriangledown}$	559.8	2	AAYPWLLER	59	*Vipera ammodytes ammodytes* AMB36344	SVSP
	0.003	54$^{\blacktriangledown}$	799.4	2	IYEMVNTLNVVFR	110	*Vipera ammodytes ammodytes* AMB36352	SVMP (PIII)
	0.002	54$^{\blacktriangledown}$	762.4	2	HGQGTGELLQVSGIK	89	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			812.4	3	FHECNLGNLICDAVIYNNLR			
	0.002	54$^{\blacktriangledown}$	860.0	2	SLEDGTLYIIEQIPK	51	*Ovophis okinavensis* BAN82155	PLB
	0.001	54$^{\blacktriangledown}$	1039.0	2	GDDIPYTPVFYAYTLLTK	128	*Notechis scutatus* XP_026530513	Aminopeptidase
60d	0.041	44$^{\blacktriangledown}$	703.9	2	FTAYAINGPPVEK	259	*Vipera ammodytes ammodytes* QBF53421	PLB
			730.9	2	QVVPESLFAWER			
			739.8	2	YGLEFSYEMoxAPR			
			541.6	3	NGYWPSYNIPFHK			
			860.0	2	SLEDGTLYIIEQIPK	224	*Ovophis okinavensis* BAN82155	PLB
			474.7	2	VADINMoxAAK	179	*Borikenophis portoricensis* AXL96594	PLB
	0.025	44$^{\blacktriangledown}$	747.7	3	IFFAGEYTANAHGWIDSTIK	129	*Vipera ammodytes ammodytes* QBF53419	LAAO
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	47	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.012	44$^{\blacktriangledown}$	559.8	2	AAYPWLLER	54	*Vipera ammodytes ammodytes* AMB36344	SVSP
60e	0.221	36$^{\blacktriangledown}$	452.3	2	TLCAGILR	267	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			455.8	2	IELGVHDK	153	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			820.4	2	PLSLPSSPPSVGSVCR	45	*Protobothrops mucrosquamatus* XP_015671564	SVSP
			504.9	3	IVGGDECNINEHR	43	*Lachesis muta rhombeata* C0HLA2	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
	0.001	36$^{\blacktriangledown}$	860.0	2	SLEDGTLYIIEQIPK	41	*Ovophis okinavensis* BAN82155	PLB
60f	0.190	31$^{\blacktriangledown}$	452.3	2	TLCAGILR	266	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.5	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			820.4	2	PLSLPSSPPSVGSVCR	81	*Ovophis okinavensis* BAN82126	SVSP
	0.004	31$^{\blacktriangledown}$	730.9	2	KVVPESLFAWER	81	*Ovophis okinavensis* BAN82155	PLB
			860.0	2	SLEDGTLYIIEQIPK			

60g	0.480	14▼	494.3	2	DHAQLLYK	288	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			768.3	2	CNSSQYFVCQSR			
			584.3	2	HLATIEWLGK	166	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			721.3	3	DQDCLPGWSFYEGHCYK	122	*Macrovipera lebetina* B4XSY8	CTL
			712.3	2	AWSDEPNCFVAK	120	*Macrovipera lebetina* B4XT06	CTL
			576.8	2	YDIVWMGLR	98	*Daboia palestinae* P0DJL5	CTL
			822.9	2	DQDCLPGWSYFEK			
			699.3	2	AWSDEPNCYGAK	98	*Vipera ammodytes ammodytes* AMB36341	CTL
			854.9	2	TSADYVWIGLWNQR	50	*Vipera ammodytes ammodytes* QBF53411	CTL
			512.8	2	HLASIEGLGK	47	*Daboia palestinae* P0DJL4	CTL
	0.022	14▼	559.8	2	AAYPWLLER	45	*Vipera ammodytes ammodytes* AMB36344	SVSP
60h	0.428	11▼	538.2	3	VFKEEMoxNWADAEK	102	*Macrovipera lebetina* AJO70723	CTL
			517.0	4	GSHLVSLHNIAEADFVVKK			
			521.8	2	ADLVWIGLR	83	*Vipera ammodytes ammodytes* APB93444	CTL
			853.9	2	VWNQCDWGWSNGAK	71	*Macrovipera lebetina* B4XT00	CTL
			609.6	3	AWAEESYCVYFSSTK			
			639.8	2	ESEIVWMGLSK	70	*Echis carinatus* Q9PSM8	CTL
			647.8	2	ESEIVWMoxGLSK			
62a	0.344	54▼	438.7	2	STTDLPSR	533	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			583.4	2	IKFEPPLPPK			
			420.9	3	FWEDDGIHGGK			
			637.8	2	TFCYPSMIQK			
			826.4	2	NVEEGWYANLGPMoxR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			463.6	3	KFWEDDGIHGGK	287	*Crotalus adamanteus* O93364	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR			
			567.3	2	YPVKPSEEGK	283	*Protobothrops mucrosquamatus* XP_015677465	LAAO
			690.9	2	SAGQLYEESLRK	259	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
	0.003	54▼	530.6	3	IIALGHSGFFEDQR	68	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
	0.002	54▼	676.9	2	NPQCILNKPLR	91	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
62b	1.015	29▼	676.9	2	NPQCILNKPLR	152	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			937.5	2	TWAHQLVNNIIVFYR			
	0.655	29▼	452.3	2	TLCAGILR	266	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
	0.039	29▼	578.6	3	YIELVIVADHSMoxVTK	109	*Macrovipera lebetina* Q3ZD74	PI-SVMP
62c	0.335	14▼	584.3	2	HLATIEWLGK	167	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			494.3	2	DHAQLLYK	130	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	95	*Macrovipera lebetina* B4XT06	CTL
	0.098	14▼	676.9	2	NPQCILNKPLR	71	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
62d	0.251	11▼	512.8	2	HLASIEGLGK	222	*Daboia palestinae* P0DJL4	CTL
			466.6	3	SWVDAEKFCQK			
			513.9	3	QSNGKHLASIEGLGK			
			1069.9	2	DQDCLPGWSFYEGNCYK			
			576.8	2	YDIVWMGLR	167	*Vipera ammodytes ammodytes* AMB36341	CTL
			699.3	2	AWSDEPNCYGAK			
			711.6	4	DGHLISLHSNEEVEFMoxTSLAFPILK			
			822.9	2	DQDCLPGWSYFEK	166	*Daboia palestinae* P0DJL5	CTL
			712.3	2	AWSDEPNCFVAK	88	*Macrovipera lebetina* B4XT06	CTL
			688.4	3	GSHLVSLHNIAEADFVVKK	39	*Macrovipera lebetina* AJO70723	CTL

63a	0.238	116▼	855.5	2	YIELVIVVDNVMFR	173	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			1007.9	2	LTPGSQCADGECCDQCR	44	*Echis carinatus sochureki* ADI47586	PIII-SVMP
63b	0.825	54▼	855.5	2	YIELVIVVDNVMFR	238	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			613.3	3	YIELVIVVDNVMFRK			
			1000.9	2	LTPGSECGDGECCDQCR			
			1007.9	2	LTPGSQCADGECCDQCR	49	*Echis carinatus sochureki* ADI47586	PIII-SVMP
	0.782	54▼	438.7	2	STTDLPSR	428	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			826.4	2	NVEEGWYANLGPMoxR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			567.3	2	YPVKPSEEGK	119	*Vipera ammodytes ammodytes* P0DI84	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	35	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.029	54▼	507.8	2	CIDNKPLR	32	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
63f	0.149	36▼	559.8	2	AAYPWLLER	218	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.6	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			604.8	2	IMoxGWGTTTPTK	46	*Crotalus scutulatus* AUS82544	SVSP
			634.8	2	AENPWLPAQSR	41	*Vipera ammodytes ammodytes* AMB36345	SVSP
63c	0.256	29▼	452.3	2	TLCAGILR	195	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
	0.062	29▼	676.9	2	NPQCILNKPLR	160	*Vipera ammodytes ammodytes* AMB36351	SVMP (PI)
			937.5	2	TWAHQLVNNIIVFYR			
63d	0.243	14▼						Unidentified
63e	0.170	11▼	621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
			853.9	2	NWDQCNWGWSNGAK	*de novo*	~*Macrovipera lebetina* B4XT02	CTL
64a	0.387	116▼	790.4	2	IYEIVNTLNVVFR	299	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			798.4	2	SAESVTLDLFGDWR			
			1000.9	2	LTPGSECGDGECCDQCR			
64b	1.359	54▼	790.4	2	IYEIVNTLNVVFR	349	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			798.4	2	SAESVTLDLFGDWR			
			570.6	3	YIELVIVVDNVMFR			
			1000.9	2	LTPGSECGDGECCDQCR			
			1007.9	2	LTPGSQCADGECCDQCR	48	*Echis carinatus sochureki* ADI47586	PIII-SVMP
	0.242	54▼	502.3	2	VTVLEASER	130	*Vipera ammodytes ammodytes* QBF53419	LAAO
			750.8	2	EDDYEEFLEIAK			
			563.8	2	FDEIVGGMoxDK	121	*Macrovipera lebetina* P81375	LAAO
64c	0.582	45▼	671.3	3	FTHSPDDPDYGMoxVDLGTK	30	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
	0.299	45▼	790.4	2	IYEIVNTLNVVFR	235	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			570.6	3	YIELVIVVDNVMFR			
	0.063	45▼	750.8	2	EDDYEEFLEIAK	31	*Vipera ammodytes ammodytes* QBF53419	LAAO
64f	0.076	29▼	559.8	2	AAYPWLLER	150	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.043	29▼	676.9	2	NPQCILNKPLR	88	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
64d	0.085	14▼	714.3	2	TWEDAENFCQK	78	*Vipera ammodytes ammodytes* AMB36338	CTL
			517.3	2	TTDNQWLR	56	*Vipera ammodytes ammodytes* APB93444	CTL
			712.3	2	AWSDEPNCFVAK	43	*Macrovipera lebetina* B4XT06	CTL
64e	0.108	11▼	798.4	2	SAESVTLDLFGDWR	55	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
65a	0.199	116▼	790.4	2	IYEIVNTLNVVFR	210	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			798.4	2	SAESVTLDLFGDWR			
			1000.9	2	LTPGSECGDGECCDQCR			
	0.098	116▼	599.8	2	ESVGIVQDHSK	50	*Echis coloratus* ADI47641	SVMP (PIII)
	0.022	116▼	826.4	2	NVEEGWYANLGPMoxR	46	*Vipera ammodytes ammodytes* QBF53419	LAAO
65b	0.323	54▼	798.4	2	SAESVTLDLFGDWR	192	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			

			671.3	3	FTHSPDDPDYGMoxVDLGTK	45	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
			528.7	2	QCVDVTTAY	35	*Protobothrops mucrosquamatus* XP_015682631	PIII-SVMP
65c	1.005	45▼	790.4	2	IYEIVNTLNVVFR	286	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			855.5	2	YIELVIVVDNVMFR			
			599.8	2	ESVGIVQDHSK	149	*Echis coloratus* ADI47630	SVMP (PIII)
			1174.6	2	GDLINVQSVVDVTLNSFGEWR			
	0.113	45▼	595.6	3	YSDFAPDYGLVDHGTK	100	*Vipera ammodytes ammodytes* AJC52543	PIII-SVMP
			671.3	3	FTHSPDDPDYGMoxVDLGTK	34	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
	0.003	45▼	1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR	159	*Vipera ammodytes ammodytes* QBF53419	LAAO
65f	0.053	29▼	452.3	2	TLCAGILR	241	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.025	29▼	676.9	2	NPQCILNKPLR	117	*Vipera ammodytes ammodytes* AMB36351	SVMP (PI)
			625.3	3	TWAHQLVNNIIVFYR			
			599.8	2	KSVGIVQDHSK	112	*Echis pyramidum leakeyi* ADI47732	SVMP (PI)
			798.4	2	SAESVTLDLFGDWR	68	*Vipera ammodytes ammodytes* AHB62069	SVMP (PI)
65d	0.061	14▼	584.3	2	HLATIEWLGK	93	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			517.3	2	TTDNQWLR	53	*Vipera ammodytes ammodytes* APB93444	CTL
			712.3	2	AWSDEPNCFVAK	47	*Macrovipera lebetina* B4XT06	CTL
	0.014	14▼	790.4	2	IYEIVNTLNVVFR	145	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
	0.006	14▼	559.8	2	AAYPWLLER	35	*Vipera ammodytes ammodytes* AMB36344	SVSP
65e	0.106	11▼	517.3	2	TTDNQWLR	52	*Vipera ammodytes ammodytes* APB93444	CTL
66a	0.068	54▼	438.7	2	STTDLPSR	206	*Protobothrops flavoviridis* BAN82013	LAAO
			567.3	2	YPVKPSEEGK			
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			826.4	2	NVEEGWYANLGPMoxR	114	*Vipera ammodytes ammodytes* QBF53419	LAAO
	0.040	54▼	501.7	2	IACAPEDVK	130	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			762.8	2	CETSYLFSDCSR			
			1007.9	2	LTPGSQCADGECCDQCR	30	*Echis carinatus sochureki* ADI47586	PIII-SVMP
66b	0.097	46▼	599.8	2	ESVGIVQDHSK	137	*Echis coloratus* ADI47630	SVMP (PIII)
			660.9	2	LVIVVDNVMYR			
	0.005	46▼	826.4	2	NVEEGWYANLGPMoxR	50	*Vipera ammodytes ammodytes* QBF53419	LAAO
66c	1.035	27▼						Unidentified
66d	0.043	14▼	714.3	2	TWEDAENFCQK	59	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	33	*Macrovipera lebetina* B4XT06	CTL
	0.012	14▼	676.9	2	NPQCILNKPLR	66	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
66e	0.069	11▼	853.9	2	VWNQCDWGWSNGAK	27	*Macrovipera lebetina* B4XT02	CTL
67a	0.229	54▼	526.8	2	SCIMoxSGILR	557	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			616.8	2	YSVGIVQDHSK			
			453.2	3	MoxPQCILNKPLK			
			762.8	2	CETSYLFSDCSR			
			805.4	2	IYEIVNTLNVIYR			
			870.9	2	NPCQIYYIPSDENK			
			991.5	2	HDNAQLLTGINFNGPSAGR			
	0.049	54▼	438.7	2	STTDLPSR	217	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			563.8	2	FDEIVGGMoxDK	187	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			460.9	3	SAGQLYEESLRK	161	*Protobothrops flavoviridis* BAN82013	LAAO
	0.005	54▼	442.3	2	INVLPEAK	144	*Daboia siamensis* AUF41660	SVMP (PIII)
			446.8	2	VTLDLFGK			
	0.001	54▼	559.8	2	AAYPWLLER	51	*Vipera ammodytes ammodytes* AMB36344	SVSP
67b	0.045	45▼	599.8	2	ESVGIVQDHSK	88	*Echis coloratus* ADI47630	SVMP (PIII)
			660.9	2	LVIVVDNVMYR			
			521.8	2	YTGNFTAIR	82	*Vipera ammodytes ammodytes* AJC52543	SVMP (PIII)

67f	0.045	36▼		452.3	2	TLCAGILR	180	*Vipera ammodytes ammodytes* AMB36344	SVSP
				559.8	2	AAYPWLLER			
				563.6	3	VLNEDEETREPTEK			
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
				455.8	2	IELGVHDK	92	*Vipera berus nikolskii* E5AJX2	SVSP
				587.8	2	VVCAGIWQGGK			
				504.9	3	IVGGDECNINEHR	48	*Lachesis muta rhombeata* C0HLA2	SVSP
				604.8	2	IMoxGWGTTTPTK	44	*Crotalus scutulatus* AUS82544	SVSP
	0.004	36▼		501.7	2	IACAPEDVK	75	*Macrovipera lebetina* Q4VM07	PIII-SVMP
				661.3	3	HDNAQLLTGINFNGPSAGR			
67g	0.046	31▼		452.3	2	TLCAGILR	314	*Vipera ammodytes ammodytes* AMB36344	SVSP
				552.8	2	VLNEDEETR			
				559.8	2	AAYPWLLER			
				563.6	3	VLNEDEETREPTEK			
				606.3	3	KVLNEDEETREPTEK			
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
67h	0.044	29▼		559.8	2	AAYPWLLER	158	*Vipera ammodytes ammodytes* AMB36344	SVSP
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.009	29▼		501.7	2	IACAPEDVK	33	*Macrovipera lebetina* Q4VM07	PIII-SVMP
67c	0.064	27▼		501.7	2	IACAPEDVK	78	*Macrovipera lebetina* Q4VM07	PIII-SVMP
				411.5	3	YSVGIVQDHSK			
	0.059	27▼		676.9	2	NPQCILNKPLR	70	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
67d	0.085	14▼		714.3	2	TWEDAENFCQK	48	*Vipera ammodytes ammodytes* AMB36338	CTL
67e	0.084	11▼		647.8	2	ESEIVWMoxGLSK	61	*Echis carinatus* Q9PSM8	CTL
				639.8	2	ESEIVWMGLSK	50	*Echis carinatus* Q9PSM8	CTL
69	1.425	46▼		430.7	2	ETDLLNR	735	*Vipera ammodytes* QBF53418	PIII-SVMP
				514.3	2	IPCAPQDVK			
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				601.8	2	WRETDLLNR			
				656.3	2	NPCQIYYTPR			
				453.2	3	MoxPQCILNKPLK			
				718.3	2	LYCFDNLPEHK			
				720.9	2	LVIVADYIMoxFLK			
				811.5	2	IYEIVNLLNVIYR			
				814.8	2	VTAMoxPKGAVKQPEQK			
				627.0	3	TRIYEIVNLLNVIYR			
				993.4	2	LTPGSQCADGECCDQCK			

Table A2.4 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL011 from Vila Chã. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
1	0.225								
2	0.185								
3	1.142			536.8	2	ZDPXDPPNPP	*de novo*		BPP
	7.644			444.3	1	ZBW	*de novo*		SVMPi
4	1.186			536.8	2	ZDPXDPPNPP	*de novo*		BPP
	0.350			472.2	1	ZRW	*de novo*		SVMPi
5	1.115			536.8	2	ZDPXDPPNPP	*de novo*		BPP
6	1.207			536.8	2	ZDPXDPPNPP	*de novo*		BPP
7	1.674	6 ▼	4435.9	418.9	3	TSXTSHYCTGK	*de novo*	~*Macrovipera lebetina obtusa* P83469	(K/R)TS disintegrin
				581.3	2	XBPAGTTCWK	*de novo*	~*Macrovipera lebetina* Q3BK14	(K/R)TS disintegrin
9	4.239			536.8	2	ZDPXDPPNPP	*de novo*		BPP
				573.3	2	ZRWPGPKVPP	*de novo*		BPP
10a	0.503	6 ▼		733.8	2	EFIYGGCHGNANK	54	*Daboia siamensis* A8Y7P1	KTSPi
				547.7	2	FYYDSASNK	50	*Vipera ammodytes ammodytes* P00991	KTSPi
				1033.1	3	FCYLPAEPGECNAYMoxPSFYYDSASNK	43	*Vipera berus nikolskii* E5AJX3	KTSPi
	0.065	6 ▼		418.9	3	TSLTSHYCTGK	44	*Macrovipera lebetina obtusa* P83469	Disintegrin

10b	1.844	5 ▼	3858.9/3930.0/3843.0/3914.0	733.8	2	EFIYGGCHGNANK	41	*Daboia siamensis* A8Y7P1	KTSPi
14	3.445	6 ▼	7522.5/7366.4/6998.2/7493.5	1033.4	3	FCYLPAEPGECNAYMoxPSFYYDSASNK	66	*Vipera berus nikolskii* E5AJX3	KTSPi
				547.7	2	FYYDSASNK	66	*Vipera ammodytes ammodytes* P00991	KTSPi
				627.8	2	HTCVASGKGIQP			
				733.8	2	EFIYGGCHGNANK	63	*Daboia siamensis* A8Y7P1	KTSPi
	0.547	6 ▼		418.9	3	TSLTSHYCTGK	30	*Macrovipera lebetina obtusa* P83469	Medium-sized disintegrin
15a	0.677	15▪	13928.7	583.3	2	FLNAGTICNR	67	*Macrovipera lebetina* P83253	Dimeric disintegrin
15b	0.096	14▪							Unidentified
16	0.426	15▪	13685.6	583.3	2	FLNAGTICNR	65	*Macrovipera lebetina* P83253	Dimeric disintegrin
17	0.043								Unidentified
18a	0.335	26 ▼		605.3	2	KGESYFYCR	144	*Vipera ammodytes ammodytes* QBF53416	DC-domain
				446.5	3	KGESYFYCRK			
	0.143	26 ▼		532.3	2	TPPAGPDVGPR	47	*Agkistrodon bilineatus* P85025	BIP
18b	0.282	22 ▼		533.2	2	HCVDVTTAY	135	*Vipera ammodytes ammodytes* QBF53416	DC-domain
				605.3	2	KGESYFYCR			
				1004.4	2	YDYSEDPDYGMoxVDHGTK			
				619.3	2	RGESYFYCR	88	*Echis ocellatus* CAJ01682	DC-domain
18c	1.795	7 ▼	14436/14408.1/14307.0	525.3	2	FLNPGTICK	205	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				1080.9	2	AMoxLDGLNDYCTGISSDCPR			
				492.2	3	RGEHCVSGPCCR	122	*Macrovipera lebetina obtusa* P0C6B0	Dimeric disintegrin
				725.6	3	TMLDGLNDYCTGVTSDCPR			
				1009.4	2	GDWNDDYCTGISSDCPR	114	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
				1088.0	2	AMoxLDGLNDYCTGISTDCPR	112	*Echis carinatus* P81631	Dimeric disintegrin
				728.6	3	AMoxLDGLHDYCTGVTSDCPR	35	*Echis carinatus* Q5EE07	Dimeric disintegrin
20a	0.099	26▪	14567.2	525.3	2	FLNPGTICK	178	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				1081.0	2	AMoxLDGLNDYCTGISSDCPR			
				895.4	2	NSANPCCDPITCKPR	130	*Macrovipera lebetina obtusa* P0C6B0	Dimeric disintegrin
20b	0.322	15▪		525.3	2	FLNPGTICK	163	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				1081.0	2	AMoxLDGLNDYCTGISSDCPR			
				598.2	3	LGEHCVSGPCCDNCK	134	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
				1009.4	2	GDWNDDYCTGISSDCPR			
21a	0.058	26▪		525.3	2	FLNPGTICK	40	*Eristicophis macmahoni* P81742	Disintegrin
21b	0.340	15▪	14418.0/14390.1	1081.0	2	AMoxLDGLNDYCTGISSDCPR	193	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				525.3	2	FLNPGTICK			
				1009.4	2	GDWNDDYCTGISSDCPR	129	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
				598.2	3	LGEHCVSGPCCDNCK			
				492.2	3	RGEHCVSGPCCR	89	*Macrovipera lebetina obtusa* P0C6B0	Dimeric disintegrin
	0.0003	15▪		1050.5	3	ETLVSILQEYPDEISDIFRPSCVAVLR	29	*Macrovipera lebetina* P82475	VEGF
22	0.142								Unidentified
23	0.693	26▪	25073.1/24689.9	1050.5	3	ETLVSILQEYPDEISDIFRPSCVAVLR	207	*Vipera aspis aspis* P83942	VEGF
				658.7	2	CSGCCTDESLK			
				564.8	2	HTVDLQIMoxR			
25a	0.408	26 ▼		836.9	2	AAAICFGENVNTYDK	296	*Vipera renardi* F8QN51	D49-PLA2
				900.9	2	AAAICFGENVNTYDKK			
				511.9	3	CCFVHDCCYGR			
				826.3	2	YYSSSHCTETEQC			
				914.9	2	VAAICFGENVNTYDKK	102	*Cerastes cerastes* P0DPS4	D49-PLA2
	0.009	26 ▼		647.3	2	IDTACVCVISR	111	*Protobothrops flavoviridis* BAP39981	VNGF
25b	0.308	18 ▼		647.3	2	IDTACVCVISR	214	*Vipera ursinii* AEH59582	VNGF
				690.3	2	ALTMoxEGNQASWR			
				703.8	2	ALTMoxEGNRASWR	139	*Tropidechis carinatus* Q3HXX8	VNGF
	0.133	18 ▼		836.9	2	AAAICFGENVNTYDK	137	*Vipera renardi* F8QN51	D49-PLA2
				601.0	3	AAAICFGENVNTYDKK			
				914.9	2	VAAICFGENVNTYDKK	42	*Cerastes cerastes* P0DPS4	D49-PLA2
25c	0.266	16 ▼		836.9	2	AAAICFGENVNTYDK	130	*Vipera renardi* F8QN51	D49-PLA2
				601.0	3	AAAICFGENVNTYDKK			
				914.9	2	VAAICFGENVNTYDKK	50	*Cerastes cerastes* P0DPS4	D49-PLA2
	0.104	16 ▼		690.3	2	ALTMoxEGNQASWR	218	*Oxyuranus microlepidotus* Q3HXZ0	VNGF
				647.3	2	IDTACVCVISR			
				549.3	2	NPNPVPSGCR			
25d	4.471	14 ▼	13569.8	826.3	2	YYSSSHCTETEQC	339	*Vipera renardi* F8QN51	D49-PLA2
				836.9	2	AAAICFGENVNTYDK			
				900.9	2	AAAICFGENVNTYDKK			

				698.0	3	AAAICFGENVNTYDKKYK			
				914.9	2	VAAICFGENVNTYDKK	144	*Cerastes cerastes* P21789	D49-PLA2
				707.3	3	VAAICFGENVNTYDKKYK			
25e	0.571	6 ▼		511.9	3	CCFVHDCCYGR	262	*Vipera renardi* F8QN51	D49-PLA2
				826.3	2	YYSSSHCTETEQC			
				836.9	2	AAAICFGENVNTYDK			
				900.9	2	AAAICFGENVNTYDKK			
				914.9	2	VAAICFGENVNTYDKK	116	*Cerastes cerastes* P0DPS4	D49-PLA2
26	0.111								Unidentified
27	1.530	15 ▼	13522.7	1039.4	2	SALFSYSDYGCYCGWGGK	243	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				736.0	3	KSALFSYSDYGCYCGWGGK			
				511.9	3	CCFVHDCCYGR			
				455.2	2	AVCECDR			
				908.4	2	VAAICFGENLSTYDKK	139	*Vipera aspis aspis* CAE47193	D49-PLA2
				806.8	2	NYPSSHCTETEQC			
28a	0.226	50 ▼		589.3	2	SVNPTASNMoxLK	171	*Vipera berus nikolskii* B7FDI0	CRISP
				777.3	2	MoxEWYPEAAANAER			
				977.0	2	YFYVCQYCPAGNIIGK	160	*Echis coloratus* P0DMT4	CRISP
	0.022	50 ▼		1039.4	2	SALFSYSDYGCYCGWGGK	45	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				908.4	2	VAAICFGENLSTYDKK	45	*Vipera aspis aspis* CAE47193	D49-PLA2
	0.004	50 ▼		830.4	2	MoxYEIVNTVNEIYR	37	*Crotalus atrox* Q90282	SVMP (PIII)
28b	2.412	26 ▼	24427.1	777.3	2	MoxEWYPEAAANAER	220	*Daboia russelii* ACE73568	CRISP
				904.7	3	SVNPTASNMoxLKMoxEWYPEAAANAER			
				705.3	3	MoxEWYPEAAANAERWAFR			
				1142.8	3	AGCAAAYCPSSKYSYFYVCQYCPAGNIIGK	217	*Protobothrops flavoviridis* Q8JI39	CRISP
				640.3	3	KPEIQNEIIDLHNSLR			
				977.5	2	YFYVCQYCPAGNIIGK	161	*Echis coloratus* P0DMT4	CRISP
28c	0.224	15 ▼		1039.4	2	SALFSYSDYGCYCGWGGK	186	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				1307.0	2	MGTYSYSFENGDIVCGGDDPCLR	148	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				908.4	2	VAAICFGENLSTYDKK	148	*Vipera aspis aspis* CAE47193	D49-PLA2
				1298.5	2	TATYSYSFENGDIVCGGDDPCLR	98	*Daboia russelii* A8CG87	D49-PLA2
				806.8	2	NYPSSHCTETEQC			
	0.034	15 ▼		769.3	2	MEWYPEAAANAER	155	*Crotalus horridus* ACE73560	CRISP
				569.8	2	SVDFDSESPR			
				589.3	2	SVNPTASNMoxLK			
				977.0	2	YFYVCQYCPAGNIIGK	105	*Echis coloratus* P0DMT4	CRISP
29	0.308	26 ▼	13676.8/13693.8	589.3	2	SVNPTASNMoxLK	276	*Vipera berus nikolskii* B7FDI0	CRISP
				777.3	2	MoxEWYPEAAANAER			
				640.3	3	KPEIQNEIIDLHNSLR			
				692.4	3	KPEIQNEIIDLHNSLRR			
				569.8	2	SVDFDSESPR	174	*Crotalus horridus* ACE73560	CRISP
				499.2	3	SKCPASCFCHNK	38	*Ophiophagus hannah* Q7ZT98	CRISP
30	5.139	14 ▼	13676.8	767.3	2	CCFVHDCCYGR	320	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				829.7	3	GKPLDATDRCCFVHDCCYGR			
				1059.4	2	YMoxLYSLFDCKEESEQC			
				1235.0	2	TGIFGIMoxSYIYYGCYCGWGGK			
				923.1	3	AVCECDRVAAICFGENMoxNTYDKK			
				1315.0	2	MoxGTYSYSFENGDIVCGGDDPCLR			
32	0.124	14 ▼	13683.8/13666.8						Unidentified
33a	0.136	66 ▼		1061.0	2	GDSGGPLICNGEIQGIVSYGK	241	*Vipera ammodytes ammodytes* AMB36343	SVSP
				437.7	2	ASYALPPR			
				457.8	2	KLCAGIPR			
				796.9	2	TLCAGILQGGIDSCK	145	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				616.3	4	VIGGDECNINEHPFLVALHTAR			
				696.4	3	FHCAGTLLNKEWVLTAAR	102	*Bitis gabonica* Q6T6S7	SVSP
33b	0.178	50 ▼		457.8	2	KLCAGIPR	80	*Vipera ammodytes ammodytes* AMB36343	SVSP
				437.7	2	ASYALPPR			
33c	1.379	38 ▼		1061.0	2	GDSGGPLICNGEIQGIVSYGK	672	*Vipera ammodytes ammodytes* AMB36343	SVSP
				759.7	3	GDSGGPLICNGEIQGIVSYGKR			
				903.4	3	IVSCKGDSGGPLICNGEIQGIVSYGK			

				955.5	3	IVSCKGDSGGPLICNGEIQGIVSYGKR			
				981.5	3	VYDYTDWIQSIIAGNTAATCPPLLYP			
				437.7	2	ASYALPPR			
				457.8	2	KLCAGIPR			
				553.3	2	KDNDIMoxLIK			
				466.6	3	TCGKNGAPSIYTK			
33d	0.397	24 ▼		821.4	3	VIGGDECNINEHPFLVALHTAR	34	*Vipera ammodytes ammodytes* P0DPS3	SVSP
	0.296	24 ▼		1313.1	2	LSTYSYSFENGDIVCGGDDPCLR	28	*Vipera aspis aspis* CAE47158	D49-PLA2
33e	3.167	14 ▼	13666.8	455.2	2	AVCECDR	462	*Vipera aspis aspis* CAE47119	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				874.9	2	VAAICFGENMoxNTYDK			
				626.3	3	VAAICFGENMoxNTYDKK			
				818.4	3	TGIFGIMoxSYIYYGCYCGWGGK			
				861.1	3	KTGIFGIMSYIYYGCYCGWGGK			
				1313.1	2	LSTYSYSFENGDIVCGGDDPCLR			
				678.3	2	YMoxLYSLFDCK	443	*Vipera ammodytes ammodytes* Q910A1	D49-PLA2
				1059.4	2	YMoxLYSLFDCKEESEQC			
34a	0.257	61 ▼		796.9	2	TLCAGILQGGIDSCK	204	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				821.4	3	VIGGDECNINEHPFLVALHTAR			
				573.3	2	EKFFCLSSK	171	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				612.8	2	IMoxGWGTITTTK			
				1044.0	2	FHCAGTLLNKEWVLTAAR	106	*Bitis gabonica* Q6T6S7	SVSP
				803.9	2	TLCAGILQGGIDTCK	66	*Macrovipera lebetina* E0Y419	SVSP
				452.3	2	TLCAGILR	37	*Echis ocellatus* ADE45140	SVSP
34b	2.298	34 ▼		612.8	2	IMoxGWGTITTTK	265	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				573.3	2	EKFFCLSSK			
				796.9	2	TLCAGILQGGIDSCK			
				433.8	2	IILGVHSK			
				892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
				821.4	3	VIGGDECNINEHPFLVALHTAR	203	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				1044.0	2	FHCAGTLLNKEWVLTAAR	127	*Bitis gabonica* Q6T6S7	SVSP
				1059.5	2	FHCTGTLINEQWVLTAAR	116	*Echis carinatu sochureki* ADI47565	SVSP
				452.3	2	TLCAGILR	77	*Echis coloratus* ADI47576	SVSP
				810.9	2	TLCAGILRGGIDSCK			
				629.8	2	NIQNEDEQIR	53	*Protobothrops mucrosquamatus* XP_015671564	SVSP
35	0.185	31 ▼		612.8	2	IMoxGWGTITTTK	250	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				796.9	2	TLCAGILQGGIDSCK			
				433.8	2	IILGVHSK			
				892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
				821.4	3	VIGGDECNINEHPFLVALHTAR	231	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				1044.0	2	FHCAGTLLNKEWVLTAAR	134	*Bitis gabonica* Q6T6S7	SVSP
36a	0.898	49 ▼		756.8	2	VIGGDECNINEHR	102	*Lachesis muta rhombeata* C0HLA1	SVSP
				485.9	3	VIGGAEFNINEHR	75	*Cerastes cerastes* AAB34493	SVSP
				714.9	4	LNSPVLNSAHIAPLSLPSSPPSVGSVCR	55	*Gloydius intermedius* ASX97878	SVSP
36b	0.067	33 ▼		587.8	2	VVCAGIWQGGK	158	*Vipera berus nikolskii* E5AJX2	SVSP
				916.0	2	VILPDVPHCANIEIIK			
				748.4	3	CAGTLINQEWVLTAAHCNGK			
				796.9	2	TLCAGILQGGIDSCK	125	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				612.8	2	IMoxGWGTITTTK			
				559.8	2	AAYPWLLER	121	*Vipera ammodytes ammodytes* AMB36344	SVSP
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
				604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
36c	0.041	31 ▼		796.9	2	TLCAGILQGGIDSCK	215	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				612.8	2	IMoxGWGTITTTK			
				433.8	2	IILGVHSK			
				616.3	4	VIGGDECNINEHPFLVALHTAR	174	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				696.4	3	FHCAGTLLNKEWVLTAAR	96	*Bitis gabonica* Q6T6S7	SVSP
				504.9	3	IVGGDECNINEHR	44	*Lachesis muta rhombeata* C0HLA2	SVSP
				587.8	2	VVCAGIWQGGK	35	*Vipera berus nikolskii* E5AJX2	SVSP
39a	0.386	81 ▼		587.8	2	VVCAGIWQGGK	188	*Vipera berus nikolskii* E5AJX2	SVSP
				916.0	2	VILPDVPHCANIEIIK			
				748.4	3	CAGTLINQEWVLTAAHCNGK			
				559.8	2	AAYPWLLER	165	*Vipera ammodytes ammodytes* AMB36344	SVSP

39b	2.052	61 ▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			563.6	3	VLNEDEETREPTEK			
			504.9	3	VIGGDECNINEHR	67	*Lachesis muta rhombeata* C0HLA1	SVSP
			803.9	2	TLCAGILQGGIDTCK	51	*Macrovipera lebetina* E0Y419	SVSP
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			587.8	2	VVCAGIWQGGK	214	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			450.2	3	YMoxKIELGVHDK			
			559.8	2	AAYPWLLER	211	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
39c	13.128	33 ▼	573.8	2	SRTLCAGILR			
			606.3	3	KVLNEDEETREPTEK			
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			634.8	2	AENPWLPAQSR	38	*Vipera ammodytes ammodytes* AMB36345	SVSP
			587.8	2	VVCAGIWQGGK	176	*Vipera berus nikolskii* E5AJX2	SVSP
			463.2	3	GRVVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			553.3	4	VILPDVPHCANIEIIKYSK			
			563.6	3	VLNEDEETREPTEK	170	*Vipera ammodytes ammodytes* AMB36344	SVSP
39d	0.442	26 ▼	606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			634.8	2	AENPWLPAQSR	41	*Vipera ammodytes ammodytes* AMB36345	SVSP
			587.8	2	VVCAGIWQGGK	230	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			455.8	2	IELGVHDK			
			552.8	2	VLNEDEETR	199	*Vipera ammodytes ammodytes* AMB36344	SVSP
41a	0.136	35 ▼	559.8	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			634.8	2	AENPWLPAQSR	38	*Vipera ammodytes ammodytes* AMB36345	SVSP
			552.8	2	VLNEDEETR	215	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	120	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
41b	0.455	31 ▼	504.9	3	VIGGDECNINEHR	99	*Agkistrodon bilineatus* AAB26159	SVSP
			496.9	3	VIGGDEHNINEHR			
			803.9	2	TLCAGILQGGIDTCK	94	*Vipera ammodytes ammodytes* AMB36345	SVSP
			634.8	2	AENPWLPAQSR			
			604.8	2	IMoxGWGTTTPTK	34	*Crotalus scutulatus* AUS82544	SVSP
			844.9	2	VLNEDEETREPTEK	221	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			916.0	2	VILPDVPHCANIEIIK	156	*Vipera berus nikolskii* E5AJX2	SVSP
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			634.8	2	AENPWLPAQSR	136	*Vipera ammodytes ammodytes* AMB36345	SVSP
42a	0.197	>116 ▼	803.9	2	TLCAGILQGGIDTCK			
			504.9	3	VIGGDECNINEHR	64	*Agkistrodon bilineatus* AAB26159	SVSP
			604.8	2	IMoxGWGTTTPTK	32	*Crotalus scutulatus* AUS82544	SVSP
			509.6	3	IIGGDECNINEHR	30	*Bothrops fonsecai* P0DMH6	SVSP
			584.3	2	HLATIEWLGK	250	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			781.2	4	ANFVAELVTLTKPETHVWIGLRVEDQR			
			494.3	2	DHAQLLYK	217	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			590.9	3	TWEDAEKFCTEQAR			
			633.6	3	KTWEDAEKFCTEQAR			
			712.3	2	AWSDEPNCFVAK	216	*Macrovipera lebetina* B4XT06	CTL

			721.3	3	DQDCLPGWSFYEGHCYK	129	*Macrovipera lebetina* B4XSY8	CTL
42b	0.050	35 ▼	552.8	2	VLNEDEETR	207	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR			
			563.6	3	VLNEDEETREPTEK			
			803.9	2	TLCAGILQGGIDTCK	95	*Macrovipera lebetina* E0Y419	SVSP
			587.8	2	VVCAGIWQGGK	86	*Vipera berus nikolskii* E5AJX2	SVSP
			611.0	3	VILPDVPHCANIEIIK			
			604.8	2	IMoxGWGTTTPTK	34	*Crotalus scutulatus* AUS82544	SVSP
	0.035	35 ▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	111	*Vipera ammodytes ammodytes* AMB36338	CTL
			781.2	4	ANFVAELVTLTKPETHVWIGLRVEDQR			
			517.3	2	TTDNQWLR	56	*Bitis rhinoceros* I7ICN3	CTL
			712.3	2	AWSDEPNCFVAK	30	*Macrovipera lebetina* B4XT06	CTL
42c	0.097	31 ▼	606.3	3	KVLNEDEETREPTEK	141	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
	0.029	31 ▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	132	*Vipera ammodytes ammodytes* AMB36338	CTL
			781.2	4	ANFVAELVTLTKPETHVWIGLRVEDQR			
			712.3	2	AWSDEPNCFVAK	73	*Macrovipera lebetina* B4XT06	CTL
			517.3	2	TTDNQWLR	166	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			494.3	2	DHAQLLYK			
42d	0.073	28 ▼	584.3	2	HLATIEWLGK	348	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			494.3	2	DHAQLLYK	259	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			768.3	2	CNSSQYFVCQSR			
			521.8	2	ADLVWIGLR			
			721.3	3	DQDCLPGWSFYEGHCYK	135	*Macrovipera lebetina* B4XSY8	CTL
			721.3	2	TWEDAEKFCQK			
			712.3	2	AWSDEPNCFVAK	115	*Macrovipera lebetina* B4XT06	CTL
	0.003	28 ▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	77	*Vipera ammodytes ammodytes* AMB36344	SVSP
			587.8	2	VVCAGIWQGGK	28	*Vipera berus nikolskii* E5AJX2	SVSP
42e	0.091	18 ▼	494.3	2	DHAQLLYK	91	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	73	*Macrovipera lebetina* B4XT06	CTL
			832.1	3	ANFVAELVTLTKPETHVWIGLR	63	*Vipera ammodytes ammodytes* AMB36338	CTL
42f	1.246	14 ▼	584.3	2	HLATIEWLGK	249	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			633.6	3	KTWEDAEKFCTEQAR	193	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			595.3	2	TTDNQWLRR			
			721.6	3	DQDCLPGWSFYEGHCYK	134	*Macrovipera lebetina* B4XSY8	CTL
43a	0.806	61 ▼	843.4	2	HDNAQLLTAIDFDGR	361	*Crotalus scutulatus* QIV64921	PIII-SVMP
			461.2	4	RHDNAQLLTAIDFDGR			
			985.5	2	KRHDNAQLLTAIDFDGR			
			742.3	3	LHSWVECESGECCEQCR			
			747.0	3	LHSWVECEIGECCDQCR	35	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			538.3	3	ENDVKIPCAPEDVK			
	0.379	61 ▼	692.9	2	LVIVVDHSMoxVEK	87	*Echis carinatus* Q9PRP9	SVMP (PIII)
43b	0.169	35 ▼	474.7	2	NAYGGLPEK	344	*Vipera ammodytes ammodytes* QBF53414	SVSP
			827.4	2	SYTLWDKDIMLIR			
			556.3	3	HPCAQPHLPAFYTK			
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR			
			980.0	4	FHCSGTLLNQEWVLTAAHCDMENMQIYLGVHNK			
			559.8	2	AAYPWLLER	208	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	127	*Vipera ammodytes ammodytes* QBF53412	SVSP

			803.9	2	TLCAGILQGGIDTCK	125	*Vipera ammodytes ammodytes* AMB36345	SVSP
			634.8	2	AENPWLPAQSR			
	0.019	35 ▼	562.6	3	HDNAQLLTAIDFDGR	74	*Crotalus scutulatus* QIV64921	SVMP (PIII)
			493.3	4	KRHDNAQLLTAIDFDGR			
			684.9	2	LVIVVDHSMVEK	71	*Echis carinatus* Q9PRP9	SVMP (PIII)
43c	0.091	31 ▼	552.8	2	VLNEDEETR	376	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			559.3	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			504.9	3	VIGGDECNINEHR	69	*Crotalus atrox* Q9PRW2	SVSP
			496.9	3	VIGGDEHNINEHR			
	0.004	31 ▼	692.9	2	LVIVVDHSMoxVEK	42	*Echis carinatus* Q9PRP9	SVMP (PIII)
			440.9	3	LVIVVDNVMYR	26	*Echis coloratus* ADI47641	SVMP (PIII)
43d	0.172	28 ▼	843.4	2	HDNAQLLTAIDFDGR	210	*Crotalus scutulatus* QIV64921	SVMP (PI)
			657.3	3	KRHDNAQLLTAIDFDGR			
			692.9	2	LVIVVDHSMoxVEK	74	*Echis carinatus* Q9PRP9	SVMP (PI)
	0.014	28 ▼	737.6	3	LHSWVKCESGECCDQCR	68	*Trimeresurus stejnegeri* Q3HTN1	SVMP fragment
	0.006	28 ▼	504.9	3	VIGGDECNINEHR	46	*Lachesis muta rhombeata* C0HLA1	SVSP
			509.6	3	IIGGDECNINEHR	33	*Bothrops fonsecai* P0DMH6	SVSP
43e	0.094	14 ▼	584.3	2	HLATIEWLGK	236	*Vipera ammodytes ammodytes* AMB36338	CTL
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			714.3	2	TWEDAENFCQK			
			494.3	2	DHAQLLYK	177	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			521.8	2	ADLVWIGLR			
			721.3	3	DQDCLPGWSFYEGHCYK	96	*Macrovipera lebetina* B4XSY8	CTL
			712.3	2	AWSDEPNCFVAK	91	*Macrovipera lebetina* B4XT06	CTL
			508.3	2	YHAWIGLR	29	*Macrovipera lebetina* AJO70721	CTL
44a	0.254	56 ▼	843.4	2	HDNAQLLTAIDFDGR	207	*Crotalus scutulatus* QIV64921	SVMP (PIII)
			657.3	3	KRHDNAQLLTAIDFDGR			
			692.9	2	LVIVVDHSMoxVEK	81	*Echis carinatus* Q9PRP9	SVMP (PIII)
			742.3	3	LHSWVECESGECCEQCR	55	*Bothrops jararaca* Q0NZX8	SVMP (PIII)
			462.3	3	LVIVVDHSMoxVEK	40	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
	0.232	56 ▼	737.6	3	LHSWVKCESGECCDQCR	69	*Trimeresurus stejnegeri* Q3HTN1	PIII-SVMP
			535.7	2	QCVDVDTAY	46	*Protobothrops mucrosquamatus* XP_029142320	PIII-SVMP
	0.043	56 ▼	504.9	3	VIGGDECNINEHR	66	*Lachesis muta rhombeata* C0HLA1	SVSP
44b	1.682	38 ▼	827.4	2	SYTLWDKDIMLIR	458	*Vipera ammodytes ammodytes* QBF53414	SVSP
			1258.6	2	VFDYTDWIQSIIAGNTFATCPP			
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR			
			980.0	4	FHCSGTLLNQEWVLTAAHCDMENMQIYLGVHNK			
			552.8	2	VLNEDEETR	200	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			929.5	2	IAPFSLPSSPPSVGSVCR	107	*Crotalus atrox* AUS82483	SVSP
			474.6	3	VIGGAEININEHR	59	*Cerastes cerastes* AAB34493	SVSP
			841.4	2	NYTLWDKDIMLIR	56	*Crotalus adamanteus* J3RY93	SVSP
45a	0.072	38 ▼	474.7	2	NAYGGLPEK	241	*Vipera ammodytes ammodytes* QBF53414	SVSP
			538.2	2	IYDYSVCR			
			557.3	3	SYTLWDKDIMoxLIR			
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR			
			559.8	2	AAYPWLLER	223	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			504.9	3	VIGGDECNINEHR	97	*Agkistrodon bilineatus* AAB26159	SVSP
			496.9	3	VIGGDEHNINEHR			
			587.8	2	VVCAGIWQGGK	95	*Vipera berus nikolskii* E5AJX2	SVSP
			803.9	2	TLCAGILQGGIDTCK	78	*Vipera ammodytes ammodytes* AMB36345	SVSP
			634.8	2	AENPWLPAQSR			

			604.8	2	IMoxGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
45b	0.078	34 ▼	552.8	2	VLNEDEETR	352	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR	124	*Vipera ammodytes ammodytes* QBF53414	SVSP
			634.8	2	AENPWLPAQSR	30	*Vipera ammodytes ammodytes* AMB36345	SVSP
45c	1.755	14 ▼	422.9	3	LFKTWEDAEK	457	*Vipera ammodytes ammodytes* AMB36340	CTL
			769.4	2	GYLEWVTLPCGDK			
			890.9	2	DKGYLEWVTLPCGDK			
			1092.9	3	FCTQQVNGCHLASIESVEEANFVAELVPK			
			508.3	2	YHAWIGLR			
			410.9	3	SKYHAWIGLR			
			757.7	3	GYLEWVTLPCGDKNAFICK			
			629.3	4	DKGYLEWVTLPCGDKNAFICK			
			884.0	3	QQCSSHWTDGSAVSYETVTDYTK			
			648.8	2	EEMoxNWEDAEK	306	*Vipera ammodytes ammodytes* AMB36339	CTL
			719.8	2	AWSDKPNCYVAK			
			816.9	2	FDLIWIGLSNLWR			
			557.6	3	VFKEEMoxNWEDAEK			
			547.8	2	TIDYQWLR			
			454.2	3	DCHWGWTDGVK			
			714.3	2	TWEDAENFCQK	177	*Vipera ammodytes ammodytes* AMB36338	CTL
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			721.3	3	DQDCLPGWSFYEGHCYK	125	*Macrovipera lebetina* C0HKZ7	CTL
			536.3	3	VFKLLKTWEDAEK	95	*Daboia siamensis* Q38L02	CTL
			630.9	3	DCPSDWSSYEGHCYK	63	*Gloydius halys* CCH35771	CTL
			521.8	2	ADIVWIGLR	58	*Echis ocellatus* B5U6Y7	CTL
	0.098	14 ▼	535.3	2	FLVALYTSR	263	*Bothrops jararacussu* Q7T229	SVSP
			559.8	2	TLCAGILEGGK			
			584.8	2	VSDYTEWIR			
			682.4	4	RPVNDSPHIAPISLPSSPPSVGSVCR			
			864.4	3	EIYPDVPHCANINILDYEVCR	122	*Crotalus atrox* AUS82483	SVSP
			1243.3	3	TLCAGVLQGGIDTCLADSGGPLICNGQLQGIVAWGR	101	*Vipera ammodytes ammodytes* QBF53414	SVSP
46a	0.054	38 ▼	474.7	2	NAYGGLPEK	187	*Vipera ammodytes ammodytes* QBF53414	SVSP
			538.2	2	IYDYSVCR			
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			573.8	2	SRTLCAGILR	151	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	63	*Vipera berus nikolskii* E5AJX2	SVSP
46b	0.065	34 ▼	559.8	2	AAYPWLLER	325	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	66	*Vipera berus nikolskii* E5AJX2	SVSP
			634.8	2	AENPWLPAQSR	40	*Vipera ammodytes ammodytes* AMB36345	SVSP
46c	0.090	19 ▼	489.3	3	IIYVNWKEGESK	27	*Daboia siamensis* ADK22831	CTL
			629.1	4	RPYCTVMoxVLKPDRIFWFNR	25	*Macrovipera lebetina* AJO70725	CTL
	0.040	19 ▼	1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	53	*Vipera ammodytes ammodytes* AMB36344	SVSP
46d	0.154	17 ▼	639.0	3	GSHLASIHSSEEEAFVSK	65	*Daboia russelii* ADK22834	CTL
			468.3	2	IIYVNWK	34	*Daboia siamensis* ADK22831	CTL
46e	0.096	15 ▼						Unidentified
46f	0.118	12 ▼	621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
			521.8	2	ADIVWIGLR	26	*Echis ocellatus* B5U6Y7	CTL
			468.3	2	IIYVNWK	26	*Daboia siamensis* ADK22831	CTL
47a	0.025	38 ▼	606.3	3	KVLNEDEETREPTEK	105	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	105	*Vipera berus nikolskii* E5AJX2	SVSP
			748.4	3	CAGTLINQEWVLTAAHCNGK			
47b	0.032	34 ▼	563.6	3	VLNEDEETREPTEK	295	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			

			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			452.3	2	TLCAGILR			
			504.9	3	IVGGDECNINEHR	48	*Lachesis muta rhombeata* C0HLA2	SVSP
47c	1.575	15 ▼	409.3	2	LAYPILK	99	*Macrovipera lebetina* B4XT06	CTL
			473.2	2	TYNFICK	89	*Vipera ammodytes ammodytes* AMB36339	CTL
			578.3	2	EMoxTWEDAEK	33	*Gloydius blomhoffii* Q9YI92	CTL
47d	1.758	12 ▼	624.4	4	ANFVAELVTLTKPETHVWIGLR	39	*Vipera ammodytes ammodytes* AMB36338	CTL
			621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
48	0.144							Unidentified
49	0.338							Unidentified
50a	0.489	>116 ▼	438.7	2	STTDLPSR	657	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			645.8	2	TFCYPSMoxIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR)			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			626.8	2	SAGQLYEESLR	180	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	129	*Macrovipera lebetina* P81375	LAAO
	0.003	>116 ▼	818.4	2	NIQSSDLYAWIGLR	66	*Bothrops jararaca* P22029	CTL
50b	4.265	56 ▼	438.7	2	STTDLPSR	943	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.3	2	IKFEPPLPPK			
			630.8	2	FWEDDGIHGGK			
			637.8	2	TFCYPSMIQK			
			431.9	3	IKFEPPLPPKK			
			818.4	2	NVEEGWYANLGPMR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			567.3	2	YPVKPSEEGK	380	*Vipera ammodytes ammodytes* P0DI84	LAAO
			498.6	3	ADDKNPLEECFR	354	*Macrovipera lebetina* P81375	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			563.8	2	FDEIVGGMoxDK			
			626.8	2	SAGQLYEESLR	287	*Bothrops pictus* X2L4E2	LAAO
			690.9	2	SAGQLYEESLRK			
			448.2	2	IFLTCNK	252	*Protobothrops elegans* BAP39915	LAAO
			512.3	2	IFLTCNKK			
			741.8	2	EPDYEEFLEIAK	123	*Thamnophis elegans* XP_032064947	LAAO
50c	0.346	39 ▼	502.3	2	VTVLEASER	483	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			431.9	3	IKFEPPLPPKK			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			567.3	2	YPVKPSEEGK	222	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			641.8	2	RFDEIVGGMoxDK	218	*Gloydius halys* Q6STF1	LAAO
			448.2	2	IFLTCNK	148	*Protobothrops elegans* BAP39915	LAAO
	0.007	39 ▼	826.4	3	VSNSEHIAPLSLPSSPPSVGSVCR	45	*Bothrops asper* Q072L6	SVSP
50d	0.113	32 ▼	502.3	2	VTVLEASER	243	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			

			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			460.9	3	SAGQLYEESLRK	85	*Cerastes cerastes* P0DQH9	LAAO
	0.025	32 ▼	552.8	2	VLNEDEETR	194	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
52	0.711							Unidentified
53	0.066							Unidentified
54a	0.253	82▪						Unidentified
54b	0.119	56▪	438.7	2	STTDLPSR	706	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			818.4	2	NVEEGWYANLGPMR			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			626.8	2	SAGQLYEESLR	265	*Bothrops pictus* X2L4E2	LAAO
			641.8	2	RFDEIVGGMoxDK			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	261	*Protobothrops flavoviridis* BAN82013	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	202	*Macrovipera lebetina* P81375	LAAO
55a	0.070	57 ▼	438.7241	2	STTDLPSR	627	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			431.9	3	IKFEPPLPPKK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			626.8	2	SAGQLYEESLR	345	*Bothrops pictus* X2L4E2	LAAO
			641.8	2	RFDEIVGGMoxDK			
			463.6	3	KFWEDDGIHGGK			
			840.4	2	NEKEGWYANLGPMoxR			
			567.3	2	YPVKPSEEGK	278	*Protobothrops flavoviridis* BAN82013	LAAO
			498.6	3	ADDKNPLEECFR	269	*Macrovipera lebetina* P81375	LAAO
55b	0.026	38 ▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	141	*Vipera ammodytes ammodytes* AMB36344	SVSP
			452.3	2	TLCAGILR			
			573.8	2	SRTLCAGILR			
			587.8	2	VVCAGIWQGGK	77	*Vipera berus nikolskii* E5AJX2	SVSP
			634.8	2	AENPWLPAQSR	31	*Vipera ammodytes ammodytes* AMB36345	SVSP
	0.003	38 ▼	571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK	70	*Vipera ammodytes ammodytes* QBF53419	LAAO
55c	0.035	34 ▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	248	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			573.8	2	SRTLCAGILR			
55d	0.164	19 ▼	578.3	2	WTDGSSVIYK	316	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			1169.6	3	FCTEQANGGHLASIESVEEAEFVAQLVSENIK			
			1178.9	3	FCTEQANGGHLVSIESVEEAEFVAQLVSENIK	200	*Macrovipera lebetina* AJO70726	CTL
55e	0.184	13 ▼	854.9	2	TSADYVWIGLWNQR	121	*Vipera ammodytes ammodytes* QBF53411	CTL
			1169.6	3	FCTEQANGGHLASIESVEEAEFVAQLVSENIK			
56a	0.160	57 ▼	502.3	2	VTVLEASER	819	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			645.8	2	TFCYPSMoxIQK			
			431.9	3	IKFEPPLPPKK			
			826.4	2	NVEEGWYANLGPMoxR			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			

			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			849.4	3	NPLEECFREDDYEEFLEIAK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			563.8	2	FDEIVGGMoxDK	388	Macrovipera lebetina P81375	LAAO
			567.3	2	YPVKPSEEGK			
			463.6	3	KFWEDDGIHGGK			
			498.6	3	ADDKNPLEECFR			
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			626.8	2	SAGQLYEESLR	275	*Protobothrops flavoviridis* BAN82013	LAAO
			564.3	2	AHGWIDSTIK	137	*Demansia vestigiata* A6MFL0	LAAO
	0.097	57 ▼	507.8	2	CILNEPLR	489	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			513.2	2	GSYYGYCR			
			521.3	2	IPCAPQDIK			
			640.3	2	LYCLNNSPGNK			
			647.8	2	LIGVEFWCDR			
			806.9	2	ATVAEDSCFEENLK			
			1090.6	2	IYEMVNTVNEIYIPLNVR			
			1072.2	4	DQFQQNGQPCLNNLGYCYNGDCPIMoxTNQCISLFGSR			
	0.023	57 ▼	972.9	2	NPVTSYGAYGCNCGVLGR	234	*Bothrops moojeni* AQQ72931	K49-PLA2
			954.4	3	MoxILQETGKNPVTSYGAYGCNCGVLGR			
	0.002	57 ▼	504.9	3	IVGGDECNINEHR	59	*Lachesis muta rhombeata* C0HLA2	SVSP
56b	0.080	38 ▼	559.8	2	AAYPWLLER	268	*Vipera ammodytes ammodytes* AMB36344	SVSP
			452.3	2	TLCAGILR			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			573.8	2	SRTLCAGILR			
			538.2	2	IYDYSVCR	107	*Vipera ammodytes ammodytes* QBF53414	SVSP
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	65	*Vipera berus nikolskii* E5AJX2	SVSP
	0.007	38 ▼	747.7	3	IFFAGEYTANAHGWIDSTIK	207	*Vipera ammodytes ammodytes* QBF53419	LAAO
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
	0.001	38 ▼	1098.6	2	IYEMoxVNTVNEIYIPLNVR	83	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
56c	0.076	34 ▼	552.8	2	VLNEDEETR	351	*Vipera ammodytes ammodytes* AMB36344	SVSP
			844.9	2	VLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			820.4	2	PLSLPSSPPSVGSVCR	97	*Ovophis okinavensis* BAN82126	SVSP
	0.020	34 ▼	502.3	2	VTVLEASER	183	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			750.8	2	EDDYEEFLEIAK			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			626.8	2	SAGQLYEESLR	92	*Cerastes cerastes* P0DQH9	LAAO
	0.011	34 ▼	806.9	2	ATVAEDSCFEENLK	88	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
56d	0.101	21 ▼	854.9	2	TSADYVWIGLWNQR	163	*Vipera ammodytes ammodytes* QBF53411	CTL
			1169.6	3	FCTEQANGGHLASIESVEEAEFVAQLVSENIK			
			521.8	2	ADLVWIGLR	117	*Vipera ammodytes ammodytes* APB93444	CTL
			494.3	2	DHAQLLYK			
			645.4	2	FITHFWIGLR	50	*Macrovipera lebetina* Q696W1	CTL
			453.7	2	TWEDAER	36	*Protobothrops elegans* BAP39929	CTL
			468.3	2	IIYVNWK	34	*Daboia siamensis* ADK22831	CTL
			430.6	3	FITHFWIGLR	30	*Macrovipera lebetina* Q696W1	CTL
56e	0.110	16 ▼	494.3	2	DHAQLLYK	282	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			768.3	2	CNSSQYFVCQSR			
			521.8	2	ADLVWIGLR			
			439.7	2	TWEDAEK			
			412.8	2	GGHLISLK			
			508.3	2	YHAWIGLR	247	*Vipera ammodytes ammodytes* AMB36340	CTL
			769.4	2	GYLEWVTLPCGDK			
			1092.9	3	FCTQQVNGCHLASIESVEEANFVAELVPK			

			594.3	3	DKGYLEWVTLPCGDK			
			584.3	2	HLATIEWLGK	201	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			547.8	2	TIDYQWLR	156	*Vipera ammodytes ammodytes* AMB36339	CTL
			549.9	3	FCTEQASGGHLLSLK			
			454.2	3	DCHWGWTDGVK			
			473.2	2	TYNFICK			
			712.3	2	AWSDEPNCFVAK	150	*Macrovipera lebetina* B4XT06	CTL
			721.3	3	DQDCLPGWSFYEGHCYK	149	*Macrovipera lebetina* B4XSY8	CTL
			854.9	2	TSADYVWIGLWNQR	76	*Macrovipera lebetina* B4XSY9	CTL
			430.6	3	FITHFWIGLR	39	*Macrovipera lebetina* Q696W1	CTL
56f	0.115	14 ▼	646.0	3	GSHLVSLHNIAEADFVVK	104	*Echis carinatus sochureki* Q6X5S9	CTL
			688.7	3	GSHLVSLHNIAEADFVVKK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR	74	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	62	*Macrovipera lebetina* B4XT06	CTL
			854.9	2	TSADYVWIGLWNQR	32	*Macrovipera lebetina* AJO70726	CTL
			853.9	2	VWNQCDWGWSNGAK	26	*Macrovipera lebetina* B4XT02	CTL
57	0.136							Unidentified
58a	0.120	68 ▼	1039.0	2	GDDIPYTPVFYAYTLLTK	834	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			1081.1	2	NLINESLLSRDQIQYINK			
			1110.5	2	EIPQENLLEDDFSPVMoxLSK			
			750.0	3	LSAYIVPNTDAHLSEYVAER			
			758.1	3	KPTAILLSGLEETAWLFNLR			
			483.7	2	QLEEEYR			
			553.3	2	VLMoxGNIDLSK			
			561.8	2	RQLEEEYR			
			675.8	2	QMDCNWELQK			
			953.9	2	EALQMoxLTAGCPESPCVK			
			1058.0	2	LSWMoxTGFSGSEGTGVITLQK			
			731.3	3	GMoxFTSIEPGYYHDGEFGIR			
			951.8	3	KLSLNEMoxYLLDSGGQYFDGTTDITR			
			475.8	2	YLVWLEK			
			1036.1	2	TLNMPEVNLVDLVWGSER	468	*Notechis scutatus* XP_026530513	Aminopeptidase
			864.9	2	TKYPVNEEPYLTFK			
58b	0.183	56 ▼	583.4	2	IKFEPPLPPK	480	*Vipera ammodytes ammodytes* QBF53419	LAAO
			441.3	3	RIKFEPPLPPK			
			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			571.3	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			859.4	3	KFGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			460.9	3	SAGQLYEESLRK			
			626.8	2	SAGQLYEESLR	182	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			463.6	3	KFWEDDGIHGGK	179	*Bothrops atrox* P0CC17	LAAO
			586.3	3	DPGLLQYPVKPSEEGK	150	*Bothriechis schlegelii* A0A024BTN9	LAAO
			472.0	4	KDPGLLQYPVKPSEEGK			
			744.6	4	ADDKNPLEECFREDDYEEFLEIAK	86	*Macrovipera lebetina* P81375	LAAO
58c	0.097	37 ▼	563.6	3	VLNEDEETREPTEK	311	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			587.8	2	VVCAGIWQGGK	204	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			538.2	2	IYDYSVCR	147	*Vipera ammodytes ammodytes* QBF53414	SVSP
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR			
			634.8	2	AENPWLPAQSR	105	*Vipera ammodytes ammodytes* AMB36345	SVSP
			803.9	2	TLCAGILQGGIDTCK			
	0.001	37 ▼	1036.1	2	TLNMPEVNLVDLVWGSER	48	*Vipera anatolica senliki* QHR82741	Aminopeptidase
			805.4	2	EAFEVFDILLNGDK	43	*Vipera anatolica senliki* QHR82741	Aminopeptidase
58d	0.133	34 ▼	563.6	3	VLNEDEETREPTEK	368	*Vipera ammodytes ammodytes* AMB36344	SVSP

			606.3	3	KVLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			559.3	2	AAYPWLLER			
			1153.6	2	KSEHIAPLSLPSSPPSVGSVCR	56	*Sistrurus catenatus edwardsi* ABG26973	SVSP
	0.007	34 ▼	502.3	2	VTVLEASER	53	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.003	34 ▼	860.0	2	SLEDGTLYIIEQIPK	37	*Ovophis okinavensis* BAN82155	PLB
58e	0.138	16 ▼	584.3	2	HLATIEWLGK	267	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			494.3	2	DHAQLLYK	259	*Vipera ammodytes ammodytes* APB93444	CTL
			517.3	2	TTDNQWLR			
			768.3	2	CNSSQYFVCQSR			
			549.9	2	FCTEQASGGHLLSLK			
			409.3	2	LAYPILK			
			412.8	2	GGHLISLK			
			769.4	2	GYLEWVTLPCGDK	234	*Vipera ammodytes ammodytes* AMB36340	CTL
			1092.9	3	FCTQQVNGCHLASIESVEEANFVAELVPK			
			508.3	2	YHAWIGLR			
			547.8	2	TIDYQWLR	210	*Vipera ammodytes ammodytes* AMB36339	CTL
			816.9	2	FDLIWIGLSNLWR			
			549.9	3	FCTEQASGGHLLSLK			
			557.6	3	VFKEEMoxNWEDAEK			
			712.3	2	AWSDEPNCFVAK	136	*Macrovipera lebetina* B4XT06	CTL
			721.3	3	DQDCLPGWSFYEGHCYK	111	*Macrovipera lebetina* B4XSY8	CTL
			854.9	2	TSADYVWIGLWNQR	43	*Macrovipera lebetina* AJO70726	CTL
			468.3	2	IIYVNWK	26	*Daboia siamensis* ADK22831	CTL
	0.008	16 ▼	1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	111	*Vipera ammodytes ammodytes* AMB36344	SVSP
	0.002	16 ▼	502.3	2	VTVIEASER	58	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
58f	0.127	14 ▼	494.3	2	DHAQLLYK	84	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			712.3	2	AWSDEPNCFVAK	81	*Macrovipera lebetina* B4XT06	CTL
			816.9	2	FDLIWIGLSNLWR	68	*Vipera ammodytes ammodytes* AMB36339	CTL
			473.2	2	TYNFICK			
			624.4	4	ANFVAELVTLTKPETHVWIGLR	47	*Vipera ammodytes ammodytes* AMB36338	CTL
			619.8	2	EEMoxNWADAEK	36	*Daboia siamensis* Q4PRD0	CTL
			516.8	4	GSHLVSLHNIAEADFVVKK	27	*Echis pyramidum leakeyi* Q6X5S3	CTL
59a	0.027	68 ▼	586.3	2	LPPPTNTIYR	437	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			772.3	2	LADDFMoxGSTWQEK			
			1039.0	2	GDDIPYTPVFYAYTLLTK			
			1110.5	2	EIPQENLLEDDFSPVMoxLSK			
			758.1	3	KPTAILLSGLEETAWLFNLR			
			411.2	2	LVESFAR			
			483.2	2	YWIQAER			
			502.3	2	VVSLVPYAR			
			561.8	2	RQLEEEYR			
			1124.6	2	LSAYIVPNTDAHLSEYVAER			
			864.9	2	TKYPVNEEPYLTFK	348	*Notechis scutatus* XP_026530513	Aminopeptidase
			1036.1	2	TLNMPEVNLVDLVWGSER			
			577.3	2	LEDVALVVPAK	315	*Panterophis guttatus* XP_034279908	Aminopeptidase
			520.3	2	QVIGPELQR	125	*Pseudonaja textilis* XP_026580739	Aminopeptidase
	0.007	68 ▼	438.7	2	STTDLPSR	66	*Vipera ammodytes ammodytes* P0DI84	LAAO
			502.3	2	VTVLEASER			
59b	0.162	56 ▼	438.7	2	STTDLPSR	979	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			532.7	2	NPLEECFR			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			630.8	2	FWEDDGIHGGK			
			647.4	2	IKFEPPLPPKK			
			750.8	2	EDDYEEFLEIAK			

			826.4	2	NVEEGWYANLGPMoxR			
			707.0	3	NVEEGWYANLGPMoxRIPEK			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			567.3	2	YPVKPSEEGK	387	*Vipera ammodytes ammodytes* P0DI84	LAAO
			626.8	2	SAGQLYEESLR	357	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			498.6	3	ADDKNPLEECFR	353	*Macrovipera lebetina* P81375	LAAO
	0.005	56 ▼	798.4	2	SAESVTLDLFGDWR	49	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
59c	0.083	37 ▼	563.6	3	VLNEDEETREPTEK	265	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			587.8	2	VVCAGIWQGGK	199	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			634.8	2	AENPWLPAQSR	129	*Vipera ammodytes ammodytes* AMB36345	SVSP
			803.9	2	TLCAGILQGGIDTCK			
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
	0.005	37 ▼	569.3	2	HDDIFAYEK	77	*Vipera ammodytes ammodytes* P0DI84	LAAO
			502.3	2	VTVLEASER			
59d	0.844	33 ▼	563.6	3	VLNEDEETREPTEK	235	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			452.3	2	TLCAGILR			
	0.031	33 ▼	549.3	2	KPQCILNKP	31	*Gloydius brevicaudus* O73795	SVMP (PIII)
	0.001	33 ▼	676.9	2	NPQCILNKPLR	71	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
59e	0.069	17 ▼	1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	29	*Vipera ammodytes ammodytes* AMB36344	SVSP
59f	0.095	15 ▼	676.9	2	NPQCILNKPLR	71	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
	0.080	15 ▼	517.3	2	TTDNQWLR	122	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			832.1	3	ANFVAELVTLTKPETHVWIGLR	92	*Vipera ammodytes ammodytes* AMB36338	CTL
			584.3	2	HLATIEWLGK			
59g	0.150	14 ▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	89	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	68	*Macrovipera lebetina* B4XT06	CTL
61a	0.059	>116▪	588.3	4	SAESVTLDLFGDWREKDLLR	119	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			1367.3	3	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
			798.4	2	SAESVTLDLFGDWR			
	0.017	>116▪	818.4	2	NIQSSDLYAWIGLR	77	*Bothrops jararaca* P22029	CTL
61b	1.152	56 ▼	790.4	2	IYEIVNTLNVVFR	196	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			618.3	3	SAESVTLDLFGDWREK			
			804.4	2	SAARVTLDLFGDWR	98	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
			840.9	2	KSAATVTLDLFGDWR			
	0.439	56 ▼	438.7	2	STTDLPSR	619	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.3	2	IKFEPPLPPK			
			630.8	2	FWEDDGIHGGK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			571.3	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1224.6	2	FGLQLNEFVQETDNGWYFIK			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			563.8	2	FDEIVGGMoxDK	375	*Macrovipera lebetina* P81375	LAAO
			463.6	3	KFWEDDGIHGGK			

			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			567.3	2	YPVKPSEEGK			
61c	0.096	37 ▼	563.6	3	VLNEDEETREPTEK	158	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	144	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			803.9	2	TLCAGILQGGIDTCK	116	*Vipera ammodytes ammodytes* AMB36345	SVSP
			634.8	2	AENPWLPAQSR			
			604.8	2	IMoxGWGTTTPTK	35	*Crotalus scutulatus* AUS82544	SVSP
	0.034	37 ▼	790.4	2	IYEIVNTLNVVFR	141	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
61d	0.137	35 ▼	552.8	2	VLNEDEETR	327	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	62	*Vipera berus nikolskii* E5AJX2	SVSP
			1153.6	2	KSEHIAPLSLPSSPPSVGSVCR	42	*Sistrurus catenatus edwardsi* ABG26973	SVSP
	0.034	35 ▼	790.4	2	IYEIVNTLNVVFR	157	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			676.9	2	NPQCILNKPLR	108	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
61e	0.053	33 ▼	563.6	3	VLNEDEETREPTEK	328	*Vipera ammodytes ammodytes* AMB36344	SVSP
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			452.3	2	TLCAGILR			
	0.037	33 ▼	790.4	2	IYEIVNTLNVVFR	187	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			676.9	2	NPQCILNKPLR	168	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			937.5	2	TWAHQLVNNIIVFYR			
61f	0.118	15 ▼	584.3	2	HLATIEWLGK	182	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR			
			521.8	2	ADLVWIGLR	140	*Vipera ammodytes ammodytes* APB93444	CTL
			494.3	2	DHAQLLYK			
			517.3	2	TTDNQWLR			
			712.3	2	AWSDEPNCFVAK	91	*Macrovipera lebetina* B4XT06	CTL
			854.9	2	TSADYVWIGLWNQR	61	*Macrovipera lebetina* B4XSY9	CTL
	0.018	15 ▼	790.4	2	IYEIVNTLNVVFR	169	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
	0.004	15 ▼	1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	64	*Vipera ammodytes ammodytes* AMB36344	SVSP
61g	0.107	14 ▼	790.4	2	IYEIVNTLNVVFR	153	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
	0.055	14 ▼	1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	40	*Vipera ammodytes ammodytes* AMB36344	SVSP
63a	0.077	57 ▼	438.7	2	STTDLPSR	644	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			630.8	2	FWEDDGIHGGK			
			431.9	3	IKFEPPLPPKK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			571.3	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			1121.5	3	EANLSPGAVDMoxIGDLLNEDSGYYVSFIESLK			
			563.8	2	FDEIVGGMoxDK	407	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			463.6	3	KFWEDDGIHGGK			
			840.4	2	NEKEGWYANLGPMoxR			
			460.9	3	SAGQLYEESLRK			
			567.3	2	YPVKPSEEGK	375	*Macrovipera lebetina* P81375	LAAO
			498.6	3	ADDKNPLEECFR			

				992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
	0.012	57 ▼		790.4	2	IYEIVNTLNVVFR	152	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
				798.4	2	SAESVTLDLFGDWR			
63b	0.059	55 ▼		798.4	2	SAESVTLDLFGDWR	106	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
				784.1	3	SAESVTLDLFGDWREKDLLR			
63c	0.950	29 ▼		676.9	2	NPKCILNKPLR	33	*Echis pyramidum leakeyi* ADI47732	SVMP (PI)
				704.9	2	SSVTXNXFGEWR	*de novo*	~*Vipera ammodytes ammodytes* AMB36349	SVMP (PI)
64	0.228	57 ▼		501.7	2	IACAPEDVK	502	*Macrovipera lebetina* Q4VM07	PIII-SVMP
				526.8	2	SCIMoxSGILR			
				762.8	2	CETSYLFSDCSR			
				805.4	2	IYEIVNTLNVIYR			
				870.9	2	NPCQIYYIPSDENK			
				661.3	3	HDNAQLLTGINFNGPSAGR			
				677.0	3	LRPGAQCGDGVCCYQCK			
				411.5	3	YSVGIVQDHSK			
	0.007	57 ▼		750.8	2	EDDYEEFLEIAK	177	*Vipera ammodytes ammodytes* QBF53419	LAAO
				826.4	2	NVKEGWYANLGPMoxR			
				438.7	2	STTDLPSR			
65	0.692	55 ▼		566.2	2	LGNEYGYCR	839	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				578.3	2	KIPCAPQDVK			
				679.4	2	MoxPQCILNKPLK			
				799.8	2	DCQNPCCNAATCK			
				811.5	2	IYEIVNLLNVIYR			
				844.4	2	SCIMoxSGTLSCEASIR			
				993.4	2	LTPGSQCADGECCDQCK			
				519.8	4	VTLDLFGKWRETDLLNR			
				831.1	3	QCISLFGASATVAQDACFQFNR			
				442.8	2	INVLPEAK			
				514.3	2	IPCAPQDVK			
				412.2	3	VTLDLFGKWR			
				718.3	2	LYCFDNLPEHK			
				682.8	4	LYCFDNLPEHKNPCQIYYTPR			
	0.024	55 ▼		805.4	2	IYEIVNTLNVIYR	157	*Macrovipera lebetina* Q4VM07	SVMP (PIII)
				798.4	2	SAESVTLDLFGDWR	68	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)

Table A2.5 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of juvenile *V. latastei* 19VL026 from Gerês. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
4	0.236								Unidentified
5	0.348								Unidentified
6	8.939			444.2	1	ZKW	*de novo*		SVMPi
	0.431			536.8	2	ZDPXDPPNPP	*de novo*	~*B. jararacussu* AAP83421	BPP
7	0.972			536.8	2	ZDPXDPPNPP	*de novo*	~*B. jararacussu* AAP83421	BPP
				481.3	2	PRVGPEIPP	*de novo*	~ *B. jararaca* P85169	BPP
8	1.344	6▼	4435.9	418.9	3	TSLTSHYCTGK	74	*Macrovipera lebetina obtusa* P83469	(K/R)TS disintegrin
11	2.350	14▼	4435.9/4467.9	583.3	2	FLNAGTICNR	77	*Macrovipera lebetina* ABC00778	(K/R)TS disintegrin
				592.6	3	NSANPCCDPVTCKPR	29	*Vipera ammodytes ammodytes* P0C6A5	(K/R)TS disintegrin
13a	0.384	7▼		547.7	2	FYYDSASNK	42	*Bitis gabonica* Q6T269	KTSPi
13b	0.563	5▼							Unidentified
15	1.214	7▼	7383.4/7367.4/7113.2/7095.2	547.7	2	FYYDSASNK	47	*Bitis gabonica* Q6T269	KTSPi
				733.8	2	EFIYGGCHGNANK	42	*Daboia siamensis* A8Y7P5	KTSPi
17	2.376	14▼	14059.8/13928.8/13911.8	587.9	3	NSGNPCCDPVTCKPR	205	*Macrovipera lebetina* P83254	Dimeric disintegrin
				990.4	2	GDDMoxNDYCTGISSDCPR			
				736.0	3	ARGDDMoxNDYCTGISSDCPR			
				590.3	2	FLNAGTICKR	181	*Macrovipera lebetina obtusa* P0C6A8	Dimeric disintegrin
				1009.4	2	GDWNDDYCTGISSDCPR	120	*Eristicophis macmahoni* AAB25266	Dimeric disintegrin
				592.6	3	NSANPCCDPVTCKPR	107	*Vipera ammodytes ammodytes* P0C6A5	Dimeric disintegrin
				1016.4	2	GDWMNNYCTGISSDCPR	97	*Vipera berus berus* P0C6A7	Dimeric disintegrin

				1024.4	2	GDWMoxNNYCTGISSDCPR			
				749.0	3	ELLQNSGNPCCDPVTCKPR			
18a	0.146	14▼	13929.7	588.2	3	NSGNPCCDPVTCKPR	150	*Macrovipera lebetina* P83254	Dimeric disintegrin
				990.4	2	GDDMoxNDYCTGISSDCPR			
				736.0	3	ARGDDMoxNDYCTGISSDCPR			
				1009.4	2	GDWNDDYCTGISSDCPR	97	*Eristicophis macmahoni* AAB25266	Dimeric disintegrin
				592.6	3	NSANPCCDPVTCKPR	68	*Vipera ammodytes ammodytes* P0C6A5	Dimeric disintegrin
18b	0.333	7▼	7047.1	583.3	2	FLNAGTICNR	53	*Macrovipera lebetina* P83253	Medium-sized disintegrin
				525.3	2	FLNPGTICK	43	*Macrovipera lebetina* ABC18317	Medium-sized disintegrin
20a	0.222	35▼		525.3	2	FLNPGTICK	91	*Macrovipera lebetina obtusa* P0C6B0	Disintegrin
				597.3	3	NSANPCCDPITCKPR			
	0.050	35▼		593.3	2	KIPCAPKDEK	73	*Daboia russelii* B8K1W0	DC-domain
				605.3	2	KGESYFYCR	51	*Vipera ammodytes ammodytes* QBF53416	DC-domain
20b	0.343	28▼		605.3	2	KGESYFYCR	112	*Vipera ammodytes ammodytes* QBF53416	DC-domain
				669.9	3	YDYSEDPDYGMoxVDHGTK			
	0.011	28▼		525.3	2	FLNPGTICK	75	*Macrovipera lebetina* ABC18317	Disintegrin
20c	0.142	25▼		541.2	2	GESYFYCR	110	*Vipera ammodytes ammodytes* QBF53416	DC-domain
				605.3	2	KGESYFYCR			
				669.9	3	YDYSEDPDYGMoxVDHGTK			
	0.097	25▼		525.3	2	FLNPGTICK	45	*Macrovipera lebetina* ABC18317	Disintegrin
20d	0.431	17▼		1073.0	2	AMLDGLNDYCTGISSDCPR	186	*Vipera ammodytes ammodytes* AMB36347	Disintegrin
				1081.0	2	AMoxLDGLNDYCTGISSDCPR			
				773.0	3	RAMoxLDGLNDYCTGISSDCPR			
				895.4	2	NSANPCCDPITCKPR	85	*Macrovipera lebetina obtusa* P0C6B0	Disintegrin
				598.2	3	LGEHCVSGPCCDNCK	38	*Vipera ammodytes ammodytes* AMB36349	Disintegrin
20e	0.795	10▼		525.3	2	FLNPGTICK	48	*Macrovipera lebetina* ABC18317	Disintegrin
26a	0.769	29▼		717.3	2	GDIVCGGDDPCLR	99	*Vipera aspis aspis* CAE47133	D49-PLA2
				511.9	3	CCFVHDCCYGR			
	0.458	29▼		569.8	2	SVDFDSESPR	110	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
26b	4.530	16▼	13553.7/13522.7	494.2	2	GKPQDATDR	202	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				767.3	2	CCFVHDCCYGR			
				1039.4	2	SALFSYSDYGCYCGWGGK			
				717.3	2	GDIVCGGDDPCLR	95	*Vipera aspis aspis* CAE47133	D49-PLA2
26c	0.902	8▼		511.9	3	CCFVHDCCYGR	42	*Azemiops feae* ABU68548	D49-PLA2
27a	0.133	68▼		569.8	2	SVDFDSESPR	113	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
				786.3	2	CGENIYMoxSPIPMoxK	67	*Gloydius blomhoffii* Q8JI40	CRISP
27b	0.295	55▼		569.8	2	SVDFDSESPR	229	*Crotalus horridus* ACE73560	CRISP
				581.3	2	SVNPTASNMLK			
				777.3	2	MoxEWYPEAAANAER			
				485.2	2	CILSHSPR	215	*Vipera berus nikolskii* B7FDI0	CRISP
				778.3	2	CGENIYMoxSPIPMK	214	*Gloydius blomhoffii* Q8JI40	CRISP
27c	0.117	45▼		569.8	2	SVDFDSESPR	171	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
				777.3	2	MoxEWYPEAAANAER			
				786.3	2	CGENIYMoxSPIPMoxK	142	*Gloydius blomhoffii* Q8JI40	CRISP
27d	1.080	28▼		569.8	2	SVDFDSESPR	166	*Crotalus horridus* ACE73560	CRISP
				445.2	3	RSVNPTASNMoxLK			
				777.3	2	MoxEWYPEAAANAER			
				778.3	2	CGENIYMSPIPMoxK	155	*Gloydius blomhoffii* Q8JI40	CRISP
				977.0	2	YFYVCQYCPAGNIIGK	102	*Echis coloratus* P0DMT4	CRISP
27e	0.048	22▼		569.8	2	SVDFDSESPR	184	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
				769.3	2	MEWYPEAAANAER			
27f	0.361	16▼	13505.7/13522.7	717.3	2	GDIVCGGDDPCLR	124	*Vipera aspis aspis* CAE47133	D49-PLA2
				511.9	3	CCFVHDCCYGR			
				1039.4	2	SALFSYSDYGCYCGWGGK	110	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
	0.032	16▼		569.8	2	SVDFDSESPR	100	*Crotalus horridus* ACE73560	CRISP
				589.3	2	SVNPTASNMoxLK			
29a	0.329	55▼		589.3	2	SVNPTASNMoxLK	237	*Vipera berus* B7FDI1	CRISP
				777.3	2	MoxEWYPEAAANAER			

				545.9	3	WTAIIHEWHGEEK			
				640.3	3	KPEIQNEIIDLHNSLR			
				524.2	2	CIYDHSPR	215	*Vipera anatolica senliki* QHR82745	CRISP
				569.8	2	SVDFDSESPR	191	*Crotalus horridus* ACE73560	CRISP
29b	2.391	28▼		445.2	3	RSVNPTASNMoxLK	359	*Vipera berus* B7FDI1	CRISP
				769.3	2	MEWYPEAAANAER			
				545.9	3	WTAIIHEWHGEEK			
				960.0	2	KPEIQNEIIDLHNSLR			
				519.5	4	KPEIQNEIIDLHNSLRR			
				583.8	2	NVDFDSESPR	298	*Echis coloratus* P0DMT4	CRISP
				524.2	2	CIYDHSPR	285	*Vipera anatolica senliki* QHR82745	CRISP
				569.8	2	SVDFDSESPR	198	*Crotalus horridus* ACE73560	CRISP
				476.5	4	KPEIQNQIVDLHNSLR	175	*Agkistrodon piscivorus piscivorus* Q7ZTA0	CRISP
				703.8	2	EWYPEAAANAER	143	*Helicops angulatus* P0DJG8	CRISP
29c	0.185	22▼	24773.4	589.3	2	SVNPTASNMoxLK	173	*Vipera berus* B7FDI1	CRISP
				777.3	2	MoxEWYPEAAANAER			
				640.3	3	KPEIQNEIIDLHNSLR			
				524.2	2	CIYDHSPR	153	*Vipera anatolica senliki* QHR82745	CRISP
				569.8	2	SVDFDSESPR	138	*Crotalus horridus* ACE73560	CRISP
29d	0.967	14▼	13648.8	486.8	2	GKPLDATDR	296	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				678.3	2	YMoxLYSLFDCK			
				874.9	2	VAAICFGENMoxNTYDK			
				626.3	3	VAAICFGENMoxNTYDKK			
				877.0	3	MoxGTYSYSFENGDIVCGGDDPCLR			
				717.3	2	GDIVCGGDDPCLR	227	*Vipera aspis aspis* CAE47133	D49-PLA2
	0.089	14▼		589.3	2	SVNPTASNMoxLK	140	*Vipera berus nikolskii* B7FDI0	CRISP
				769.3	2	MEWYPEAAANAER			
				640.3	3	KPEIQNEIIDLHNSLR			
30a	0.381	36▼		569.8	2	SVDFDSESPR	43	*Daboia russelii* P86537	CRISP
30b	0.954	26▼		631.3	2	IVCGGDDPCLR	36	*Vipera aspis aspis* CAE47133	D49-PLA2
30c	4.263	14▼	13708.9/13679.8/13648.8	486.8	2	GKPLDATDR	367	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				670.3	2	YMLYSLFDCK			
				866.9	2	VAAICFGENMNTYDK			
				930.9	2	VAAICFGENMNTYDKK			
				877.0	3	MoxGTYSYSFENGDIVCGGDDPCLR			
				717.3	2	GDIVCGGDDPCLR	278	*Vipera aspis aspis* CAE47133	D49-PLA2
				873.9	2	VAAICFAENMNTYDK	244	*Vipera renardi* F8QN52	D49-PLA2
				625.6	3	VAAICFAENMNTYDKK			
				631.3	2	IVCGGDDPCLR	150	*Daboia siamensis* Q7T3T5	D49-PLA2
30d	0.688	6▼		866.9	2	VAAICFGENMNTYDK	86	*Vipera ammodytes ruffoi* Q910A1	D49-PLA2
				751.8	2	RCFVHDCCYGK	28	*Vipera aspis aspis* CAE47284	D49-PLA2
32a	0.444	>116▼		433.8	2	IILGVHSK	119	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				444.7	2	FFCLSSK			
				465.2	2	FFCLNTK	86	*Macrovipera lebetina* Q9PT41	SVSP
				653.3	3	HAWCEALYPWVPADSR			
				511.3	3	FPNGLDKDIMLIR	67	*Daboia siamensis* P18964	SVSP
				516.6	3	FPNGLDKDIMoxLIR			
				629.8	2	NIQNEDEQIR	66	*Protobothrops mucrosquamatus* XP_015671564	SVSP
32b	0.471	66▼		444.7	2	FFCLSSK	238	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				603.3	2	WDKDIMoxLIR			
				604.8	2	IMGWGTITTTK			
				796.9	2	TLCAGILQGGIDSCK			
				616.3	4	VIGGDECNINEHPFLVALHTAR	176	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				696.4	3	FHCAGTLLNKEWVLTAAR	109	*Bitis gabonica* Q6T6S7	SVSP
				629.8	2	NIQNEDEQIR	94	*Protobothrops mucrosquamatus* XP_015671564	SVSP
				511.3	3	FPNGLDKDIMLIR	85	*Daboia siamensis* P18964	SVSP
				465.2	2	FFCLNTK	80	*Macrovipera lebetina* Q9PT41	SVSP
				653.3	3	HAWCEALYPWVPADSR			
32c	2.729	36▼		433.8	2	IILGVHSK	416	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				444.7	2	FFCLSSK			
				573.3	2	EKFFCLSSK			
				595.3	2	WDKDIMLIR			
				612.8	2	IMoxGWGTITTTK			

			796.9	2	TLCAGILQGGIDSCK			
			571.0	3	TYTRWDKDIMLIR			
			892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
			821.4	3	VIGGDECNINEHPFLVALHTAR	346	*Vipera ammodytes ammodytes* P0DPS3	SVSP
			696.4	3	FHCAGTLLNKEWVLTAAR	220	*Bitis gabonica* Q6T6S7	SVSP
			803.9	2	TLCAGILQGGIDTCK	144	*Macrovipera lebetina* E0Y419	SVSP
			511.3	3	FPNGLDKDIMLIR	91	*Daboia siamensis* P18964	SVSP
			653.3	3	HAWCEALYPWVPADSR	54	*Macrovipera lebetina* Q9PT41	SVSP
32d	0.289	30$^{\blacktriangledown}$	511.3	3	FPNGLDKDIMLIR	91	*Daboia siamensis* P18964	SVSP
			696.4	3	FHCAGTLLNKEWVLTAAR	84	*Bitis gabonica* Q6T6S7	SVSP
			629.8	2	NIQNEDEQIR	68	*Protobothrops mucrosquamatus* XP_015671564	SVSP
			452.3	2	TLCAGILR	50	*Echis ocellatus* ADE45140	SVSP
			612.8	2	IMoxGWGTITTTK	32	*Macrovipera lebetina* Q9PT40	SVSP
35a	0.111	66$^{\blacksquare}$	552.8	2	VLNEDEETR	186	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			455.8	2	IELGVHDK	145	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			803.9	2	TLCAGILQGGIDTCK	93	*Macrovipera lebetina* E0Y419	SVSP
			596.8	2	IMGWGTTTPTK	39	*Crotalus scutulatus* AUS82544	SVSP
			604.8	2	IMoxGWGTTTPTK	33	*Crotalus scutulatus* AUS82544	SVSP
35b	0.405	37$^{\blacktriangledown}$	559.8	2	AAYPWLLER	271	*Vipera ammodytes ammodytes* AMB36344	SVSP
			844.9	2	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			444.7	2	FFCLSSK	198	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			604.8	2	IMoxGWGTTTPTK	47	*Crotalus scutulatus* AUS82544	SVSP
			892.9	2	VIGGDECNINEHPFLA	42	*Daboia russelii* P86530	
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			629.8	2	NIQNEDEQIR	37	*Protobothrops mucrosquamatus* XP_015671564	SVSP
			504.9	3	IVGGDECNINEHR	36	*Lachesis muta rhombeata* C0HLA2	SVSP
35c	0.181	34$^{\blacktriangledown}$	559.3	2	AAYPWLLER	143	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			444.7	2	FFCLSSK	122	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			611.0	3	VILPDVPHCANIEIIK			
			629.8	2	NIQNEDEQIR	50	*Protobothrops mucrosquamatus* XP_015671564	SVSP
36a	0.747	>116$^{\blacktriangledown}$	447.6	3	LVIVVDHSMVTK	67	*Echis coloratus* ADI47606	SVMP (PIII)
			702.9	2	LVIVVYHSMoxVTK			
	0.320	>116$^{\blacktriangledown}$	452.3	2	TLCAGILR	162	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
36b	0.293	116$^{\blacktriangledown}$	702.9	2	LVIVVYHSMoxVTK	30	*Echis coloratus* ADI47606	SVMP (PIII)
36c	0.946	60$^{\blacktriangledown}$	447.6	3	LVIVVDHSMVTK	107	*Echis coloratus* ADI47606	SVMP (PIII)
			694.9	2	LVIVVFHSMoxVTK			
			702.9	2	LVIVVYHSMoxVTK			
	0.183	60$^{\blacktriangledown}$	742.3	3	LHSWVECESGECCQQCR	65	*Echis coloratus* ADI47638	PIII-SVMP
			737.6	3	LHSWVKCESGECCDQCR	64	*Trimeresurus stejnegeri* Q3HTN1	PIII-SVMP
			953.7	3	RSECDIAESCTGQSDDCPTDDFHR	60	*Crotalus atrox* QIV64940	PIII-SVMP
36d	0.374	36$^{\blacktriangledown}$	702.9	2	LVIVVYHSMoxVTK	31	*Echis coloratus* ADI47606	SVMP (PIII)
	0.242	36$^{\blacktriangledown}$	452.3	2	TLCAGILR	73	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
36e	0.367	34$^{\blacktriangledown}$	452.3	2	TLCAGILR	192	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.340	34$^{\blacktriangledown}$	737.6	3	LHSWVKCESGECCDQCR	91	*Trimeresurus stejnegeri* Q3HTN1	PIII-SVMP
			953.7	3	RSECDIAESCTGQSDDCPTDDFHR	70	*Crotalus atrox* QIV64940	PIII-SVMP

	0.117	34▼	702.9	2	LVIVVYHSMoxVTK	34	*Echis coloratus* ADI47606	SVMP (PIII)
38a	0.208	>116▼	684.9	2	LVIVVDHSMVEK	96	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
	0.099	>116▼	849.9	2	TDIVSPPVCGNGLLEK	65	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	35	*Echis carinatus sochureki* ADI47590	PIII-SVMP
38b	0.223	75▼	684.9	2	LVIVVDHSMVEK	61	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
			692.4	2	LVIVVDHSMoxVEK	57	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
			456.9	3	LVIVVDHSMVEK	51	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
			462.3	3	LVIVVDHSMoxVEK	50	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
	0.029	75▼	849.9	2	TDIVSPPVCGNGLLEK	61	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	32	*Echis carinatus sochureki* ADI47590	PIII-SVMP
38c	1.092	55▼	820.4	2	ENDVPIPCAPEDRK	100	*Vipera ammodytes ammodytes* QBF53417	PIII-SVMP
			849.9	2	TDIVSPPVCGNGLLEK	70	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	36	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.854	55▼	684.9	2	LVIVVDHSMVEK	137	*Echis carinatus* Q9PRP9	SVMP (PIII)
			713.4	2	LVIVVDHSMVWK			
38d	0.221	46▼	849.9	2	TDIVSPPVCGNGLLEK	61	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	39	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			571.6	3	TDIVSPPVCGNALLEK	29	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.086	46▼	684.9	2	LVIVVDHSMVEK	95	*Echis carinatus* Q9PRP9	SVMP (PIII)
38e	0.332	41▼	849.9	2	TDIVSPPVCGNGLLEK	57	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	33	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.159	41▼	692.9	2	LVIVVDHSMoxVEK	72	*Echis carinatus* Q9PRP9	SVMP (PIII)
38f	0.716	34▼	849.9	2	TDIVSPPVCGNGLLEK	52	*Echis coloratus* ADI47619	PIII-SVMP
			571.6	3	TDIVSPPVCGNALLEK	43	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			733.0	3	LHSWVECESGECCEQCK	34	*Crotalus atrox* QIV64940	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	31	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.368	34▼	456.9	3	LVIVVDHSMVEK	44	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
			692.4	2	LVIVVDHSMoxVEK	33	*Echis pyramidum leakeyi* ADI47673	SVMP (PIII)
	0.009	34▼	552.8	2	VLNEDEETR	61	*Vipera ammodytes ammodytes* AMB36344	SVSP
38g	0.758	28▼	684.9	2	LVIVVDHSMVEK	123	*Echis carinatus* Q9PRP9	SVMP (PI)
			706.4	2	LVIVVDHSMoxVRK			
			440.9	3	LVIVVDNVMYR	30	*Echis coloratus* ADI47641	SVMP (PI)
	0.021	28▼	849.9	2	TDIVSPPVCGNGLLEK	50	*Echis coloratus* ADI47619	SVMP fragment
38h	0.361	25▼	462.3	3	LVIVVDHSMoxVEK	52	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
38i	0.268	21▼	849.9	2	TDIVSPPVCGNGLLEK	37	*Echis coloratus* ADI47619	SVMP fragment
39a	0.393	>116▼	562.6	3	HDNAQLLTAIDFDGR	135	*Crotalus scutulatus* QIV64921	SVMP (PIII)
			657.4	3	KRHDNAQLLTAIDFDGR			
			684.9	2	LVIVVDHSMVEK	113	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
	0.239	>116▼	849.9	2	TDIVSPPVCGNGLLEK	57	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	33	*Echis carinatus sochureki* ADI47590	PIII-SVMP
	0.221	>116▼	504.9	3	VIGGDECNINEHR	66	*Lachesis muta rhombeata* C0HLA1	SVSP
			538.2	2	IYDYSVCR	39	*Vipera ammodytes ammodytes* QBF53414	SVSP
39b	0.312	116▼	692.9	2	LVIVVDHSMoxVEK	118	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
			562.6	3	HDNAQLLTAIDFDGR	54	*Crotalus scutulatus* QIV64921	SVMP (PIII)
	0.061	116▼	538.2	2	IYDYSVCR	45	*Vipera ammodytes ammodytes* QBF53414	SVSP
			504.9	3	IVGGDECNINEHR	31	*Lachesis muta rhombeata* C0HLA2	SVSP
	0.092	116▼	849.9	2	TDIVSPPVCGNGLLEK	63	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	34	*Echis carinatus sochureki* ADI47590	PIII-SVMP
39c	1.803	56▼	562.6	3	HDNAQLLTAIDFDGR	151	*Crotalus scutulatus* QIV64921	SVMP (PIII)
			657.3	3	KRHDNAQLLTAIDFDGR			
			684.9	2	LVIVVDHSMVEK	76	*Echis carinatus* Q9PRP9	SVMP (PIII)
			440.9	3	LVIVVDNVMYR	40	*Echis coloratus* ADI47641	SVMP (PIII)
	0.286	56▼	849.9	2	TDIVSPPVCGNGLLEK	139	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	36	*Echis carinatus sochureki* ADI47590	PIII-SVMP
			953.7	3	RSECDIAESCTGQSDDCPTDDFHR	31	*Crotalus atrox* QIV64940	PIII-SVMP
			944.7	3	ASECDLPEYCTGQSADCPTDHFDR	30	*Vipera ammodytes ammodytes* QBF53417	PIII-SVMP
39d	1.101	34▼	843.4	2	HDNAQLLTAIDFDGR	152	*Crotalus scutulatus* QIV64921	SVMP (PIII)
			657.3	3	KRHDNAQLLTAIDFDGR			
			456.9	3	LVIVVDHSMVEK	136	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			

	0.139	34▼	559.8	2	AAYPWLLER	158	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			538.2	2	IYDYSVCR	41	*Vipera ammodytes ammodytes* QBF53414	SVSP
	0.136	34▼	849.9	2	TDIVSPPVCGNGLLEK	57	*Echis coloratus* ADI47619	PIII-SVMP
			856.9	2	TDIVSPPVCGNALLEK	31	*Echis carinatus sochureki* ADI47590	PIII-SVMP
39e	0.225	28▼	562.6	3	HDNAQLLTAIDFDGR	74	*Crotalus scutulatus* QIV64921	SVMP (PI)
			684.9	2	LVIVVDHSMVEK	65	*Echis carinatus* Q9PRP9	SVMP (PI)
	0.074	28▼	535.7	2	QCVDVDTAY	30	*Protobothrops mucrosquamatus* XP_029142320	SVMP fragment
39f	0.207	25▼	462.3	3	LVIVVDHSMoxVEK	48	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
			456.9	3	LVIVVDHSMVEK	41	*Echis pyramidum leakeyi* ADI47673	SVMP (PI)
	0.066	25▼	856.9	2	TDIVSPPVCGNALLEK	30	*Echis carinatus sochureki* ADI47590	SVMP fragment
			953.4	3	RSECDIAESCTGQSDDCPTDDFHR	30	*Crotalus atrox* QIV64940	SVMP fragment
42	0.856	56▼	438.7	2	STTDLPSR	627	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			750.8	2	EDDYEEFLEIAK			
			818.4	2	NVEEGWYANLGPMR			
			894.9	2	EQIKTFCYPSMoxIQK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGH			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR.I			
			563.8	2	FDEIVGGMoxDK	366	*Gloydius halys* Q6STF1	LAAO
			567.3	2	YPVKPSEEGK			
			641.8	2	RFDEIVGGMoxDK			
			463.6	3	KFWEDDGIHGGK	345	*Macrovipera lebetina* P81375	LAAO
			498.6	3	ADDKNPLEECFR			
			460.9	3	SAGQLYEESLRK	327	*Bothrops pictus* X2L4E2	LAAO
			564.3	2	AHGWIDSTIK	112	*Demansia vestigiata* A6MFL0	LAAO
43	0.906	56▼	438.7	2	STTDLPSR	496	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			502.3	2	VTVLEASER			
			532.7	2	NPLEECFR			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			555.8	2	FDEIVGGMDK	368	*Gloydius halys* Q6STF1	LAAO
			567.3	2	YPVKPSEEGK			
			641.8	2	RFDEIVGGMoxDK			
			626.8	2	SAGQLYEESLR	351	*Bothrops pictus* X2L4E2	LAAO
			460.9	3	SAGQLYEESLRK			
			498.6	3	ADDKNPLEECFR	348	*Cerastes cerastes* P0DQH9	LAAO
			564.3	2	AHGWIDSTIK	49	*Demansia vestigiata* A6MFL0	LAAO
44a	0.314	56▼	438.7	2	STTDLPSR	207	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			818.4	2	NVEEGWYANLGPMR			
44b	0.366	21▼						Unidentified
44c	0.325	18▼						Unidentified
44d	0.266	12▼						Unidentified
45a	0.081	>116▼	578.3	2	WTDGSSVIYK	132	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
	0.058	>116▼	562.8	2	TLGMoxLMoxEGLK	294	*Macrovipera lebetina* W8E7D1	PDE
			583.8	2	QPLPETLQLK			
			678.3	2	AATYFWPGSEVK			
			724.8	2	DFYTFDSEGIVR			
			507.3	3	SMoxQAIFLAHGPGFK			
			785.9	2	SPPTSVPPSASDCLR			
	0.005	>116▼	640.3	2	LYCLNNSPGNK	89	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			647.8	2	LIGVEFWCDR			

45b	0.355	56▼		513.2	2	GSYYGYCR	304	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
				521.3	2	IPCAPQDIK			
				585.3	2	KIPCAPQDIK			
				640.3	2	LYCLNNSPGNK			
				647.8	2	LIGVEFWCDR			
				806.9	2	ATVAEDSCFEENLK			
				534.3	2	QCISLFGSR	146	*Macrovipera lebetina* Q7T046	PIII-SVMP
45c	0.399	21▼		630.8	2	CGDDYPFVCK	146	*Vipera ammodytes ammodytes* QBF53411	CTL
				854.9	2	TSADYVWIGLWNQR			
				468.3	2	IIYVNWK	33	*Daboia siamensis* ADK22831	CTL
45d	0.435	18▼		435.7	2	AQYCISK	187	*Vipera ammodytes ammodytes* QBF53411	CTL
				578.3	2	WTDGSSVIYK			
				630.8	2	CGDDYPFVCK			
				854.9	2	TSADYVWIGLWNQR			
45e	0.597	12▼		611.8	2	EEMNWADAEK	142	*Macrovipera lebetina* AJO70723	CTL
				538.2	3	VFKEEMoxNWADAEK			
				646.0	3	GSHLVSLHNIAEADFVVK			
46a	0.234	>116▼		507.8	2	CILNEPLR	297	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
				513.2	2	GSYYGYCR			
				640.3	2	LYCLNNSPGNK			
				647.8	2	LIGVEFWCDR			
				806.9	2	ATVAEDSCFEENLK			
	0.143	>116▼		534.3	2	QCISLFGSR	115	*Macrovipera lebetina* Q7T046	PIII-SVMP
				813.9	2	ATVAEDSCFQENQK			
				591.3	2	NQCISLFGSR	81	*Daboia siamensis* Q7LZ61	PIII-SVMP
46b	0.280	97▼		513.2	2	GSYYGYCR	401	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
				521.3	2	IPCAPQDIK			
				585.3	2	KIPCAPQDIK			
				640.3	2	LYCLNNSPGNK			
				647.8	2	LIGVEFWCDR			
				806.9	2	ATVAEDSCFEENLK			
				527.0	4	TAVIMoxAHELGHNLGMSHDR			
				534.3	2	QCISLFGSR	226	*Macrovipera lebetina* Q7T046	PIII-SVMP
				813.9	2	ATVAEDSCFQENQK			
	0.009	97▼		430.6	3	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
				645.4	2	FITHFWIGLR	30	*Macrovipera lebetina* Q696W1	CTL
46c	0.360	73▼		507.8	2	CILNEPLR	399	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
				513.2	2	GSYYGYCR			
				521.3	2	IPCAPQDIK			
				585.3	2	KIPCAPQDIK			
				640.3	2	LYCLNNSPGNK			
				647.8	2	LIGVEFWCDR			
				806.9	2	ATVAEDSCFEENLK			
	0.158	73▼		534.3	2	QCISLFGSR	230	*Macrovipera lebetina* Q7T046	PIII-SVMP
				813.9	2	ATVAEDSCFQENQK			
	0.013	73▼		645.4	2	FITHFWIGLR	39	*Macrovipera lebetina* Q696W1	CTL
				430.6	3	FITHFWIGLR	36	*Macrovipera lebetina* Q696W1	CTL
46d	2.281	56▼	459825	513.2	2	GSYYGYCR	737	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			293287	585.3	2	KIPCAPQDIK			
				658.4	2	FVELLIVVDLR			
				800.3	2	DCQNPCCDAATCK			
				806.9	2	ATVAEDSCFEENLK			
				970.4	2	LTPGAECGNGLCCENCK			
				697.0	3	TAVIMAHELGHNLGMSHDR			
				716.3	3	DECDVPEHCTGQSAECPR			
				1090.6	2	IYEMVNTVNEIYIPLNVR			
				534.3	2	QCISLFGSR	233	*Macrovipera lebetina* Q7T046	PIII-SVMP
				813.9	2	ATVAEDSCFQENQK			
				591.3	2	NQCISLFGSR	177	*Daboia siamensis* Q7LZ61	PIII-SVMP
	0.241	56▼		569.3	2	HDDIFAYEK	160	*Vipera ammodytes ammodytes* QBF53419	LAAO
				750.8	2	EDDYEEFLEIAK			
				1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
				563.8	2	FDEIVGGMoxDK	116	*Macrovipera lebetina* P81375	LAAO

	0.039	56▼	622.3	2	NDQLLWLWR	92	*Echis ocellatus* A3QVN2	Hyaluronidase
			635.3	3	HSDSNAFLHLFPESFR			
	0.026	56▼	430.6	3	FITHFWIGLR	40	*Macrovipera lebetina* Q696W1	CTL
46e	0.321	42▼	507.8	2	CILNEPLR	272	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			513.2	2	GSYYGYCR			
			585.3	2	KIPCAPQDIK			
			647.8	2	LIGVEFWCDR			
			490.9	3	SVGVVKEHNINFK			
			534.3	2	QCISLFGSR	120	*Macrovipera lebetina* Q7T046	PIII-SVMP
46f	0.679	37▼	507.8	2	CILNEPLR	356	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			513.2	2	GSYYGYCR			
			571.8	2	CILNEPLRK			
			585.3	2	KIPCAPQDIK			
			647.8	2	LIGVEFWCDR			
			806.9	2	ATVAEDSCFEENLK			
			523.0	4	TAVIMAHELGHNLGMSHDR			
			534.3	2	QCISLFGSR	146	*Macrovipera lebetina* Q7T046	PIII-SVMP
	0.073	37▼	430.6	3	FITHFWIGLR	53	*Macrovipera lebetina* Q696W1	CTL
			645.4	2	FITHFWIGLR	45	*Macrovipera lebetina* Q696W1	CTL
	0.009	37▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	74	*Vipera ammodytes ammodytes* AMB36344	SVSP
46g	0.311	28▼	585.3	2	KIPCAPQDIK	186	*Vipera ammodytes ammodytes* QBF53415	SVMP fragment
			806.9	2	ATVAEDSCFEENLK			
			534.3	2	QCISLFGSR	117	*Macrovipera lebetina* Q7T046	SVMP fragment
46h	0.855	20▼	640.3	2	LYCLNNSPGNK	103	*Vipera ammodytes ammodytes* QBF53415	SVMP fragment
			647.8	2	LIGVEFWCDR			
			534.3	2	QCISLFGSR	82	*Macrovipera lebetina* Q7T046	SVMP fragment
	0.540	20▼	630.8	2	CGDDYPFVCK	52	*Macrovipera lebetina* AJO70726	CTL
			645.4	2	FITHFWIGLR	46	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
46i	0.804	17▼	430.6	3	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
46j	0.184	15▼	521.3	2	IPCAPQDIK	161	*Macrovipera lebetina* Q7T046	SVMP fragment
			534.3	2	QCISLFGSR			
			585.3	2	KIPCAPQDIK			
	0.035	15▼	430.6	3	FITHFWIGLR	36	*Macrovipera lebetina* Q696W1	CTL
			645.4	2	FITHFWIGLR	35	*Macrovipera lebetina* Q696W1	CTL
47a	1.350	200▼	677.4	2	NPQCIINKPLR	175	*Echis coloratus* ADI47654	SVMP (PIII)
	0.149	200▼	529.3	2	IPCAPKDEK	193	*Echis ocellatus* Q2UXQ5	PIII-SVMP
			593.3	2	KIPCAPKDEK			
			1106.4	2	LHSWVECESGECCDQCR			
			806.9	2	VCSNGQCVDLNIAY	156	*Daboia russelii* B8K1W0	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	36	*Echis carinatus sochureki* ADI47595	PIII-SVMP
	0.003	200▼	730.9	2	KVVPESLFAWER	61	*Crotalus adamanteus* F8S101	PLB
47b	0.393	>116▼	677.3	2	NPQCIINKPLR	78	*Echis coloratus* ADI47654	SVMP (PIII)
			647.8	2	LIGVEFWCDR	71	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
	0.036	>116▼	529.3	2	IPCAPKDEK	109	*Daboia russelii* B8K1W0	PIII-SVMP
			593.3	2	KIPCAPKDEK			
			742.6	3	LHSWVECESGECCEQCR	53	*Protobothrops mucrosquamatus* XP_015683679	PIII-SVMP
	0.003	>116▼	569.3	2	HDDIFAYEK	31	*Calloselasma rhodostoma* P81382	LAAO
	0.000	>116▼	730.9	2	KVVPESLFAWER	57	*Crotalus adamanteus* F8S101	PLB
47c	0.634	116▼	529.3	2	IPCAPKDEK	172	*Echis coloratus* ADI47654	PIII-SVMP
			677.4	2	NPQCIINKPLR			
			737.9	3	LHSWVECESGECCDQCR			
			593.3	2	KIPCAPKDEK	169	*Echis ocellatus* Q2UXQ5	PIII-SVMP
			885.9	2	TDIVSPPVCGNELLEK	137	*Echis ocellatus* CAJ01687	PIII-SVMP
			742.6	3	LHSWVECESGECCEQCR	74	*Bothrops jararaca* Q0NZX8	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	34	*Echis carinatus sochureki* ADI47595	PIII-SVMP
47d	0.435	77▼	677.3	2	NPQCIINKPLR	80	*Echis coloratus* ADI47654	SVMP (PIII)
	0.074	77▼	411.2	2	LVESFAR	173	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			483.2	2	YWIQAER			
			545.3	2	VLMGNIDLSK			
			945.9	2	EALQMLTAGCPESPCVK			
			750.4	2	YPVNEEPYLTFK	123	*Notechis scutatus* XP_026530513	Aminopeptidase

			520.3	2	QVIGPELQR	52	*Pseudonaja textilis* XP_026580739	Aminopeptidase
	0.068	77▼	529.3	2	IPCAPKDEK	117	*Daboia russelii* B8K1W0	PIII-SVMP
			593.3	2	KIPCAPKDEK			
			806.9	2	VCSNGQCVDLNIAY			
			742.6	3	LHSWVECESGECCEQCR	69	*Bothrops jararaca* Q0NZX8	PIII-SVMP
			885.9	2	TDIVSPPVCGNELLEK	50	*Echis ocellatus* ADW54351	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	34	*Echis carinatus sochureki* ADI47595	PIII-SVMP
47e	2.876	65▼	677.3	2	NPQCIINKPLR	162	*Echis coloratus* ADI47654	SVMP (PIII)
	0.392	65▼	529.3	2	IPCAPKDEK	164	*Echis ocellatus* Q2UXQ5	PIII-SVMP
			593.3	2	KIPCAPKDEK			
			738.3	3	LHSWVECESGECCDQCR			
			885.9	2	TDIVSPPVCGNELLEK	145	*Echis ocellatus* CAJ01687	PIII-SVMP
			806.9	2	VCSNGQCVDLNIAY	131	*Daboia russelii* B8K1W0	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	35	*Echis carinatus sochureki* ADI47595	PIII-SVMP
47f	0.969	42▼	593.3	2	KIPCAPKDEK	145	*Echis ocellatus* Q2UXQ5	PIII-SVMP
			737.9	3	LHSWVECESGECCDQCR			
			885.9	2	TDIVSPPVCGNELLEK	116	*Echis ocellatus* CAJ01687	PIII-SVMP
			742.6	3	LHSWVECESGECCEQCR	53	*Protobothrops mucrosquamatus* XP_015683679	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	34	*Echis carinatus sochureki* ADI47595	PIII-SVMP
	0.291	42▼	703.9	2	FTAYAINGPPVEK	173	*Vipera ammodytes ammodytes* QBF53421	PLB
			730.9	2	QVVPESLFAWER			
			541.6	3	NGYWPSYNIPFHK			
	0.092	42▼	451.9	3	NPQCIINKPLR	130	*Echis coloratus* ADI47654	SVMP
47g	0.567	31▼	677.3	2	NPQCIINKPLR	99	*Echis coloratus* ADI47654	PIII-SVMP
			737.9	3	LHSWVECESGECCDQCR			
47h	0.330	27▼	806.9	2	VCSNGQCVDLNIAY	84	*Daboia russelii* B8K1W0	SVMP fragment
47i	0.342	23▼	677.3	2	NPKCILNKPLR	41	*Echis pyramidum leakeyi* ADI47744	SVMP (PI)
47j	0.140	14▼	529.3	2	IPCAPKDEK	114	*Echis coloratus* ADI47654	SVMP fragment
			676.9	2	NPQCIINKPLR			
			806.9	2	VCSNGQCVDLNIAY	83	*Daboia russelii* B8K1W0	SVMP fragment
	0.015	14▼	703.9	2	FTAYAINGPPVEK	66	*Drysdalia coronoides* F8J2D3	PLB
49a	0.404	>116▼	535.2	2	QCVDVNTAY	375	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			1367.6	3	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
			529.3	2	IPCAPKDEK	125	*Echis coloratus* ADI47654	PIII-SVMP
			618.3	2	VTLDLFGEWR	96	*Echis carinatus sochureki* ADI47585	PIII-SVMP
			885.9	2	TDIVSPPVCGNELLEK			
	0.396	>116▼	676.9	2	NPQCILNKPLR	185	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
			507.3	2	CILNKPLR	127	*Echis pyramidum leakeyi* ADI47732	SVMP (PIII)
	0.020	>116▼	778.6	4	HDNAQLLTAIDFDGDTVGLAHVGGMoxCQLK	32	*Agkistrodon contortrix laticinctus* ACV83930	SVMP fragment
49b	0.276	116▼	535.2	2	QCVDVNTAY	214	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			529.3	2	IPCAPKDEK	79	*Daboia russelii* B8K1W0	PIII-SVMP
	0.029	116▼	677.8	2	NPQCILNEPLR	58	*Crotalus atrox* QIV64944	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR	47	*Vipera ammodytes ammodytes* AMB36349	SVMP (PIII)
			937.5	2	TWAHQLVNNIIVFYR	31	*Vipera ammodytes ammodytes* AMB36349	SVMP (PIII)
49c	1.336	66▼	535.2	2	QCVDVNTAY	194	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			800.7	3	CFNNNLQGTENFHCGMENGR			
			529.3	2	IPCAPKDEK	110	*Echis coloratus* ADI47654	PIII-SVMP
			676.9	2	NPQCIINKPLR			
			806.9	2	VCSNGQCVDLNIAY	99	*Daboia russelii* B8K1W0	PIII-SVMP
			893.0	2	TDIVSPPVCGNDLLER	34	*Echis carinatus sochureki* ADI47595	PIII-SVMP
49d	0.346	42▼	635.3	2	SSVGLIQDYCK	211	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			529.3	2	IPCAPKDEK	158	*Echis coloratus* ADI47654	PIII-SVMP
			676.9	2	NPQCIINKPLR			
			737.9	3	LHSWVECESGECCDQCR			

			885.9	2	TDIVSPPVCGNELLEK	118	*Echis ocellatus* CAJ01687	PIII-SVMP
			806.9	2	VCSNGQCVDLNIAY	72	*Daboia russelii* B8K1W0	PIII-SVMP
	0.013	42▼	447.6	2	LVIVVDHSMVTK	92	*Vipera ammodytes ammodytes* AMB36352	SVMP (PIII)
	0.003	42▼	730.9	2	KVVPESLFAWER	42	*Crotalus adamanteus* F8S101	PLB
49e	1.944	34▼	937.5	2	TWAHQLVNNIIVFYR	160	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			507.3	2	CILNKPLR	103	*Echis pyramidum leakeyi* ADI47732	SVMP (PIII)
			584.0	3	YIELVIVADNVMoxVKK	33	*Crotalus horridus* QIS79142	SVMP (PIII)
	0.075	34▼	552.8	2	VLNEDEETR	65	*Vipera ammodytes ammodytes* AMB36344	SVSP
49f	0.158	26▼	937.5	2	TWAHQLVNNIIVFYR	114	*Macrovipera lebetina* Q3ZD74	PI-SVMP
49g	0.461	16▼	676.9	2	NPQCILNKPLR	172	*Vipera ammodytes ammodytes* AMB36351	SVMP fragment
			937.5	2	TWAHQLVNNIIVFYR			
49h	0.519	14▼	676.9	2	NPQCILNKPLR	134	*Vipera ammodytes ammodytes* AMB36351	SVMP fragment
			625.3	3	TWAHQLVNNIIVFYR			
51a	0.559	>116▼	535.2	2	QCVDVNTAY	388	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			1367.6	3	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
	0.029	>116▼	676.9	2	NPQCILNKPLR	95	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
	0.004	>116▼	750.8	2	EDDYEEFLEIAK	49	*Daboia russelii* G8XQX1	LAAO
51b	0.346	116▼	535.2	2	QCVDVNTAY	401	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			790.4	2	IYEIVNTLNVVFR			
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
	0.011	116▼	676.9	2	NPQCILNKPLR	109	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			647.8	2	LIGVEFWCDR	33	*Daboia russelii russelii* ADJ67475	SVMP (PIII)
51c	1.606	67▼	535.2	2	QCVDVNTAY	372	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			855.5	2	YIELVIVVDNVMFR			
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			1025.7	4	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
			1007.9	2	LTPGSQCADGECCDQCR	46	*Echis carinatus sochureki* ADI47586	PIII-SVMP
	0.011	67▼	677.3	2	NPKCILNKPLR	41	*Echis pyramidum leakeyi* ADI47744	SVMP (PIII)
51d	0.438	56▼	635.3	2	SSVGLIQDYCK	257	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			1007.9	2	LTPGSQCADGECCDQCR	39	*Echis carinatus sochureki* ADI47586	PIII-SVMP
	0.120	56▼	502.3	2	VTVLEASER	113	*Vipera ammodytes ammodytes* QBF53419	LAAO
			818.4	2	NVEEGWYANLGPMR			
			460.9	3	SAGQLYEESLRK	83	*Cerastes cerastes* P0DQH9	LAAO
	0.017	56▼	647.8	2	LIGVEFWCDR	67	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
51e	0.559	53▼	635.3	2	SSVGLIQDYCK	333	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			790.4	2	IYEIVNTLNVVFR			
			798.4	2	SAESVTLDLFGDWR			
			1000.9	2	LTPGSECGDGECCDQCR			
			671.3	3	FTHSPDDPDYGMoxVDLGTK	36	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
51f	0.263	42▼	635.3	2	SSVGLIQDYCK	149	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
51g	0.295	37▼	635.3	2	SSVGLIQDYCK	188	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			790.4	2	IYEIVNTLNVVFR			
			1000.9	2	LTPGSECGDGECCDQCR			
51h	0.298	34▼	676.9	2	NPQCILNKPLR	107	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
	0.005	34▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	79	*Vipera ammodytes ammodytes* AMB36344	SVSP
51i	0.298	30▼	535.2	2	QCVDVNTAY	93	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
	0.036	30▼	676.9	2	NPKCILNKPLR	59	*Echis pyramidum leakeyi* ADI47744	SVMP (PI)
51j	0.262	27▼	635.3	2	SSVGLIQDYCK	96	*Vipera ammodytes ammodytes* AHB62069	SVMP (PI)
53a	0.143	>116▼	635.3	2	SSVGLIQDYCK	66	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
53b	0.198	116▼	635.3	2	SSVGLIQDYCK	111	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			

53c	0.558	66▼	535.2	2	QCVDVNTAY	202	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			1000.9	2	LTPGSECGDGECCDQCR			
			885.9	2	TDIVSPPVCGNELLEK	30	*Echis ocellatus* CAJ01687	PIII-SVMP
53d	0.294	56▼	635.3	2	SSVGLIQDYCK	201	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			790.4	2	IYEIVNTLNVVFR			
			1000.9	2	LTPGSECGDGECCDQCR			
	0.241	56▼	502.3	2	VTVLEASER	93	*Cerastes cerastes* P0DQH9	LAAO
			460.9	3	SAGQLYEESLRK			
	0.179	56▼	647.8	2	LIGVEFWCDR	152	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
			806.9	2	ATVAEDSCFEENLK			
53e	0.476	53▼	635.3	2	SSVGLIQDYCK	347	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			790.4	2	IYEIVNTLNVVFR			
			798.4	2	SAESVTLDLFGDWR			
			1000.9	2	LTPGSECGDGECCDQCR			
			671.3	3	FTHSPDDPDYGMoxVDLGTK	40	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
53f	0.329	37▼	635.3	2	SSVGLIQDYCK	212	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			798.4	2	SAESVTLDLFGDWR			
53g	0.173	34▼	676.9	2	NPQCILNKPLR	89	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
53h	0.189	30▼	676.9	2	NPQCILNKPLR	84	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
54a	0.143	>116▪	535.2	2	QCVDVNTAY	192	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			1000.9	2	LTPGSECGDGECCDQCR			
			501.7	2	IACAPEDVK	37	*Macrovipera lebetina* Q4VM07	PIII-SVMP
54b	0.093	81▪	647.8	2	LIGVEFWCDR	108	*Vipera ammodytes ammodytes* QBF53415	SVMP (PIII)
			800.3	2	DCQNPCCDAATCK			
54c	0.219	26▪	676.9	2	NPQCILNKPLR	83	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
55a	0.127	>116▼	501.7	2	IACAPEDVK	292	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			526.8	2	SCIMoxSGILR			
			453.2	3	MoxPQCILNKPLK			
			762.8	2	CETSYLFSDCSR			
			661.3	3	HDNAQLLTGINFNGPSAGR			
			677.0	3	LRPGAQCGDGVCCYQCK			
	0.024	>116▼	676.9	2	NPQCILNKPLR	67	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
	0.010	>116▼	555.8	2	TLDSFGEWR	41	*Echis ocellatus* ADW54338	SVMP (PIII)
55b	0.294	56▼	501.7	2	IACAPEDVK	531	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			526.8	2	SCIMoxSGILR			
			411.5	3	YSVGIVQDHSK			
			453.2	3	MoxPQCILNKPLK			
			762.8	2	CETSYLFSDCSR			
			805.4	2	IYEIVNTLNVIYR			
			870.9	2	NPCQIYYIPSDENK			
			661.3	3	HDNAQLLTGINFNGPSAGR			
	0.056	56▼	647.8	2	LIGVEFWCDR	61	*Daboia russelii russelii* ADJ67475	SVMP (PIII)
			555.8	2	TLDSFGEWR	57	*Echis ocellatus* ADW54338	SVMP (PIII)
55c	0.612	30▼	676.9	2	NPQCILNKPLR	68	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
57a	0.114	>116▪	430.7	2	ETDLLNR	344	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			566.2	2	LGNEYGYCR			
			578.3	2	KIPCAPQDVK			
			617.9	2	VTLDLFGKWR			
			993.4	2	LTPGSQCADGECCDQCK			
			682.8	4	LYCFDNLPEHKNPCQIYYTPR			
57b	0.172	116▪	430.7	2	ETDLLNR	459	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			442.3	2	INVLPEAK			
			514.3	2	IPCAPQDVK			
			578.3	2	KIPCAPQDVK			
			656.3	2	NPCQIYYTPR			
			679.4	2	MoxPQCILNKPLK			
			799.8	2	DCQNPCCNAATCK			
			993.4	2	LTPGSQCADGECCDQCK			
57c	0.897	96▪	430.7	2	ETDLLNR	1028	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			514.3	2	IPCAPQDVK			

				566.2	2	LGNEYGYCR			
				412.2	3	VTLDLFGKWR			
				656.3	2	NPCQIYYTPR			
				718.3	2	LYCFDNLPEHK			
				720.9	2	LVIVADYIMoxFLK			
				799.8	2	DCQNPCCNAATCK			
				811.5	2	IYEIVNLLNVIYR			
				844.4	2	SCIMoxSGTLSCEASIR			
				627.0	3	TRIYEIVNLLNVIYR			
				993.4	2	LTPGSQCADGECCDQCK			
				1072.6	2	VLNIYIALVGLEIWNNGDK			
				831.1	3	QCISLFGASATVAQDACFQFNR			
				961.8	3	TDIVSPAVCGNYLVELGEDCDCGSPR			
57d	0.942	53▼		430.7	2	ETDLLNR	1115	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				514.3	2	IPCAPQDVK			
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				601.8	2	WRETDLLNR			
				412.2	3	VTLDLFGKWR			
				671.4	2	MPQCILNKPLK			
				712.9	2	LVIVADYIMFLK			
				718.3	2	LYCFDNLPEHK			
				799.8	2	DCQNPCCNAATCK			
				811.5	2	IYEIVNLLNVIYR			
				836.4	2	SCIMSGTLSCEASIR			
				627.0	3	TRIYEIVNLLNVIYR			
				993.4	2	LTPGSQCADGECCDQCK			
				1072.6	2	VLNIYIALVGLEIWNNGDK			
				831.1	3	QCISLFGASATVAQDACFQFNR			
				910.4	3	LYCFDNLPEHKNPCQIYYTPR			
				961.8	3	TDIVSPAVCGNYLVELGEDCDCGSPR			
57e	0.113	37▼		430.7	2	ETDLLNR	463	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				442.3	2	INVLPEAK			
				446.8	2	VTLDLFGK			
				514.3	2	IPCAPQDVK			
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				479.2	3	LYCFDNLPEHK			
				720.9	2	LVIVADYIMoxFLK			
				799.8	2	DCQNPCCNAATCK			
				811.5	2	IYEIVNLLNVIYR			
57f	0.132	14▼		430.7	2	ETDLLNR	208	*Vipera ammodytes ammodytes* AGL45259	SVMP fragment
				442.3	2	INVLPEAK			
				446.8	2	VTLDLFGK			
				720.9	2	LVIVADYIMoxFLK			

Table A2.6 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 18VL258 from Gerês. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
1	11.358			430.2	1	ZNW	*de novo*		SVMPi
				444.2	1	ZBW	*de novo*		SVMPi
3	1.568			536.8	2	ZDPXDPPNPP	*de novo*		BPP
				809.4	1	QPWPGPK	*de novo*	~*Vipera aspis* P31351	BPP
4	3.135	6■	4435.9	581.3	2	LKPAGTTCWK	190	*Macrovipera lebetina obtusa* P83469	(K/R)TS disintegrin
				627.8	2	TSLTSHYCTGK			
				600.0	4	LKPAGTTCWKTSLTSHYCTGK			
6	2.815			536.8	2	ZDPXDPPNPP	*de novo*		BPP
7	1.745	6▼	7085.2/ 7028.2/ 6980.2/6923.2	547.7	2	FYYDSASNK	86	*Macrovipera lebetina transmediterranea* I2G9B4	KTSPi

				461.5	3	FYYDSASNKCK			
8	2.206	6▼	7423.4/ 7366.4/ 7318.4	547.7	2	FYYDSASNK	67	*Vipera ammodytes ammodytes* AMH40736	KTSPi
				733.8	2	EFIYGGCHGNANK	56	*Daboia siamensis* A8Y7P5	KTSPi
10	1.049	17■	13986.8/ 13929.8	583.3	2	FLNAGTICNR	139	*Macrovipera lebetina* ABC00778	Dimeric disintegrin
				784.4	2	NCKFLNAGTICNR			
				587.9	3	NSGNPCCDPVTCKPR	44	*Macrovipera lebetina* P83254	Dimeric disintegrin
11	0.803	13■	7162.2/ 7105.2/ 7056.2/ 6999.2	733.8	2	EFIYGGCHGNANK	48	*Daboia siamensis* A8Y7P5	KTSPi
				547.7	2	FYYDSASNK	48	*Vipera ammodytes ammodytes* AMH40736	KTSPi
12	0.195								Unidentified
13a	0.180	53■		597.6	3	NSANPCCDPITCKPR	222	*Macrovipera lebetina obtusa* P0C6B0	Disintegrin
				402.6	3	FLNPGTICKR			
				525.3	2	FLNPGTICK			
				536.9	3	NCKFLNPGTICKR			
13b	0.299	36■		1009.4	2	GDWNDDYCTGISSDCPR	102	*Vipera ammodytes ammodytes* AMB36349	Disintegrin
				598.2	3	LGEHCVSGPCCDNCK			
				525.3	2	FLNPGTICK	49	*Macrovipera lebetina* Q3BK13	Disintegrin
13c	1.003	26■		895.9	2	NSANPCCDPITCKPR	66	*Macrovipera lebetina obtusa* P0C6B0	Disintegrin
				525.3	2	FLNPGTICK			
13d	1.338	19■		515.8	2	XGFCPPSPR	*de novo*	*Notechis scutatus* XP_026546510	KTSPi
13e	2.926	16■		1009.4	2	GDWNDDYCTGISSDCPR	121	*Vipera ammodytes ammodytes* AMB36349	Disintegrin
				598.2	3	LGEHCVSGPCCDNCK			
				895.9	2	NSANPCCDPITCKPR	41	*Macrovipera lebetina transmediterranea* CAK12626	Disintegrin
15	1.492	16■		895.9	2	NSANPCCDPITCKPR	39	*Macrovipera lebetina transmediterranea* CAK12626	Disintegrin
18a	0.132	26■	14475.1/ 14418.1/ 14361.1	525.3	2	FLNPGTICK	50	*Macrovipera lebetina* Q3BK13	Dimeric disintegrin
	0.010	26■		658.7	2	CSGCCTDESLK	43	*Vipera ammodytes ammodytes* P67863	VEGF
18b	0.646	16■		525.3	2	FLNPGTICK	48	*Macrovipera lebetina* Q3BK13	Disintegrin
19a	0.131	26■		525.3	2	FLNPGTICK	50	*Macrovipera lebetina* Q3BK13	Disintegrin
	0.037	26■		658.7	2	CSGCCTDESLK	61	*Vipera ammodytes ammodytes* P67863	VEGF
19b	0.265	16■		525.3	2	FLNPGTICK	34	*Macrovipera lebetina* Q3BK13	Disintegrin
				598.2	3	LGEHCVSGPCCDNCK	25	*Vipera ammodytes ammodytes* AMB36349	Disintegrin
21a	0.816	16▼		658.7	2	CSGCCTDESLK	104	*Vipera ammodytes ammodytes* P67863	VEGF
				556.8	2	HTVDLQIMR			
21b	0.786	13▼		1050.5	3	ETLVSILQEYPDEISDIFRPSCVAVLR	222	*Vipera aspis aspis* P83942	VEGF
				658.7	2	CSGCCTDESLK			
				521.9	3	FTEHTACECRPR			
				556.8	2	HTVDLQIMR			
				439.9	3	IFRPSCVAVLR	42	*Bitis arietans* C0K3N1	VEGF
24	1.767	16▼	13579.7/ 13522.7	1039.4	2	SALFSYSDYGCYCGWGGK	339	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				736.0	3	KSALFSYSDYGCYCGWGGK			
				767.3	2	CCFVHDCCYGR			
				494.2	2	GKPQDATDR			
				455.2	2	AVCECDR			
				871.7	3	MGTYSYSFQNGDIVCGGDDPCLR	187	*Echis coloratus* Q910A0	D49-PLA2
				717.3	2	GDIVCGGDDPCLR	175	*Vipera aspis aspis* CAE47133	D49-PLA2
				806.8	2	NYPSSHCTETEQC	173	*Vipera ammodytes ammodytes* P34180	D49-PLA2
				877.4	3	MoxGTYSYSFENGDIVCGGDDPCLR	163	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				463.6	3	NLYQFGKMIFK	128	*Cerastes cerastes* P21789	D49-PLA2
				745.8	2	GNIVCGRNNGCLR	31	*Daboia siamensis* Q02471	D49-PLA2
	0.012	16▼		775.8	2	SGCAAAYCPSSEYK	47	*Vipera berus* B7FDI1	CRISP
25a	1.145	28▼		640.3	3	KPEIQNEIIDLHNSLR	294	*Vipera berus nikolskii* B7FDI0	CRISP
				769.3	2	MEWYPEAAANAER			
				589.3	2	SVNPTASNMoxLK			
				485.2	2	CILSHSPR			
				445.2	3	RSVNPTASNMoxLK			
				977.0	2	YFYVCQYCPAGNIIGK	229	*Echis coloratus* P0DMT4	CRISP
				569.8	2	SVDFDSESPR	222	*Crotalus horridus* ACE73560	CRISP
				778.3	2	CGENIYMoxSPIPMK	207	*Gloydius blomhoffii* Q8JI40	CRISP
				526.2	2	VDFDSESPR	46	*Daboia russelii* P86537	CRISP
25b	0.721	16▼	13497.8/ 24500.1	1039.4	2	SALFSYSDYGCYCGWGGK	156	*Vipera ammodytes meridionalis* CAE47236	D49-PLA2
				767.3	2	CCFVHDCCYGR			
				463.6	3	NLYQFGKMIFK	101	*Cerastes cerastes* P21789	D49-PLA2

				806.8	2	NYPSSHCTETEQC	88	*Vipera ammodytes ammodytes* P34180	D49-PLA2
	0.042	16▼		569.8	2	SVDFDSESPR	45	*Daboia russelii* P86537	CRISP
26	1.193	28▼	24742.4	960.0	2	KPEIQNEIIDLHNSLR	473	*Vipera berus* B7FDI1	CRISP
				775.8	2	SGCAAAYCPSSEYK			
				924.1	3	DFVYGQGASPANAVVGHYTQIVWYK			
				777.3	2	MoxEWYPEAAANAER			
				581.3	2	SVNPTASNMLK			
				1001.4	2	YFYVCQYCPAGNMoxQGK			
				545.9	3	WTAIIHEWHGEEK			
				977.0	2	YFYVCQYCPAGNIIGK	233	*Echis coloratus* P0DMT4	CRISP
				569.8	2	SVDFDSESPR	186	*Crotalus horridus* ACE73560	CRISP
				778.3	2	CGENIYMSPIPMoxK	157	*Gloydius blomhoffii* Q8JI40	CRISP
				703.8	2	EWYPEAAANAER	113	*Helicops angulatus* P0DJG8	CRISP
				856.3	3	EGPKCGDCPDACENGLCTNPCR	85	*Causus rhombeatus A7X4T8*	CRISP
				526.2	2	VDFDSESPR	53	*Daboia russelii* P86537	CRISP
27a	0.336	28▼		640.3	3	KPEIQNEIIDLHNSLR	468	*Vipera berus* B7FDI1	CRISP
				924.1	3	DFVYGQGASPANAVVGHYTQIVWYK			
				769.3	2	MEWYPEAAANAER			
				775.8	2	SGCAAAYCPSSEYK			
				589.3	2	SVNPTASNMoxLK			
				545.9	3	WTAIIHEWHGEEK			
				569.8	2	SVDFDSESPR	201	*Crotalus horridus* ACE73560	CRISP
				778.3	2	CGENIYMSPIPMoxK	166	*Gloydius blomhoffii* Q8JI40	CRISP
				550.8	2	YTQIVWYK	117	*Helicops angulatus* P0DJG8	CRISP
				856.3	3	EGPKCGDCPDACENGLCTNPCR	71	*Causus rhombeatus A7X4T8*	CRISP
				526.2	2	VDFDSESPR	53	*Daboia russelii* P86537	CRISP
27b	0.455	16▼	13734.8/ 13706.8/ 13676.8 /13648.8	866.9	2	VAAICFGENMNTYDK	420	*Vipera ammodytes meridionalis* CAE47179	D49-PLA2
				877.0	3	MoxGTYSYSFENGDIVCGGDDPCLR			
				626.3	3	VAAICFGENMoxNTYDKK			
				670.3	2	YMLYSLFDCK			
				486.8	2	GKPLDATDR			
				511.9	3	CCFVHDCCYGR			
				455.2	2	AVCECDR			
				631.3	2	IVCGGDDPCLR	158	*Daboia siamensis* Q7T3T5	D49-PLA2
29a	0.160	28▼	13677.9 /13649.8	631.3	2	IVCGGDDPCLR	89	*Daboia siamensis* Q7T3T5	D49-PLA2
				678.3	2	YMoxLYSIFDCK			
	0.132	28▼		485.2	2	CILSHSPR	117	*Vipera berus nikolskii* B7FDI0	CRISP
				640.3	3	KPEIQNEIIDLHNSLR			
				569.8	2	SVDFDSESPR	77	*Crotalus horridus* ACE73560	CRISP
29b	10.985	16▼		874.9	2	VAAICFGENMoxNTYDK	102	*Macrovipera lebetina* C3W4R6	D49-PLA2
				626.3	3	VAAICFGENMoxNTYDKK			
29c	1.323	9▼		866.9	2	VAAICFGENMNTYDK	389	*Vipera ammodytes ammodytes* Q910A1	D49-PLA2
				626.3	3	VAAICFGENMoxNTYDKK			
				670.3	2	YMLYSLFDCK			
				511.9	3	CCFVHDCCYGR			
				486.8	2	GKPLDATDR			
				1059.4	2	YMoxLYSLFDCKEESEQC			
				717.3	2	GDIVCGGDDPCLR	72	*Vipera aspis aspis* CAE47133	D49-PLA2
				631.3	2	IVCGGDDPCLR	67	*Daboia siamensis* Q7T3T5	D49-PLA2
30a	0.429	45▼		1061.0	2	GDSGGPLICNGEIQGIVSYGK	332	*Vipera ammodytes ammodytes* AMB36343	SVSP
				437.7	2	ASYALPPR			
				457.8	2	KLCAGIPR			
				553.3	2	KDNDIMoxLIK			
				475.8	2	NGAPSIYTK			
				756.8	2	VIGGDECNINEHR	73	*Lachesis muta rhombeata* C0HLA1	SVSP
30b	0.348	37▼		796.9	2	TLCAGILQGGIDSCK	286	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				612.8	2	IMoxGWGTITTTK			
				892.4	3	VTYPDVPHCADINMoxFDYSVCQK			
				433.8	2	IILGVHSK			
				444.7	2	FFCLSSK			
				616.3	4	VIGGDECNINEHPFLVALHTAR	209	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				437.7	2	ASYALPPR	118	*Vipera ammodytes ammodytes* AMB36343	SVSP

			696.4	3	FHCAGTLLNKEWVLTAAR	102	*Bitis gabonica* Q6T6S7	SVSP
			803.9	2	TLCAGILQGGIDTCK	89	*Macrovipera lebetina* E0Y419	SVSP
			504.9	3	VIGGDECNINEHR	89	*Gloydius shedaoensis* Q6T5L0	SVSP
	0.021	37▼	569.8	2	SVDFDSESPR	160	*Crotalus horridus* ACE73560	CRISP
			589.3	2	SVNPTASNMoxLK			
			777.3	2	MoxEWYPEAAANAER			
30c	0.628	26▼	612.8	2	IMoxGWGTITTTK	221	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			573.3	2	EKFFCLSSK			
			595.3	2	WDKDIMLIR			
			433.8	2	IILGVHSK			
			892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
			821.4	3	VIGGDECNINEHPFLVALHTAR	197	*Vipera ammodytes ammodytes* P0DPS3	SVSP
			696.4	3	FHCAGTLLNKEWVLTAAR	120	*Bitis gabonica* Q6T6S7	SVSP
31a	0.654	37▼	796.9	2	TLCAGILQGGIDSCK	328	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			612.8	2	IMoxGWGTITTTK			
			595.3	2	WDKDIMLIR			
			886.7	3	VTYPDVPHCADINMFDYSVCQK			
			433.8	2	IILGVHSK			
			444.7	2	FFCLSSK			
			821.4	3	VIGGDECNINEHPFLVALHTAR	312	*Vipera ammodytes ammodytes* P0DPS3	SVSP
			1044.0	2	FHCAGTLLNKEWVLTAAR	186	*Bitis gabonica* Q6T6S7	SVSP
			757.4	2	VTYPDVPHCANIK			
			629.8	2	NIQNEDEQIR	103	*Protobothrops mucrosquamatus* XP_015671564	SVSP
			511.3	3	FPNGLDKDIMLIR	91	*Daboia siamenis* P18964	SVSP
			803.9	2	TLCAGILQGGIDTCK	82	*Macrovipera lebetina* E0Y419	SVSP
			587.8	2	VVCAGIWQGGK	75	*Vipera berus nikolskii* E5AJX2	SVSP
			653.3	3	HAWCEALYPWVPADSR	64	*Macrovipera lebetina* Q9PT41	SVSP
			604.8	2	IMoxGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	39	*Crotalus scutulatus* AUS82544	SVSP
31b	0.025	32▼	683.4	4	RPVNDSTHIAPLSLPSSPPSVGSVCR	243	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			612.8	2	IMoxGWGTITTTK			
			433.8	2	IILGVHSK			
			402.5	3	WDKDIMoxLIR			
			696.4	3	FHCAGTLLNKEWVLTAAR	101	*Bitis gabonica* Q6T6S7	SVSP
			629.8	2	NIQNEDEQIR	78	*Protobothrops mucrosquamatus* XP_015671564	SVSP
			452.3	2	TLCAGILR	31	*Echis ocellatus* ADE45140	SVSP
31c	0.061	26▼	612.8	2	IMoxGWGTITTTK	151	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			444.7	2	FFCLSSK			
			892.1	3	VTYPDVPHCADINMoxFDYSVCQK			
			696.4	3	FHCAGTLLNKEWVLTAAR	98	*Bitis gabonica* Q6T6S7	SVSP
			757.4	2	VTYPDVPHCANIK			
			455.8	2	IELGVHDK	76	*Vipera berus nikolskii* E5AJX2	SVSP
			452.3	2	TLCAGILR	31	*Echis ocellatus* ADE45140	SVSP
31d	0.019	21▼	612.8	2	IMoxGWGTITTTK	157	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			433.8	2	IILGVHSK			
			444.7	2	FFCLSSK			
			696.4	3	FHCAGTLLNKEWVLTAAR	67	*Bitis gabonica* Q6T6S7	SVSP
34a	0.577	78▼	748.4	3	CAGTLINQEWVLTAAHCNGK	233	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			587.8	2	VVCAGIWQGGK			
			444.7	2	FFCLSSK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR	230	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			559.8	2	AAYPWLLER			
			452.3	2	TLCAGILR			
			455.0	4	KVLNEDEETREPTEK			
			803.9	2	TLCAGILQGGIDTCK	113	*Macrovipera lebetina* E0Y419	SVSP
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
34b	7.924	37▼	563.6	3	VLNEDEETREPTEK	204	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR			

			916.0	2	VILPDVPHCANIEIIK	149	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			455.8	2	IELGVHDK			
			504.9	3	IVGGDECNINEHR	54	*Lachesis muta rhombeata* C0HLA1	SVSP
			634.8	2	AENPWLPAQSR	41	*Vipera ammodytes ammodytes* AMB36345	SVSP
34c	0.380	30▼	748.7	3	CAGTLINQEWVLTAAHCNGK	301	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			587.8	2	VVCAGIWQGGK			
			444.7	2	FFCLSSK			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR	260	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			504.9	3	VIGGDECNINEHR	103	*Gloydius shedaoensis* Q6T5L0	SVSP
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
34d	0.428	26▼	748.4	3	CAGTLINQEWVLTAAHCNGK	217	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			455.8	2	IELGVHDK			
			444.7	2	FFCLSSK			
			552.8	2	VLNEDEETR	216	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.9	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			504.9	2	VIGGDECNINEHR	84	*Gloydius shedaoensis* Q6T5L0	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			604.8	2	IMoxGWGTTTPTK	40	*Crotalus scutulatus* AUS82544	SVSP
34e	0.197	17▼	748.4	3	CAGTLINQEWVLTAAHCNGK	281	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			444.7	2	FFCLSSK			
			455.8	2	IELGVHDK			
			559.8	2	AAYPWLLER	67	*Vipera ammodytes ammodytes* AMB36344	SVSP
			452.3	2	TLCAGILR			
			892.9	2	VIGGDECNINEHPFLA	44	*Daboia russelii* P86530	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
	0.007	17▼	690.3	2	ALTMoxEGNQASWR	108	*Tropidechis carinatus* Q3HXX4	VNGF
			549.3	2	NPNPVPSGCR			
35a	0.059	60▼	737.6	3	LHSWVKCESGECCDQCR	72	*Trimeresurus stejnegeri* Q3HTN1	PIII-SVMP
	0.014	60▼	452.3	2	TLCAGILR	29	*Echis ocellatus* ADE45140	SVSP
35b	0.075	40▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	304	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			748.4	3	CAGTLINQEWVLTAAHCNGK	257	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			444.7	2	FFCLSSK			
			455.8	2	IELGVHDK			
			611.0	3	VILPDVPHCANIEIIK			
			803.9	2	TLCAGILQGGIDTCK	161	*Vipera ammodytes ammodytes* AMB36345	SVSP
			634.8	2	AENPWLPAQSR			
			504.9	3	VIGGDECNINEHR	110	*Gloydius shedaoensis* Q6T5L0	SVSP
			509.6	3	IIGGDECNINEHR	79	*Gloydius blomhoffii* P81176	SVSP
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
35c	0.210	33▼	751.1	3	TSTHIAPLSLPSSPPSVGSVCR	255	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	133	*Vipera berus nikolskii* E5AJX2	SVSP

			748.4	3	CAGTLINQEWVLTAAHCNGK			
			444.7	2	FFCLSSK			
			611.0	3	VILPDVPHCANIEIIK			
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
36a	0.277	55▼	684.9	2	LVIVVDHSMVEK	75	*Echis carinatus* Q9PRP9	SVMP (PIII)
	0.063	55▼	849.9	2	TDIVSPPVCGNGLLEK	67	*Echis carinatus* ADI47592	PIII-SVMP
	0.049	55▼	559.8	2	AAYPWLLER	38	*Vipera ammodytes ammodytes* AMB36344	SVSP
36b	0.481	40▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	224	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			606.3	3	KVLNEDEETREPTEK			
			563.6	3	VLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			756.8	2	VIGGDECNINEHR	143	*Gloydius shedaoensis* Q6T5L0	SVSP
			841.4	2	NYTLWDKDIMLIR			
			587.8	2	VVCAGIWQGGK	115	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			611.0	3	VILPDVPHCANIEIIK			
			929.5	2	IAPFSLPSSPPSVGSVCR	105	*Crotalus atrox* AUS82483	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			995.5	3	LDRPVRKSAHIAPLSLPSSPPSVGSVCR	41	*Protobothrops mucrosquamatus* Q91507	SVSP
			892.9	2	VIGGDECNINEHPFLA	36	*Daboia russelii* P86530	SVSP
36c	0.375	32▼	1125.6	2	TSTHIAPLSLPSSPPSVGSVCR	188	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			452.3	2	TLCAGILR			
			504.9	3	IVGGDECNINEHR	46	*Lachesis muta rhombeata* C0HLA2	SVSP
37a	0.902	55▼	462.3	3	LVIVVDHSMoxVEK	77	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
	0.041	55▼	856.9	2	TDIVSPPVCGNALLEK	32	*Echis carinatus* ADI47592	PIII-SVMP
	0.030	55▼	559.8	2	AAYPWLLER	37	*Vipera ammodytes ammodytes* AMB36344	SVSP
37b	0.216	40▼	552.8	2	VLNEDEETR	205	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			559.8	2	AAYPWLLER			
			452.3	2	TLCAGILR			
			929.5	2	IAPFSLPSSPPSVGSVCR	98	*Crotalus atrox* AUS82483	SVSP
			587.8	2	VVCAGIWQGGK	72	*Vipera berus nikolskii* E5AJX2	SVSP
			504.9	3	IVGGDECNINEHR	58	*Lachesis muta rhombeata* C0HLA2	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			995.5	3	LNIPVRNSEHIAPLSLPSSPPSVGSVCR	35	*Crotalus molossus* AUS82531	SVSP
	0.019	40▼	471.3	3	LVIVVDHSMoxVRK	34	*Echis carinatus* Q9PRP9	SVMP (PIII)
37c	0.348	32▼	1125.6	2	TSTHIAPLSLPSSPPSVGSVCR	249	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			452.3	2	TLCAGILR			
38a	0.168	55▼	481.3	3	LVIVVDHSMoxVWK	149	*Echis carinatus* Q9PRP9	SVMP (PIII)
			471.3	3	LVIVVDHSMoxVRK			
			692.4	2	LVIVVDHSMoxVEK			
	0.106	55▼	733.0	3	LHSWVECESGECCEQCK	43	*Crotalus adamanteus* AEJ31992	PIII-SVMP
			535.7	2	QCVDVDTAY	36	*Protobothrops mucrosquamatus* XP_015683144	PIII-SVMP
	0.011	55▼	559.8	2	AAYPWLLER	52	*Vipera ammodytes ammodytes* AMB36344	SVSP
38b	0.433	40▼	452.3	2	TLCAGILR	140	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			929.5	2	IAPFSLPSSPPSVGSVCR	58	*Crotalus atrox* AUS82483	SVSP
			995.5	3	LNIPVRNSEHIAPLSLPSSPPSVGSVCR	33	*Crotalus molossus* AUS82531	SVSP
38c	0.228	32▼	452.3	2	TLCAGILR	189	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			581.3	2	WDKDIMLIK	153	*Macrovipera lebetina* E0Y420	SVSP
			504.9	3	VIGGNECNINEHR	51	*Crotalus atrox* Q9PRW2	SVSP
39a	0.949	53■	547.8	2	TIDYQWLR	361	*Vipera ammodytes ammodytes* AMB36339	CTL

			648.8	2	EEMoxNWEDAEK			
			680.8	2	DCHWGWTDGVK			
			816.9	2	FDLIWIGLSNLWR			
			824.4	2	FCTEQASGGHLLSLK			
			557.6	3	VFKEEMoxNWEDAEK			
			439.7	2	TWEDAEK	156	*Vipera ammodytes ammodytes* AMB36340	CTL
			508.3	2	YHAWIGLR			
			769.4	2	GYLEWVTLPCGDK			
	0.003	53■	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	48	*Macrovipera lebetina* E0Y420	SVSP
39b	0.523	32▼	547.8	2	TIDYQWLR	354	*Vipera ammodytes ammodytes* AMB36339	CTL
			648.8	2	EEMoxNWEDAEK			
			680.8	2	DCHWGWTDGVK			
			719.8	2	AWSDKPNCYVAK			
			816.9	2	FDLIWIGLSNLWR			
			549.9	3	FCTEQASGGHLLSLK			
			827.9	2	VFKEEMNWEDAEK			
			439.7	2	TWEDAEK	75	*Macrovipera lebetina* C0HKZ7	CTL
			409.3	2	LAYPILK	72	*Macrovipera lebetina* B4XT05	CTL
			508.3	2	YHAWIGLR	64	*Daboia siamensis* Q38L02	CTL
	0.380	32▼	452.3	2	TLCAGILR	175	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
	0.018	32▼	569.3	2	HDDIFAYEK	97	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
39c	4.207	17▼	473.2	2	TYNFICK	447	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			680.8	2	DCHWGWTDGVK			
			719.8	2	AWSDKPNCYVAK			
			816.9	2	FDLIWIGLSNLWR			
			824.4	2	FCTEQASGGHLLSLK			
			835.9	2	VFKEEMoxNWEDAEK			
			571.3	3	TIDYQWLRVDCSR			
			508.3	2	YHAWIGLR	286	*Vipera ammodytes ammodytes* AMB36340	CTL
			769.4	2	GYLEWVTLPCGDK			
			890.9	2	DKGYLEWVTLPCGDK			
			1092.9	3	FCTQQVNGCHLASIESVEEANFVAELVPK			
42a	0.105	32▼	452.3	2	TLCAGILR	159	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.053	32▼	473.2	2	TYNFICK	90	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			454.2	3	DCHWGWTDGVK			
			508.3	2	YHAWIGLR	41	*Macrovipera lebetina* AJO70721	CTL
			409.3	2	LAYPILK	39	*Vipera ammodytes ammodytes* APB93444	CTL
42b	0.111	23▼	468.3	2	IIYVNWK	38	*Daboia siamensis* ADK22831	CTL
42c	1.110	18▼	547.8	2	TIDYQWLR	224	*Vipera ammodytes ammodytes* AMB36339	CTL
			454.2	3	DCHWGWTDGVK			
			719.4	2	AWSDKPNCYVAK			
			549.9	3	FCTEQASGGHLLSLK			
			552.3	3	VFKEEMNWEDAEK			
			439.7	2	TWEDAEK	88	*Macrovipera lebetina* C0HKZ7	CTL
			409.3	2	LAYPILK	65	*Macrovipera lebetina* B4XT05	CTL
			484.9	4	DCPSDWSSHEEHCYK	56	*Macrovipera lebetina* C0HKZ6	CTL
			508.3	2	YHAWIGLR	37	*Macrovipera lebetina* AJO70721	CTL
42d	1.131	14▼	639.8	2	ESEIVWMGLSK	71	*Echis carinatus* Q9PSM8	CTL
43a	0.124	31▼	452.3	2	TLCAGILR	152	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.039	31▼	473.2	2	TYNFICK	81	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			439.7	2	TWEDAEK	70	*Daboia siamensis* Q38L02	CTL
			508.3	2	YHAWIGLR			

43b	1.521	16▼	508.3	2	YHAWIGLR	157	*Vipera ammodytes ammodytes* AMB36340	CTL
			769.4	2	GYLEWVTLPCGDK			
			890.9	2	DKGYLEWVTLPCGDK			
			547.8	2	TIDYQWLR	123	*Vipera ammodytes ammodytes* AMB36339	CTL
			454.2	3	DCHWGWTDGVK			
			816.9	2	FDLIWIGLSNLWR			
			549.9	3	FCTEQASGGHLLSLK			
			409.3	2	LAYPILK	29	*Vipera ammodytes ammodytes* APB93444	CTL
43c	1.309	14▼	639.8	2	ESEIVWMGLSK	54	*Echis carinatus* Q9PSM8	CTL
			647.8	2	ESEIVWMoxGLSK	39	*Echis carinatus* Q9PSM8	CTL
46a	0.170	>116▼	502.3	2	VTVLEASER	299	*Cerastes cerastes* P0DQH9	LAAO
			567.3	2	YPVKPSEEGK			
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			747.3	2	ADDKNPLEECFR			
			563.8	2	FDEIVGGMoxDK	297	*Macrovipera lebetina* P81375	LAAO
			569.3	2	HDDIFAYEK			
			463.6	3	KFWEDDGIHGGK			
			583.4	2	IKFEPPLPPK	265	*Gloydius halys* Q6STF1	LAAO
			826.4	2	NVKEGWYANLGPMoxR	101	*Daboia russelii* G8XQX1	LAAO
46b	2.565	55▼	438.7	2	STTDLPSR	469	*Bothrops pictus* X2L4E2	LAAO
			555.8	2	FDEIVGGMDK			
			569.3	2	HDDIFAYEK			
			626.8	2	SAGQLYEESLR			
			630.8	2	FWEDDGIHGGK			
			633.8	2	RFDEIVGGMDK			
			431.9	3	HDDIFAYEKR			
			690.9	2	SAGQLYEESLRK			
			694.8	2	KFWEDDGIHGGK			
			583.4	2	IKFEPPLPPK	425	*Bothrops atrox* P0CC17	LAAO
			498.6	3	ADDKNPLEECFR	409	*Macrovipera lebetina* P81375	LAAO
			750.8	2	EDDYEEFLEIAK			
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			826.4	2	NVKEGWYANLGPMoxR	357	*Daboia russelii* G8XQX1	LAAO
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			605.1	4	RFDEIVGGMDQLPTSMoxYEAIK	309	*Crotalus adamanteus* O93364	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR			
			502.3	2	VTVLEASER	288	*Vipera ammodytes ammodytes* P0DI84	LAAO
			469.2	2	IFLTCKR	192	*Crotalus durissus terrificus* C0HJE7	LAAO
46c	0.305	50▼	438.7	2	STTDLPSR	325	*Protobothrops flavoviridis* BAN82013	LAAO
			567.3	2	YPVKPSEEGK			
			569.3	2	HDDIFAYEK			
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			750.8	2	EDDYEEFLEIAK	306	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			502.3	2	VTVLEASER	289	*Vipera ammodytes ammodytes* P0DI84	LAAO
			583.4	2	IQFEPPLPPK			
			431.9	3	IQFEPPLPPKK			
			564.3	2	AHGWIDSTIK	105	*Demansia vestigiata* A6MFL0	LAAO
46d	0.264	47▼	438.7	2	STTDLPSR	495	*Bothrops pictus* X2L4E2	LAAO
			563.8	2	FDEIVGGMoxDK			
			569.3	2	HDDIFAYEK			
			626.8	2	SAGQLYEESLR			
			630.8	2	FWEDDGIHGGK			
			633.8	2	RFDEIVGGMDK			
			460.9	3	SAGQLYEESLRK			
			694.8	2	KFWEDDGIHGGK			
			583.4	2	IKFEPPLPPK	470	*Bothrops atrox* P0CC17	LAAO
			567.3	2	YPVKPSEEGK	429	*Protobothrops flavoviridis* BAN82013	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	345	*Crotalus adamanteus* O93364	LAAO

			818.4	2	NVKEGWYANLGPMR	238	*Daboia russelii* G8XQX1	LAAO
			564.3	2	AHGWIDSTIK	178	*Demansia vestigiata* A6MFL0	LAAO
	0.005	47▼	559.8	2	AAYPWLLER	160	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
46e	0.110	33▼	532.7	2	NPLEECFR	337	*Macrovipera lebetina* P81375	LAAO
			563.8	2	FDEIVGGMoxDK			
			567.3	2	YPVKPSEEGK			
			569.3	2	HDDIFAYEK			
			498.6	3	ADDKNPLEECFR			
			750.8	2	EDDYEEFLEIAK			
			744.6	4	ADDKNPLEECFREDDYEEFLEIAK			
			438.7	2	STTDLPSR	309	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			583.4	2	IKFEPPLPPK	284	*Gloydius halys* Q6STF1	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	283	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			826.4	2	NVKEGWYANLGPMoxR	259	*Daboia russelii* G8XQX1	LAAO
	0.040	33▼	452.3	2	TLCAGILR	229	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
46f	0.069	31▼	438.7	2	STTDLPSR	339	*Bothrops pictus* X2L4E2	LAAO
			555.8	2	FDEIVGGMDK			
			569.3	2	HDDIFAYEK			
			626.8	2	SAGQLYEESLR			
			690.9	2	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	334	*Protobothrops flavoviridis* BAN82013	LAAO
			583.4	2	IKFEPPLPPK	282	*Bothrops atrox* P0CC17	LAAO
			750.8	2	EDDYEEFLEIAK	276	*Macrovipera lebetina* P81375	LAAO
			826.4	2	NVKEGWYANLGPMoxR	221	*Daboia russelii* G8XQX1	LAAO
			564.3	2	AHGWIDSTIK	105	*Demansia vestigiata* A6MFL0	LAAO
	0.018	31▼	452.3	2	TLCAGILR	148	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
46g	0.110	29▼	563.8	2	FDEIVGGMoxDK	289	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			569.3	2	HDDIFAYEK			
			750.8	2	EDDYEEFLEIAK			
			438.7	2	STTDLPSR	267	*Bothrops atrox* P0CC17	LAAO
			462.8	2	FEPPLPPK			
			583.4	2	IKFEPPLPPK			
			626.8	2	SAGQLYEESLR	267	*Protobothrops flavoviridis* BAN82013	LAAO
			502.3	2	VTVLEASER	248	*Vipera ammodytes ammodytes* P0DI84	LAAO
			826.4	2	NVKEGWYANLGPMoxR	189	*Daboia russelii* G8XQX1	LAAO
			564.3	2	AHGWIDSTIK	89	*Demansia vestigiata* A6MFL0	LAAO
	0.001	29▼	559.8	2	AAYPWLLER	33	*Vipera ammodytes ammodytes* AMB36344	SVSP
46h	0.085	22▼	578.3	2	WTDGSSVIYK	126	*Macrovipera lebetina* AJO70726	CTL
			854.9	2	TSADYVWIGLWNQR			
			630.8	2	CGDDYPFVCK	98	*Bitis arietans* AOE43148	CTL
			468.3	2	IIYVNWK	90	*Vipera ammodytes ammodytes* APB93442	CTL
	0.022	22▼	438.7	2	STTDLPSR	140	*Vipera ammodytes ammodytes* P0DI84	LAAO
			502.3	2	VTVLEASER			
			567.3	2	YPVKPSEEGK			
			460.9	3	SAGQLYEESLRK	132	*Cerastes cerastes* P0DQH9	LAAO
			738.8	2	WDYVSCAEQYR	88	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR			
46i	0.170	18▼	532.7	2	NPLEECFR	247	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			498.6	3	ADDKNPLEECFR			
			750.8	2	EDDYEEFLEIAK			
			744.6	4	ADDKNPLEECFREDDYEEFLEIAK			

			438.7	2	STTDLPSR	221	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR	193	*Cerastes cerastes* P0DQH9	LAAO
			502.3	2	VTVLEASER			
	0.001	18▼	630.8	2	CGDDYPFVCK	32	*Macrovipera lebetina* AJO70726	CTL
48a	0.291	55▼	438.7	2	STTDLPSR	575	*Vipera ammodytes ammodytes* QBF53419	LAAO
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			818.4	2	NVEEGWYANLGPMR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			849.4	3	NPLEECFREDDYEEFLEIAK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			563.8	2	FDEIVGGMoxDK.L	360	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR.K			
			633.8	2	RFDEIVGGMDK.L			
			690.9	2	SAGQLYEESLRK.A			
			694.8	2	KFWEDDGIHGGK.S			
			567.3	2	YPVKPSEEGK	317	*Macrovipera lebetina* P81375	LAAO
			498.6	3	ADDKNPLEECFR			
			744.6	4	ADDKNPLEECFREDDYEEFLEIAK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	310	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			448.2	2	IFLTCNK	209	*Protobothrops elegans* BAP39915	LAAO
	0.116	55▼	423.3	2	LTTLGVNK	680	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			476.3	2	VGIIGYTTK			
			513.8	2	ASGNPILLNK			
			566.8	2	VVSLNVLCTK			
			653.9	2	QVPVVQAYAFGK			
			508.6	3	HGQGTGELLQVSGIK			
			792.4	2	IQLQNYYSQEIGK			
			530.6	3	IIALGHSGFFEDQR			
			859.9	2	ETPVLSNPGPYLEFR			
			640.3	3	VLLPSFLATGGDGYHMLK			
			812.4	3	FHECNLGNLICDAVIYNNLR			
			604.0	3	GSFELTILHTNDVHAR	476	*Naja atra* A0A2I4HXH5	5'-nucleotidase
			653.0	3	YLGYLNVVFDDKGNVIK	316	*Vipera anatolica senliki* QHR82712	5'-nucleotidase
	0.002	55▼	738.8	2	WDYVSCAEQYR	31	*Vipera ammodytes ammodytes* APB93442	CTL
48b	0.415	22▼	434.2	2	NCFGLEK	324	*Vipera ammodytes ammodytes* QBF53411	CTL
			578.3	2	WTDGSSVIYK			
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			1169.6	3	FCTEQANGGHLASIESVEEAEFVAQLVSENIK			
			738.8	2	WDYVSCAEQYR	54	*Vipera ammodytes ammodytes* APB93442	CTL
	0.001	22▼	438.7	2	STTDLPSR	75	*Vipera ammodytes ammodytes* QBF53419	LAAO
			567.1	4	HIVVVGAGMSGLSAAYVLAGAGHK			
48c	0.389	18▼	434.2	2	NCFGLEK	202	*Vipera ammodytes ammodytes* QBF53411	CTL
			578.3	2	WTDGSSVIYK			
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			413.7	2	SVSFVCK	104	*Macrovipera lebetina* AJO70725	CTL
			958.0	2	GSHLASIHSSEEEAFVSK			
			473.2	2	TYNFICK	70	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			409.3	2	LAYPILK	39	*Vipera ammodytes ammodytes* APB93444	CTL
			468.3	2	IIYVNWK	38	*Vipera ammodytes ammodytes* APB93442	CTL
	0.040	18▼	502.3	2	VTVLEASER	222	*Vipera ammodytes ammodytes* QBF53419	LAAO
			750.8	2	EDDYEEFLEIAK			
			818.4	2	NVEEGWYANLGPMR			
48d	0.388	14▼	571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK	29	*Vipera ammodytes ammodytes* QBF53419	LAAO
49a	0.037	55▼	502.3	2	VTVLEASER	522	*Vipera ammodytes ammodytes* QBF53419	LAAO
			532.7	2	NPLEECFR			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			

			826.4	2	NVEEGWYANLGPMoxR			
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			563.8	2	FDEIVGGMoxDK	396	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			463.6	3	KFWEDDGIHGGK			
			498.6	3	ADDKNPLEECFR			
			626.8	2	SAGQLYEESLR	311	*Cerastes cerastes* P0DQH9	LAAO
			460.9	3	SAGQLYEESLRK			
	0.0005	55▼	504.9	3	IVGGDECNINEHR	44	*Lachesis muta rhombeata* C0HLA2	SVSP
49b	0.010	33▼	452.3	2	TLCAGILR	221	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.001	33▼	578.3	2	WTDGSSVIYK	79	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
	0.0003	33▼	761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK	51	*Vipera ammodytes ammodytes* QBF53419	LAAO
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK	49	*Vipera ammodytes ammodytes* QBF53419	LAAO
49c	0.068	22▼	434.2	2	NCFGLEK	236	*Vipera ammodytes ammodytes* QBF53411	CTL
			578.3	2	WTDGSSVIYK			
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			468.3	2	IIYVNWK	88	*Vipera ammodytes ammodytes* APB93442	CTL
			738.8	2	WDYVSCAEQYR			
			430.6	3	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
49d	0.027	18▼	413.7	2	SVSFVCK	76	*Macrovipera lebetina* AJO70725	CTL
			639.0	3	GSHLASIHSSEEEAFVSK			
			578.3	2	WTDGSSVIYK	72	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			547.8	2	TIDYQWLR	45	*Vipera ammodytes ammodytes* AMB36339	CTL
	0.002	18▼	438.7	2	STTDLPSR	79	*Vipera ammodytes ammodytes* QBF53419	LAAO
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
49e	0.036	16▼	473.2	2	TYNFICK	156	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			680.8	2	DCHWGWTDGVK			
			630.8	2	CGDDYPFVCK	43	*Macrovipera lebetina* AJO70726	CTL
			508.3	2	YHAWIGLR	36	*Macrovipera lebetina* AJO70721	CTL
			468.3	2	IIYVNWK	33	*Daboia siamensis* ADK22831	CTL
49f	0.074	14▼	611.8	2	EEMNWADAEK	72	*Macrovipera lebetina* AJO70723	CTL
			619.8	2	EEMoxNWADAEK			
			633.3	2	ERMoxNWADAEK	39	*Echis carinatus* Q7T247	CTL
50a	0.036	60▼	438.7	2	STTDLPSR	223	*Gloydius halys* Q6STF1	LAAO
			563.8	2	FDEIVGGMoxDK			
			567.3	2	YPVKPSEEGK			
			583.4	2	IKFEPPLPPK			
			460.9	3	SAGQLYEESLRK	146	*Protobothrops flavoviridis* BAN82013	LAAO
	0.002	60▼	630.8	2	CGDDYPFVCK	37	*Vipera ammodytes ammodytes* QBF53411	CTL
50b	0.057	31▼	452.3	2	TLCAGILR	86	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
50c	0.111	21▼	854.9	2	TSADYVWIGLWNQR	106	*Vipera ammodytes ammodytes* QBF53411	CTL
			468.3	2	IIYVNWK	35	*Daboia siamensis* ADK22831	CTL
	0.018	21▼	559.8	2	AAYPWLLER	30	*Vipera ammodytes ammodytes* AMB36344	SVSP
50d	0.160	13▼	619.8	2	EEMoxNWADAEK	27	*Daboia siamensis* Q4PRD0	CTL
51a	0.058	97▼	490.7	2	CSSITDLGK	945	*Macrovipera lebetina* W8E7D1	PDE
			554.8	2	TLGMoxLMEGLK			
			567.8	2	NPFYNPSPAK			
			583.8	2	QPLPETLQLK			
			678.3	2	AATYFWPGSEVK			
			722.8	2	VDFFMoxYEGPAPR			
			724.8	2	DFYTFDSEGIVR			
			744.9	2	LWNYFHGTLLPK			
			500.2	3	CNGGTHGYDNEFK			
			507.3	3	SMoxQAIFLAHGPGFK			

			785.9	2	SPPTSVPPSASDCLR			
			795.4	2	VNLMVDQQWMAVR			
			908.4	2	MANVLCSCSEDCLEK			
			926.4	2	AGYLETWDSLMPNINK			
			934.0	2	FGPVSGEIIMoxALQMoxADR			
			580.3	4	AERPDFVTLYIEEPDTTGHK			
			403.2	2	SVPFEAR	315	*Protobothrops flavoviridis* BAN82021	PDE
			778.0	3	EQSSPLSCPFGPVPSPDVSGCK	258	*Crotalus adamanteus* J3SBP3	PDE
	0.0002	97▼	826.4	2	NVEEGWYANLGPMoxR	55	*Vipera ammodytes ammodytes* QBF53419	LAAO
51b	0.072	55▼	532.7	2	NPLEECFR	343	*Macrovipera lebetina* P81375	LAAO
			555.8	2	FDEIVGGMDK			
			567.3	2	YPVKPSEEGK			
			569.3	2	HDDIFAYEK			
			498.6	3	ADDKNPLEECFR			
			750.8	2	EDDYEEFLEIAK			
			438.7	2	STTDLPSR	306	*Vipera ammodytes ammodytes* QBF53419	LAAO
			826.4	2	NVEEGWYANLGPMoxR			
			626.8	2	SAGQLYEESLR	286	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
	0.003	55▼	678.3	2	AATYFWPGSEVK	87	*Macrovipera lebetina* W8E7D1	PDE
			724.8	2	DFYTFDSEGIVR			
51c	0.018	33▼	452.3	2	TLCAGILR	210	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.002	33▼	630.8	2	CGDDYPFVCK	69	*Bitis arietans* AOE43148	CTL
51d	0.108	22▼	578.3	2	WTDGSSVIYK	225	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
51e	0.129	14▼	619.8	2	EEMoxNWADAEK	175	*Macrovipera lebetina* AJO70723	CTL
			538.2	3	VFKEEMoxNWADAEK			
			646.0	3	GSHLVSLHNIAEADFVVK			
			630.8	2	CGDDYPFVCK	104	*Vipera ammodytes ammodytes* QBF53411	CTL
			854.9	2	TSADYVWIGLWNQR			
			633.3	2	ERMoxNWADAEK	50	*Echis carinatus* Q7T247	CTL
52a	0.434	55▼	438.7	2	STTDLPSR	686	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			1017.5	3	YAMoxGAITTFTPYQFQHFSEALTAPEGR			
			563.8	2	FDEIVGGMoxDK	435	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			463.6	3	KFWEDDGIHGGK			
			498.6	3	ADDKNPLEECFR			
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			626.8	2	SAGQLYEESLR	330	*Protobothrops flavoviridis* BAN82013	LAAO
			460.9	3	SAGQLYEESLRK			
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR	273	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
	0.142	55▼	513.2	2	GSYYGYCR	454	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			521.3	2	IPCAPQDIK			
			571.8	2	CILNEPLRK			
			585.3	2	KIPCAPQDIK			
			640.3	2	LYCLNNSPGNK			
			647.8	2	LIGVEFWCDR			
			806.9	2	ATVAEDSCFEENLK			
			716.3	3	DECDVPEHCTGQSAECPR			
			534.3	2	QCISLFGSR	319	*Macrovipera lebetina* Q7T046	PIII-SVMP
			813.9	2	ATVAEDSCFQENQK			

			833.4	2	LTPGAECGNGLCCEK			
	0.001	55▼	646.0	3	GSHLVSLHNIAEADFVVK	32	*Echis pyramidum leakeyi* Q6X5S3	CTL
52b	0.072	46▼	452.3	2	TLCAGILR	251	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			444.7	2	FFCLSSK	148	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			587.8	2	VVCAGIWQGGK			
			611.0	3	VILPDVPHCANIEIIK			
			634.8	2	AENPWLPAQSR	75	*Vipera ammodytes ammodytes* AMB36345	SVSP
			538.2	2	IYDYSVCR	67	*Vipera ammodytes ammodytes* QBF53414	SVSP
			556.3	3	HPCAQPHLPAFYTK			
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			604.8	2	IMoxGWGTTTPTK	38	*Crotalus scutulatus* AUS82544	SVSP
	0.004	46▼	647.8	2	LIGVEFWCDR	150	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			806.9	2	ATVAEDSCFEENLK			
	0.004	46▼	502.3	2	VTVLEASER	115	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			826.4	2	NVEEGWYANLGPMoxR			
52c	0.060	36▼	452.3	2	TLCAGILR	228	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.0004	36▼	571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK	30	*Vipera ammodytes ammodytes* QBF53419	LAAO
52d	0.085	33▼	452.3	2	TLCAGILR	251	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
	0.001	33▼	569.3	2	HDDIFAYEK	46	*Calloselasma rhodostoma* P81382	LAAO
52e	0.211	22▼	578.3	2	WTDGSSVIYK	194	*Vipera ammodytes ammodytes* QBF53411	CTL
			630.8	2	CGDDYPFVCK			
			854.9	2	TSADYVWIGLWNQR			
			468.3	2	IIYVNWK	66	*Vipera ammodytes ammodytes* APB93442	CTL
			738.8	2	WDYVSCAEQYR			
			645.4	2	FITHFWIGLR	56	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	42	*Macrovipera lebetina* Q696W1	CTL
52f	0.119	18▼	578.3	2	WTDGSSVIYK	80	*Macrovipera lebetina* B4XSY9	CTL
			854.9	2	TSADYVWIGLWNQR			
			473.2	2	TYNFICK	65	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			430.6	3	FITHFWIGLR	42	*Macrovipera lebetina* Q696W1	CTL
			645.4	3	FITHFWIGLR	30	*Macrovipera lebetina* Q696W1	CTL
	0.024	18▼	750.8	2	EDDYEEFLEIAK	143	*Vipera ammodytes ammodytes* QBF53419	LAAO
			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
52g	0.318	16▼	473.2	2	TYNFICK	183	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			680.8	2	DCHWGWTDGVK			
			480.2	3	AWSDKPNCYVAK			
			439.7	2	TWEDAEK	134	*Vipera ammodytes ammodytes* AMB36340	CTL
			508.3	2	YHAWIGLR			
			769.4	2	GYLEWVTLPCGDK			
			430.6	3	FITHFWIGLR	29	*Macrovipera lebetina* Q696W1	CTL
	0.003	16▼	559.8	2	AAYPWLLER	30	*Vipera ammodytes ammodytes* AMB36344	SVSP
52h	0.240	14▼	639.8	2	ESEIVWMGLSK	58	*Echis carinatus* Q9PSM8	CTL
			619.8	2	EEMoxNWADAEK	37	*Daboia siamensis* Q4PRD0	CTL
53a	0.052	67▼	411.2	2	LVESFAR	585	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			483.2	2	YWIQAER			
			483.7	2	QLEEEYR			
			545.3	2	VLMGNIDLSK			
			561.8	2	RQLEEEYR			

			586.3	2	LPPPTNTIYR			
			764.3	2	LADDFMGSTWQEK			
			1039.0	2	GDDIPYTPVFYAYTLLTK			
			731.3	3	GMoxFTSIEPGYYHDGEFGIR			
			1102.5	2	EIPQENLLEDDFSPVMLSK			
			758.1	3	KPTAILLSGLEETAWLFNLR			
			750.4	2	YPVNEEPYLTFK	402	*Notechis scutatus* XP_026530513	Aminopeptidase
			577.3	2	LEDVALVVPAK	349	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
53b	0.167	55▼	438.7	2	STTDLPSR	765	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			431.9	3	IKFEPPLPPKK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			555.8	2	FDEIVGGMDK	390	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			641.8	2	RFDEIVGGMoxDK			
			460.9	3	SAGQLYEESLRK			
			463.6	3	KFWEDDGIHGGK			
			567.3	2	YPVKPSEEGK	373	*Gloydius halys* Q6STF1	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	349	*Macrovipera lebetina* P81375	LAAO
			609.1	4	RFDEIVGGMoxDQLPTSMoxYEAIK	323	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			1034.2	3	EATVTYQTSANEMoxSSVTADYVIVCTTSR			
			448.2	2	IFLTCNK	247	*Protobothrops elegans* BAP39915	LAAO
			564.3	2	AHGWIDSTIK	104	*Demansia vestigiata* A6MFL0	LAAO
	0.002	55▼	647.8	2	LIGVEFWCDR	139	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			806.9	2	ATVAEDSCFEENLK			
			534.3	2	QCISLFGSR	30	*Echis coloratus* ADI47635	PIII-SVMP
	0.002	55▼	504.9	3	IVGGDECNINEHR	62	*Lachesis muta rhombeata* C0HLA2	SVSP
53c	0.063	46▼	444.7	2	FFCLSSK	282	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			559.8	2	AAYPWLLER	272	*Vipera ammodytes ammodytes* AMB36344	SVSP
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			538.2	2	IYDYSVCR	133	*Vipera ammodytes ammodytes* QBF53414	SVSP
			995.5	3	LNSPVTYNTHIAPFSLPSSPPSVGSVCR	123	*Macrovipera lebetina* E0Y419	SVSP
			803.9	2	TLCAGILQGGIDTCK			
			509.6	3	IIGGDECNINEHR	68	*Bothrops fonsecai* P0DMH6	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			892.9	2	VIGGDECNINEHPFLA	31		
			596.8	2	IMGWGTTTPTK	30	*Crotalus scutulatus* AUS82544	SVSP
	0.0003	46▼	826.4	2	NVEEGWYANLGPMoxR	76	*Vipera ammodytes ammodytes* QBF53419	LAAO
53d	0.043	36▼	559.8	2	AAYPWLLER	298	*Vipera ammodytes ammodytes* AMB36344	SVSP
			844.9	2	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			1027.1	3	GGIDTCQADSGGPLICNGQLQGIVSWGYR			
			504.9	3	IVGGDECNINEHR	43	*Lachesis muta rhombeata* C0HLA1	SVSP
	0.001	36▼	502.3	2	VTVLEASER	170	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			755.7	3	HIVVVGAGMSGLSAAYVLAGAGHK			
			626.8	2	SAGQLYEESLR	103	*Cerastes cerastes* P0DQH9	LAAO
53e	0.051	33▼	452.3	2	TLCAGILR	241	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			

			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
			581.3	2	WDKDIMLIK	120	*Macrovipera lebetina* E0Y420	SVSP
	0.0004	$33^{\blacktriangledown}$	409.3	2	LAYPILK	26	*Vipera ammodytes ammodytes* APB93444	CTL
53f	0.226	$16^{\blacktriangledown}$	473.2	2	TYNFICK	263	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			680.8	2	DCHWGWTDGVK			
			816.9	2	FDLIWIGLSNLWR			
			549.9	3	FCTEQASGGHLLSLK			
			552.3	3	VFKEEMNWEDAEK			
			452.3	2	TLCAGILR	81	*Vipera ammodytes ammodytes* APB93444	CTL
			559.8	2	AAYPWLLER			
			508.3	2	YHAWIGLR	79	*Vipera ammodytes ammodytes* AMB36340	CTL
			769.4	2	GYLEWVTLPCGDK			
			484.9	4	DCPSDWSSHEEHCYK	52	*Macrovipera lebetina* C0HKZ6	CTL
53g	0.147	$14^{\blacktriangledown}$	647.8	2	ESEIVWMoxGLSK	61	*Echis carinatus* Q9PSM8	CTL
			639.8	2	ESEIVWMGLSK	58	*Echis carinatus* Q9PSM8	CTL
			547.8	2	TIDYQWLR	40	*Vipera ammodytes ammodytes* AMB36339	CTL
55a	0.114	$55^{\blacktriangledown}$	438.7	2	STTDLPSR	510	*Vipera ammodytes ammodytes* QBF53419	LAAO
			462.8	2	FEPPLPPK			
			502.3	2	VTVLEASER			
			532.7	2	NPLEECFR			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			563.8	2	FDEIVGGMoxDK	335	*Gloydius halys* Q6STF1	LAAO
			567.3	2	YPVKPSEEGK			
			626.8	2	SAGQLYEESLR	325	*Protobothrops flavoviridis* BAN82013	LAAO
			690.9	2	SAGQLYEESLRK			
	0.0003	$55^{\blacktriangledown}$	534.3	2	QCISLFGSR	37	*Echis coloratus* ADI47635	PIII-SVMP
	0.0003	$55^{\blacktriangledown}$	647.8	2	LIGVEFWCDR	29	*Daboia russelii russelii* ADJ67475	SVMP (PIII)
55b	0.388	$33^{\blacktriangledown}$	452.3	2	TLCAGILR	29	*Echis ocellatus* ADE45140	SVSP
	0.116	$33^{\blacktriangledown}$	571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK	59	*Vipera ammodytes ammodytes* QBF53419	LAAO
			761.1	3	HIVVVGAGMoxSGLSAAYVLAGAGHK	40	*Vipera ammodytes ammodytes* QBF53419	LAAO
55c	0.133	$16^{\blacktriangledown}$	473.2	2	TYNFICK	99	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			454.2	3	DCHWGWTDGVK			
			409.3	2	LAYPILK	72	*Macrovipera lebetina* B4XT05	CTL
			439.7	2	TWEDAEK			
55d	0.103	$14^{\blacktriangledown}$	647.8	2	ESEIVWMoxGLSK	31	*Echis carinatus* Q9PSM8	CTL
56a	0.094	$>116^{\blacktriangledown}$	535.2	2	QCVDVNTAY	110	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
	0.015	$>116^{\blacktriangledown}$	826.4	2	NVEEGWYANLGPMoxR	43	*Vipera ammodytes ammodytes* QBF53419	LAAO
56b	0.233	$60^{\blacktriangledown}$	635.3	2	SSVGLIQDYCK	343	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1000.9	2	LTPGSECGDGECCDQCR			
			805.7	3	CFNNNLQGTENFHCGMENGR			
56c	0.893	$55^{\blacktriangledown}$	438.7	2	STTDLPSR	409	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			583.3	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			1012.1	3	YAMGAITTFTPYQFQHFSEALTAPEGR			
			567.3	2	YPVKPSEEGK	264	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			463.6	3	KFWEDDGIHGGK			
			563.8	2	FDEIVGGMoxDK	246	*Macrovipera lebetina* P81375	LAAO
56d	0.064	$46^{\blacktriangledown}$	452.3	2	TLCAGILR	269	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			

			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			455.8	2	IELGVHDK	175	*Vipera berus nikolskii* E5AJX2	SVSP
			587.8	2	VVCAGIWQGGK			
			916.0	2	VILPDVPHCANIEIIK			
			748.4	3	CAGTLINQEWVLTAAHCNGK			
			504.9	3	VIGGDECNINEHR	94	*Gloydius shedaoensis* Q6T5L0	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
56e	0.089	33▼	452.3	2	TLCAGILR	236	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.001	33▼	676.9	2	NPQCILNKPLR	89	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
56f	0.138	16▼	473.2	2	TYNFICK	68	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
	0.013	16▼	559.8	2	AAYPWLLER	34	*Vipera ammodytes ammodytes* AMB36344	SVSP
56g	0.114	14▼	639.8	2	ESEIVWMGLSK	45	*Echis carinatus* Q9PSM8	CTL
			647.8	2	ESEIVWMoxGLSK	37	*Echis carinatus* Q9PSM8	CTL
			547.8	2	TIDYQWLR	30	*Vipera ammodytes ammodytes* AMB36339	CTL
57a	0.204	>116▼	635.3	2	SSVGLIQDYCK	54	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
57b	0.339	60▼	635.3	2	SSVGLIQDYCK	188	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			805.7	3	CFNNNLQGTENFHCGMoxENGR			
			1025.7	4	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
			1007.9	2	LTPGSQCADGECCDQCR	32	*Echis carinatus sochureki* ADI47586	PIII-SVMP
57c	0.890	55▼	502.3	2	VTVLEASER	135	*Vipera ammodytes ammodytes* QBF53419	LAAO
			750.8	2	EDDYEEFLEIAK			
	0.002	55▼	798.4	2	SAESVTLDLFGDWR	32	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
57d	0.362	50▼	563.8	2	FDEIVGGMoxDK	89	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			463.6	3	KFWEDDGIHGGK			
	0.212	50▼	500.2	3	VVGGDECNINEHR	50	*Bothrops cotiara* P0DMH5	SVSP
	0.144	50▼	790.4	2	IYEIVNTLNVVFR	167	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
57e	0.101	46▼	452.3	2	TLCAGILR	165	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	42	*Vipera anatolica senliki* QHR82809	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
57f	0.093	33▼	452.3	2	TLCAGILR.G	234	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
57g	0.162	16▼	547.8	2	TIDYQWLR	36	*Vipera ammodytes ammodytes* AMB36339	CTL
57h	0.116	14▼	647.8	2	ESEIVWMoxGLSK	50	*Echis carinatus* Q9PSM8	CTL
			639.8	2	ESEIVWMGLSK	46	*Echis carinatus* Q9PSM8	CTL
			853.9	2	VWNQCDWGWSNGAK	34	*Macrovipera lebetina* B4XT02	CTL
58a	0.072	>116▼	750.8	2	EDDYEEFLEIAK	41	*Daboia russelii* G8XQX1	LAAO
	0.014	>116▼	798.4	2	SAESVTLDLFGDWR	36	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
58b	0.197	55▼	502.3	2	VTVLEASER	240	*Vipera ammodytes ammodytes* QBF53419	LAAO
			637.8	2	TFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK			
			826.4	2	NVEEGWYANLGPMoxR			
			571.1	4	HIVVVGAGMoxSGLSAAYVLAGAGHK			
			567.3	2	YPVKPSEEGK	238	*Cerastes cerastes* P0DQH9	LAAO
			626.8	2	SAGQLYEESLR			
			498.6	3	ADDKNPLEECFR			
			463.6	3	KFWEDDGIHGGK	236	*Macrovipera lebetina* P81375	LAAO
58c	0.349	50▼	790.4	2	IYEIVNTLNVVFR	226	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			570.6	3	YIELVIVVDNVMFR			
	0.229	50▼	445.6	3	FVTAGTVCRPAR	126	*Vipera ammodytes ammodytes* AJC52543	PIII-SVMP

58d	0.074	33▼	559.8	2	AAYPWLLER	165	*Vipera ammodytes ammodytes* AMB36344	SVSP
			1125.6	2	TSTHIAPLSLPSSPPSVGSVCR			
	0.001	33▼	790.4	2	IYEIVNTLNVVFR	181	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			570.6	3	YIELVIVVDNVMFR	30	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
58e	0.086	16▼	473.2	2	TYNFICK	142	*Vipera ammodytes ammodytes* AMB36339	CTL
			547.8	2	TIDYQWLR			
			680.8	2	DCHWGWTDGVK			
			508.3	2	YHAWIGLR	36	*Macrovipera lebetina* AJO70721	CTL
	0.017	16▼	452.3	2	TLCAGILR	86	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
	0.001	16▼	790.4	2	IYEIVNTLNVVFR	118	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
58f	0.093	14▼	472.2	3	(330.6)AYDQHCYK	*de novo*	*Vipera ammodytes ammodytes* QBF53411	CTL
			621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
59a	0.085	55▼	690.9	2	SAGQLYEESLRK	46	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
59b	0.044	50▼	438.7	2	STTDLPSR	200	*Vipera ammodytes ammodytes* QBF53419	LAAO
			502.3	2	VTVLEASER			
			569.3	2	HDDIFAYEK			
			826.4	2	NVEEGWYANLGPMoxR			
	0.041	50▼	442.3	2	INVLPEAK	116	*Daboia siamensis* AUF41660	SVMP (PIII)
			446.8	2	VTLDLFGK			
			578.3	2	KIPCAPQDVK			
59c	0.406	29▼	676.9	2	NPQCILNKPLR	71	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
	0.043	29▼	559.8	2	AAYPWLLER	35	*Vipera ammodytes ammodytes* AMB36344	SVSP
60a	0.328	55▼	526.8	2	SCIMoxSGILR	595	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			616.8	2	YSVGIVQDHSK			
			671.4	2	MPQCILNKPLK			
			805.4	2	IYEIVNTLNVIYR			
			870.9	2	NPCQIYYIPSDENK			
			991.5	2	HDNAQLLTGINFNGPSAGR			
			677.0	3	LRPGAQCGDGVCCYQCK			
			713.4	3	RHDNAQLLTGINFNGPSAG			
	0.0005	55▼	647.8	2	LIGVEFWCDR	61	*Daboia russelii russelii* ADJ67475	SVMP (PIII)
	0.124	55▼	438.7	2	STTDLPSR	305	*Vipera ammodytes ammodytes* QBF53419	LAAO
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK			
			637.8	2	TFCYPSMIQK			
			818.4	2	NVEEGWYANLGPMR			
			567.1	4	HIVVVGAGMSGLSAAYVLAGAGHK			
			555.8	2	FDEIVGGMDK	289	*Gloydius halys* Q6STF1	LAAO
			567.3	2	YPVKPSEEGK			
			690.9	2	SAGQLYEESLRK	232	*Bothrops pictus* X2L4E2	LAAO
	0.001	55▼	559.8	2	AAYPWLLER	37	*Vipera ammodytes ammodytes* AMB36344	SVSP
60b	0.050	46▼	452.3	2	TLCAGILR	170	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			563.6	3	VLNEDEETREPTEK			
			444.7	2	FFCLSSK	120	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			587.8	2	VVCAGIWQGGK			
			538.2	2	IYDYSVCR	34	*Vipera ammodytes ammodytes* QBF53414	SVSP
	0.027	46▼	501.7	2	IACAPEDVK	309	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			616.8	2	YSVGIVQDHSK			
			805.4	2	IYEIVNTLNVIYR			
			870.9	2	NPCQIYYIPSDENK			
			661.3	3	HDNAQLLTGINFNGPSAGR			
60c	0.872	29▼	676.9	2	NPQCILNKPLR	83	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
	0.224	29▼	559.8	2	AAYPWLLER	59	*Vipera ammodytes ammodytes* AMB36344	SVSP
	0.202	29▼	501.7	2	IACAPEDVK	32	*Macrovipera lebetina* Q4VM07	PIII-SVMP
	0.060	29▼	1087.5	2	HDNAQLLTGMoxIFNETIEGR	29	*Crotalus adamanteus* J9Z332	SVMP (PI)
			725.4	3	HDNAQLLTGMoxIFNETIEGR	27	*Crotalus adamanteus* J9Z332	SVMP (PI)
60d	0.065	16▼	680.8	2	DCHWGWTDGVK	53	*Vipera ammodytes ammodytes* AMB36339	CTL

				508.3	2	YHAWIGLR	33	*Macrovipera lebetina* AJO70721	CTL
	0.044	16▼		559.8	2	AAYPWLLER	35	*Vipera ammodytes ammodytes* AMB36344	SVSP
	0.041	16▼		502.3	2	VTVLEASER	74	*Vipera ammodytes ammodytes* P0DI84	LAAO
60e	0.116	14▼		647.8	2	ESEIVWMoxGLSK	50	*Echis carinatus* Q9PSM8	CTL
61a	0.416	>116▼		514.3	2	IPCAPQDVK	541	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				412.2	3	VTLDLFGKWR			
				656.3	3	NPCQIYYTPR			
				718.3	2	LYCFDNLPEHK			
				799.8	2	DCQNPCCNAATCK			
				993.4	2	LTPGSQCADGECCDQCK			
	0.003	>116▼		438.7	2	STTDLPSR	41	*Notechis scutatus* XP_026538830	LAAO
61b	0.072	97▼		430.7	2	ETDLLNR	367	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				442.3	2	INVLPEAK			
				446.8	2	VTLDLFGK			
				514.3	2	IPCAPQDVK			
				566.2	2	LGNEYGYCR			
				656.3	2	NPCQIYYTPR			
				799.8	2	DCQNPCCNAATCK			
61c	0.675	50▼		514.3	2	IPCAPQDVK	658	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				412.2	3	VTLDLFGKWR			
				656.3	2	NPCQIYYTPR			
				671.4	2	MPQCILNKPLK			
				718.3	2	LYCFDNLPEHK			
				799.8	2	DCQNPCCNAATCK.L			
				811.5	2	IYEIVNLLNVIYR.V			
				627.0	3	TRIYEIVNLLNVIYR.V			
				993.4	2	LTPGSQCADGECCDQCK			
61d	0.111	46▼		430.7	2	ETDLLNR	540	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
				442.3	2	INVLPEAK			
				446.8	2	VTLDLFGK			
				514.3	2	IPCAPQDVK			
				566.2	2	LGNEYGYCR			
				578.3	2	KIPCAPQDVK			
				656.3	2	NPCQIYYTPR			
				453.2	3	MoxPQCILNKPLK			
				718.3	2	LYCFDNLPEHK			
				799.8	2	DCQNPCCNAATCK			
	0.014	46▼		559.8	2	AAYPWLLER	193	*Vipera ammodytes ammodytes* AMB36344	SVSP
				563.6	3	VLNEDEETREPTEK			
				750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
				444.7	2	FFCLSSK	100	*Macrovipera lebetina* E0Y420	SVSP
				604.8	2	IMoxGWGTTTPTK	36	*Crotalus scutulatus* AUS82544	SVSP

Table A2.7 MS/MS identification of proteins fractionated by reverse-phase HPLC and SDS-PAGE from the venom of adult *V. latastei* 19VL029 from Gerês. ■ = non-reduced; ▼= reduced.

Spot ID	%	MW (kDa)	ESI-MS (ave)	m/z	z	Peptide sequence	Score	Best NCBI match	Protein family
3	9.771			444.3	1	ZBW	*de novo*		SVMPi
				536.8	2	ZDPXDPPNPP	*de novo*		BPP
4	0.817			536.8	2	ZDPXDPPNPP	*de novo*		BPP
				481.3	2	ZBNBXGPPP	*de novo*	~*Bothrops jararaca* P0DM54	BPP
5	1.014			536.8	2	ZDPXDPPNPP	*de novo*		BPP
				481.3	2	ZBNBXGPPP	*de novo*	~*Bothrops jararaca* P0DM54	BPP
6	0.695	6▼	4435.8	418.9	3	TSLTSHYCTGK	61	*Macrovipera lebetina obtusa* P83469	(K/R)TS disintegrin
				649.8	2	TSRTSHYCTGK	24	*Daboia palestinae* P0C6E2	(K/R)TS disintegrin

7	2.793		4435.8/3661.6						Unidentified
8	3.002	7▼	7028.0/7085.1	733.8	2	EFIYGGCHGNANK	57	*Daboia siamensis* A8Y7P1	KTSPi
				1033.1	3	FCYLPAEPGECNAYMoxPSFYYDSASNK	32	*Vipera berus nikolskii* E5AJX3	KTSPi
				1037.4	3	FCYLPADPGRCLAYMoxPSFYYDSASNK	28	*Vipera ammodytes ammodytes* P00992	KTSPi
10a	0.273	14■		733.8	2	EFIYGGCHGNANK	52	*Daboia siamensis* A8Y7P1	KTSPi
10b	0.655	10■	7103.1/6681.9	733.8	2	EFIYGGCHGNANK	75	*Daboia siamensis* A8Y7P1	KTSPi
				843.8	2	NYTGRFYYDSASNK	27	*Bitis gabonica* Q6T269	KTSPi
11	0.978	13▼	13986.4/13871.1	583.3	2	FLNAGTICNR	97	*Macrovipera lebetina* P83253	Dimeric disintegrin
				491.9	3	RGEHCVSGPCCR			
				525.3	2	FLNPGTICK	34	*Macrovipera lebetina* ABC18317	Dimeric disintegrin
				592.9	3	NSANPCCDPVTCKPR	31	*Vipera ammodytes ammodytes* P0C6A5	Dimeric disintegrin
13a	0.232	31▼		501.8	2	IACAPEDVK	48	*Macrovipera lebetina* Q4VM07	DC-domain
13b	0.585	27▼		605.3	2	KGESYFYCR	137	*Echis coloratus* ADI47610	DC-domain
				541.2	2	GESYFYCR			
				533.2	2	HCVDVTTAY			
				619.3	2	RGESYFYCR	125	*Echis ocellatus* CAJ01682	DC-domain
	0.054	27▼		525.3	2	FLNPGTICK	34	*Eristicophis macmahoni* P81742	Disintegrin
13c	0.502	23▼		605.3	2	KGESYFYCR	99	*Echis coloratus* ADI47610	DC-domain
				541.2	2	GESYFYCR			
				533.2	2	HCVDVTTAY			
				619.3	2	RGESYFYCR	94	*Echis ocellatus* CAJ01682	DC-domain
	0.158	23▼		1004.4	2	YDYSEDPDYGMoxVDHGTK	40	*Ovophis okinavensis* T2HS56	Disintegrin
				664.6	3	YDYSEDPDYGMVDHGTK	39	*Ovophis okinavensis* T2HS56	Disintegrin
13d	1.085	20▼		605.3	2	KGESYFYCR	67	*Echis coloratus* ADI47610	DC-domain
				619.3	2	RGESYFYCR	50	*Echis ocellatus* Q2UXQ7	DC-domain
13e	4.048	12▼		1080.9	2	AMoxLDGLNDYCTGISSDCPR	263	*Vipera ammodytes ammodytes* AMB36347	Disintegrin
				402.6	3	FLNPGTICKR			
				525.3	2	FLNPGTICK			
				482.9	3	KGEHCVSGPCCR			
				597.6	3	NSANPCCDPITCKPR	180	*Macrovipera lebetina transmediterranea* CAK12655	Disintegrin
				496.9	3	RGEHCISGPCCR	109	*Cerastes vipera* Q3BK16	Disintegrin
				1085.4	2	ARGDNLNDYCTGISSDCPR	100	*Echis carinatus sochureki* ADI47727	Disintegrin
				1009.4	2	GDWNDDYCTGISSDCPR	76	*Vipera ammodytes ammodytes* AMB36349	Disintegrin
				1079.9	2	AMLDGLNDYCTGISTDCPR	52	*Echis carinatus* P81631	Disintegrin
14a	0.154	27▼		678.4	2	DVXXPCAEPDVK	*de novo*	~*Echis coloratus* ADI47648	DC-domain
14b	0.173	22▼		605.3	2	KGESYFYCR	33	*Echis coloratus* ADI47610	DC-domain
				545.7	2	(273.1)GDFYCR	*de novo*	~*Echis ocellatus* ADW54336	DC-domain
14c	0.940	12▼	14535.8/14518.8	1081.4	2	AMoxLDGLNDYCTGISSDCPR	154	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				525.3	2	FLNPGTICK			
				737.3	2	RGEHCVSGPCCR	99	*Macrovipera lebetina obtusa* P0C6B0	Dimeric disintegrin
15a	0.041	64▼							Unidentified
15b	0.143	28▼		678.4	2	DVXXPCAEPDVK	*de novo*	~*Echis coloratus* ADI47648	DC-domain
15c	0.639	12▼	14417.7/14475.8	1080.9	2	AMoxLDGLNDYCTGISSDCPR	277	*Vipera ammodytes ammodytes* AMB36347	Dimeric disintegrin
				525.3	2	FLNPGTICK			
				773.0	3	RAMoxLDGLNDYCTGISSDCPR			
				402.6	3	FLNPGTICKR			
				496.9	3	RGEHCISGPCCR	125	*Cerastes vipera* Q3BK16	Dimeric disintegrin
				1087.9	2	AMoxLDGLNDYCTGISTDCPR	91	*Echis carinatus* P81631	Dimeric disintegrin
				1085.4	2	ARGDNLNDYCTGISSDCPR	72	*Echis carinatus sochureki* ADI47727	Dimeric disintegrin
				1009.4	2	GDWNDDYCTGISSDCPR	69	*Vipera ammodytes ammodytes* AMB36349	Dimeric disintegrin
16a	0.103	29▼		678.4	2	DVXXPCAEPDVK	*de novo*	~*Echis coloratus* ADI47648	DC-domain
16b	0.122	17■		525.3	2	FLNPGTICK	38	*Eristicophis macmahoni* P81742	Disintegrin
20a	0.163	26▼		836.9	2	AAAICFGENVNTYDK	161	*Vipera renardi* F8QN51	D49-PLA2
				601.0	3	AAAICFGENVNTYDKK			
				826.3	2	YYSSSHCTETEQC			
				850.9	2	VAAICFGENVNTYDK	138	*Cerastes cerastes* P21789	D49-PLA2
				914.9	2	VAAICFGENVNTYDKK			
	0.004	26▼		569.8	2	SVDFDSESPR	67	*Crotalus horridus* ACE73560	CRISP
20b	0.949	17▼		836.9	2	AAAICFGENVNTYDK	234	*Vipera renardi* F8QN51	D49-PLA2
				601.0	3	AAAICFGENVNTYDKK			
				826.3	2	YYSSSHCTETEQC			
				914.9	2	VAAICFGENVNTYDKK	88	*Cerastes cerastes* P0DPS4	D49-PLA2

	0.020	17▼		690.3	2	ALTMoxEGNQASWR	176	*Bothrops jararacussu* Q90W38	VNGF
				647.3	2	IDTACVCVISR			
20c	7.271	14▼	13569.6/13626.6	836.9	2	AAAICFGENVNTYDK	241	*Vipera renardi* F8QN51	D49-PLA2
				900.9	2	AAAICFGENVNTYDKK			
				826.3	2	YYSSSHCTETEQC			
				914.9	2	VAAICFGENVNTYDKK	173	*Cerastes cerastes* P0DPS4	D49-PLA2
				850.9	2	VAAICFGENVNTYDK			
20d	0.561	5▼		836.9	2	AAAICFGENVNTYDK	206	*Vipera renardi* F8QN51	D49-PLA2
				900.9	2	AAAICFGENVNTYDKK			
				914.9	2	VAAICFGENVNTYDKK	106	*Cerastes cerastes* P0DPS4	D49-PLA2
				850.9	2	VAAICFGENVNTYDK			
23a	2.384	27▼		976.9	2	YFYVCQYCPAGNIIGK	168	*Echis coloratus* P0DMT4	CRISP
				777.3	2	MoxEWYPEAAANAER			
				583.8	2	NVDFDSESPR			
				569.8	2	SVDFDSESPR	120	*Crotalus horridus* ACE73560	CRISP
				484.7	2	CILSHSPR	114	*Vipera berus nikolskii* B7FDI0	CRISP
				703.8	2	EWYPEAAANAER	104	*Helicops angulatus* P0DJG8	CRISP
23b	0.102	21▼		589.3	2	SVNPTASNMoxLK	161	*Crotalus horridus* ACE73560	CRISP
				569.8	2	SVDFDSESPR			
				777.3	2	MoxEWYPEAAANAER			
			24500.0/24557.6/24614.3	583.7	2	NVDFDSESPR	160	*Echis coloratus* P0DMT4	CRISP
				976.9	2	YFYVCQYCPAGNIIGK			
				777.3	2	MoxEWYPEAAANAER			
24	1.262	28▼	24773.1/24830.0/24887.1	640.3	3	KPEIQNEIIDLHNSLR	188	*Echis coloratus* P0DMT4	CRISP
				519.5	4	KPEIQNEIIDLHNSLRR			
				583.8	2	NVDFDSESPR			
				767.4	4	NVDFDSESPRKPEIQNEIIDLHNSLR			
				589.3	2	SVNPTASNMoxLK	170	*Vipera berus nikolskii* B7FDI0	CRISP
				569.8	2	SVDFDSESPR	111	*Crotalus horridus* ACE73560	CRISP
				703.8	2	EWYPEAAANAER	48	*Protobothrops mucrosquamatus* P79845	CRISP
	0.004	28▼		836.9	2	AAAICFGENVNTYDK	37	*Vipera renardi* F8QN51	D49-PLA2
25	0.438	14▼	13666.5/13723.5	874.9	2	VAAICFGENMoxNTYDK	183	*Macrovipera lebetina* C3W4R6	D49-PLA2
				678.3	2	YMoxLYSLFDCK			
				626.3	3	VAAICFGENMoxNTYDKK			
				631.3	2	IVCGGDDPCLR	100	*Daboia siamensis* Q7T3T5	D49-PLA2
27a	2.707	37▼		796.9	2	TLCAGILQGGIDSCK	349	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				612.8	2	IMoxGWGTITTTK			
				892.4	3	VTYPDVPHCADINMoxFDYSVCQK			
				573.3	2	EKFFCLSSK			
				433.8	2	IILGVHSK			
				444.7	2	FFCLSSK			
				821.4	3	VIGGDECNINEHPFLVALHTAR	286	*Vipera ammodytes ammodytes* P0DPS3	SVSP
				1044.0	2	FHCAGTLLNKEWVLTAAR	161	*Bitis gabonica* Q6T6S7	SVSP
				629.8	2	NIQNEDEQIR	60	*Protobothrops mucrosquamatus* XP_015671564	SVSP
				819.9	2	NIRNEDEQIRVPR	41	*Daboia siamensis* ADP88558	SVSP
				452.3	2	TLCAGILR	34	*Echis ocellatus* ADE45140	SVSP
27b	4.892	14▼	12772.9/13666.5/13723.5	1313.0	2	LSTYSYSFQNGDIVCGGDDPCLR	356	*Vipera aspis aspis* CAE47119	D49-PLA2
				866.9	2	VAAICFGENMNTYDK			
				930.9	2	VAAICFGENMNTYDKK			
				455.2	2	AVCECDR			
				670.3	2	YMLYSLFDCK	331	*Macrovipera lebetina* C3W4R6	D49-PLA2
				970.9	2	YMLYSLFDCKEESEK			
				1059.4	2	YMoxLYSLFDCKEESEKC			
				1320.5	2	LSTYSYSFENGDIICGGDDPCLR	42	*Vipera aspis aspis* CAE47160	D49-PLA2
27c	0.615	6▼		875.7	3	LSTYSYSFQNGDIVCGGDDPCLR	57	*Vipera aspis aspis* CAE47158	D49-PLA2
				631.3	2	IVCGGDDPCLR	*de novo*	~*Daboia siamensis* Q7T3T5	D49-PLA2
28a	1.118	>116▼		766.4	2	FPNGLDKDIMLIR	190	*Daboia siamensis* P18964	SVSP
				820.4	2	NIRNEDEQIRVPR			
				643.8	2	NIRNEDEQIR			
				612.8	2	IMoxGWGTITTTK	110	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
				796.9	2	TLCAGILQGGIDSCK			
				433.8	2	IILGVHSK			
				653.3	3	HAWCEALYPWVPADSR	121	*Macrovipera lebetina* Q9PT41	SVSP

			629.8	2	NIQNEDEQIR	57	*Daboia siamensis* P18964	SVSP
			530.3	3	KDDVLDKDIMoxLIR	36	*Bothrops jararaca* P81824	SVSP
28b	0.555	36▼	629.8	2	NIQNEDEQIR	37	*Daboia siamensis* P18964	SVSP
			516.6	3	FPNGLDKDIMoxLIR	29	*Daboia siamensis* P18964	SVSP
28c	0.331	30▼	774.4	2	FPNGLDKDIMoxLIR	120	*Daboia siamensis* P18964	SVSP
			643.8	2	NIRNEDEQIR			
			653.3	3	HAWCEALYPWVPADSR	111	*Macrovipera lebetina* Q9PT41	SVSP
			604.8	2	IMGWGTITTTK	89	*Echis coloratus* ADI47560	SVSP
			797.4	2	TLCAGILEGGIDSCK			
			629.8	2	NIQNEDEQIR	57	*Daboia siamensis* P18964	SVSP
			631.3	2	NMoxPNEDEQIR	36	*Echis coloratus* E9JG23	SVSP
29a	0.653	60▼	763.8	2	IIGGDECNINEHR	92	*Bothrops fonsecai* P0DMH6	SVSP
			792.3	2	ILGDDECNINEHR	34	*Gloydius halys* AGK44857	SVSP
					(304.2)XGXHNXR	*de novo*	*Macrovipera lebetina* E0Y421	SVSP
29b	0.059	38▼	796.9	2	TLCAGILQGGIDSCK	145	*Vipera ammodytes ammodytes* P0DPS3	SVSP
			616.3	4	VIGGDECNINEHPFLVALHTAR			
			444.7	2	FFCLSSK	131	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			643.8	2	NIRNEDEQIR	100	*Daboia siamensis* P18964	SVSP
			516.6	3	FPNGLDKDIMoxLIR			
			629.8	2	NIQNEDEQIR	68	*Daboia siamensis* P18964	SVSP
			500.2	3	VVGGDECNINEHR	47	*Agkistrodon bilineatus* P33588	SVSP
			559.8	2	AAYPWLLER	35	*Vipera ammodytes ammodytes* AMB36344	SVSP
29c	0.077	33▼	796.9	2	TLCAGILQGGIDSCK	241	*Vipera ammodytes ammodytes* A0A1I9KNP0	SVSP
			612.8	2	IMoxGWGTITTTK			
			433.8	2	IILGVHSK			
			444.7	2	FFCLSSK			
			616.3	4	VIGGDECNINEHPFLVALHTAR	170	*Vipera ammodytes ammodytes* P0DPS3	SVSP
			643.8	2	NIRNEDEQIR	86	*Daboia siamensis* P18964	SVSP
			516.6	3	FPNGLDKDIMoxLIR			
			629.8	2	NIQNEDEQIR	63	*Daboia siamensis* P18964	SVSP
			500.2	3	VIGGVECDINEHR	37	*Deinagkistrodon acutus* P0DJG7	SVSP
31a	0.091	81▼	552.8	2	VLNEDEETR	197	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			587.8	2	VVCAGIWQGGK	177	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			444.7	2	FFCLSSK			
			455.8	2	IELGVHDK			
			504.9	3	VIGGDECNINEHR	134	*Agkistrodon bilineatus* AAB26159	SVSP
			496.9	3	VIGGDEHNINEHR			
			803.9	2	TLCAGILQGGIDTCK	97	*Macrovipera lebetina* E0Y419	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
			604.8	2	IMoxGWGTTTPTK	36	*Crotalus scutulatus* AUS82544	SVSP
31b	2.470	40▼	552.8	2	VLNEDEETR	331	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			606.3	3	KVLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	153	*Vipera berus nikolskii* E5AJX2	SVSP
			916.0	2	VILPDVPHCANIEIIK			
			444.7	2	FFCLSSK			
			504.9	3	VIGGDECNINEHR	126	*Gloydius shedaoensis* Q6T5L0	SVSP
			506.2	3	VIGGDEYNINEHR	117	*Agkistrodon bilineatus* AAB26159	SVSP
			803.9	2	TLCAGILQGGIDTCK	110	*Macrovipera lebetina* E0Y419	SVSP
			604.8	2	IMoxGWGTTTPTK	42	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	39	*Crotalus scutulatus* AUS82544	SVSP
31c	0.503	33▼	602.3	2	SRTLCAGILGR	105	*Echis pyramidum leakeyi* ADI47546	SVSP
			480.8	2	TLCAGILGR			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR	83	*Vipera ammodytes ammodytes* AMB36344	SVSP
31d	0.152	30▼						Unidentified

31e	0.178	26▼	552.8	2	VLNEDEETR	261	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	147	*Vipera berus nikolskii* E5AJX2	SVSP
			444.7	2	FFCLSSK			
			455.8	2	IELGVHDK			
			611.0	3	VILPDVPHCANIEIIK			
			504.9	3	VIGGDECNINEHR	100	*Gloydius shedaoensis* Q6T5L0	SVSP
			604.8	2	IMoxGWGTTTPTK	43	*Crotalus scutulatus* AUS82544	SVSP
			596.8	2	IMGWGTTTPTK	41	*Crotalus scutulatus* AUS82544	SVSP
32a	1.524	64▼	566.2	2	EGKGDFYCR	89	*Echis coloratus* ADI47625	PIII-SVMP
32b	0.271	40▼	552.8	2	VLNEDEETR	244	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			587.8	2	VVCAGIWQGGK	133	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			444.7	2	FFCLSSK			
			611.3	3	VILPDVPHCANIEIIK			
32c	0.356	34▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	302	*Vipera ammodytes ammodytes* AMB36344	SVSP
			552.8	2	VLNEDEETR			
			559.8	2	AAYPWLLER			
			563.6	3	VLNEDEETREPTEK			
			452.3	2	TLCAGILR			
			587.8	2	VVCAGIWQGGK	116	*Vipera berus nikolskii* E5AJX2	SVSP
			455.8	2	IELGVHDK			
			611.3	3	VILPDVPHCANIEIIK			
32d	0.172	30▼	535.3	2	QCVDVNTAY	63	*Protobothrops flavoviridis* Q8JIR2	PIII-SVMP
	0.142	30▼	552.8	2	VLNEDEETR	124	*Vipera ammodytes ammodytes* AMB36344	SVSP
			452.3	2	TLCAGILR			
			563.6	3	VLNEDEETREPTEK			
33a	0.240	>116▼						Unidentified
33b	0.983	15▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	258	*Vipera ammodytes ammodytes* AMB36338	CTL
			584.3	2	HLATIEWLGK			
			714.3	2	TWEDAENFCQK			
			517.3	2	TTDNQWLR	193	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			494.3	2	DHAQLLYK			
			412.8	2	GGHLISLK			
			721.3	3	DQDCLPGWSFYEGHCYK	134	*Macrovipera lebetina* B4XSY8	CTL
			712.8	2	AWSDEPNCFVAK	126	*Macrovipera lebetina* B4XT06	CTL
34a	5.224	64▼	849.9	2	TDIVSPPVCGNGLLEK	115	*Echis carinatus sochureki* ADI47592	PIII-SVMP
			742.3	3	LHSWVECESGECCEQCR	41	*Protobothrops flavoviridis* Q8JIR2	PIII-SVMP
			535.7	2	QCVDVDTAY	33	*Vipera ammodytes ammodytes* QBF53418	PIII-SVMP
	2.070	64▼	706.4	2	LVIVVDHSMoxVRK	105	*Vipera ammodytes ammodytes* AMB36352	SVMP (PIII)
			462.3	3	LVIVVDHSMoxVEK			
	0.074	64▼	624.3	4	ANFVAELVTLTKPETHVWIGLR	52	*Vipera ammosyted ammodytes* AMB36338	CTL
34b	0.270	51▼	462.3	3	LVIVVDHSMoxVEK	40	*Echis carinatus* Q9PRP9	SVMP (PIII)
	0.205	51▼	849.9	2	TDIVSPPVCGNGLLEK	107	*Echis carinatus sochureki* ADI47592	PIII-SVMP
	0.080	51▼	504.9	3	IVGGDECNINEHR	51	*Gloydius halys* P80899	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR	48	*Macrovipera lebetina* E0Y420	SVSP
34c	0.800	38▼	995.5	3	LDRPVRKSAHIAPLSLPSSPPSVGSVCR	39	*Crotalus molossus* AUS82531	SVSP
			452.3	2	TLCAGILR	30	*Echis ocellatus* ADE45140	SVSP
34d	0.448	34▼	474.6	3	VIGGAEININEHR	51	*Cerastes cerastes* AAB34493	SVSP
			452.3	2	TLCAGILR	27	*Echis ocellatus* ADE45140	SVSP
	0.372	34▼	849.9	2	TDIVSPPVCGNGLLEK	42	*Echis carinatus sochureki* ADI47592	PIII-SVMP
	0.252	34▼	706.4	2	LVIVVDHSMoxVRK	67	*Echis carinatus* Q9PRP9	SVMP (PIII)
34e	0.646	30▼						Unidentified
34f	0.452	15▼	1069.9	2	DQDCLPGWSFYEGNCYK	176	*Daboia palestinae* P0DJL4	CTL
			512.8	2	HLASIEGLGK			
			449.9	3	EPQIHVWIGLR			

			417.7	2	SWVDAEK			
			517.3	2	TTDNQWLR	160	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			714.3	2	TWEDAENFCQK	129	*Vipera ammodytes ammodytes* AMB36338	CTL
			584.3	2	HLATIEWLGK			
			822.8	2	DQDCLPGWSYFEK	121	*Daboia palestinae* P0DJL5	CTL
			576.8	2	YDIVWMGLR			
			721.3	3	DQDCLPGWSFYEGHCYK	115	*Macrovipera lebetina* B4XSY8	CTL
			712.3	2	AWSDEPNCFVAK	114	*Macrovipera lebetina* B4XT06	CTL
			699.3	2	AWSDEPNCYGAK	95	*Vipera ammodytes ammodytes* AMB36341	CTL
35a	0.071	64▼						Unidentified
35b	0.076	33▼	824.4	2	FCTEQASGGHLLSLK	86	*Vipera ammodytes ammodytes* AMB36339	CTL
			473.2	2	TYNFICK			
			769.4	2	GYLEWVTLPCGDK	42	*Vipera ammodytes ammodytes* AMB36340	CTL
			409.3	2	LAYPILK	39	*Macrovipera lebetina* B4XT05	CTL
	0.016	33▼	552.8	2	VLNEDEETR	196	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			563.6	3	VLNEDEETREPTEK			
	0.003	33▼	567.3	2	YPVKPSEEGK	55	*Cerastes cerastes* P0DQH9	LAAO
35c	0.149	15▼						Unidentified
36a	0.024	64▼	567.3	2	YPVKPSEEGK	92	*Vipera ammodytes ammodytes* P0DI84	LAAO
			502.3	2	VTVLEASER			
	0.007	64▼	500.2	3	VVGGDECNINEHR	32	*Bothrops cotiara* P0DMH5	SVSP
36b	0.240	20▼						Unidentified
36c	0.173	16▼	521.8	2	ADIVWIGLR	50	*Echis ocellatus* B5U6Y7	CTL
			468.3	2	IIYVNWK	23	*Vipera ammodytes ammodytes* APB93442	CTL
36d	0.230	13▼	621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
37a	0.139	>116▼	621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
	0.046	>116▼	438.7	2	STTDLPSR	32	*Trimeresurus stejnegeri* AAQ16182	LAAO
	0.023	>116▼	552.8	2	VLNEDEETR	52	*Vipera ammodytes ammodytes* AMB36344	SVSP
37b	0.078	64▼						Unidentified
37c	1.047	20▼	639.0	3	GSHLASIHSSEEEAFVSK	72	*Macrovipera lebetina* AJO70725	CTL
			413.7	2	SVSFVCK			
			468.3	2	IIYVNWK	38	*Vipera ammodytes ammodytes* APB93442	CTL
37d	1.365	15▼	517.3	2	TTDNQWLR	108	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			468.3	2	IIYVNWK	38	*Vipera ammodytes ammodytes* APB93442	CTL
37e	1.499	13▼	468.3	2	IIYVNWK	34	*Vipera ammodytes ammodytes* APB93442	CTL
			853.9	2	VWNQCDWGWSNGAK	33	*Macrovipera lebetina* B4XT00	CTL
40a	0.091	>116▼	775.7	3	ISHDNAQLLTAVVFDQQTIGR	118	*Bothrops jararacussu* Q7T1T4	SVMP (PIII)
			547.8	2	YNSNLNTIR			
			818.9	2	YIELVVVADHGMoxFK	84	*Bothrops leucurus* P84907	SVMP (PIII)
40b	0.075	>116▼	626.8	2	SAGQLYEESLR	294	*Cerastes cerastes* P0DQH9	LAAO
			498.6	3	ADDKNPLEECFR			
			567.3	2	YPVKPSEEGK			
			502.3	2	VTVLEASER			
			460.9	3	SAGQLYEESLRK			
			438.7	2	STTDLPSR	260	*Bothrops pictus* X2L4E2	LAAO
			832.4	2	NEKEGWYANLGPMR			
			555.8	2	FDEIVGGMDK			LAAO
			750.8	2	EDDYEEFLEIAK	225	*Macrovipera lebetina* P81375	LAAO
			894.9	2	EEIQTFCYPSMoxIQK	181	*Gloydius halys* Q6STF1	LAAO
			741.8	2	EPDYEEFLEIAK	89	*Echis ocellatus* B5U6Y8	LAAO
40c	1.618	60▼	750.8	2	EDDYEEFLEIAK	376	*Macrovipera lebetina* P81375	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			567.3	2	YPVKPSEEGK			
			463.6	3	KFWEDDGIHGGK			
			498.6	3	ADDKNPLEECFR			
			630.8	2	FWEDDGIHGGK			
			626.8	2	SAGQLYEESLR	313	*Bothrops pictus* X2L4E2	LAAO
			832.4	2	NEKEGWYANLGPMR			

			690.9	2	SAGQLYEESLRK			
			1066.0	2	NEKEGWYANLGPMRLPEK			
			747.7	3	IFFAGEYTANAHGWIDSTIK	296	*Vipera berus berus* P0C2D7	LAAO
			647.4	2	IKFEPPLPPKK	282	*Bothrops atrox* P0CC17	LAAO
			583.3	2	IKFEPPLPPK			
			502.3	2	VTVLEASER	273	*Cerastes cerastes* P0DQH9	LAAO
			567.3	4	HVVVVGAGMoxSGLSAAYVLAGAGHK	262	*Vipera ammodytes ammodytes* P0DI84	LAAO
			886.9	2	EEIQTFCYPSMIQK	260	*Gloydius halys* Q6STF1	LAAO
			436.7	2	VVEELKR			
			629.0	3	KDPGLLQYPVKPSEEGK	220	*Bothriechis schlegelii* A0A024BTN9	LAAO
			826.4	2	NVKEGWYANLGPMoxR	217	*Daboia russelii* G8XQX1	LAAO
			741.8	2	EPDYEEFLEIAK	95	*Echis ocellatus* B5U6Y8	LAAO
40d	0.076	45▼	567.3	2	YPVKPSEEGK	214	*Gloydius halys* Q6STF1	LAAO
			438.7	2	STTDLPSR			
			555.8	2	FDEIVGGMDK			
			569.3	2	HDDIFAYEK			
			886.9	2	EEIQTFCYPSMIQK			
			502.3	2	VTVLEASER	197	*Vipera ammodytes ammodytes* P0DI84	LAAO
			750.8	2	EDDYEEFLEIAK	194	*Daboia russelii* G8XQX1	LAAO
			423.2	2	AVEELKR			
			747.7	3	IFFAGEYTANAHGWIDSTIK			
			626.8	2	SAGQLYEESLR	192	*Cerastes cerastes* P0DQH9	LAAO
			741.8	2	EPDYEEFLEIAK	99	*Echis ocellatus* B5U6Y8	LAAO
40e	0.109	17▼	750.8	2	EDDYEEFLEIAK	142	*Vipera berus berus* P0C2D7	LAAO
			747.3	2	ADDKNPLEECFR			
			438.7	2	STTDLPSR	113	*Daboia russelii* G8XQX1	LAAO
			502.3	2	VTVLEASER	112	*Cerastes cerastes* P0DQH9	LAAO
			832.4	2	NEKEGWYANLGPMR	102	*Bothrops atrox* P0CC17	LAAO
			741.8	2	EPDYEEFLEIAK	98	*Echis ocellatus* B5U6Y8	LAAO
	0.014	17▼	854.9	2	TSADYVWIGLWNQR	95	*Macrovipera lebetina* B4XSY9	CTL
			468.3	2	IIYVNWK	34	*Vipera ammodytes ammodytes* APB93442	CTL
40f	0.070	15▼	502.3	2	VTVLEASER	97	*Vipera ammodytes ammodytes* P0DI84	LAAO
			438.7	2	STTDLPSR			
40g	0.075	13▼	853.9	2	VWNQCDWGWSNGAK	26	*Macrovipera lebetina* B4XT00	CTL
			621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
40h	0.035	34▼	567.3	2	YPVKPSEEGK	228	*Cerastes cerastes* P0DQH9	LAAO
			498.6	3	ADDKNPLEECFR			
			502.3	2	VTVLEASER			
			626.8	2	SAGQLYEESLR			
			750.8	2	EDDYEEFLEIAK	207	*Macrovipera lebetina* P81375	LAAO
			438.7	2	STTDLPSR	150	*Vipera ammodytes ammodytes* P0DI84	LAAO
			832.4	2	NEKEGWYANLGPMR	126	*Bothrops pictus* X2L4E2	LAAO
			741.8	2	EPDYEEFLEIAK	110	*Echis ocellatus* B5U6Y8	LAAO
	0.025	34▼	552.8	2	VLNEDEETR	240	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			452.3	2	TLCAGILR			
40i	0.056	30▼						Unidentified
42a	0.028	80▼	567.3	2	YPVKPSEEGK	153	*Cerastes cerastes* P0DQH9	LAAO
			502.3	2	VTVLEASER			
			626.8	2	SAGQLYEESLR			
			460.9	3	SAGQLYEESLRK			
			886.9	2	EEIQTFCYPSMIQK	80	*Gloydius halys* Q6STF1	LAAO
	0.004	80▼	476.3	2	VGIIGYTTK	324	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			859.9	2	ETPVLSNPGPYLEFR			
			566.8	2	VVSLNVLCTK			
			792.4	2	IQLQNYYSQEIGK			
			661.3	2	VPTYVPLEMoxEK			
			812.4	3	FHECNLGNLICDAVIYNNLR			
			513.8	2	ASGNPILLNK			
			723.4	2	YLGYLNVVFDDK	90	*Vipera anatolica senliki* QHR82712	5'-nucleotidase
42b	0.075	60▼	438.7	2	STTDLPSR	195	*Vipera ammodytes ammodytes* P0DI84	LAAO
			567.3	2	YPVKPSEEGK			

			502.3	2	VTVLEASER			
			431.9	3	IQFEPPLPPKK			
			460.9	3	SAGQLYEESLRK	190	*Cerastes cerastes* P0DQH9	LAAO
			498.6	3	ADDKNPLEECFR			
			750.8	2	EDDYEEFLEIAK	153	*Macrovipera lebetina* P81375	LAAO
			840.4	2	NEKEGWYANLGPMoxR	139	*Bothrops pictus* X2L4E2	LAAO
			741.8	2	EPDYEEFLEIAK	108	*Echis ocellatus* B5U6Y8	LAAO
	0.067	60$^{\blacktriangledown}$	812.4	3	FHECNLGNLICDAVIYNNLR	668	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			530.6	3	IIALGHSGFFEDQR			
			859.9	2	ETPVLSNPGPYLEFR			
			792.4	2	IQLQNYYSQEIGK			
			476.3	2	VGIIGYTTK			
			566.8	2	VVSLNVLCTK			
			513.8	2	ASGNPILLNK			
			437.7	2	VFPAVEGR			
			661.3	2	VPTYVPLEMoxEK			
			423.3	2	LTTLGVNK			
			863.1	3	YDAMALGNHEFDNGLAGLLDPLLK	335	*Ovophis okinavensis* BAN89427	5'-nucleotidase
42c	0.050	20$^{\blacktriangledown}$						Unidentified
42d	0.217	17$^{\blacktriangledown}$	445.8	2	VFDEPBR	*de novo*	~*T. albolabris* P81114	CTL
42e	0.039	15$^{\blacktriangledown}$	832.1	3	ANFVAELVTLTKPETHVWIGLR	106	*Vipera ammodytes ammodytes* AMB36338	CTL
			714.3	2	TWEDAENFCQK			
			521.8	2	ADLVWIGLR	100	*Vipera ammodytes ammodytes* APB93444	CTL
			494.3	2	DHAQLLYK			
			712.3	2	AWSDEPNCFVAK	81	*Macrovipera lebetina* B4XT06	CTL
			854.9	2	TSADYVWIGLWNQR	36	*Macrovipera lebetina* B4XSY9	CTL
			468.3	2	IIYVNWK	34	*Vipera ammodytes ammodytes* APB93442	CTL
42f	0.049	13$^{\blacktriangledown}$	566.8	2	VVSLNVLCTK	113	*Macrovipera lebetina* AHJ80886	5'-nucleotidase
			476.3	2	VGIIGYTTK			
			423.3	2	LTTLGVNK			
	0.018	13$^{\blacktriangledown}$	516.8	4	GSHLVSLHNIAEADFVVKK	35	*Echis carinatus sochureki* Q6X5S9	CTL
45a	0.027	>116$^{\blacktriangledown}$	502.3	2	VTVLEASER	53	*Cerastes cerastes* P0DQH9	LAAO
	0.005	>116$^{\blacktriangledown}$	834.9	2	DVELLTGLNFYSGLK	68	*Crotalus adamanteus* J3SBP3	PDE
45b	0.043	>116$^{\blacktriangledown}$	785.9	2	SPPTSVPPSASDCLR	539	*Macrovipera lebetina* W8E7D1	PDE
			834.9	2	DVELLTGLNFYSGLK			
			724.8	2	DFYTFDSEGIVR			
			773.4	3	AERPDFVTLYIEEPDTTGHK			
			678.3	2	AATYFWPGSEVK			
			583.8	2	QPLPETLQLK			
			642.0	3	VRDVELLTGLNFYSGLK			
			933.9	2	FGPVSGEIIMoxALQMoxADR			
			934.4	2	AGYLETWDSLMoxPNINK			
			988.8	3	NGLNVISGPIFDYNYDGHFDSYDTIK			
			531.3	2	SVQPQVSCR	271	*Protobothrops mucrosquamatus* XP_015675291	PDE
			404.2	2	STPFEAR	151	*Notechis scutatus* XP_026521895	PDE
	0.009	>116$^{\blacktriangledown}$	438.7	2	STTDLPSR	135	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			750.8	2	EDDYEEFLEIAK	127	*Daboia russelii* G8XQX1	LAAO
			502.3	2	VTVLEASER	120	*Vipera ammodytes ammodytes* P0DI84	LAAO
45c	0.165	60$^{\blacktriangledown}$	463.6	3	KFWEDDGIHGGK	334	*Macrovipera lebetina* P81375	LAAO
			567.3	2	YPVKPSEEGK			
			750.8	2	EDDYEEFLEIAK			
			563.8	2	FDEIVGGMoxDK			
			569.3	2	HDDIFAYEK			
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			626.8	2	SAGQLYEESLR	314	*Bothrops pictus* X2L4E2	LAAO
			460.9	3	SAGQLYEESLRK			
			633.8	2	RFDEIVGGMDK			
			886.9	2	EEIQTFCYPSMIQK	282	*Gloydius halys* Q6STF1	LAAO
			583.4	2	IKFEPPLPPK			
			502.3	2	VTVLEASER	235	*Cerastes cerastes* P0DQH9	LAAO
			818.4	2	NVKEGWYANLGPMR	207	*Daboia russelii* G8XQX1	LAAO

			747.7	3	IFFAGEYTANAHGWIDSTIK			
			564.3	2	AHGWIDSTIK	97	*Demansia vestigiata* A6MFL0	LAAO
	0.015	60▼	800.3	2	DCQNPCCDAATCK	125	*Macrovipera lebetina* Q7T046	PIII-SVMP
			513.2	2	GSYYGYCR			
			806.8	2	ATVAEDSCFKDNQK	104	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
45d	0.285	20▼	854.9	2	TSADYVWIGLWNQR	144	*Macrovipera lebetina* B4XSY9	CTL
			578.3	2	WTDGSSVIYK			
			630.8	2	CGDDYPFVCK	98	*Bitis arietans* AOE43148	CTL
			645.4	2	FITHFWIGLR	47	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	42	*Macrovipera lebetina* Q696W1	CTL
			453.7	2	TWEDAER	40	*Protobothrops jerdonii* D1MGU0	CTL
45e	0.223	17▼	854.9	2	TSADYVWIGLWNQR	187	*Macrovipera lebetina* AJO70726	CTL
			578.3	2	WTDGSSVIYK			
			435.7	2	AQYCISK			
			630.8	2	CGDDYPFVCK	148	*Bitis arietans* AOE43148	CTL
			860.9	2	SSPDYVWIGLWNQR			
			639.0	3	GSHLASIHSSEEEAFVSK	67	*Macrovipera lebetina* AJO70725	CTL
			413.7	2	SVSFVCK			
			468.3	2	IIYVNWK	34	*Vipera ammodytes ammodytes* APB93442	CTL
			430.6	3	FITHFWIGLR	24	*Macrovipera lebetina* Q696W1	CTL
	0.011	17▼	750.8	2	EDDYEEFLEIAK	70	*Vipera berus berus* P0C2D7	LAAO
			502.3	2	VTVLEASER	41	*Cerastes cerastes* P0DQH9	LAAO
45f	0.088	15▼	854.9	2	TSADYVWIGLWNQR	102	*Macrovipera lebetina* B4XSY9	CTL
			630.8	2	CGDDYPFVCK	78	*Bitis arietans* AOE43148	CTL
			639.9	3	CGDDYPFVCKFPPRC			
			712.3	2	AWSDEPNCFVAK	48	*Macrovipera lebetina* B4XT06	CTL
45g	0.588	13▼	1420.1	2	DGVIWMoxGLNDVWNECNWGWTDGAK	427	*Macrovipera lebetina* AJO70723	CTL
			968.5	2	GSHLVSLHNIAEADFVVK			
			798.9	2	VFKEEMNWADAEK			
			688.7	3	GSHLVSLHNIAEADFVVKK			
			619.8	2	EEMoxNWADAEK			
			854.9	2	TSADYVWIGLWNQR	110	*Macrovipera lebetina* B4XSY9	CTL
			578.3	2	WTDGSSVIYK			
46a	0.038	>116▼	641.8	2	RFDEIVGGMoxDK	224	*Bothrops pictus* X2L4E2	LAAO
			569.3	2	HDDIFAYEK			
			626.8	2	SAGQLYEESLR			
			438.7	2	STTDLPSR			
			460.9	3	SAGQLYEESLRK	27		
			502.3	2	VTVLEASER	173	*Vipera ammodytes ammodytes* P0DI84	LAAO
	0.017	>116▼	968.5	2	GSHLVSLHNIAEADFVVK	106	*Echis pyramidum leakeyi* Q6X5S2	CTL
	0.001	>116▼	806.9	2	ATVAEDSCFEENLK	42	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
46b	0.058	80▼	626.8	2	SAGQLYEESLR	204	*Bothrops pictus* X2L4E2	LAAO
			690.9	2	SAGQLYEESLRK			
			438.7	2	STTDLPSR			
			563.8	2	FDEIVGGMoxDK			
			750.8	2	EDDYEEFLEIAK	177	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR			
			502.3	2	VTVLEASER	170	*Cerastes cerastes* P0DQH9	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	134	*Macrovipera lebetina* P81375	LAAO
	0.046	80▼	806.9	2	ATVAEDSCFEENLK	90	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			513.2	2	GSYYGYCR	86	*Macrovipera lebetina* Q7T046	PIII-SVMP
			585.3	2	KIPCAPQDIK			
			813.9	2	ATVAEDSCFQENQK			
			807.3	2	TCRDPCCDAATCK	31	*Crotalus atrox* Q92043	PIII-SVMP
	0.004	80▼	507.8	2	CILNEPLR	29	*Crotalus adamanteus* J3S830	SVMP (PIII)
	0.004	80▼	968.5	2	GSHLVSLHNIAEADFVVK	89	*Echis pyramidum leakeyi* Q6X5S2	CTL
			854.9	2	TSADYVWIGLWNQR	52	*Macrovipera lebetina* B4XSY9	CTL
46c	0.676	60▼	800.3	2	DCQNPCCDAATCK	271	*Macrovipera lebetina* Q7T046	PIII-SVMP
			878.4	3	ATVAEDSCFQENQKGSYYGYCR			
			534.3	2	QCISLFGSR			
			513.2	2	GSYYGYCR			
			521.3	2	IPCAPQDIK			

			806.8	2	ATVAEDSCFEENLK	86	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			807.3	2	TCRDPCCDAATCK	33	*Crotalus atrox* Q92043	PIII-SVMP
	0.510	60▼	438.7	2	STTDLPSR	96	*Gloydius halys* Q6STF1	LAAO
			894.9	2	EEIQTFCYPSMoxIQK			
			502.3	2	VTVLEASER	96	*Vipera ammodytes ammodytes* P0DI84	LAAO
			472.0	4	KDPGLLQYPVKPSEEGK	95	*Bothriechis schlegelii* A0A024BTN9	LAAO
			460.9	3	SAGQLYEESLRK	94	*Sistrurus catenatus edwardsi* B0VXW0	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK	46	*Macrovipera lebetina* P81375	LAAO
	0.011	60▼	968.5	2	GSHLVSLHNIAEADFVVK	57	*Echis pyramidum leakeyi* Q6X5S3	CTL
46d	0.666	20▼	453.7	2	TWEDAER	40	*Protobothrops jerdonii* D1MGU0	CTL
			646.0	3	GSHLVSLHNIAEADFVVK	32	*Echis carinatus sochureki* Q6X5S9	CTL
			854.9	2	TSADYVWIGLWNQR	27	*Macrovipera lebetina* B4XSY9	CTL
46e	0.532	17▼	854.9	2	TSADYVWIGLWNQR	138	*Macrovipera lebetina* B4XSY9	CTL
			578.3	2	WTDGSSVIYK			
			738.8	2	WDYVSCAEQYR	78	*Vipera ammodytes ammodytes* APB93442	CTL
			468.3	2	IIYVNWK			
			630.8	2	CGDDYPFVCK	69	*Bitis arietans* AOE43148	CTL
			645.4	2	FITHFWIGLR	57	*Macrovipera lebetina* Q696W1	CTL
			430.6	3	FITHFWIGLR	39	*Macrovipera lebetina* Q696W1	CTL
			639.0	3	GSHLASIHSSEEEAFVSK	36	*Macrovipera lebetina* AJO70725	CTL
46f	0.197	15▼	832.1	3	ANFVAELVTLTKPETHVWIGLR	219	*Vipera ammodytes ammodytes* AMB36338	CTL
			896.7	3	QQCSSHWTDGSAVSYENVVYNTR			
			714.3	2	TWEDAENFCQK			
			584.3	2	HLATIEWLGK			
			854.9	2	TSADYVWIGLWNQR	79	*Macrovipera lebetina* B4XSY9	CTL
			712.3	2	AWSDEPNCFVAK	71	*Macrovipera lebetina* B4XT06	CTL
			822.8	2	DQDCLPGWSYFEK	65	*Daboia palestinae* P0DJL5	CTL
			430.6	3	FITHFWIGLR	42	*Macrovipera lebetina* Q696W1	CTL
			645.4	2	FITHFWIGLR	41	*Macrovipera lebetina* Q696W1	CTL
46g	0.176	13▼	646.0	3	GSHLVSLHNIAEADFVVK	209	*Macrovipera lebetina* AJO70723	CTL
			619.7	2	EEMoxNWADAEK			
			516.8	4	GSHLVSLHNIAEADFVVKK			
			1420.1	2	DGVIWMoxGLNDVWNECNWGWTDGAK			
47a	0.025	83▼	1058.0	2	LSWMoxTGFSGSEGTGVITLQK	858	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
			764.3	2	LADDFMGSTWQEK			
			903.7	3	LSLNEMYLLDSGGQYFDGTTDITR			
			1110.5	2	EIPQENLLEDDFSPVMoxLSK			
			750.0	3	LSAYIVPNTDAHLSEYVAER			
			586.3	2	LPPPTNTIYR			
			945.9	2	EALQMLTAGCPESPCVK			
			483.7	2	QLEEEYR			
			758.1	3	KPTAILLSGLEETAWLFNLR			
			561.8	2	RQLEEEYR			
			545.3	2	VLMGNIDLSK			
			1081.0	2	NLINESLLSRDQIQYINK			
			472.2	3	TIHWGEPTAFQK			
			731.3	3	GMoxFTSIEPGYYHDGEFGIR			
			411.2	2	LVESFAR			
			1039.0	2	GDDIPYTPVFYAYTLLTK			
			1036.0	2	TLNMPEVNLVDLVWGSER	389	*Notechis scutatus* XP_026530513	Aminopeptidase
			864.9	2	TKYPVNEEPYLTFK			
	0.003	83▼	438.7	2	STTDLPSR	168	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			567.3	2	YPVKPSEEGK			
			569.3	2	HDDIFAYEK			
			460.9	3	SAGQLYEESLRK			
			502.3	2	VTVLEASER	156	*Vipera ammodytes ammodytes* P0DI84	LAAO
	0.002	83▼	646.0	3	GSHLVSLHNIAEADFVVK	72	*Echis pyramidum leakeyi* Q6X5S2	CTL
47b	0.076	60▼	463.6	3	KFWEDDGIHGGK	477	*Bothrops pictus* X2L4E2	LAAO
			626.8	2	SAGQLYEESLR			
			633.8	2	RFDEIVGGMDK			
			438.7	2	STTDLPSR			

			690.9	2	SAGQLYEESLRK			
			555.8	2	FDEIVGGMDK			
			569.3	2	HDDIFAYEK			
			583.4	2	IKFEPPLPPK	450	*Bothrops atrox* P0CC17	LAAO
			431.9	3	IKFEPPLPPKK			
			567.3	2	YPVKPSEEGK	426	*Gloydius halys* Q6STF1	LAAO
			886.9	2	EEIQTFCYPSMIQK			
			750.8	2	EDDYEEFLEIAK	360	*Macrovipera lebetina* P81375	LAAO
			992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
			502.3	2	VTVLEASER	304	*Vipera ammodytes ammodytes* P0DI84	LAAO
			826.4	2	NVKEGWYANLGPMoxR	259	*Daboia russelii* G8XQX1	LAAO
			469.3	2	IFLTCKR	176	*Crotalus durissus terrificus* C0HJE7	LAAO
	0.010	60▼	800.3	2	DCQNPCCDAATCK	184	*Macrovipera lebetina* Q7T046	PIII-SVMP
			513.2	2	GSYYGYCR			
			813.9	2	ATVAEDSCFQENQK			
			716.3	3	DECDVPEHCTGQSAECPR	97	*Daboia siamensis* Q7LZ61	PIII-SVMP
			806.9	2	ATVAEDSCFEENLK	91	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
	0.001	60▼	1036.0	2	TLNMPEVNLVDLVWGSER	130	*Notechis scutatus* XP_026530513	Aminopeptidase
			1102.5	2	EIPQENLLEDDFSPVMLSK			
			1039.0	2	GDDIPYTPVFYAYTLLTK			
			758.1	3	KPTAILLSGLEETAWLFNLR	76	*Protobothrops mucrosquamatus* XP_015676063	Aminopeptidase
	0.001	60▼	507.8	2	CILNEPLR	46	*Crotalus adamanteus* J3S830	SVMP (PIII)
	0.001	60▼	860.0	2	SLEDGTLYIIEQIPK	50	*Ovophis okinavensis* BAN82155	PLB
47c	0.008	46▼	703.9	2	FTAYAINGPPVEK	216	*Ovophis okinavensis* BAN82155	PLB
			730.9	2	KVVPESLFAWER			
			859.9	2	SLEDGTLYIIEQIPK			
			953.9	2	QNSGTYNNQYMoxILDTK			
			590.8	2	SPVPAGCYDSK	211	*Vipera ammodytes ammodytes* QBF53421	PLB
			478.9	3	YNNYKEDPYTK	196	*Vipera ammodytes ammodytes* QBF53421	PLB
	0.005	46▼	626.8	2	SAGQLYEESLR	149	*Protobothrops flavoviridis* BAN82014	LAAO
			569.3	2	HDDIFAYEK			
			567.3	2	YPVKPSEEGK			
			502.3	2	VTVLEASER	148	*Cerastes cerastes* P0DQH9	LAAO
	0.002	46▼	806.8	2	ATVAEDSCFEENLK	86	*Vipera ammodytes ammodytes* QBF53415	PIII-SVMP
			800.3	2	DCQNPCCDAATCK	57	*Macrovipera lebetina* Q7T046	PIII-SVMP
	0.002	46▼	500.2	3	VVGGDECNINEHR	42	*Agkistrodon bilineatus* P33588	SVSP
47d	0.032	20▼	854.9	2	TSADYVWIGLWNQR	78	*Macrovipera lebetina* B4XSY9	CTL
			738.8	2	WDYVSCAEQYR	78	*Vipera ammodytes ammodytes* APB93442	CTL
			468.3	2	IIYVNWK			
			639.0	3	GSHLASIHSSEEEAFVSK	50	*Macrovipera lebetina* AJO70725	CTL
	0.009	20▼	750.8	2	EDDYEEFLEIAK	124	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR			
			502.3	2	VTVLEASER	45	*Cerastes cerastes* P0DQH9	LAAO
47e	0.074	15▼	517.3	2	TTDNQWLR	200	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			439.7	2	TWEDAEK			
			494.3	2	DHAQLLYK			
			832.1	3	ANFVAELVTLTKPETHVWIGLR	153	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	134	*Macrovipera lebetina* B4XT06	CTL
			854.9	2	TSADYVWIGLWNQR	77	*Macrovipera lebetina* B4XSY9	CTL
	0.003	15▼	559.8	2	AAYPWLLER	46	*Vipera ammodytes ammodytes* AMB36344	SVSP
47f	0.057	13▼	688.7	3	GSHLVSLHNIAEADFVVKK	31	*Echis carinatus sochureki* Q6X5S9	CTL
			853.9	2	VWNQCDWGWSNGAK	23	*Macrovipera lebetina* B4XT00	CTL
49a	0.185	>116▼	1000.8	2	LTPGSECGDGECCDQCR	414	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			798.4	2	SAESVTLDLFGDWR			
			863.5	2	YIELVIVVDNVMoxFR			
			535.2	2	QCVDVNTAY			
			1007.8	2	LTPGSQCADGECCDQCR	32	*Echis ocellatus* Q2UXR0	PIII-SVMP
	0.045	>116▼	626.8	2	SAGQLYEESLR	181	*Bothrops pictus* X2L4E2	LAAO
			569.3	2	HDDIFAYEK			
			438.7	2	STTDLPSR			
			460.9	3	SAGQLYEESLRK			

				563.8	2	FDEIVGGMoxDK			
				502.3	2	VTVLEASER	134	*Cerastes cerastes* P0DQH9	LAAO
				826.4	2	NVKEGWYANLGPMoxR	130	*Daboia russelii* G8XQX1	LAAO
49b	0.245	64▼		635.3	2	SSVGLIQDYCK	224	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
				1000.8	2	LTPGSECGDGECCDQCR			
				855.5	2	YIELVIVVDNVMFR			
	0.126047966	64▼		676.9	2	NPQCILNKPLR	113	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
				625.3	2	TWAHQLVNNIIVFYR			
49c	0.240	60▼		641.8	2	RFDEIVGGMoxDK	346	*Glydius halys* Q6STF1	LAAO
				583.4	2	IKFEPPLPPK			
				438.7	2	STTDLPSR			
				569.3	2	HDDIFAYEK			
				567.3	2	YPVKPSEEGK			
				894.9	2	EEIQTFCYPSMoxIQK			
				563.8	2	FDEIVGGMoxDK			
				626.8	2	SAGQLYEESLR	338	*Bothrops pictus* X2L4E2	LAAO
				460.9	3	SAGQLYEESLRK			
				463.6	3	KFWEDDGIHGGK			
				750.8	2	EDDYEEFLEIAK	253	*Macrovipera lebetina* P81375	LAAO
				992.4	3	ADDKNPLEECFREDDYEEFLEIAK			
				502.3	2	VTVLEASER	252	*Vipera ammodytes ammodytes* P0DI84	LAAO
				826.4	2	NVKEGWYANLGPMoxR	218	*Daboia russelii* G8XQX1	LAAO
	0.034	60▼		937.5	2	TWAHQLVNNIIVFYR	150	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
				676.9	2	NPQCILNKPLR			
	0.027	60▼		1000.8	2	LTPGSECGDGECCDQCR	326	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
				635.3	2	SSVGLIQDYCK			
				798.4	2	SAESVTLDLFGDWR			
				863.5	2	YIELVIVVDNVMoxFR			
				806.9	2	ATVAEDSCFEENLK	85	*Echis coloratus* ADI47643	PIII-SVMP
				521.3	2	IPCAPQDIK	33	*Agkistrodon laticinctus* O42138	PIII-SVMP
	0.006	60▼		750.7	3	TSTHIAPLSLPSSPPSVGSVCR	43	*Macrovipera lebetina* E0Y420	SVSP
49d	2.061	32▼		937.5	2	TWAHQLVNNIIVFYR	161	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
				676.9	2	NPQCILNKPLR			
				549.3	2	KPQCILNKP	24	*Gloydius brevicaudus* O73795	SVMP (PIII)
				790.4	2	IYEIVNTLNVVFR	39	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
	0.790	32▼		559.8	2	AAYPWLLER	120	*Vipera ammodytes ammodytes* AMB36344	SVSP
				606.3	3	KVLNEDEETREPTEK			
				563.6	3	VLNEDEETREPTEK			
49e	0.256	20▼	18373	937.5	2	TWAHQLVNNIIVFYR	110	*Vipera ammodytes ammodytes* AMB36351	SVMP (PI)
			713	676.9	2	NPQCILNKPLR			
	0.063	20▼	4734	854.9	2	TSADYVWIGLWNQR	39	*Macrovipera lebetina* B4XSY9	CTL
49f	0.276	15▼	23820	676.9	2	NPQCILNKPLR	70	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
	0.101	15▼		832.1	3	ANFVAELVTLTKPETHVWIGLR	123	*Vipera ammodytes ammodytes* AMB36338	CTL
				517.3	2	TTDNQWLR	74	*Vipera ammodytes ammodytes* APB93444	CTL
				494.3	2	DHAQLLYK			
				712.3	2	AWSDEPNCFVAK	31	*Macrovipera lebetina* B4XT06	CTL
49g	0.139	13▼		619.8	2	EEMoxNWADAEK	37	*Macrovipera lebetina* AJO70723	CTL
				853.9	2	VWNQCDWGWSNGAK	21	*Macrovipera lebetina* B4XT00	CTL
				621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
50a	0.248	>116▼		1000.8	2	LTPGSECGDGECCDQCR	529	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
				798.4	2	SAESVTLDLFGDWR			
				635.3	2	SSVGLIQDYCK			
				790.4	2	IYEIVNTLNVVFR			
				805.6	3	CFNNNLQGTENFHCGMoxENGR			
				535.2	2	QCVDVNTAY			
	0.035	>116▼		804.4	2	SAARVTLDLFGDWR	127	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
				671.3	3	FTHSPDDPDYGMoxVDLGTK			
	0.005	>116▼		992.4	3	ADDKNPLEECFREDDYEEFLEIAK	33	*Macrovipera lebetina* P81375	LAAO
50b	1.192	64▼		1000.8	2	LTPGSECGDGECCDQCR	447	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
				800.3	3	CFNNNLQGTENFHCGMENGR			
				635.3	2	SSVGLIQDYCK			
				1025.7	4	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			

			863.5	2	YIELVIVVDNVMoxFR			
			699.4	2	DSPDYGMVDXGTK	*de novo*	~*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
50c	1.154	48▼	798.4	2	SAESVTLDLFGDWR	269	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
			804.4	2	SAARVTLDLFGDWR	56	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
	0.005	48▼	598.7	2	DPCCDAATCK	*de novo*	~*Protobothrops flavoviridis* Q90ZI3	PIII-SVMP
50d	0.265	32▼	937.5	2	TWAHQLVNNIIVFYR	158	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			676.9	2	NPQCILNKPLR			
			798.4	2	SAESVTLDLFGDWR	208	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
			745.1	3	DLINVTSAANVTLDLFGEWR	40	*Daboia russelii* B8K1W0	SVMP (PIII)
	0.143	32▼	559.8	2	AAYPWLLER	194	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			606.3	3	KVLNEDEETREPTEK			
			563.6	3	VLNEDEETREPTEK			
50e	0.114	20▼	798.4	2	SAESVTLDLFGDWR	232	*Vipera ammodytes ammodytes* AHB62069	SVMP (PI)
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
			625.3	3	TWAHQLVNNIIVFYR	47	*Vipera ammodytes ammodytes* AMB36349	SVMP (PI)
			937.5	2	TWAHQLVNNIIVFYR	48	*Vipera ammodytes ammodytes* AMB36349	SVMP (PI)
	0.013	20▼	854.9	2	TSADYVWIGLWNQR	47	*Macrovipera lebetina* B4XSY9	CTL
50f	0.093	15▼	517.3	2	TTDNQWLR	97	*Vipera ammodytes ammodytes* APB93444	CTL
			521.8	2	ADLVWIGLR			
			832.1	3	ANFVAELVTLTKPETHVWIGLR	79	*Vipera ammodytes ammodytes* AMB36338	CTL
			712.3	2	AWSDEPNCFVAK	69	*Macrovipera lebetina* B4XT06	CTL
	0.060	15▼	790.4	2	IYEIVNTLNVVFR	208	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
			863.5	2	YIELVIVVDNVMoxFR			
50g	0.132	13▼	853.9	2	VWNQCDWGWSNGAK	22	*Macrovipera lebetina* B4XT00	CTL
			621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
	0.023	13▼	798.4	2	SAESVTLDLFGDWR	215	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
			745.1	3	DLINVTSAANVTLDLFGEWR	35	*Daboia russelii* B8K1W0	SVMP fragment
51a	0.514	>116▼	671.3	3	FTHSPDDPDYGMoxVDLGTK	41	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
			903.7	3	(953.4)CTGBSAECPTDVFBR	*de novo*	~*Echis coloratus* ADI47650	PIII-SVMP
	0.029	>116▼	798.4	2	SAESVTLDLFGDWR	101	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
51b	0.313	65▼	1000.8	2	LTPGSECGDGECCDQCR	686	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			1367.2	3	IQTAGTECRPAWDECDVPEYCTGQSAECPTDVLQR			
			635.3	2	SSVGLIQDYCK			
			790.4	2	IYEIVNTLNVVFR			
			798.4	2	SAESVTLDLFGDWR			
			805.6	3	CFNNNLQGTENFHCGMoxENGR			
			535.2	2	QCVDVNTAY			
			671.3	3	FTHSPDDPDYGMoxVDLGTK	79	*Vipera ammodytes ammodytes* P0DJE2	PIII-SVMP
			1007.9	2	LTPGSQCADGECCDQCR	35	*Echis ocellatus* Q2UXR0	PIII-SVMP
51c	2.276	50▼	798.4	2	SAESVTLDLFGDWR	239	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			863.5	2	YIELVIVVDNVMoxFR			
			527.3	3	IYEIVNTLNVVFR			
			1000.8	2	LTPGSECGDGECCDQCR			
			840.9	2	KSAATVTLDLFGDWR	118	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
			855.4	2	KSAAMVTLDLFGDWR			
			817.9	2	KSAAGVTLDLFGDWR			
51d	0.121	32▼	790.4	2	IYEIVNTLNVVFR	204	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR			
			875.4	2	YIELVIVADNVMoxVKK	31	*Agkistrodon piscivorus leucostoma* C9E1S0	SVMP (PIII)
			676.9	2	NPQCILNKPLR	173	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			937.5	2	TWAHQLVNNIIVFYR			
	0.037	32▼	552.8	2	VLNEDEETR	174	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			606.3	3	KVLNEDEETREPTEK			

51e	0.125	15▼	798.4	2	SAESVTLDLFGDWR	173	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			790.4	2	IYEIVNTLNVVFR			
			676.9	2	NPQCILNKPLR	54	*Agkistrodon piscivorus leucostoma* B7U492	SVMP fragment
	0.009	15▼	712.3	2	AWSDEPNCFVAK	25	*Macrovipera lebetina* B4XT06	CTL
51f	0.125	13▼	798.4	2	SAESVTLDLFGDWR	88	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
52a	0.072	>116▼	790.4	2	IYEIVNTLNVVFR	364	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			798.4	2	SAESVTLDLFGDWR			
			1000.8	2	LTPGSECGDGECCDQCR			
			635.3	2	SSVGLIQDYCK			
			863.5	2	YIELVIVVDNVMoxFR			
	0.002	>116▼	460.9	3	SAGQLYEESLRK	21	*Cerastes cerastes* P0DQH9	LAAO
52b	0.158	64▼	1000.8	2	LTPGSECGDGECCDQCR	458	*Vipera ammodytes ammodytes* AHB62069	PIII-SVMP
			635.3	2	SSVGLIQDYCK			
			798.4	2	SAESVTLDLFGDWR			
			805.6	3	CFNNNLQGTENFHCGMoxENGR			
			855.5	2	YIELVIVVDNVMFR			
			535.2	2	QCVDVNTAY			
			1007.8	2	LTPGSQCADGECCDQCR	32	*Echis ocellatus* Q2UXR0	PIII-SVMP
	0.010	64▼	750.8	2	EDDYEEFLEIAK	64	*Daboia russelii* G8XQX1	LAAO
52c	0.229	48▼	798.4	2	SAESVTLDLFGDWR	292	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			855.5	2	YIELVIVVDNVMFR			
			613.0	3	TRIYEIVNTLNVVFR			
			804.4	2	SAARVTLDLFGDWR	71	*Vipera ammodytes ammodytes* P0DJE2	SVMP (PIII)
			671.3	3	FTHSPDDPDYGMoxVDLGTK			
			676.9	2	NPQCILNKPLR	87	*Agkistrodon piscivorus leucostoma* B7U492	SVMP (PIII)
	0.012	48▼	500.2	3	VVGGDECNINEHR	56	*Agkistrodon bilineatus* P33588	SVSP
52d	0.055	32▼	798.4	2	SAESVTLDLFGDWR	213	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			855.5	2	YIELVIVVDNVMFR			
			875.4	2	YIELVIVADNVMoxVKK	46	*Agkistrodon piscivorus leucostoma* C9E1S0	SVMP (PIII)
			676.9	2	NPQCILNKPLR	108	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			625.3	3	TWAHQLVNNIIVFYR			
	0.025	32▼	552.8	2	VLNEDEETR	139	*Vipera ammodytes ammodytes* AMB36344	SVSP
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
			563.6	3	VLNEDEETREPTEK			
	0.014	32▼	676.9	2	NPQCILNKPLR	70	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
52e	0.873	28▼	676.9	2	NPQCILNKPLR	70	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
	0.051	28▼	798.4	2	SAESVTLDLFGDWR	131	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			1000.8	2	LTPGSECGDGECCDQCR			
	0.038	28▼	1571.0	3	DEYBTFXTNR	*de novo*	*Vipera ammodytes ammodytes* AMB36349	SVMP (PI)
52f	0.069	15▼					Unidentified	Unidentified
52g	0.044	13▼	853.9	2	VWNQCDWGWSNGAK	31	*Macrovipera lebetina* B4XT00	CTL
	0.009	13▼	798.4	2	SAESVTLDLFGDWR	112	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			790.4	2	IYEIVNTLNVVFR			
			676.9	2	NPQCILNKPLR	39	*Echis pyramidum leakeyi* ADI47744	SVMP fragment
53a	0.013	60▼	1196.1	3	AGTVCRPANGECDVSDLCTGQSAECPTDQFQR	942	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			991.5	2	HDNAQLLTGINFNGPSAGR			
			805.4	2	IYEIVNTLNVIYR			
			535.3	4	RHDNAQLLTGINFNGPSAGR			
			762.8	2	CETSYLFSDCSR			
			836.4	3	QCISLFGASATVAQDSCFQFNR			
			567.3	4	KRHDNAQLLTGINFNGPSAGR			
			870.9	2	NPCQIYYIPSDENK			
			453.3	3	MoxPQCILNKPLK			
			676.9	3	LRPGAQCGDGVCCYQCK			
			411.6	3	YSVGIVQDHSK			
			501.8	2	IACAPEDVK			
			526.8	2	SCIMoxSGILR			
	0.002	60▼	567.3	2	YPVKPSEEGK	160	*Protobothrops flavoviridis* BAN82013	LAAO
			626.8	2	SAGQLYEESLR			
			438.7	2	STTDLPSR			

			460.9	3	SAGQLYEESLRK			
			750.8	2	EDDYEEFLEIAK	154	*Daboia russelii* G8XQX1	LAAO
			826.4	2	NVKEGWYANLGPMoxR			
	0.0001	60▼	798.4	2	SAESVTLDLFGDWR	83	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
53b	0.072	50▼	991.5	2	HDNAQLLTGINFNGPSAGR	539	*Macrovipera lebetina* Q4VM07	PIII-SVMP
			805.4	2	IYEIVNTLNVIYR			
			762.8	2	CETSYLFSDCSR			
			567.3	4	KRHDNAQLLTGINFNGPSAGR			
			518.8	2	SCIMSGILR			
			870.9	2	NPCQIYYIPSDENK			
			501.8	2	IACAPEDVK			
			411.6	3	YSVGIVQDHSK			
			811.5	2	IYEIVNLLNVIYR	245	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			446.8	2	VTLDLFGK			
			430.7	2	ETDLLNR			
			442.3	2	INVLPEAK			
			479.2	3	LYCFDNLPEHK			
	0.045	50▼	798.4	2	SAESVTLDLFGDWR	210	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
	0.013	50▼	750.8	2	EDDYEEFLEIAK	102	*Daboia russelii* G8XQX1	LAAO
			438.7	2	STTDLPSR			
			569.3	2	HDDIFAYEK			
53c	0.026	32▼	552.8	2	VLNEDEETR	179	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			750.7	3	TSTHIAPLSLPSSPPSVGSVCR			
	0.021	32▼	805.4	2	IYEIVNTLNVIYR	280	*Macrovipera lebetina* Q4VM07	SVMP (PIII)
			661.3	3	HDNAQLLTGINFNGPSAGR			
			762.8	2	CETSYLFSDCSR			
			501.8	2	IACAPEDVK			
			798.4	2	SAESVTLDLFGDWR	209	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
			790.4	2	IYEIVNTLNVVFR			
			863.5	2	YIELVIVVDNVMoxFR			
			676.9	2	NPQCILNKPLR	159	*Vipera ammodytes ammodytes* AMB36351	SVMP (PIII)
			937.5	2	TWAHQLVNNIIVFYR			
53d	0.077	28▼	762.8	2	CETSYLFSDCSR	208	*Macrovipera lebetina* Q4VM07	SVMP fragment
			567.3	4	KRHDNAQLLTGINFNGPSAGR			
			805.4	2	IYEIVNTLNVIYR			
			501.8	2	IACAPEDVK			
	0.006	28▼	676.9	2	NPQCILNKPLR	70	*Agkistrodon piscivorus leucostoma* B7U492	PI-SVMP
	0.002	28▼	798.4	2	SAESVTLDLFGDWR	71	*Vipera ammodytes ammodytes* AHB62069	SVMP (PI)
53e	0.028	16▼	790.4	2	IYEIVNTLNVVFR	141	*Vipera ammodytes ammodytes* AHB62069	SVMP (PI)
			798.4	2	SAESVTLDLFGDWR			
			676.9	2	NPKCILNKPLR	48	*Echis pyramidum leakeyi* ADI47744	SVMP (PI)
53f	0.034	13▼	853.9	2	VWNQCDWGWSNGAK	24	*Macrovipera lebetina* B4XT00	CTL
			621.3	2	SYCVYFSSTK	*de novo*	*Macrovipera lebetina* B4XT02	CTL
	0.002	13▼	790.4	2	IYEIVNTLNVVFR	96	*Vipera ammodytes ammodytes* AHB62069	SVMP fragment
			798.4	2	SAESVTLDLFGDWR			
55a	0.407	>116▼	1191.5	3	AGTVCRPANGECDVSDVCTGQSAECPTDQFQR	1404	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			1246.0	2	QCISLFGASATVAQDACFQFNR			
			961.7	3	TDIVSPAVCGNYLVELGEDCDCGSPR			
			844.4	2	SCIMoxSGTLSCEASIR			
			993.4	2	LTPGSQCADGECCDQCK			
			811.5	2	IYEIVNLLNVIYR			
			720.9	2	LVIVADYIMoxFLK			
			679.4	2	MoxPQCILNKPLK			
			566.2	2	LGNEYGYCR			
			799.8	2	DCQNPCCNAATCK			
			656.3	2	NPCQIYYTPR			
			940.0	2	TRIYEIVNLLNVIYR			
			430.7	2	ETDLLNR			
			578.3	2	KIPCAPQDVK			
			718.3	2	LYCFDNLPEHK			

			1072.6	2	VLNIYIALVGLEIWNNGDK			
			442.3	2	INVLPEAK			
			514.3	2	IPCAPQDVK			
			617.8	2	VTLDLFGKWR			
55b	1.743	50▼	811.5	2	IYEIVNLLNVIYR	1084	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			831.0	3	QCISLFGASATVAQDACFQFNR			
			961.7	3	TDIVSPAVCGNYLVELGEDCDCGSPR			
			993.4	2	LTPGSQCADGECCDQCK			
			799.8	2	DCQNPCCNAATCK			
			720.9	2	LVIVADYIMoxFLK			
			656.3	2	NPCQIYYTPR			
			453.3	3	MoxPQCILNKPLK			
			519.8	4	VTLDLFGKWRETDLLNR			
			430.7	2	ETDLLNR			
			446.8	2	VTLDLFGK			
			578.3	2	KIPCAPQDVK			
			718.3	2	LYCFDNLPEHK			
			514.3	2	IPCAPQDVK			
			1072.6	2	VLNIYIALVGLEIWNNGDK			
			627.0	3	TRIYEIVNLLNVIYR			
	0.021	50▼	814.8	2	VTAMoxPKGAVKQPEQK	772	*Macrovipera lebetina* Q4VM08	SVMP (PIII)
			798.4	2	SAESVTLDLFGDWR	84	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
55c	0.180	36▼	1246.0	2	QCISLFGASATVAQDACFQFNR	836	*Vipera ammodytes ammodytes* AGL45259	PIII-SVMP
			712.9	2	LVIVADYIMFLK			
			656.3	2	NPCQIYYTPR			
			993.4	2	LTPGSQCADGECCDQCK			
			811.5	2	IYEIVNLLNVIYR			
			799.8	2	DCQNPCCNAATCK			
			446.8	2	VTLDLFGK			
			430.7	2	ETDLLNR			
			566.2	2	LGNEYGYCR			
			514.3	2	IPCAPQDVK			
			718.3	2	LYCFDNLPEHK			
			453.3	3	MoxPQCILNKPLK			
			442.3	2	INVLPEAK			
			1072.6	2	VLNIYIALVGLEIWNNGDK			
	0.037	36▼	750.7	3	TSTHIAPLSLPSSPPSVGSVCR	82	*Vipera ammodytes ammodytes* AMB36344	SVSP
			559.8	2	AAYPWLLER			
			587.8	2	VVCAGIWQGGK	27	*Vipera berus nikolskii* E5AJX2	SVSP
	0.003	36▼	798.4	2	SAESVTLDLFGDWR	75	*Vipera ammodytes ammodytes* AHB62069	SVMP (PIII)
55d	0.187	13▼	811.5	2	IYEIVNILNVIYR	87	*Macrovipera lebetina* Q4VM08	SVMP fragment

Table A2.8 Final binary matrix of the 34 peaks considered for statistical testing. The elution time (min) of every peak is reported above each peak column. The total number of peaks of each chromaographic profile considered for analysis is reported in the column "Total peaks".

	8	9.5	10	11	11.5	12	12.5	14	16.5	17	17.5	21	21.5	23	24	25.5	26.5	27	29.5	30.5	31.5	32	33	35.5	36.5	37	37.5	39.5	40.5	41	41.5	42	42.5	42.8	
Specimen	**P1**	**P2**	**P3**	**P4**	**P5**	**P6**	**P7**	**P8**	**P9**	**P10**	**P11**	**P12**	**P13**	**P14**	**P15**	**P16**	**P17**	**P18**	**P19**	**P20**	**P21**	**P22**	**P23**	**P24**	**P25**	**P26**	**P27**	**P28**	**P29**	**P30**	**P31**	**P32**	**P33**	**P34**	**Total peaks**
19VL026	1	1	1	1	0	1	0	0	0	0	0	0	1	1	0	0	1	0	1	0	1	0	0	0	0	1	0	1	1	1	1	1	1	0	17
18VL258	1	1	1	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	1	0	0	1	1	0	1	1	1	0	18
18VL259	0	1	0	1	0	0	1	0	1	0	0	1	1	1	0	0	1	0	1	0	1	0	0	0	1	0	0	1	1	1	1	1	1	0	17
18VL261	0	1	0	1	0	0	0	0	1	0	0	0	1	1	0	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	1	1	1	0	16
19VL011	1	1	0	1	0	0	1	0	1	0	0	1	0	1	0	0	1	1	1	0	1	0	0	0	1	0	0	1	1	1	1	1	1	1	19
19VL012	1	1	0	1	1	0	0	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	1	0	0	1	1	1	1	1	1	1	18
19VL016	1	1	1	1	1	0	1	0	1	0	0	1	0	1	0	0	1	0	0	0	1	0	1	0	0	1	0	1	1	1	1	1	1	1	20
19VL017	1	1	0	1	1	0	1	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	1	1	1	0	1	1	0	1	1	1	19
19VL018	1	1	1	1	1	0	1	0	1	0	0	0	1	1	0	0	1	1	1	0	1	0	1	0	0	1	0	1	1	1	1	1	1	1	22
19VL019	1	1	0	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	1	0	0	0	1	1	1	1	1	0	17
19VL025	1	1	1	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	1	0	1	1	0	1	1	1	1	1	1	0	20

19VL027	1	1	1	1	1	1	0	0	1	0	0	0	1	1	0	0	1	1	1	0	1	0	1	0	1	1	0	1	1	1	0	1	1	0	21
19VL028	1	1	1	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	1	1	0	0	19
19VL030	1	1	1	1	1	1	1	0	1	0	0	1	1	1	0	0	1	0	0	1	1	0	0	0	1	0	0	1	1	1	1	1	1	0	21
19VL035	1	1	0	1	0	1	1	0	1	0	0	1	0	1	0	0	1	0	0	0	1	0	1	0	1	0	0	1	1	1	0	1	1	0	17
19VL179	1	1	0	1	0	1	1	0	1	0	0	0	1	1	0	0	1	1	0	0	1	0	1	1	1	0	0	1	1	1	1	1	1	0	20
19VL454	1	1	1	1	1	1	1	0	1	0	0	1	0	1	0	0	1	0	0	1	1	1	1	1	1	0	0	1	1	1	1	1	1	0	23
19VL455	1	1	0	1	1	1	0	0	0	1	0	0	1	1	1	0	1	0	0	0	1	0	1	0	0	1	0	1	1	1	1	1	1	0	19
19VL457	1	1	1	1	1	1	0	0	0	1	0	0	1	1	1	0	1	0	0	0	1	0	1	0	0	1	0	1	1	1	1	0	1	0	19
19VL029	1	1	0	1	0	1	1	0	0	1	1	0	0	1	1	1	1	1	1	0	1	0	0	0	1	1	1	1	1	1	1	1	1	0	23
19VL459	1	1	0	1	0	1	0	0	1	1	1	0	1	1	1	1	1	0	0	0	1	0	1	0	0	1	1	1	1	1	1	1	0	0	21
19VL013	0	1	0	1	0	0	0	0	0	0	0	1	0	1	0	0	1	0	1	0	1	0	0	0	1	0	0	1	1	0	1	0	0	0	11
18VL007	0	1	1	0	1	1	0	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	1	1	1	1	1	1	0	0	20
18VL008	0	1	0	0	1	1	1	0	1	0	0	1	0	1	0	0	1	0	0	0	1	1	0	0	1	0	0	1	1	1	0	1	1	0	16
18VL253	0	1	0	1	1	0	1	0	1	0	0	0	1	1	0	0	1	0	0	1	0	1	1	0	1	0	1	1	1	1	1	1	0	0	18
18VL264	0	1	1	0	1	1	0	1	1	0	0	0	1	1	0	0	1	0	0	0	1	1	1	1	1	0	0	0	1	1	0	1	0	0	17
18VL303	1	1	0	1	0	1	0	0	1	0	0	1	0	1	0	0	1	0	0	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	20
18VL304	1	1	0	1	0	1	0	0	0	0	0	1	0	1	0	0	1	0	0	1	1	0	0	0	1	0	0	1	1	1	1	1	1	0	16
18VL305	0	1	1	1	0	1	1	0	1	0	0	0	1	1	0	0	1	0	0	1	1	1	1	1	1	0	0	1	1	1	1	1	0	0	20
19VL003	0	1	0	0	1	1	1	0	1	0	0	0	1	1	0	0	1	0	1	1	1	0	1	0	1	0	0	1	1	1	1	1	0	0	18
19VL008	0	1	0	1	1	0	0	0	1	0	0	0	1	1	0	0	1	0	0	0	1	0	0	0	1	0	0	1	1	1	0	1	1	0	14
19VL009	0	1	0	1	0	1	0	0	1	0	0	0	1	1	0	0	1	0	0	1	0	1	0	0	1	0	0	1	1	1	1	1	0	0	15
19VL020	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	0	1	0	0	1	1	1	0	0	1	0	0	1	1	0	1	1	0	0	17
19VL033	0	0	0	1	0	0	0	1	1	0	0	1	0	1	0	0	1	0	0	1	0	1	1	0	1	0	0	1	1	1	0	0	1	0	14
19VL066	1	0	0	1	0	0	0	0	1	0	0	1	1	1	0	0	1	0	0	0	1	1	0	0	1	0	0	1	1	1	0	0	1	0	14
19VL068	1	1	0	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0	0	1	1	0	0	1	0	0	1	1	0	1	0	1	1	18
19VL071	1	1	0	0	1	0	0	0	1	0	0	1	1	1	0	0	1	1	0	1	1	0	0	0	1	0	0	1	1	0	1	1	1	1	18
19VL180	1	1	0	1	0	1	0	0	1	0	0	1	1	1	0	0	1	0	1	0	1	0	0	0	1	0	0	1	1	1	0	1	1	0	17
18VL003	1	1	1	0	1	1	0	0	1	1	0	0	1	1	0	1	1	0	0	1	0	1	0	0	1	0	0	1	1	1	1	1	1	1	21
18VL009	1	1	0	0	1	0	0	1	1	1	0	0	1	1	0	1	1	0	0	1	1	1	0	0	1	0	0	1	1	1	0	1	0	0	18
18VL010	1	1	1	0	1	0	1	0	1	1	0	0	1	1	0	1	1	0	0	1	1	1	0	1	1	0	0	1	1	1	0	1	1	0	21
18VL011	1	1	0	0	1	1	1	0	0	1	0	0	1	1	0	1	1	0	0	1	1	1	1	1	1	0	0	1	1	1	1	1	0	0	21
18VL028	1	1	0	1	0	1	1	1	1	1	0	0	1	1	0	1	1	0	0	1	0	1	1	0	1	0	0	1	1	1	1	1	0	0	21
18VL306	0	1	0	1	0	0	1	0	1	1	0	0	1	1	0	1	1	0	0	1	1	0	1	1	1	0	0	0	1	1	0	1	0	0	17
19VL001	0	1	0	0	1	0	1	0	1	1	0	0	1	1	0	1	1	0	1	1	1	1	1	0	1	0	0	1	1	1	0	1	0	0	19
19VL005	0	1	0	0	1	0	1	0	0	1	0	0	1	1	0	1	1	0	0	1	0	1	0	0	1	0	0	1	1	1	1	1	0	0	16
19VL006	0	1	0	1	0	0	0	0	1	1	0	0	0	0	0	1	1	0	0	1	0	1	1	0	1	0	0	1	1	1	0	1	0	0	14
19VL007	0	1	0	0	1	0	1	0	1	1	0	0	1	1	0	1	1	0	1	0	0	1	0	0	1	0	0	1	1	1	0	1	0	0	16
19VL021	0	1	1	0	1	0	1	0	1	1	0	1	0	1	0	1	0	0	0	1	1	1	0	0	1	1	0	1	1	1	1	1	0	0	19
19VL022	0	1	0	1	0	0	1	0	1	1	0	1	1	1	0	1	0	0	0	1	1	1	0	0	1	0	0	0	1	1	0	1	0	0	16
19VL067	1	1	1	1	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	1	1	1	0	1	1	0	1	1	1	0	1	0	0	17
19VL070	1	1	0	0	1	0	0	0	0	1	0	1	1	1	1	1	1	0	0	0	1	0	0	0	1	0	0	1	1	1	0	1	1	0	17
19VL181	1	1	1	1	1	0	0	0	1	1	0	0	1	1	0	1	0	0	0	1	0	1	1	0	1	0	0	1	1	0	1	1	1	0	19
19VL397	0	0	0	0	1	0	0	1	1	1	0	0	1	1	0	1	1	0	0	0	1	0	1	0	1	0	0	1	0	0	1	1	1	0	15

Table A2.9 List of binomial GLMs testing the probability of occurrence of eleven specific chromatographic peaks. The models relate the occurrence of peaks 1, 6, 7, 16, 19, 20, 22, 23, 26, 31, and 33 in each chromatogram with the selected independent variables: snout-vent length (SVL), sex (Sex), day of the year in which the venom sample was collected (in its quadratic term; Day year^2), and population of origin (i.e., Gerês or Vila Chã). The best-fitting model is reported in bold. The table reports the number of parameters in the model (K), the information score of the model (Akaike's Information Criterion corrected for small sample sizes; AICc), the difference in AICc score between the best model and the model being compared (ΔAICc), and the AICc weight (i.e., proportion of the total amount of predictive power provided by the full set of models contained in the model being assessed; wAICc).

Peak	Model	K	AICc	ΔAICc	wAICc
Peak 1	**Population + Day year^2**	**4**	**52.77**	**0**	**0.97**
	Population	2	60.9	8.12	0.02
	Day year^2 + SVL	4	62.68	9.9	0.01
	Day year^2	3	63.78	11	0
	SVL	2	68.44	15.66	0
	Null	1	70.39	17.62	0
Peak 6	**Population + SVL**	**3**	**69.78**	**0**	**0.82**
	Null	1	72.76	2.99	0.18

Peak 7	**Population + Day year^2**	**4**	**69.6**	**0**	**0.42**
	Population	2	70.01	0.41	0.34
	Day year^2	3	72.04	2.44	0.12
	Null	1	72.29	2.69	0.11
Peak 16	**Population**	**2**	**56.45**	**0**	**0.99**
	Null	1	67.01	10.56	1
Peak 19	**SVL**	**2**	**44.34**	**0**	**0.99**
	Population	2	53.37	9.03	0.01
	Null	1	55.26	10.92	0
Peak 20	**Population + SVL**	**3**	**55.82**	**0**	**0.6**
	Population	2	56.79	0.96	0.37
	SVL	2	62.06	6.23	0.03
	Null	1	72.61	16.78	0
Peak 22	**Population**	**2**	**48.07**	**0**	**0.999**
	SVL	2	63.23	15.15	0.001
	Null	1	72.76	24.69	0
Peak 23	**Population + Day year^2 + SVL + Sex**	**6**	**59.7**	**0**	**0.56**
	Population + Sex	3	60.51	0.8	0.38
	Day year^2 + Sex	4	66	6.3	0.02
	Sex	2	66.58	6.87	0.02
	Population + SVL	3	68	8.29	0.01
	Population	2	68.04	8.34	0.01
	Null	1	71.19	11.48	0
Peak 26	**Population**	**2**	**50.03**	**0**	**0.93**
	Null	1	55.26	5.24	0.07
Peak 31	**Population + Sex**	**3**	**64.61**	**0**	**0.51**
	Population	2	65.06	0.45	0.41
	Null	1	68.3	3.69	0.08
Peak 33	**Population + Day year^2**	**4**	**52.15**	**0**	**0.82**
	Population	2	55.32	3.16	0.17
	SVL + Day year^2	4	62.98	10.83	0
	SVL	2	64.01	11.86	0
	Day year^2	3	68.33	16.18	0
	Null	1	70.39	18.24	0

Table A2.10 Best binomial GLMs explaining the probability of occurrence of peaks 1, 6, 7, 16, 19, 20, 22, 23, 26, 31, and 33 in a chromatogram. The table shows each peak as response variable (Response), related explanatory variables, coefficient estimate (β), Standard Error (SE), Z value (Z), and associated p-values. Significant p-values are in bold.

Response	Explanatory variables	β	SE	Z	p-value
Peak 1	Population Vila Chã	-2.822	0.924	-3.054	**0.002**
	Day year	8.37	2.897	2.89	**0.004**
	Day year^2	-8.687	2.96	-2.935	**0.003**
Peak 6	Population Vila Chã	-2.027	0.911	-2.226	**0.026**
	SVL	0.947	0.449	2.106	**0.035**
Peak 7	Population Vila Chã	-1.4	0.67	-2.091	**0.037**
	Day year	-0.465	0.308	-1.509	0.131
	Day year^2	0.506	0.315	1.608	0.108
Peak 16	Population Vila Chã	2.89	1.087	2.66	**0.008**
Peak 19	SVL	-1.466	0.483	-3.039	**0.002**
Peak 20	Population Vila Chã	2.356	0.888	2.654	**0.008**
	SVL	0.842	0.494	1.704	0.088
Peak 22	Population Vila Chã	3.989	1.106	3.608	**<0.001**
Peak 23	Population Vila Chã	-3.679	1.399	-2.63	**0.009**
	Sex	-2.89	1.062	-2.721	**0.007**
	SVL	0.898	0.562	1.598	0.11
	Day year	0.768	0.41	1.873	0.061
	Day year^2	0.621	0.443	1.4	0.161
Peak 26	Population Vila Chã	3.989	1.106	3.608	**<0.001**
Peak 31	Population Vila Chã	-1.765	0.757	-2.332	**0.02**
	Sex	-1.062	0.664	-1.598	0.11
Peak 33	Population Vila Chã	-3.538	1.125	-3.144	**0.002**
	Day year	0.219	0.406	0.54	0.589
	Day year^2	-0.928	0.374	-2.481	**0.013**

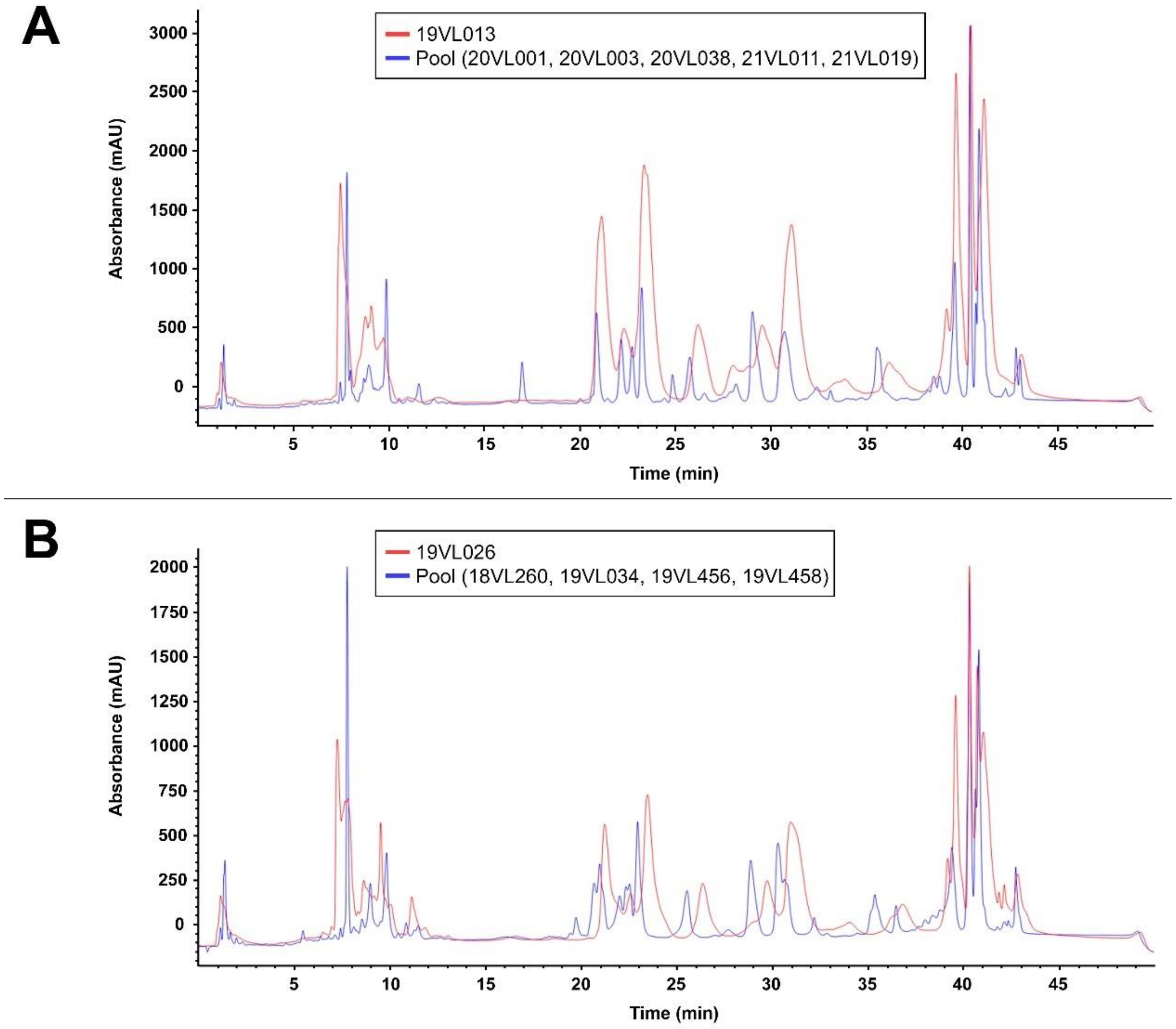
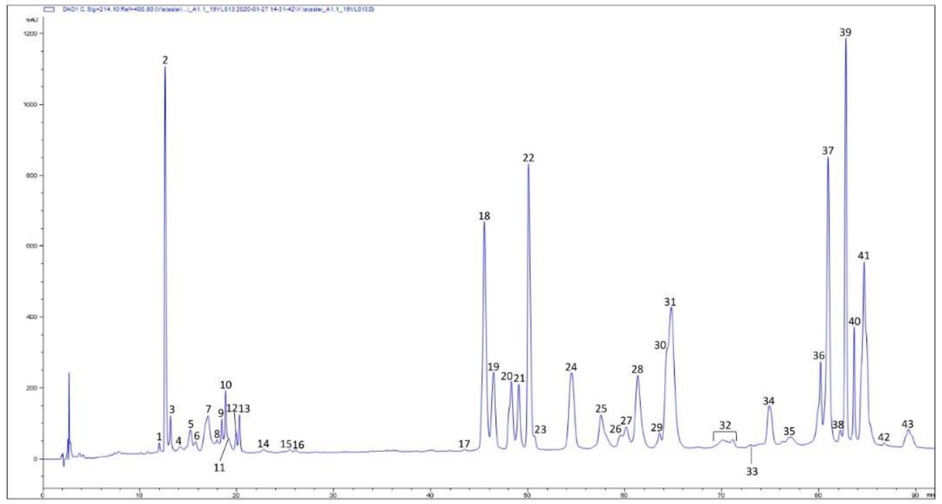
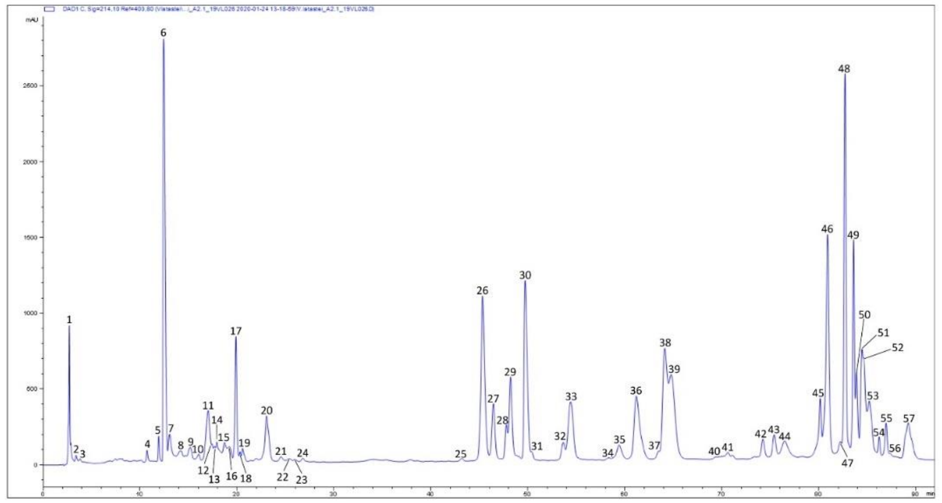


Figure A2.1 Comparison between the chromatographic profiles of venoms from single juvenile individuals and juvenile venom pools. In panel A, the overlapped chromatograms correspond to the venom of specimens from the Vila Chã population, namely 19VL013 (red profile) and the pooled venoms of specimens 20VL001, 20VL003, 20VL038, 21VL011, and 21VL019 (blue profile). In panel B, the overlapped chromatograms correspond to the venom of specimens from the Gerês population, namely 19VL026 (red profile) and the pooled venoms of specimens 18VL260, 19VL034, 19VL456, and 19VL458 (blue profile).

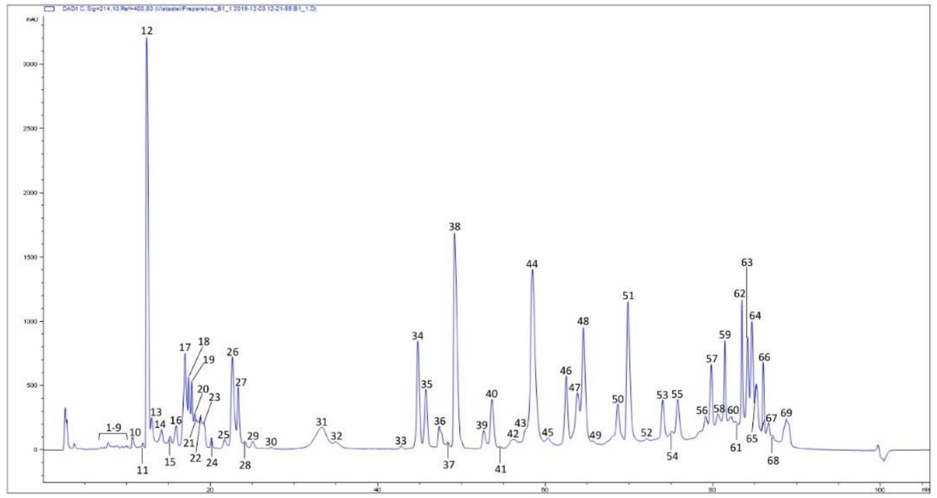
19VL013 (juvenile) - Vila Chã



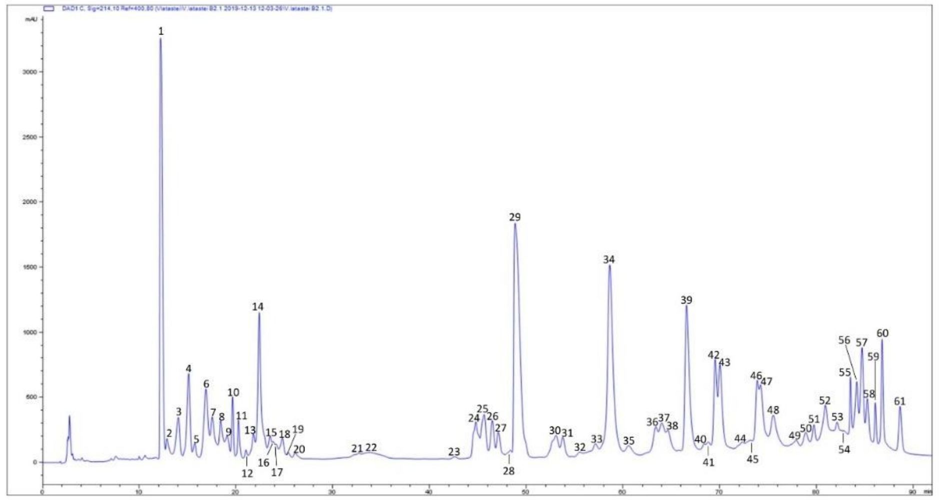
19VL026 (juvenile) - Gerês



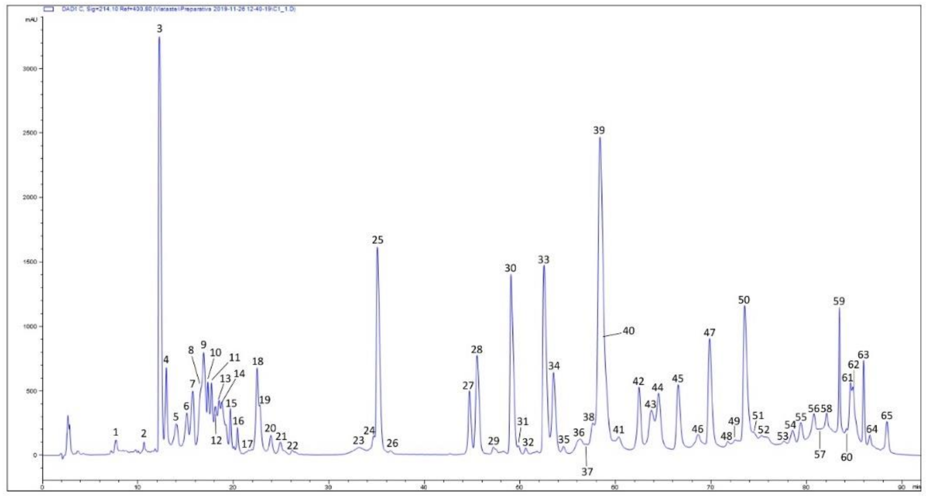
18VL253 (adult) - Vila Chã



18VL258 (adult) - Gerês



18VL011 (adult) - Vila Chã



19VL029 (adult) - Gerês

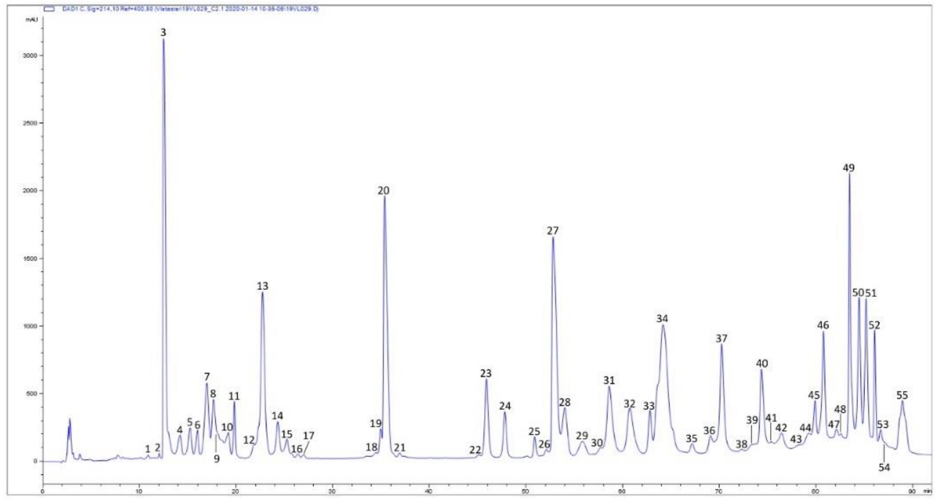


Figure A2.2 RP- HPLC profile of the *V. latastei* venoms used to produce the six venom proteomes by bottom-up venomics. Above each chromatogram, code, age class, and population of origin (i.e., Vila Chã or Gerês) of the corresponding viper are reported. The numbers linked to the peaks correspond to the numbers of the Spot IDs in Tables A2.2-A2.7.

Supplementary Information for Chapter 6

Venomics of the Iberian adder (*Vipera seoanei*)

List of Supplementary Tables and Figures

Table A3.1 List of the *V. seoanei* specimens considered in the present work. Latitude, longitude, locality and country of origin, snout-vent length (SVL), sex, colour phenotype and date of collection of each specimen are reported. Codes in bold correspond to the 20 specimens from which genetic information used to build the genetic distance matrix was obtained.

Table A3.2 Final binary matrix of the 10 polymorphic bands considered for statistical testing. The approximate molecular mass of every band is reported above each band column. The total number of polymorphic bands of each SDS-PAGE profile is reported in the column "Total polymorphic bands". The column "Total bands" reports the total number of bands (polymorphic + fixed) retrieved from each SDS-PAGE profile.

Table A3.3 List of the 65 *V. seoanei* specimens considered to produce the matrix of uncorrected p-distances estimated for cyt b and ND4 sequences. For each specimen, code, latitude, longitude, and GenBank accession numbers for ND4 and cyt b sequences are reported.

Table A3.4 Quantification of the *V. seoanei* venom pool proteome. Fraction numbers and band IDs are based, respectively, on the RP-HPLC chromatogram and on the SDS-PAGE profile in Figure 6.2.

Table A3.5 Results of the single predictor binomial GLMs performed. The models relate the occurrence of each of the 10 polymorphic SDS-PAGE bands with each of the selected 14 predictors. For each predictor tested, Likelihood Ratio Chi-square (LR χ^2), degrees of freedom (Df), and associated p-values (*p*) are reported. Significant predictors and corresponding p-values are in bold. The asterisks (*) indicate unreliable model fit.

Figure A3.1 The five geographically structured colour phenotypes currently recognised within *V. seoanei*. Viper pictures modified from Martínez-Freiría et al., 2017.

Figure A3.2 Geographic genetic variation in *V. seoanei*. First (a) and second (b) components of the Spatial Principal Component Analysis performed on the calculated genetic distances. Sampling localities are reported.

Figure A3.3 Whole venom profiles of the 49 *V. seoanei* specimens pooled to produce the reference proteome, under reducing conditions. Venom sample 20VS016 was loaded twice because of the low quality of the profile obtained with the first electrophoretic run (code reported in grey). Localities of collection of the samples are reported.

Figure A3.4 Model predictions of occurrence of bands 1, 2, 4, 8, 9 and 10 in individual SDS-PAGE venom profiles in relation to the continuous predictors tested in single predictor GLMs. The panels display the predicted probability of occurrence of: band 1 in relation to SVL (A); band 2 in relation to FOREST (B); band 4 in relation to AGRIC (C); band 8 in relation to SVL (D), BIO5 (E), and BIO12 (F); band 9 in relation to GEN2 (G); band 10 in relation to BIO5 (H) and FOREST (I).

Table A3.1 List of the *V. seoanei* specimens considered in the present work. Latitude, longitude, locality and country of origin, snout-vent length (SVL), sex, colour phenotype and date of collection of each specimen are reported. Codes in bold correspond to the 20 specimens from which genetic information used to build the genetic distance matrix was obtained.

Specimen code	Latitude	Longitude	Locality of origin	Country	SVL (mm)	Sex	Colour phenotype	Collection date
18VS076	42.90	-3.83	Alto Ebro	Spain	440	F	*melanistic*	03/06/2018
18VS077	42.90	-3.83	Alto Ebro	Spain	420	F	*classic*	03/06/2018
20VS130	42.92	-3.84	Alto Ebro	Spain	375	M	*melanistic*	29/09/2020
20VS131	42.92	-3.84	Alto Ebro	Spain	475	F	*classic*	29/09/2020
20VS132	42.93	-3.83	Alto Ebro	Spain	370	M	*melanistic*	29/09/2020
21VS072	42.00	-8.27	Peneda-Gerês National Park (PGNP)	Portugal	385	M	*melanistic*	28/05/2021
19VS074	41.99	-8.27	Peneda-Gerês National Park (PGNP)	Portugal	465	F	*melanistic*	24/05/2019
19VS075	41.99	-8.27	Peneda-Gerês National Park (PGNP)	Portugal	440	F	*melanistic*	24/05/2019
19VS076	42.03	-8.17	Peneda-Gerês National Park (PGNP)	Portugal	420	F	*cantabrica*	24/05/2019
19VS077	41.99	-8.26	Peneda-Gerês National Park (PGNP)	Portugal	465	F	*melanistic*	24/05/2019
19VS188	43.27	-4.98	Covadonga	Spain	445	F	*bilineata*	08/08/2019
19VS189	43.27	-4.98	Covadonga	Spain	435	M	*classic*	08/08/2019
19VS192	43.27	-4.98	Covadonga	Spain	365	F	*bilineata*	09/08/2019
19VS196	43.27	-4.98	Covadonga	Spain	370	M	*bilineata*	09/08/2019
19VS197	43.27	-4.98	Covadonga	Spain	425	F	*bilineata*	09/08/2019
19VS178	43.24	-7.55	Cospeito	Spain	395	M	*classic*	12/06/2019
19VS183	43.24	-7.56	Cospeito	Spain	385	F	*bilineata*	07/08/2019
19VS184	43.24	-7.56	Cospeito	Spain	405	F	*classic*	07/08/2019
19VS185	43.24	-7.55	Cospeito	Spain	400	F	*classic*	07/08/2019
20VS016	43.33	-8.42	A Coruña	Spain	400	F	*classic*	18/06/2020
20VS018	43.33	-8.42	A Coruña	Spain	515	F	*classic*	18/06/2020
21VS041	43.30	-8.46	A Coruña	Spain	426	F	*classic*	27/06/2020
21VS042	43.33	-8.42	A Coruña	Spain	425	F	*classic*	05/07/2020
21VS043	43.33	-8.42	A Coruña	Spain	413	F	*classic*	24/07/2020
21VS004	42.41	-8.84	Sanxenxo	Spain	410	M	*classic*	17/03/2021
21VS005	42.41	-8.84	Sanxenxo	Spain	360	M	*classic*	17/03/2021
21VS006	42.41	-8.84	Sanxenxo	Spain	370	M	*classic*	17/03/2021
21VS007	42.41	-8.84	Sanxenxo	Spain	410	M	*classic*	17/03/2021
21VS008	42.41	-8.84	Sanxenxo	Spain	325	M	*classic*	17/03/2021
19VS137	42.85	-5.35	Mata de la Riba	Spain	480	F	*cantabrica*	31/05/2019
19VS175	43.53	-5.37	Rodiles	Spain	475	F	*bilineata*	11/06/2019
19VS447	42.54	-7.10	Courel	Spain	355	M	*cantabrica*	28/09/2019
20VS007	42.67	-8.34	Brañas de Xestoso	Spain	345	F	*classic*	05/06/2020
20VS037	42.49	-8.38	Seixo	Spain	410	F	*classic*	26/06/2020
20VS113	43.08	-5.27	Puerto Señales	Spain	400	M	*cantabrica*	23/09/2020
20VS165	42.99	-2.83	Gorbea	Spain	497	F	*uniform*	22/08/2020
20VS217	42.91	-6.18	Cabrillanes	Spain	405	M	*cantabrica*	22/07/2020
21VS060	42.16	-8.69	Zamáns	Spain	395	F	*melanistic*	14/05/2021
21VS053	42.27	-7.27	Manzaneda	Spain	455	F	*cantabrica*	08/05/2021
19VS450	42.70	-7.07	Cebreiro	Spain	400	M	*cantabrica*	29/09/2019
19VS451	42.70	-7.07	Cebreiro	Spain	415	M	*cantabrica*	29/09/2019
20VS019	43.70	-7.86	Ortigueira	Spain	410	F	*classic*	19/06/2020
20VS020	43.70	-7.86	Ortigueira	Spain	455	F	*classic*	19/06/2020
20VS021	43.48	-7.54	Valadouro	Spain	364	F	*bilineata*	19/06/2020
20VS024	43.48	-7.53	Valadouro	Spain	360	M	*classic*	19/06/2020
20VS026	42.62	-5.59	León	Spain	490	F	*cantabrica*	22/06/2020
21VS020	42.62	-5.59	León	Spain	500	M	*cantabrica*	05/04/2021
21VS021	42.62	-5.59	León	Spain	500	F	*cantabrica*	05/04/2021
21VS022	42.62	-5.59	León	Spain	420	M	*cantabrica*	05/04/2021

Table A3.2 Final binary matrix of the 10 polymorphic bands considered for statistical testing. The approximate molecular mass of every band is reported above each band column. The total number of polymorphic bands of each SDS-PAGE profile is reported in the column "Total polymorphic bands". The column "Total bands" reports the total number of bands (polymorphic + fixed) retrieved from each SDS-PAGE profile.

	150 kDa	130 kDa	100 kDa	60 kDa	37 kDa	32 kDa	27 kDa	26 kDa	22.5 kDa	20 kDa		
Specimen code	**Band1**	**Band2**	**Band3**	**Band4**	**Band5**	**Band6**	**Band7**	**Band8**	**Band9**	**Band10**	**Total polymorphic bands**	**Total bands**
18VS076	0	0	0	0	1	1	1	1	1	0	5	14
18VS077	1	0	0	1	1	1	0	1	1	0	6	15
20VS130	1	0	0	1	1	1	0	1	1	0	6	15
20VS131	1	0	0	1	1	1	0	1	1	0	6	15
20VS132	1	0	0	1	1	1	1	1	1	0	7	16
21VS072	0	0	0	1	1	1	0	1	1	0	5	14
19VS074	1	0	0	0	1	1	0	1	1	0	5	14
19VS075	1	1	0	1	1	1	0	1	1	0	7	16
19VS076	0	0	0	0	0	1	1	1	1	0	4	13
19VS077	1	0	1	1	1	1	0	1	1	0	7	16
19VS188	1	0	0	1	1	1	0	1	1	1	7	16
19VS189	1	0	0	1	1	1	0	1	1	0	6	15
19VS192	1	0	1	1	1	1	0	1	1	0	7	16
19VS196	0	0	0	1	1	1	0	1	1	0	5	14
19VS197	0	0	0	1	1	1	0	1	1	0	5	14
19VS178	1	0	1	1	1	1	0	1	1	1	8	17
19VS183	1	0	0	1	1	1	0	1	1	1	7	16
19VS184	1	0	0	1	1	1	0	1	1	0	6	15
19VS185	1	0	0	0	1	0	0	1	1	0	4	13
20VS016	1	1	0	1	1	1	0	1	1	0	7	16
20VS018	1	0	0	1	1	1	1	1	1	0	7	16
21VS041	1	0	0	0	1	1	1	1	1	0	6	15
21VS042	1	1	0	1	1	1	0	1	1	0	7	16
21VS043	1	0	0	1	1	1	0	1	1	0	6	15
21VS004	0	0	1	1	1	1	0	1	0	0	5	14
21VS005	0	0	0	1	1	1	0	1	0	0	4	13
21VS006	0	0	0	1	1	1	0	1	0	0	4	13
21VS007	0	0	1	1	1	1	1	1	0	0	6	15
21VS008	1	0	1	1	1	1	1	1	1	0	8	17
19VS137	1	0	1	1	1	1	1	1	1	0	8	17
19VS175	1	0	0	0	1	1	1	1	1	1	7	16
19VS447	0	0	0	1	1	1	1	1	1	0	6	15
20VS007	1	0	0	1	1	1	1	1	1	0	7	16
20VS037	1	0	1	1	1	1	1	1	1	0	8	17
20VS113	1	0	1	1	1	1	1	1	1	0	8	17
20VS165	1	0	0	1	1	1	1	1	1	1	8	17
20VS217	1	1	0	1	1	1	1	0	1	0	7	16
21VS060	1	0	1	1	1	1	1	1	1	0	8	17
21VS053	1	0	0	1	1	1	1	1	1	0	7	16
19VS450	1	0	1	1	1	1	1	1	1	1	9	18
19VS451	1	1	1	1	1	0	1	1	1	1	9	18
20VS019	1	0	0	1	1	0	0	1	1	0	5	14
20VS020	1	0	0	1	1	0	1	1	1	0	6	15
20VS021	0	0	1	1	1	1	0	1	1	1	7	16
20VS024	1	0	0	1	1	0	1	1	1	0	6	15
20VS026	1	0	0	1	1	1	1	1	1	1	8	17
21VS020	1	0	1	1	1	1	1	0	1	0	7	16
21VS021	1	0	1	1	1	1	1	0	1	1	8	17
21VS022	1	1	1	1	1	1	0	1	1	1	9	18

Table A3.3 List of the 65 *V. seoanei* specimens considered to produce the matrix of uncorrected p-distances estimated for cyt b and ND4 sequences. For each specimen, code, latitude, longitude, and GenBank accession numbers for ND4 and cyt b sequences are reported.

Specimen code	Latitude	Longitude	GenBank Acc Nº - ND4	GenBank Acc Nº - cyt b
10VS001	41.91	-7.93	KM213672	KM213685
10VS013	42.07	-8.14	KM213673	KM213686
10VS015	42.78	-8.75	KM213672	KM213685
11VS001	43.04	-6.72	KM213674	KM213686
11VS005	41.73	-7.81	KM213672	KM213688
11VS007	42.62	-8.72	KM213676	KM213690
11VS008	43.15	-7.71	KM213677	KM213691
11VS009	42.16	-6.73	KM213678	KM213686
12VS001	43.14	-5.06	KM213672	KM213689
12VS003	42.65	-7.33	KM213674	KM213686
12VS004	43.39	-4.42	KM213672	KM213692
12VS005	43.47	-5.14	KM213672	KM213689
12VS006	43.38	-5.99	KM213679	KM213686
12VS007	43.55	-6.28	KM213680	KM213690
12VS008	43.02	-6.01	KM213681	KM213686
12VS011	42.83	-5.04	KM213681	KM213686
12VS012	42.93	-4.67	KM213672	KM213689
12VS013	42.91	-4.36	KM213672	KM213693
12VS014	43.13	-3.73	KM213672	KM213689
12VS016	42.86	-6.85	KM213674	KM213686
12VS017	43.34	-7.01	KM213674	KM213686
12VS018	42.94	-5.46	KM213681	KM213686
12VS019	43.42	-4.09	KM213672	KM213689
12VS021	43.48	-3.55	KM213672	KM213689
12VS022	43.13	-3.45	KM213672	KM213689
12VS023	43.36	-3.19	KM213672	KM213694
12VS026	43.28	-6.26	KM213682	KM213689
12VS028	43.25	-4.76	KM213672	KM213689
12VS029	43.52	-5.36	KM213672	KM213689
19VS137	42.85	-5.35	KM213672	KM213686
19VS175	43.53	-5.37	KM213675	KM213686
19VS178	43.24	-7.55	KM213672	KM213700
19VS197	43.27	-4.98	KM213672	KM213686
19VS447	42.54	-7.10	KM213672	KM213700
19VS451	42.70	-7.07	KM213672	KM213700
20VS007	42.67	-8.34	KM213680	OQ791313
20VS008	42.46	-8.49	OQ791314	KM213686
20VS018	43.33	-8.42	KM213672	KM213700
20VS020	43.70	-7.86	KM213672	KM213686
20VS024	43.48	-7.53	KM213681	KM213686
20VS037	42.49	-8.38	KM213672	KM213686
20VS113	43.08	-5.27	OQ791315	OQ791313
20VS131	42.92	-3.84	KM213672	KM213700
20VS165	42.99	-2.83	OQ791316	KM213686
20VS217	42.91	-6.18	KM213681	KM213686
21VS008	42.41	-8.84	KM213675	KM213686
21VS022	42.62	-5.59	KM213672	KM213700
21VS053	42.27	-7.27	KM213675	KM213686
21VS060	42.16	-8.69	KM213675	KM213686
21VS072	42.00	-8.27	KM213672	OQ791313
5VS143	42.79	-3.93	KM213672	KM213689
6VS200	43.15	-4.61	KM213672	KM213696
VSAR001	43.01	-2.33	KM213672	KM213689
VSAR1990	43.21	-1.79	KM213672	KM213697
VSAR1993	43.06	-2.71	KM213672	KM213689
VSAR4768	43.28	-1.98	KM213672	KM213689
VSCB_005	41.87	-8.51	KM213683	KM213700
VSE2AR1	43.32	-7.92	KM213672	KM213686
X-001	43.13	-6.99	KM213672	KM213686

X-034	42.86	-9.02	KM213672	KM213686
X-062	43.01	-7.43	KM213674	KM213686
12VS024	43.23	-4.32	KM213672	KM213692
12VS002	42.26	-7.36	KM213672	KM213686
11VS006	43.38	-5.99	KM213679	KM213686
VSAR_4494	43.32	-1.79	KM213672	KM213689

Table A3.4 Quantification of the *V. seoanei* venom pool proteome. Fraction numbers and band IDs are based, respectively, on the RP-HPLC chromatogram and on the SDS-PAGE profile in Figure 6.2.

				QUANTIFICATION									**MS IDENTIFIED PEPTIDES**	
					HPLC		**SDS PAGE**							
HPLC peak	**SDS-PAGE band**	**Molecular mass (kDa)**	**Toxin family**	**Band %**	**Peak intensity**	**Peak %**	**Band area**	**Band density**	**Blank area**	**Blank density**	**Control**	**%**	**Main peak mass (in m/z with z=1)**	**Main peptide**
1		-	peptides	**0.13%**	990.10	0.13%							484.2	240.09-PE
2		-	peptides	**0.08%**	583.90	0.08%							355.26	240.09-P
3		-	peptides	**0.04%**	270.50	0.04%							482.27	211.11-RP
4		-	peptides	**0.20%**	1539.10	0.20%							547.22	GGGGGGW
5		-	peptides	**0.32%**	2435.50	0.32%							814.35	pERGGGGGGW
6	6a	10	SVMPi	**5.00%**	37776.60	5.00%							444.22	pEKW
7	7a	10	SVMPi	**2.21%**	16688.60	2.21%							472.23	pERW
8	8a	10	peptides	**0.17%**	1280.70	0.17%							1072.581	pERRPPEIPP
9	9a	10	SVMPi	**0.72%**	5436.10	0.72%							430.17	pENW
10	10a	10	peptides	**1.48%**	11197.10	1.48%							851.45	pERWPGPK
11	11a	10	KUN	**0.12%**	929.30	0.12%								
12	12a	10	KUN	**0.73%**	5501.20	0.73%								
13	13a	10	KUN	**0.10%**	724.00	0.10%								
14					3050.70	0.40%								
	14a	12	DISI	**0.17%**			4292.00	78575.00	1967.00	19057.00	36992.57	0.43		
	14b	10	KUN	**0.23%**			5520.00	102288.00	1967.00	19057.00	48808.26	0.57		
											85800.83	1.00		
15					17997.50	2.38%								
	15a	12	DISI	**1.77%**			7956.00	437590.00	1836.00	19382.00	353601.33	0.74		
	15b	<8	NP	**0.61%**			9126.00	217769.00	1836.00	19382.00	121429.06	0.26		
											475030.39	1.00		
16					3987.50	0.53%								
	16a	12	DISI	**0.42%**			8806.00	640322.00	1605.00	17452.00	544569.78	0.80		
	16b	<8	NP	**0.10%**			8120.00	222327.00	1605.00	17452.00	134034.02	0.20		
											678603.80	1.00		
17					15311.20	2.03%								
	17a	12	DISI	**1.70%**			9660.00	586975.00	1248.00	13227.00	484592.93	0.84		
	17b	<8	NP	**0.33%**			8664.00	186008.00	1248.00	13227.00	94182.10	0.16		
											578775.03	1.00		
18					6752.20	0.89%								
	18a	12	DISI	**0.89%**			1.00	2.00	1.00	1.00	1.00	1.00		
											1.00	1.00		
19					14894.40	1.97%								
	19a	12	DISI	**1.97%**			1.00	2.00	1.00	1.00	1.00	1.00		
											1.00	1.00		
20					17964.60	2.38%								
	20a	12	DISI	**2.38%**			1.00	2.00	1.00	1.00	1.00	1.00		
											1.00	1.00		
21					8743.20	1.16%								
	21a	15	VEGF	**0.05%**			3535.00	42837.00	990.00	9406.00	9250.93	0.04		
	21b	12	DISI	**1.11%**			8874.00	287752.00	990.00	9406.00	203440.04	0.96		
											212690.97	1.00		
22					8848.90	1.17%								

	22a	15	VEGF	**0.07%**			3570.00	58735.00	940.00	8310.00	27174.68	0.06
	22b	13	DISI	**0.35%**			3672.00	165535.00	940.00	8310.00	133072.96	0.30
	22c	11	DISI	**0.75%**			6180.00	336051.00	940.00	8310.00	281417.17	0.64
											441664.81	1.00
23					10717.60	1.42%						
	23a	25	NA	**0.03%**			4173.00	48122.00	1352.00	11689.00	12043.45	0.02
	23b	15	VEGF	**0.14%**			3335.00	94529.00	1352.00	11689.00	65695.56	0.10
	23c	13	DISI	**0.36%**			3850.00	208285.00	1352.00	11689.00	174999.02	0.26
	23d	11	DISI	**0.89%**			7085.00	491164.00	1352.00	11689.00	429909.14	0.63
											682647.17	1.00
24					9805.30	1.30%						
	24a	14	VEGF	**0.26%**			4872.00	313378.00	1188.00	11549.00	266015.43	0.20
	24b	12	DISI	**0.97%**			10368.00	1100602.00	1188.00	11549.00	999810.73	0.75
	24c	9	DISI	**0.07%**			5160.00	118183.00	1188.00	11549.00	68020.68	0.05
											1333846.84	1.00
25					7665.50	1.01%						
	25a	14	VEGF	**0.34%**			6042.00	515468.00	1200.00	12033.00	454881.85	0.33
	25b	12	DISI	**0.63%**			8733.00	937613.00	1200.00	12033.00	850042.84	0.63
	25c	9	DISI	**0.04%**			3648.00	91033.00	1200.00	12033.00	54452.68	0.04
											1359377.37	1.00
26					37694.40	4.99%						
	26a	28	PLA2	**0.31%**			5328.00	190693.00	1040.00	9968.00	139626.17	0.06
	26b	14	PLA2	**3.61%**			14807.00	1758095.00	1040.00	9968.00	1616175.60	0.72
	26c	12	VEGF	**1.07%**			5047.00	525388.00	1040.00	9968.00	477014.45	0.21
											2232816.22	1.00
27					9198.40	1.22%						
	27a	28	SVMP	**0.05%**			3900.00	115228.00	880.00	9024.00	75235.27	0.04
	27b	20	SVMP	**0.05%**			3400.00	112152.00	880.00	9024.00	77286.55	0.04
	27c	14	PLA2	**0.31%**			4134.00	483115.00	880.00	9024.00	440722.71	0.25
	27d	13	VEGF	**0.41%**			4773.00	643905.00	880.00	9024.00	594960.05	0.34
	27e	12	VEGF	**0.39%**			6095.00	619596.00	880.00	9024.00	557094.55	0.32
											1745299.13	1.00
28					7810.90	1.03%						
	28a	32	SVMP	**0.01%**			4950.00	73261.00	747.00	7165.00	25782.08	0.01
	28b	28	SVMP	**0.07%**			4223.00	158192.00	747.00	7165.00	117686.25	0.06
	28c	20	SVMP	**0.36%**			6780.00	703379.00	747.00	7165.00	638347.27	0.35
	28d	18	SVMP	**0.04%**			3850.00	105887.00	747.00	7165.00	68958.95	0.04
	28e	14	PLA2	**0.07%**			2550.00	142198.00	747.00	7165.00	117739.16	0.06
	28f	13	VEGF	**0.34%**			5650.00	648978.00	747.00	7165.00	594784.89	0.33
	28g	12	VEGF	**0.15%**			3030.00	285708.00	747.00	7165.00	256645.15	0.14
											1819943.77	1.00
29					8910.00	1.18%						
	29a	32	SVMP	**0.01%**			4653.00	66953.00	756.00	7001.00	23863.51	0.01
	29b	28	SVMP	**0.13%**			5250.00	269005.00	756.00	7001.00	220386.94	0.11
	29c	20	SVMP	**0.46%**			7597.00	847039.00	756.00	7001.00	776686.36	0.39
	29d	18	SVMP	**0.04%**			3456.00	107960.00	756.00	7001.00	75955.43	0.04
	29e	14	PLA2	**0.05%**			2700.00	110929.00	756.00	7001.00	85925.43	0.04
	29f	13	VEGF	**0.34%**			5700.00	625852.00	756.00	7001.00	573066.68	0.29
	29g	12	VEGF	**0.15%**			3348.00	284589.00	756.00	7001.00	253584.57	0.13
											2009468.93	1.00
30					7054.80	0.93%						
	30a	28	SVMP	**0.15%**			4700.00	278459.00	729.00	7737.00	228577.11	0.16
	30b	20	SVMP	**0.29%**			6283.00	515701.00	729.00	7737.00	449018.46	0.31
	30c	14	PLA2	**0.04%**			2525.00	82606.00	729.00	7737.00	55807.75	0.04
	30d	13	VEGF	**0.32%**			5452.00	554148.00	729.00	7737.00	496285.00	0.35
	30e	12	VEGF	**0.13%**			3456.00	236952.00	729.00	7737.00	200272.89	0.14
											1429961.21	1.00
31					4487.50	0.59%						
	31a	28	SVMP	**0.07%**			5406.00	190621.00	810.00	8457.00	134178.36	0.12
	31b	25	SVMP	**0.04%**			2352.00	94845.00	810.00	8457.00	70288.38	0.06
	31c	20	SVMP	**0.09%**			4922.00	223387.00	810.00	8457.00	171997.67	0.15
	31d	14	PLA2	**0.02%**			2730.00	72869.00	810.00	8457.00	44365.78	0.04

	31e	13	VEGF	**0.25%**			5778.00	538948.00	810.00	8457.00	478621.40	0.43
	31f	12	VEGF	**0.12%**			3850.00	261905.00	810.00	8457.00	221708.15	0.20
											1121159.73	1.00
32					36901.30	4.88%						
	32a	25	PLA2	**0.20%**			6048.00	140178.00	1001.00	10979.00	73843.34	0.04
	32b	17	VNGF	**0.53%**			4633.00	242919.00	1001.00	10979.00	192104.11	0.11
	32c	13	PLA2	**3.03%**			10164.00	1207745.00	1001.00	10979.00	1096265.92	0.62
	32d	11	VEGF	**1.11%**			4337.00	450259.00	1001.00	10979.00	402690.65	0.23
											1764904.02	1.00
33					29799.80	3.94%						
	33a	70	NA	**0.05%**			3392.00	58702.00	4576.00	44662.00	25595.90	0.01
	33b	55	NA	**0.05%**			2970.00	52698.00	4576.00	44662.00	23710.64	0.01
	33c	25	PLA2	**0.09%**			5096.00	97181.00	930.00	9855.00	43179.84	0.02
	33d	17	VNGF	**0.24%**			4922.00	168336.00	930.00	9855.00	116178.68	0.06
	33e	13	PLA2	**2.42%**			10492.00	1270400.00	930.00	9855.00	1159218.65	0.61
	33f	11	PLA2	**1.09%**			6138.00	586479.00	930.00	9855.00	521436.00	0.28
											1889319.71	1.00
34					1437.20	0.19%						
	34a	13	PLA2	**0.19%**			6912.00	519922.00	1344.00	14478.00	445463.71	1.00
											445463.71	1.00
35					1640.80	0.22%						
	35a	25	CRISP	**0.07%**			6741.00	208894.00	600.00	5541.00	146640.87	0.31
	35b	15	PLA2	**0.01%**			3105.00	56677.00	600.00	5541.00	28002.33	0.06
	35c	14	PLA2	**0.14%**			7380.00	373498.00	600.00	5541.00	305343.70	0.64
											479986.89	1.00
36					21470.00	2.84%						
	36a	40	CRISP	**0.11%**			4725.00	103691.00	1060.00	9756.00	60203.17	0.04
	36b	25	CRISP	**1.91%**			11440.00	1197624.00	1060.00	9756.00	1092332.83	0.67
	36c	17	CRISP	**0.07%**			4469.00	83499.00	1060.00	9756.00	42367.34	0.03
	36d	15	PLA2	**0.08%**			3120.00	72058.00	1060.00	9756.00	43342.23	0.03
	36e	14	PLA2	**0.67%**			7168.00	451520.00	1060.00	9756.00	385547.35	0.24
											1623792.91	1.00
37					5243.20	0.69%						
	37a	25	CRISP	**0.35%**			7700.00	675733.00	940.00	9833.00	595186.09	0.50
	37b	13	PLA2	**0.35%**			7750.00	670795.00	940.00	9833.00	589725.05	0.50
											1184911.14	1.00
38					1357.90	0.18%						
	38a	25	CRISP	**0.10%**			7488.00	387052.00	828.00	8271.00	312253.39	0.53
	38b	13	PLA2	**0.08%**			6042.00	337266.00	828.00	8271.00	276911.67	0.47
											589165.07	1.00
39					6232.20	0.82%						
	39a	42	SVSP	**0.02%**			3978.00	51323.00	1010.00	9490.00	13945.55	0.02
	39b	35	SVSP	**0.02%**			3737.00	51156.00	1010.00	9490.00	16043.00	0.02
	39c	25	CRISP	**0.09%**			6300.00	142957.00	1010.00	9490.00	83761.95	0.12
	39d	13	PLA2	**0.70%**			7800.00	687224.00	1010.00	9490.00	613934.89	0.84
											727685.40	1.00
40					47313.30	6.26%						
	40a	55	SVMP	**0.18%**			5562.00	142198.00	1410.00	13152.00	90317.56	0.03
	40b	42	SVSP	**0.99%**			5830.00	557326.00	1410.00	13152.00	502945.74	0.16
	40c	35	SVSP	**1.25%**			6840.00	697205.00	1410.00	13152.00	633403.81	0.20
	40d	29	SVSP	**0.14%**			2808.00	94987.00	1410.00	13152.00	68794.93	0.02
	40e	25	CRISP	**0.34%**			6264.00	229852.00	1410.00	13152.00	171423.54	0.05
	40f	13	PLA2	**3.37%**			15762.00	1857739.00	1410.00	13152.00	1710716.43	0.54
											3177602.01	1.00
41					26791.00	3.54%						
	41a	120	SVMP	**0.01%**			2538.00	48486.00	672.00	10129.00	10230.94	0.00
	41b	100	SVMP	**0.01%**			3040.00	54761.00	672.00	10129.00	8939.33	0.00
	41c	70	SVMP	**0.00%**			2871.00	45250.00	672.00	10129.00	1975.66	0.00
	41d	55	SVMP	**0.97%**			9164.00	862902.00	672.00	10129.00	724773.79	0.27
	41e	42	SVSP	**0.52%**			5616.00	471235.00	672.00	10129.00	386585.50	0.15
	41f	35	SVSP	**0.81%**			7056.00	713590.00	672.00	10129.00	607235.50	0.23
	41g	29	SVSP	**0.13%**			2800.00	142839.00	672.00	10129.00	100634.83	0.04

	41h	25	SVSP	**0.11%**			3330.00	130056.00	672.00	10129.00	79863.19	0.03
	41i	13	PLA2	**0.98%**			9315.00	869178.00	672.00	10129.00	728773.78	0.28
											2649012.52	1.00
42					7319.10	0.97%						
	42a	55	SVMP	**0.42%**			6588.00	552291.00	665.00	6323.00	489650.51	0.43
	42b	35	SVSP	**0.27%**			5029.00	363259.00	665.00	6323.00	315441.91	0.28
	42c	28	LAAO	**0.22%**			4815.00	297914.00	665.00	6323.00	252131.68	0.22
	42d	13	PLA2	**0.06%**			4752.00	115357.00	665.00	6323.00	70173.70	0.06
											1127397.79	1.00
43					25732.10	3.40%						
	43a	70	SVSP	**0.02%**			1900.00	27517.00	534.00	4811.00	10399.21	0.00
	43b	55	SVMP	**0.48%**			4900.00	372390.00	534.00	4811.00	328244.12	0.14
	43c	35	SVSP	**0.93%**			6780.00	696909.00	534.00	4811.00	635825.52	0.27
	43d	30	SVSP	**0.29%**			2376.00	220477.00	534.00	4811.00	199070.75	0.09
	43e	28	LAAO	**0.64%**			5439.00	484164.00	534.00	4811.00	435162.07	0.19
	43f	20	SVSP	**0.06%**			3780.00	77878.00	534.00	4811.00	43822.61	0.02
	43g	16	CTL	**0.15%**			4982.00	149463.00	534.00	4811.00	104578.35	0.04
	43h	15	CTL	**0.84%**			7680.00	643322.00	534.00	4811.00	574130.09	0.25
											2331232.72	1.00
44					36796.50	4.87%						
	44a	70	SVSP	**0.01%**			2231.00	29351.00	1196.00	11534.00	7835.65	0.00
	44b	55	SVMP	**0.23%**			3978.00	162096.00	1196.00	11534.00	123732.91	0.05
	44c	45	SVSP	**0.07%**			3000.00	67738.00	1196.00	11534.00	38806.56	0.01
	44d	35	SVSP	**1.83%**			10375.00	1097180.00	1196.00	11534.00	997125.44	0.38
	44e	30	SVSP	**0.73%**			3712.00	433174.00	1196.00	11534.00	397376.17	0.15
	44f	28	SVSP	**0.56%**			3270.00	335951.00	1196.00	11534.00	304415.73	0.12
	44g	20	SVSP	**0.11%**			4116.00	102073.00	1196.00	11534.00	62379.07	0.02
	44h	16	CTL	**0.55%**			6489.00	362589.00	1196.00	11534.00	300010.30	0.11
	44i	15	CTL	**0.76%**			8140.00	493424.00	1196.00	11534.00	414923.36	0.16
											2646605.20	1.00
45					15876.00	2.10%						
	45a	70	SVSP	**0.01%**			2880.00	35793.00	558.00	4851.00	10755.58	0.01
	45b	55	SVMP	**0.06%**			3876.00	85100.00	558.00	4851.00	51403.81	0.03
	45c	45	SVSP	**0.02%**			2678.00	46237.00	558.00	4851.00	22955.68	0.01
	45d	35	SVSP	**0.59%**			6893.00	610810.00	558.00	4851.00	550885.37	0.28
	45e	30	SVSP	**0.66%**			6095.00	671189.00	558.00	4851.00	618201.82	0.32
	45f	28	LAAO	**0.19%**			2958.00	204947.00	558.00	4851.00	179231.48	0.09
	45g	20	SVSP	**0.01%**			2828.00	36857.00	558.00	4851.00	12271.65	0.01
	45h	16	CTL	**0.10%**			5085.00	138432.00	558.00	4851.00	94225.31	0.05
	45i	15	CTL	**0.45%**			9204.00	495652.00	558.00	4851.00	415636.58	0.21
											1955567.27	1.00
46					9042.00	1.20%						
	46a	60	SVMP	**0.13%**			6038.00	322275.00	450.00	4902.00	256501.05	0.11
	46b	55	SVSP	**0.24%**			7104.00	550613.00	450.00	4902.00	473226.76	0.20
	46c	35	SVSP	**0.17%**			3630.00	380451.00	450.00	4902.00	340908.20	0.14
	46d	31	LAAO	**0.14%**			4066.00	312548.00	450.00	4902.00	268255.71	0.11
	46e	28	LAAO	**0.02%**			3264.00	78714.00	450.00	4902.00	43158.16	0.02
	46f	16	VNGF	**0.06%**			4902.00	180144.00	450.00	4902.00	126744.88	0.05
	46g	15	CTL	**0.24%**			6144.00	537615.00	450.00	4902.00	470686.36	0.20
	46h	14	CTL	**0.20%**			4032.00	441168.00	450.00	4902.00	397246.08	0.17
											2376727.20	1.00
47					15795.60	2.09%						
	47a	60	SVMP	**0.13%**			2511.00	125243.00	658.00	6916.00	98850.79	0.06
	47b	55	SVSP	**0.06%**			2392.00	70786.00	658.00	6916.00	45644.55	0.03
	47c	42	SVSP	**0.15%**			3960.00	160838.00	658.00	6916.00	119215.87	0.07
	47d	35	SVSP	**0.20%**			3774.00	198611.00	658.00	6916.00	158943.85	0.10
	47e	31	SVSP	**0.09%**			2600.00	94394.00	658.00	6916.00	67066.34	0.04
	47f	28	SVSP	**0.35%**			5106.00	325051.00	658.00	6916.00	271383.68	0.17
	47g	16	VNGF	**0.04%**			4104.00	75968.00	658.00	6916.00	32832.34	0.02
	47h	15	CTL	**0.57%**			5808.00	504756.00	658.00	6916.00	443710.21	0.27
	47i	14	CTL	**0.51%**			4560.00	448432.00	658.00	6916.00	400503.49	0.24
											1638151.13	1.00

48					10669.00	1.41%								
	48a	60	SVMP	**0.02%**			2068.00	38776.00	810.00	7899.00	18609.17	0.02		
	48b	45	SVSP	**0.08%**			3920.00	108855.00	810.00	7899.00	70627.74	0.06		
	48c	35	SVSP	**0.31%**			4600.00	316787.00	810.00	7899.00	271928.48	0.22		
	48d	31	SVSP	**0.07%**			1974.00	76404.00	810.00	7899.00	57153.84	0.05		
	48e	28	SVSP	**0.30%**			4601.00	307678.00	810.00	7899.00	262809.73	0.21		
	48f	16	VNGF	**0.05%**			3939.00	78400.00	810.00	7899.00	39987.46	0.03		
	48g	15	CTL	**0.32%**			4368.00	327555.00	810.00	7899.00	284958.91	0.23		
	48h	14	CTL	**0.26%**			4408.00	274675.00	810.00	7899.00	231688.84	0.19		
											1237764.17	1.00		
49					18507.10	2.45%								
	49a	120	NA	**0.01%**			2548.00	33111.00	616.00	6708.00	5364.27	0.00		
	49b	100	NA	**0.01%**			2772.00	36497.00	616.00	6708.00	6311.00	0.00		
	49c	50	LAAO	**0.62%**			7147.00	606036.00	616.00	6708.00	528207.95	0.26		
	49d	45	LAAO	**0.11%**			2835.00	120886.00	616.00	6708.00	90013.95	0.04		
	49e	35	SVSP	**0.38%**			4600.00	370467.00	616.00	6708.00	320374.79	0.15		
	49f	31	SVSP	**0.12%**			2178.00	125412.00	616.00	6708.00	101694.43	0.05		
	49g	28	SVSP	**0.44%**			5170.00	431310.00	616.00	6708.00	375010.71	0.18		
	49h	20	LAAO	**0.07%**			3880.00	98257.00	616.00	6708.00	56005.31	0.03		
	49i	16	CTL	**0.25%**			5123.00	268595.00	616.00	6708.00	212807.53	0.10		
	49k	15	CTL	**0.44%**			8360.00	464845.00	616.00	6708.00	373807.86	0.18		
											2069597.81	1.00		
50					18729.00	2.48%								
	50a	50	LAAO	**0.33%**			5474.00	311998.00	616.00	6607.00	253285.80	0.13		
	50b	45	SVSP	**0.04%**			2375.00	54727.00	616.00	6607.00	29253.58	0.02		
	50c	35	SVSP	**0.14%**			3102.00	139931.00	616.00	6607.00	106660.04	0.06		
	50d	31	SVSP	**0.14%**			2744.00	138835.00	616.00	6607.00	109403.82	0.06		
	50e	28	SVSP	**0.41%**			4752.00	359665.00	616.00	6607.00	308696.71	0.16		
	50f	17	CTL	**0.08%**			3234.00	97032.00	616.00	6607.00	62345.25	0.03		
	50g	16	CTL	**0.29%**			4968.00	269942.00	616.00	6607.00	216656.97	0.12		
	50h	15	CTL	**0.62%**			5883.00	536723.00	616.00	6607.00	473624.00	0.25		
	50i	13	CTL	**0.42%**			4560.00	370247.00	616.00	6607.00	321338.04	0.17		
											1881264.21	1.00		
51					13946.70	1.85%								
	51a	110	NA	**0.01%**			2208.00	36805.00	870.00	8921.00	14164.12	0.01		
	51b	50	LAAO	**0.16%**			4784.00	342290.00	870.00	8921.00	293234.75	0.16	0.560698335	51c
			SVMP	**0.13%**									0.439301665	
	51c	45	SVSP	**0.03%**			2700.00	55610.00	870.00	8921.00	27924.14	0.02		
	51d	35	SVSP	**0.07%**			3069.00	105957.00	870.00	8921.00	74487.40	0.04		
	51e	31	SVSP	**0.09%**			3232.00	124401.00	870.00	8921.00	91260.00	0.05		
	51f	28	SVSP	**0.26%**			4264.00	304289.00	870.00	8921.00	260565.85	0.14		
	51g	17	CTL	**0.26%**			4305.00	301902.00	870.00	8921.00	257758.43	0.14		
	51h	16	CTL	**0.22%**			3922.00	259345.00	870.00	8921.00	219128.72	0.12		
	51i	15	CTL	**0.36%**			5123.00	412433.00	870.00	8921.00	359901.64	0.20		
	51k	13	CTL	**0.24%**			4400.00	287161.00	870.00	8921.00	242043.30	0.13		
											1840468.35	1.00		
52					18237.90	2.41%								
	52a	70	NA	**0.02%**			2511.00	39483.00	332.00	3211.00	15197.39	0.01		
	52b	50	LAAO	**0.13%**			5151.00	278137.00	332.00	3211.00	228318.14	0.10	0.52927242	52c
			SVMP	**0.12%**									0.47072758	
	52c	45	SVSP	**0.05%**			3441.00	78990.00	332.00	3211.00	45709.73	0.02		
	52d	35	SVSP	**0.09%**			3705.00	122646.00	332.00	3211.00	86812.40	0.04		
	52e	31	SVSP	**0.09%**			2688.00	105120.00	332.00	3211.00	79122.51	0.04		
	52f	28	SVSP	**0.30%**			4410.00	320170.00	332.00	3211.00	277517.86	0.13		
	52g	25	SVSP	**0.06%**			3045.00	80653.00	332.00	3211.00	51202.71	0.02		
	52h	17	CTL	**0.22%**			4700.00	243121.00	332.00	3211.00	197664.07	0.09		
	52i	16	CTL	**0.19%**			4056.00	214083.00	332.00	3211.00	174854.64	0.08		
	52k	15	CTL	**0.61%**			6000.00	613890.00	332.00	3211.00	555859.88	0.25		
	52l	13	CTL	**0.55%**			6069.00	558704.00	332.00	3211.00	500006.53	0.23		
											2212265.87	1.00		
53					7322.10	0.97%								
	53a	60	LAAO	**0.21%**			5664.00	462541.00	475.00	4641.00	407200.74	0.22		

	53b	40	SVSP	**0.04%**			4158.00	122562.00	475.00	4641.00	81936.15	0.04
	53c	35	SVSP	**0.04%**			3672.00	115567.00	475.00	4641.00	79689.63	0.04
	53d	31	SVSP	**0.04%**			3328.00	111818.00	475.00	4641.00	79301.69	0.04
	53e	28	SVSP	**0.15%**			4558.00	328001.00	475.00	4641.00	283466.94	0.15
	53f	25	SVSP	**0.02%**			2943.00	65562.00	475.00	4641.00	36807.34	0.02
	53g	17	CTL	**0.02%**			3572.00	71189.00	475.00	4641.00	36288.68	0.02
	53h	16	CTL	**0.03%**			4343.00	96201.00	475.00	4641.00	53767.60	0.03
	53i	15	CTL	**0.23%**			5424.00	488362.00	475.00	4641.00	435366.67	0.23
	53k	13	CTL	**0.19%**			5244.00	418475.00	475.00	4641.00	367238.36	0.20
											1861063.80	1.00
54					43318.90	5.73%						
	54a	110	SVMP	**0.14%**			3131.00	132235.00	316.00	4021.00	92394.02	0.03
	54b	80	SVMP	**0.13%**			4142.00	135383.00	316.00	4021.00	82677.36	0.02
	54c	60	SVMP	**0.45%**			4104.00	342209.00	316.00	4021.00	289986.90	0.08
	54d	50	SVMP	**2.02%**			11468.00	1434056.00	316.00	4021.00	1288129.33	0.35
	54e	35	SVSP	**0.50%**			4214.00	371926.00	316.00	4021.00	318304.18	0.09
	54f	31	SVSP	**0.33%**			2626.00	245681.00	316.00	4021.00	212265.98	0.06
	54g	28	SVSP	**0.77%**			5100.00	556706.00	316.00	4021.00	491810.11	0.13
	54h	25	SVMP	**0.19%**			2304.00	149903.00	316.00	4021.00	120585.33	0.03
	54i	17	CTL	**0.06%**			3330.00	80945.00	316.00	4021.00	38571.80	0.01
	54k	16	CTL	**0.11%**			3939.00	118864.00	316.00	4021.00	68741.47	0.02
	54l	15	CTL	**0.65%**			5830.00	490230.00	316.00	4021.00	416045.09	0.11
	54m	13	CTL	**0.38%**			4928.00	305970.00	316.00	4021.00	243262.76	0.07
											3662774.34	1.00
55					50098.70	6.63%						
	55a	110	SVMP	**0.08%**			3298.00	86321.00	837.00	10757.00	43935.59	0.01
	55b	80	SVMP	**0.09%**			4242.00	107126.00	837.00	10757.00	52608.44	0.01
	55c	60	SVMP	**0.18%**			3132.00	141275.00	837.00	10757.00	101023.00	0.03
	55d	50	SVMP	**2.06%**			11424.00	1311402.00	837.00	10757.00	1164582.44	0.31
	55e	35	SVSP	**0.44%**			3955.00	301548.00	837.00	10757.00	250718.93	0.07
	55f	31	SVSP	**0.43%**			3240.00	283686.00	837.00	10757.00	242046.00	0.06
	55g	25	SVMP	**2.02%**			13908.00	1320604.00	837.00	10757.00	1141860.44	0.30
	55h	17	CTL	**0.12%**			3400.00	112863.00	837.00	10757.00	69166.70	0.02
	55i	16	CTL	**0.21%**			3762.00	164382.00	837.00	10757.00	116033.33	0.03
	55k	15	CTL	**0.80%**			5562.00	523454.00	837.00	10757.00	451972.00	0.12
	55l	13	CTL	**0.21%**			4160.00	170080.00	837.00	10757.00	116616.30	0.03
											3750563.19	1.00
				100.00%	755824.70	100.00%						

Table A3.5 Results of the single predictor binomial GLMs performed. The models relate the occurrence of each of the 10 polymorphic SDS-PAGE bands with each of the selected 14 predictors. For each predictor tested, Likelihood Ratio Chi-square (LR χ^2), degrees of freedom (Df), and associated p-values (*p*) are reported. Significant predictors and corresponding p-values are in bold. The asterisks (*) indicate unreliable model fit.

Band	**Predictor**	**LR χ^2**	**Df**	***p***
Band 1	**SVL**	5.251	1	**0.022**
	SEX	3.619	1	0.057
	COLOUR	1.852	3	0.604
	POPULATION	25.947	19	0.132
	GEN1	1.593	1	0.207
	GEN2	0.236	1	0.627
	BIO1	0.192	1	0.661
	BIO5	1.518	1	0.218
	BIO12	2.589	1	0.108
	BIO14	0.039	1	0.843
	AGRIC	0.373	1	0.542
	FOREST	3.571	1	0.059
	MOOR	0.329	1	0.566
	PASTURE	0.245	1	0.621
Band 2	SVL	< 0.001	1	0.993
	SEX	0.355	1	0.551
	COLOUR	3.437	3	0.329
	POPULATION	17.429	19	0.561
	GEN1	0.003	1	0.953
	GEN2	0.544	1	0.461
	BIO1	0.061	1	0.805
	BIO5	0.299	1	0.584
	BIO12	0.097	1	0.756
	BIO14	0.758	1	0.384
	AGRIC	1.250	1	0.264
	FOREST	2.876	1	0.089
	MOOR	0.012	1	0.915
	PASTURE	0.833	1	0.361
Band 3	SVL	0.037	1	0.846
	SEX	3.023	1	0.082
	COLOUR	4.379	3	0.223
	POPULATION	33.398	19	**0.021**
	GEN1	0.285	1	0.594
	GEN2	1.068	1	0.301
	BIO1	0.049	1	0.825
	BIO5	1.619	1	0.203
	BIO12	0.461	1	0.497
	BIO14	0.856	1	0.355
	AGRIC	1.069	1	0.301
	FOREST	1.373	1	0.241
	MOOR	0.055	1	0.815
	PASTURE	0.043	1	0.836
Band 4	SVL	1.342	1	0.247
	SEX	6.409	1	**0.011**
	COLOUR	1.338	3	0.720
	POPULATION	15.197	19	0.711
	GEN1	0.028	1	0.867
	GEN2	0.082	1	0.775
	BIO1	0.269	1	0.604
	BIO5	0.005	1	0.943
	BIO12	0.039	1	0.842
	BIO14	0.339	1	0.561
	AGRIC	4.934	1	**0.026**
	FOREST	1.208	1	0.272

	MOOR	1.016	1	0.313
	PASTURE	0.219	1	0.639
Band 5	SVL	0.003	1	0.958
	SEX	0.994	1	0.319
	COLOUR	2.837	3	0.417
	POPULATION	4.759	19	0.999
	GEN1	0.005	1	0.941
	GEN2	0.637	1	0.425
	BIO1	0.196	1	0.658
	BIO5	0.002	1	0.962
	BIO12	1.182	1	0.277
	BIO14	1.398	1	0.237
	AGRIC	0.691	1	0.406
	FOREST*	2.558	1	0.109
	MOOR*	0.411	1	0.522
	PASTURE*	1.135	1	0.287
Band 6	SVL	0.265	1	0.607
	SEX	0.003	1	0.953
	COLOUR	4.743	3	0.192
	POPULATION	22.252	19	0.272
	GEN1	2.851	1	0.091
	GEN2	0.071	1	0.791
	BIO1	0.789	1	0.374
	BIO5	0.563	1	0.453
	BIO12	0.200	1	0.655
	BIO14	0.170	1	0.680
	AGRIC	0.111	1	0.739
	FOREST	0.059	1	0.807
	MOOR*	2.154	1	0.142
	PASTURE	0.970	1	0.325
Band 7	SVL	1.990	1	0.158
	SEX	0.166	1	0.684
	COLOUR	15.338	3	**0.002**
	POPULATION	32.670	19	**0.026**
	GEN1	2.650	1	0.104
	GEN2	0.593	1	0.441
	BIO1	0.104	1	0.747
	BIO5	1.909	1	0.167
	BIO12	0.012	1	0.914
	BIO14	0.359	1	0.549
	AGRIC	1.210	1	0.271
	FOREST	3.562	1	0.059
	MOOR	1.950	1	0.163
	PASTURE	0.021	1	0.884
Band 8	**SVL**	4.118	1	**0.042**
	SEX	1.016	1	0.313
	COLOUR	8.948	3	**0.029**
	POPULATION	17.026	19	0.588
	GEN1	0.004	1	0.946
	GEN2	0.057	1	0.811
	BIO1	0.513	1	0.474
	BIO5	6.817	1	**0.009**
	BIO12	4.971	1	**0.026**
	BIO14	1.583	1	0.208
	AGRIC*	5.046	1	**0.025**
	FOREST	1.311	1	0.252
	MOOR	0.259	1	0.610
	PASTURE	0.077	1	0.782
Band 9	SVL	2.193	1	0.139
	SEX	8.152	1	**0.004**
	COLOUR	7.086	3	0.069
	POPULATION	22.704	19	0.251

	GEN1	0.597	1	0.439
	GEN2	4.256	1	**0.039**
	BIO1*	22.704	1	**< 0.001**
	BIO5	0.244	1	0.621
	BIO12	3.601	1	0.058
	BIO14	2.161	1	0.142
	AGRIC	1.282	1	0.258
	FOREST	0.053	1	0.818
	MOOR*	1.702	1	0.192
	PASTURE*	4.742	1	**0.029**
Band 10	SVL	2.141	1	0.143
	SEX	0.035	1	0.852
	COLOUR	15.225	3	**0.002**
	POPULATION	34.368	19	**0.017**
	GEN1	0.017	1	0.895
	GEN2	0.949	1	0.329
	BIO1	0.123	1	0.726
	BIO5	4.131	1	**0.042**
	BIO12	2.646	1	0.104
	BIO14	0.298	1	0.585
	AGRIC	0.008	1	0.930
	FOREST	8.147	1	**0.004**
	MOOR*	5.135	1	**0.023**
	PASTURE	0.084	1	0.772

Figure A3.1 The five geographically structured colour phenotypes currently recognised within *V. seoanei*. Viper pictures modified from Martínez-Freiría et al., 2017.

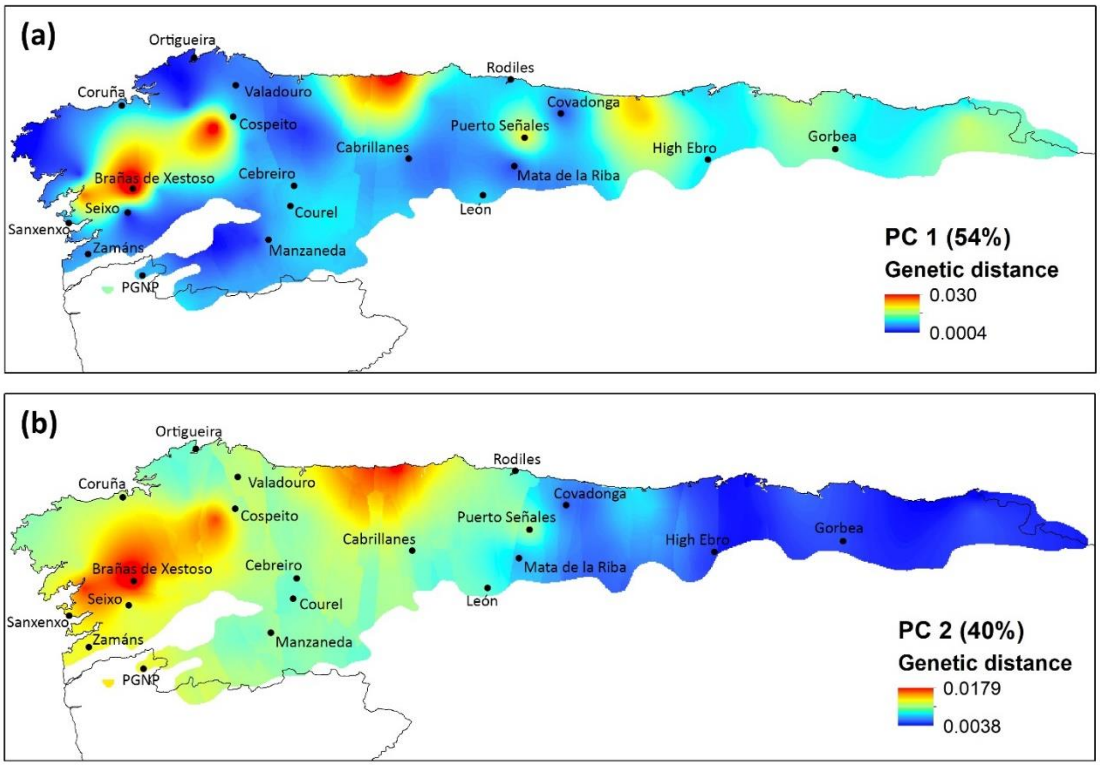


Figure A3.2 Geographic genetic variation in *V. seoanei*. First (a) and second (b) components of the Spatial Principal Component Analysis performed on the calculated genetic distances. Sampling localities are reported.

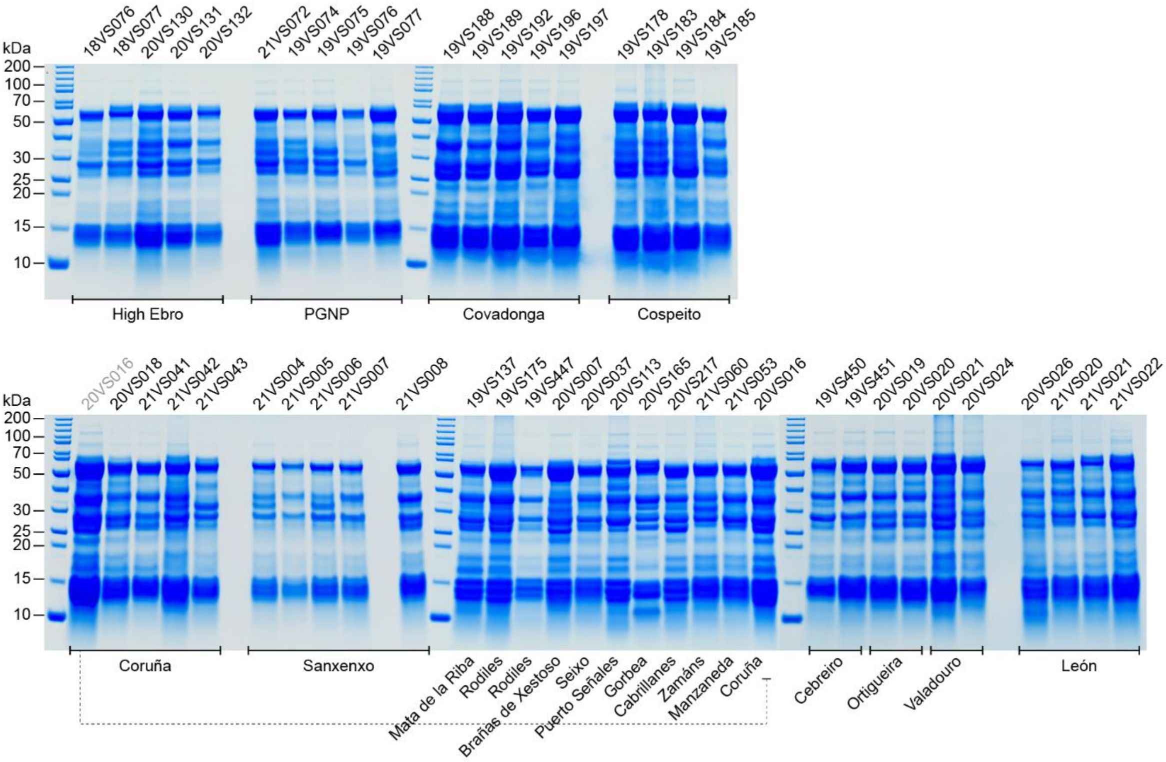


Figure A3.3 Whole venom profiles of the 49 *V. seoanei* specimens pooled to produce the reference proteome, under reducing conditions. Venom sample 20VS016 was loaded twice because of the low quality of the profile obtained with the first electrophoretic run (code reported in grey). Localities of collection of the samples are reported

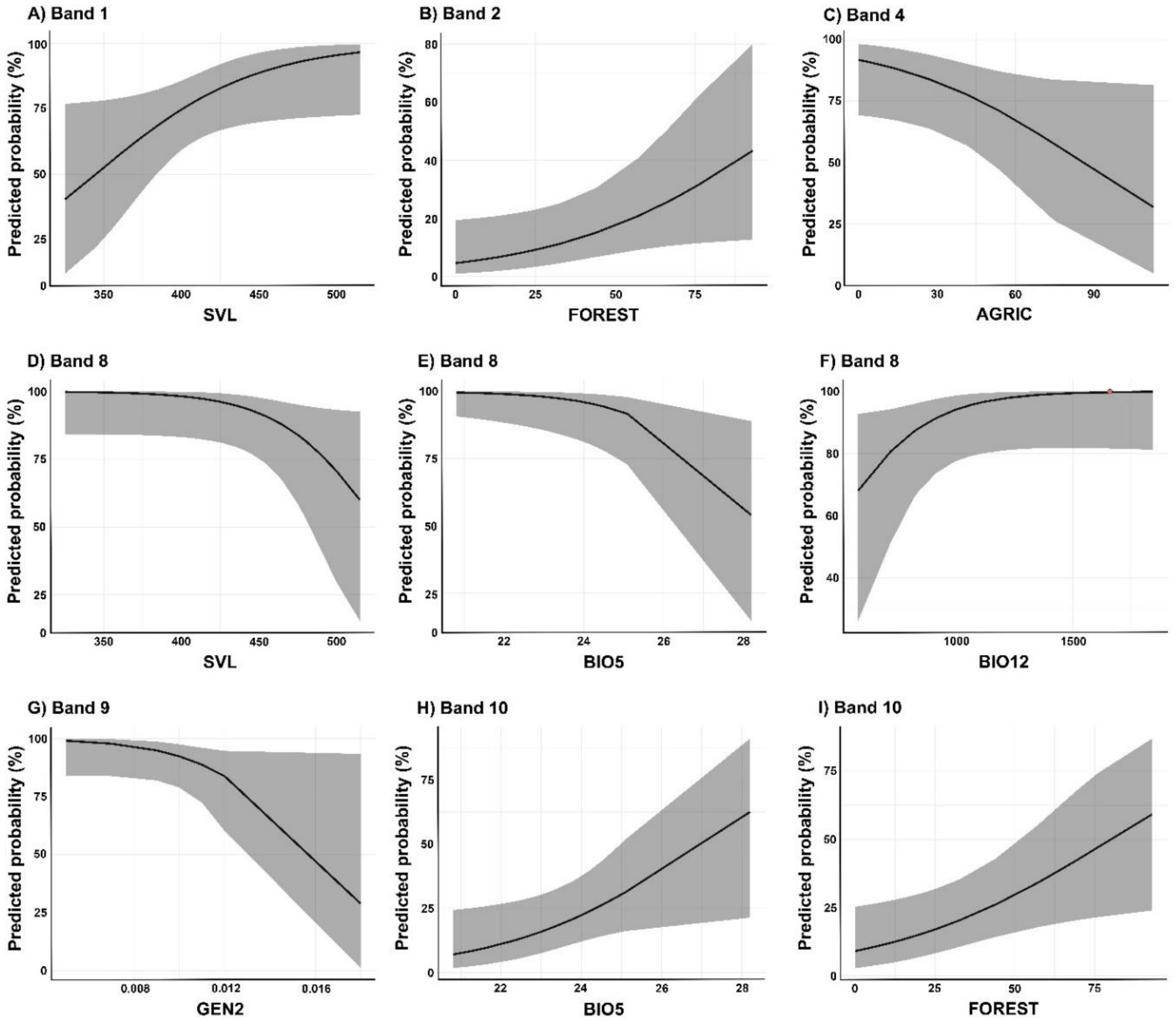


Figure A3.4 Model predictions of occurrence of bands 1, 2, 4, 8, 9 and 10 in individual SDS-PAGE venom profiles in relation to the continuous predictors tested in single predictor GLMs. The panels display the predicted probability of occurrence of: band 1 in relation to SVL (A); band 2 in relation to FOREST (B); band 4 in relation to AGRIC (C); band 8 in relation to SVL (D), BIO5 (E), and BIO12 (F); band 9 in relation to GEN2 (G); band 10 in relation to BIO5 (H) and FOREST (I).