

Concise Chemoenzymatic Total Synthesis and Identification of Cellular Targets of Cepafungin I

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Concise Chemoenzymatic Total Synthesis and Identification of Cellular Targets of Cepafungin I

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Abstract: The natural product cepafungin I was recently reported to be one of the most potent covalent inhibitors of the 20S proteasome core particle through a series of in vitro activity assays. Here, we report a short chemoenzymatic total synthesis of cepafungin I featuring the use of a regioselective enzymatic oxidation to prepare a key hydroxylated amino acid building block in a scalable fashion. The strategy developed herein enabled access to a chemoproteomic probe, which in turn revealed the exceptional selectivity and potency of cepafungin I towards the β 2 and β 5 subunits of the proteasome. Further structure-activity relationship studies suggest the key role of the hydroxyl group in the macrocycle and the identity of the lipid tail in modulating the potency of this natural product family. This study lays the groundwork for further medicinal chemistry exploration to fully realize the anticancer potential of cepafungin I.

Introduction

Cepafungin I and glidobactin A are two macrolactams belonging to a larger family of natural products called the syrbactins (Fig. 1). Members of this family share a common 12-membered macrolactam core consisting of a vinylogous amino acid and a lysine residue that may exist in various oxidation states. Further diversity can be found within the tail portion of the natural products: while the cepafungins and the glidobactins possess unsaturated fatty acid tails, all syrbactins contain a Val-Val unit that is linked via a unique ureido moiety.¹ Initial biological evaluation suggested that the glidobactins and the cepafungins exhibit moderate antifungal activity and potent antitumor activity against P388 leukemia in mice.^{2a,b} More recently, it has been determined that the latter activity arises from inhibition of the 20S proteasome core particle (CP) via covalent engagement of two distinct catalytically-active Thr10^y residues by the unsaturated lactam motif of the macrocycle.³ Cepafungin I, in particular, exhibits remarkably strong inhibitory activity relative to all known proteasome inhibitors to date (IC₅₀ of 4 nM against the β 5 subunit of yeast CP).⁴ The proteasome is a multiprotein complex that plays a critical role in protein degradation. Given the centrality of the proteasome in the regulation of cell cycle and apoptosis, its inhibition constitutes a promising modality for cancer therapy. In support of this notion, three proteasome inhibitors, bortezomib, carfilzomib and ixazomib, have been approved by the U.S. Food and Drug Administration for the treatment of multiple myeloma. However, both bortezomib and carfilzomib have been reported to exhibit several side effects such as thrombocytopenia and high occurrence of relapse and chemoresistance have also been reported.⁵ Thus, there is still an urgent need to advance new proteasome inhibitors as drug candidates that will address these issues.

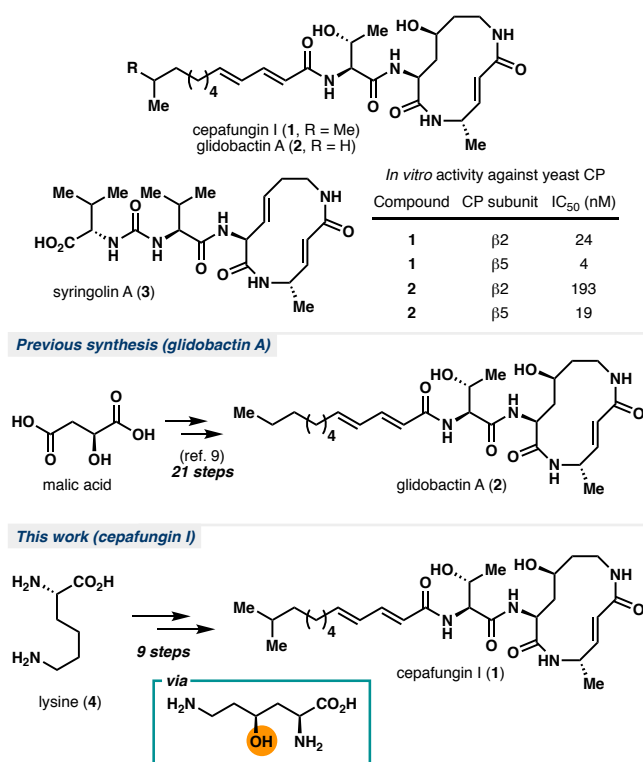


Figure 1. The syrbactins family of natural products, their respective inhibitory activities on the 20S proteasome, prior approach to glidobactin A and our synthetic strategy towards cepafungin I.

Similar to bortezomib, the syrbactins trigger apoptosis by eliciting p53 accumulation and inhibiting NF- κ B activity.¹ Pioneering studies by Bachmann and co-workers using a syrbactin derivative additionally showed that while this compound exhibited cytotoxic effects on cancer cell lines, the effect was most pronounced in multiple myeloma.⁶ Recent research has begun to elucidate certain resistance mechanisms in multiple myeloma. While current proteasome inhibitors primarily inhibit the β 5 subunit, it has been shown that co-inhibition of the β 2 subunit prevents recovery of proteasome activity by causing aggregation/inactivation of the proteasomal transcription factor Nrf1. Notably, the cytotoxicities of bortezomib and carfilzomib towards solid tumor cells (e.g., triple negative breast cancer) are significantly enhanced in this manner, whereas either drug had otherwise not shown clinical efficacy on its own. Moreover, co-inhibition of β 5 with β 2 provides a stronger antineoplastic effect than with β 1, highlighting the importance of advancing new proteasome inhibitors with equipotent activity for these subunits.^{7,8} Cepafungin I, with its low nanomolar activity towards β 5 and β 2 (IC₅₀ = 4 nM and 24 nM, respectively), stands as an attractive candidate for such purpose.

A seminal work by Schmidt and coworkers in 1992 established the first total synthesis of glidobactin A.⁹ Starting from malic acid, the synthesis of the natural product was achieved in 21 steps. While a landmark achievement, this approach suffers from high step count due to inefficient functional group interconversions and extraneous protecting group manipulations. For example, the synthesis of the key 4-hydroxylysine moiety took place in 12 steps from malic acid, featuring HWE homologation, asymmetric hydrogenation and displacement of the terminal alcohol with NaN₃. Efforts by Ichikawa,^{10a,b,c} Pirrung,¹¹ Stephenson¹² and others^{13a,b,c,d} have established viable synthetic routes to the syrbactins. However, these routes would not be amenable to the introduction of the key 2° alcohol within the embedded lysine unit.

Results and Discussion

Similar to previous studies, we recognized that an efficient route to 4-hydroxylysine (or its synthetic equivalent) would hold the key to the development of a practical synthesis of cepafungin I. If such a route could be identified, iterative condensations with alanine and an acetate equivalent would rapidly generate the macrocyclic core of the natural product. We have previously established the biosynthetic origin of the 4-hydroxylysine moiety of glidobactin A.¹⁴ Within the pathway, a nonheme dioxygenase, GlbB, catalyzes the direct C-H hydroxylation of free-standing lysine at the C4 position prior to loading of the product onto the nonribosomal peptide synthetase assembly line. Substrate scope examination of GlbB revealed that while the enzyme exhibits a narrow substrate specificity, it is able to hydroxylate lysine with remarkably high catalytic efficiency. In our hands, however, large-scale biocatalytic hydroxylation with purified GlbB was hampered by poor scalability as the reaction gave poor conversion when conducted at > 100 mg scale. While this issue could be solved by conducting the reaction with clarified lysate of cells expressing GlbB, the poor soluble expression of GlbB led to sub-optimal titer (Fig. 2). Gratifyingly, co-expression of chaperones GroES/EL was found to increase soluble expression of GlbB, which translates to ca. 5-fold improvement in reaction conversion and yield on small scale. For large scale reactions, ca. 6–7 g of lysine could be fully converted to its C4-hydroxylated counterpart in a single pass with 1 L of clarified cell lysate (final OD₆₀₀ = 12.5), corresponding to a titer of ca. 6–7 g/L based on the original volume of the expression culture.

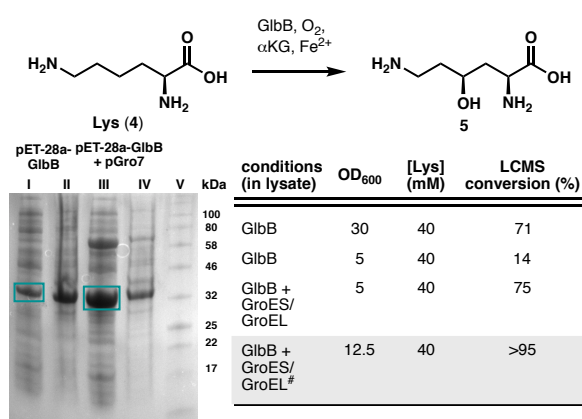
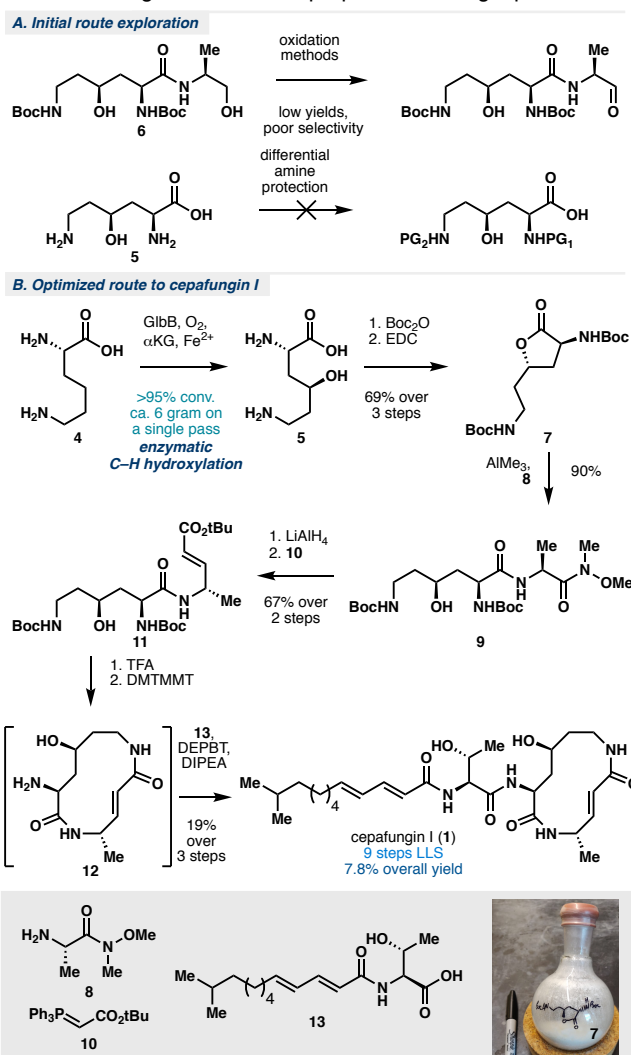


Figure 2. Optimization of preparative scale hydroxylation of **4** with GlbB. Co-expression of chaperones GroES/GroEL was found to improve the soluble

expression of GlbB, resulting in ca. 5-fold improvement in reaction conversion. Lanes (I) and (III): soluble fraction, lanes (II) and (IV): insoluble fraction, lane (V): protein ladder. [#]Reaction conducted at 6 gram scale.

Having solved the material throughput issue for the production of **5**, we turned our attention to its conversion to the macrocyclic core of **1**. We have previously described the conversion of **5** to intermediate **6** by way of coupling with alaninol.¹⁴ However, attempts to selectively oxidize the 1° alcohol of **6** were beset by low yields and poor selectivity (**Scheme 1A**). Similarly, attempts to effect differential protections of the α - and ϵ -amine proved problematic due to the presence of the C4-OH. An alternative route was thus devised to circumvent these issues (**Scheme 1B**). Lactone **7**, prepared routinely on multi-gram scale in 3 steps from lysine, was reacted with Weinreb amide **8** in the presence of AlMe₃ to afford dipeptide **9** in 90% yield. Treatment of **9** with LiAlH₄ effected a clean reduction of the Weinreb amide moiety to the corresponding aldehyde without any observable over-reduction or side reactivity with any of the carbonyl groups in the molecule. Olefination with Wittig reagent **10** furnished enoate **11**, which constitutes the protected linear form of the target macrocyclic core. As a testament to the robustness of the route, more than 1.5 g of **11** could be prepared in a single pass.



Scheme 1. Chemoenzymatic total synthesis of cepafungin I (**1**) starting from **4**. (A). Failed routes towards **1** from **5** or **6**. (B) Final synthetic route to **1** featuring AlMe₃-assisted aminolysis of lactone **7**.

While global deprotection of **11** could be achieved cleanly under acidic conditions, the subsequent macrolactamization step required extensive optimization (See **Table S1** for optimization). This observation was in line with previous efforts in the total synthesis of glidobactin A and the syrbactins where late-stage macrolactamization typically proceeded in less than 30% yield.^{9,12,13a,c,d} Eventually, DMTMMT was identified as the optimal coupling reagent, providing ~60% NMR yield of the desired macrolactam.¹⁵ Due to the high polarity of **12**, we elected to bypass any purification step and used the compound in a crude form for subsequent coupling with the fully elaborated tail fragment **13**. Extensive screening of peptide coupling conditions (**Table S2**) eventually identified DEPBT as an optimal coupling reagent for this step, leading to the formation of the target natural product in 19% yield from **11**. Overall, our chemoenzymatic synthesis of cepafungin I proceeded in 9 steps (longest linear sequence) and 7.9% overall yield from lysine. By virtue of this chemoenzymatic strategy, our route provides exceptionally rapid access to the key hydroxylysine residue and overcomes longstanding challenges associated with synthetic access to syrbactins bearing 2° alcohol at the L-lysine fragment. This route also highlights DMTMMT as a superior macrolactamization reagent to construct the strained 12-membered ring. Finally, the modularity of this route enables the rapid construction of synthetic analogs and chemoproteomic probes for further biological evaluation (*vide infra*).

Multiple myeloma (MM) has remained the main indication for clinical trials of novel proteasome inhibitor drug candidates since the FDA approval of the first-in-class drug Velcade (bortezomib) in 2003.¹⁶ Accordingly, we started our biological investigations with cytotoxicity measurements of **1** in the commonly used MM cell lines RPMI 8226 and MM1.R to evaluate its potential as a cancer drug candidate. Cells were treated with various concentrations of **1** for 24 h or 48 h and the percentage of viable cells was determined via the WST-1 assay (**Fig. 3A**). Indeed, **1** proved potently toxic and the measured cytotoxicity after 48 h treatment (EC₅₀s of 31 nM for RPMI 8226 and 23 nM for MM1.R) aligned well with the previously reported data for clinical proteasome inhibitor drugs bortezomib (30 nM for RPMI 8226; 3 nM for MM1.R¹⁷) and carfilzomib (5 nM for RPMI 8226¹⁸). Although **1** and structurally related natural products have previously been shown to inhibit proteasomal subunits PSMB2 (β2) and PSMB5 (β5) in purified yeast⁴ and mammalian¹⁹ proteasomes, direct target engagement of proteasomes by the syrbactins in mammalian cells has not yet been shown. Accordingly, we decided to perform a deep profiling of cellular targets of **1** using a classical chemoproteomics approach. For this purpose, we synthesized probe **14**, an alkyne-tagged derivative of **1** (**Fig. 3**). RPMI 8226 lysates were treated with increasing concentrations of **14** for 1 h at r.t. and the probe-labeled proteins were then conjugated to TAMRA azide using copper(I)-catalyzed alkyne-azide cycloaddition (CuAAC)²⁰, separated by SDS-PAGE and visualized by in-gel fluorescence scanning (**Fig. S1A**). The gel profile revealed only a few bands, thus suggesting low proteomic promiscuity of **14**. To examine whether **14** can be used as a clickable analog of **1**, we performed a gel-based competitive profiling experiment. RPMI 8226 cells were treated *in situ* with

various concentrations of **1** for 6 h, lysed, and then treated with 10 μM **14** for 1 h, followed by TAMRA conjugation and protein visualization, as described above (**Figs. 3B, S1B**). Excitingly, only a few bands were successfully competed at nanomolar concentrations, suggesting high potency and selectivity of **1** towards its targets. To identify the competed protein targets, we performed an *in situ* competitive LC-MS/MS-based experiment. Briefly, RPMI 8226 cells were treated with 100 nM **1** for 6 hours, lysed, then treated with 10 μM **14** followed by CuAAC-mediated conjugation of biotin azide, enrichment with streptavidin beads, trypsin digestion, and LC-MS/MS analysis. Out of 764 proteins enriched by **14**, only 5 were >50% competed by **1** (**Figs. 3C, 3D; Table S1**). Strikingly, all 5 identified targets were 20S proteasome subunits: PSMB5, PSMB10, PSMA5, PSMB1, and PSMB2. Such high selectivity is remarkable, especially considering that the structure of **1** contains two electrophilic α, β-unsaturated amides that could potentially engage hundreds of reactive cysteines.²¹

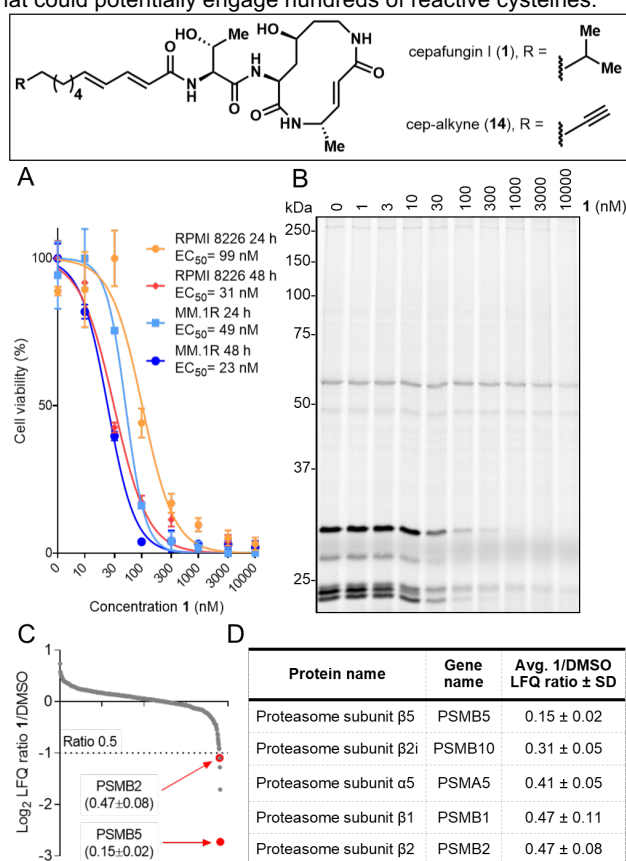


Figure 3. Cytotoxicity and cellular target identification of cepafungin I. (A) Cytotoxicity curves of RPMI 8226 and MM1.R cells treated with indicated concentrations of **1** for 24 or 48 hours. Quantification was performed using the WST-1 assay (relative values ± SD and EC₅₀s; *n* = 3). (B) Gel-based competitive *in situ* profiling of targets of **1**. RPMI 8226 cells were treated with various concentrations of **1** for 6 h, lysed, and treated with 10 μM **14**. (C) Log₂ LFQ ratios of proteins identified from the *in situ* competitive pull-down experiment with 100 nM **1** or DMSO and with 10 μM **14** (*n* = 6, three biologicals and two technicals each). (D) Cellular targets of **1** (>50% competition) in RPMI 8226 cells. Quantification was performed using the label-free quantification (LFQ) method (*n* = 6).

We chose to further validate the engagement of PSMB2 (Proteasome 20S Subunit β2) and PSMB5 (Proteasome 20S Subunit β5) by **1**, because their chemical co-inhibition has been

shown to be particularly cytotoxic in proteasome inhibitor-resistant MM cells and has therefore emerged as a promising therapeutic strategy.²² To confirm PSMB2 and PSMB5 as targets, both proteins were cloned as FLAG-tagged versions and overexpressed in HEK293T cells. PSMB2 and PSMB5-expressing cells were lysed and the lysates labeled with 30 μ M **14** for 1 h, followed by conjugation to TAMRA azide, separation by SDS-PAGE, and visualization of probe-bound proteins by in-gel fluorescence scanning (Figs. 4A, S2). A new labeled band was clearly seen in the overexpressed lane of both gels, indicating successful labeling of both overexpressed proteins, PSMB2-F and PSMB5-F. Having confirmed both proteins as targets of cepafungin I, we successfully assigned the fluorescence bands in the gel profile of **14** to respective proteasome subunits as previously described^{18,23,24} and quantified the *in situ* IC₅₀ values of **1** for the endogenously expressed proteasome subunits, yielding IC₅₀s of 7.5 nM for PSMB5 and 35 nM for PSMB2 (Figs. S3A, B). Interestingly, these values only slightly deviate from previously reported IC₅₀s for inhibition of purified yeast proteasome subunits by **1** (PSMB5: 4 nM; PSMB2: 24 nM⁴). In order to gain more insight into the structure-activity relationship between **1** and PSMB5, we synthesized several derivatives of **1** (Fig. 4) and compared their ability to inhibit β 5 activity in RPMI 8226 cells. Cells were treated with various concentrations of compounds for 6 hours, then lysed and treated with the fluorogenic β 5 subunit-selective fluorogenic substrate Suc-LLVY-AMC.²⁵ Release of the 7-Amino-4-methylcoumarin (AMC) fluorophore via proteolytic cleavage by β 5 was followed over time and quantified to obtain IC₅₀ values (Fig. 4B). From all compounds tested, **1** most potently inhibited the β 5 subunit activity. In agreement with prior work,⁴ terminal methyl branching in **1** leads to a nearly fivefold increase in β 5 inhibitory activity compared to **2** (glidobactin A). The difference in potency between **15** (desoxycepafungin) and **1**, over tenfold loss, is in agreement with a recently reported potency difference between **2** and its corresponding desoxy-macrocyclic variant luminmycin A.¹⁹ Additionally, **16** (saturated cepafungin) demonstrated a fourteen-fold loss in potency compared to **1**. These results suggest that the secondary alcohol on the macrocycle and the 2,4-dienamide motif on the tail region of **1** are critical for the β 5 inhibitory activity. Next, we sought to investigate if **1** mediates the expected biological downstream response similar to other proteasome inhibitors. One of the key cellular responses of proteasome inhibition is the accumulation of polyubiquitinated proteins, gradually leading to dysfunction and apoptosis.²⁶ Indeed, Western blot of lysates from **1**-treated RPMI 8226 cells using a mono-/poly-ubiquitin-conjugate specific antibody showed a concentration-dependent increase in ubiquitinated proteins (Fig. 4C). Next, we probed the same lysates by Western blot for Poly(ADP-Ribose) Polymerase (PARP-1) and observed PARP-1 cleavage in **1**-treated samples, indicating that **1** induced apoptotic cell death (Fig. 4C).²⁷ Finally, we performed a global proteomics experiment to identify proteins that accumulate or are upregulated in RPMI 8226 cells upon **1** treatment in comparison to the treatment with the clinical proteasome inhibitor drug bortezomib (BTZ). Cells were treated for 14 h with either **1** or BTZ at concentrations matching their corresponding EC₅₀ values at the 24 h timepoint (Figs. 3A, S4). Cells were lysed, proteins digested, and peptides analyzed by LC-MS/MS. Out of 3700 quantified proteins, 88 proteins were significantly upregulated (FDR 0.05; S₀ 0.01) in **1**-treated samples and 25 in BTZ-treated samples compared to

DMSO control samples (Figs. 4D, S5; Table S4). Indeed, 19 of 25 proteins upregulated in BTZ-treated samples, were also upregulated in proteomic samples from **1**-treated cells, thus confirming highly similar mode of action for these two compounds. Notably, 11 out of these 19 common targets have previously been reported to be upregulated upon proteasome inhibition in general (HERPUD1,²⁸ KIAA0101, RRM2,²⁹ CDC6,³⁰ CCNB1,³¹ NUSAP1,³² ORC1,³³ CYBA,³⁴ CKAP2,³⁵ KRT18,³⁶ TPX2³⁷) and 5 more targets (BAG3,³⁸ SRXN1, HMOX1, SQSMT1,³⁹ HSPA1A/B⁴⁰) specifically upon bortezomib treatment. Altogether, our data show that **1** is a potent and highly selective covalent inhibitor of the 20S proteasome that mediates downstream effects similar to the clinical drug BTZ in multiple myeloma cells.

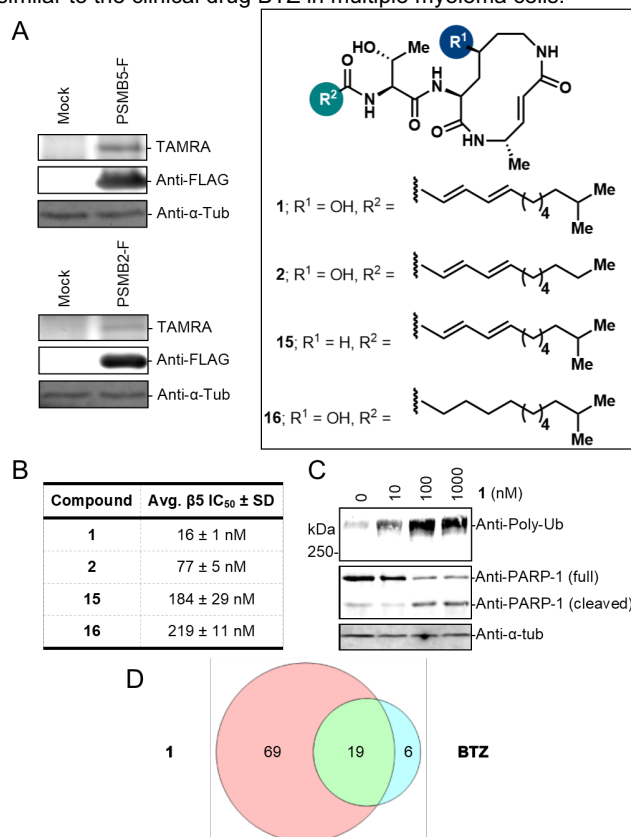


Figure 4. Validation of target engagement, structure-activity relationship, and downstream effects of **1**. (A) Labeling of mock and overexpressed PSMB2-FLAG and PSMB5-FLAG in HEK293T lysate with 30 μ M **14**. Shown are the TAMRA fluorescence profile of **14** (top), Western blot membrane probed for FLAG (middle), and α -tubulin as a loading control (bottom). See also Fig. S2. (B) *In situ* inhibition of chymotrypsin-like (β 5) proteasome activity by **1** and its derivatives. RPMI 8226 cells were treated with various concentrations of compounds for 6 h, lysed, treated with 100 μ M fluorogenic substrate Suc-LLVY-AMC, and incubated for 2 hours at 37 $^{\circ}$ C. IC₅₀ values were quantified based on A_{360EX}/A_{460EM} readouts ($n = 3$). (C) Western blotting of lysates obtained from RPMI 8226 cells treated with various concentrations of **1** for 6 h. Membranes were probed for mono- and poly-ubiquitin, PARP-1, and α -tubulin as a loading control. (D) Venn diagram representing the overlap in significantly upregulated proteins (FDR 0.05; S₀ 0.01) upon 14 h treatment of RPMI 8226 cells with 100 nM **1** or 2.5 nM BTZ versus vehicle. Quantification was performed using label-free quantification (LFQ) method ($n = 6$).

Conclusion

By harnessing the ability of G1bB to hydroxylate L-lysine in a selective and efficient fashion, we have developed a concise chemoenzymatic synthesis of cepafungin I. Despite challenges in the late-stage macrocyclization and amide coupling steps, cepafungin I could be obtained in ca. 8% yield over 9 steps (longest linear sequence). The modularity of this route allowed the development of a chemoproteomic probe to interrogate the cellular targets of cepafungin I. Our chemoproteomics studies revealed that cepafungin I is able to covalently engage 20S proteasome subunits PSMB2 and PSMB5 with exceptional selectivity and that cepafungin I elicit many similar downstream biological responses to the clinically-approved proteasome inhibitor drug bortezomib. Contemporaneous to our efforts, Böttcher and co-workers reported the development of an activity-based probe by derivatization of syringolin A that was obtained from its native producer and showed the ability of the syrbactins to coinhibit PSMB2 and PSMB5 with high potency.¹⁹ Complementary to Böttcher's findings, our work provides the first proteome-wide identification of syrbactin protein targets in cancer cells and validation of their downstream biological effects via in-depth quantitative proteomics analyses. Moreover, the synthetic strategy developed herein enabled access to both natural and unnatural cepafungin analogs for initial structure-activity relationship studies. Especially notable in this regard is the observation that the macrocyclic secondary alcohol, as well as the degree of unsaturation and the terminal branching of the lipid tail, are critical for high inhibitory potency. Further medicinal chemistry exploration featuring the use of other hydroxylated amino acids⁴¹ and alternative lipid tails is ongoing in our laboratory.

Acknowledgements

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Keywords: syrbactin • natural product • proteasome inhibitor • covalent inhibitor • chemoproteomics

- [1] D. Krahn, C. Ottmann, M. Kaiser, *Nat. Prod. Rep.* **2011**, *28*, 1854–1867.
- [2] (a) M. Oka, Y. Nishiyama, S. Ohta, H. Kamei, M. Konishi, T. Miyaki, T. Oki, H. Kawaguchi, *J. Antibiot.* **1988**, *41*, 1331–1337; (b) J. Shoji, H. Hino, T. Kato, T. Hattori, K. Hirooka, K. Tawara, O. Shiratori, Y. Terui, *J. Antibiot.* **1990**, *43*, 783–787.
- [3] M. Groll, B. Schellenberg, A. S. Bachmann, C. R. Archer, R. Huber, T. K. Powell, S. Lindow, M. Kaiser, R. A. Dudler, *Nature* **2008**, *452*, 755–758.
- [4] M. L. Stein, P. Beck, M. Kaiser, R. Dudler, C. F. W. Becker, M. Groll, *Proc. Natl. Acad. Sci. USA* **2012**, *109*, 18367–18371.
- [5] T. A. Guerrero-Garcia, S. Gandolfi, J. P. Laubach, T. Hideshima, D. Chauhan, C. Mitsiades, K. C. Anderson, P. G. Richardson, *Expert Rev. Proteomics* **2018**, *15*, 1033–1052.
- [6] C. R. Archer, M. Groll, M. L. Stein, B. Schellenberg, J. Clerc, M. Kaiser, T. P. Kondratyuk, J. M. Pezzuto, R. Dudler, A. S. Bachmann, *Biochemistry* **2012**, *51*, 6880–6888.
- [7] E. S. Weyburne, O. M. Wilkins, Z. Sha, D. A. Williams, A. A. Pletnev, G. de Bruin, H. S. Overkleeft, A. L. Goldberg, M. D. Cole, A. F. Kisselev, *Cell. Chem. Biol.* **2017**, *24*, 218–230.
- [8] R. Oerlemans, N. E. Franke, Y. G. Assaraf, J. Cloos, I. Van Zantwijk, C. R. Berkens, G. L. Scheffer, K. Debipersad, K. Votjekova, C. Lemos, J. W. van der Heijden, B. Ylstra, G. J. Peters, G. L. Kaspers, B. A. Dijkmans, R. J. Scheper, G. Jansen, *Blood* **2008**, *112*, 2489–2499.
- [9] U. Schmidt, A. Kleefeldt, R. Mangold, *J. Chem. Soc. Chem. Commun.* **1992**, 1687–1689.
- [10] (a) T. Chiba, H. Hosono, K. Nakagawa, M. Asaka, H. Takeda, A. Matsuda, S. Ichikawa, *Angew. Chem. Int. Ed.* **2014**, *53*, 4836–4839; (b) S. Kitahata, F. Yakushiji, S. Ichikawa, *Chem. Sci.* **2017**, *8*, 6959–6963; (c) S. Kitahata, T. Chiba, T. Yoshida, M. Ri, S. Iida, A. Matsuda, S. Ichikawa, *Org. Lett.* **2016**, *18*, 2312–2315.
- [11] M. C. Pirrung, G. Biswas, T. R. Ibarra-Rivera, *Org. Lett.* **2010**, *12*, 2402–2405.
- [12] C. Dai, C. R. J. Stephenson, *Org. Lett.* **2010**, *12*, 3453–3455.
- [13] (a) M. Oka, K. Yaginuma, K. Numata, M. Konishi, T. Oki, H. Kawaguchi, *J. Antibiot.* **1988**, *41*, 1338–1350; (b) M. Oka, K.-I. Iwata, Y. Nishiyama, H. Kamei, M. Konishi, T. Oki, H. Kawaguchi, *J. Antibiot.* **1988**, *41*, 1812–1822; (c) J. Clerc, M. Groll, D. J. Ilich, A. S. Bachmann, R. Huber, B. Schellenberg, R. Dudler, M. Kaiser, *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 6507–6512; (d) J. Clerc, B. Schellenberg, M. Groll, A. S. Bachmann, R. Huber, R. Dudler, M. Kaiser, *Eur. J. Org. Chem.* **2010**, 3991–4003.
- [14] A. Amatuni, H. Renata, *Org. Biomol. Chem.* **2019**, *17*, 1736–1739.
- [15] Z. J. Kamiński, B. Kolesińska, G. Sabatino, M. Chelli, P. Rovero, M. Blaszczak, M. L. Głowska, A. M. Papini, *J. Am. Chem. Soc.* **2005**, *127*, 16912–16920.
- [16] E. E. Manasanch, R. Z. Orlowski, *Nat. Rev. Clin. Oncol.* **2017**, *14*, 417–433.
- [17] T. Hideshima, P. Richardson, D. Chauhan, V. J. Palombella, P. J. Elliott, J. Adams, K. C. Anderson, *Cancer Res.* **2001**, *61*, 3071–3076.
- [18] D. J. Kuhn, Q. Chen, P. M. Voorhees, J. S. Strader, K. D. Shenk, C. M. Sun, S. D. Demo, M. K. Bennett, F. W. van Leeuwen, A. A. Chanan-Khan, R. Z. Orlowski, *Blood* **2007**, *110*, 3281–3290.
- [19] A. Pawar, M. Basler, H. Goebel, G. O. Alvarez Salinas, M. Groettrup, T. Böttcher, *ACS Cent. Sci.* **2020** DOI:10.1021/acscentsci.9b01170.
- [20] A. E. Speers, B. F. Cravatt, *Chem. Biol.* **2004**, *11*, 535–546.
- [21] D. Abegg, R. Frei, K. Cerato, D. Prasad Hari, C. Wang, J. Waser, A. Adibekian, *Angew. Chem. Int. Ed.* **2015**, *54*, 10852–10857.
- [22] A. Besse, L. besse, M. Kraus, M. Mendez-Lopez, J. Bader, B.-T. Xin, G. de Bruin, E. Maurits, H. S. Overkleeft, C. Driessen, *Cell Chem. Biol.* **2019**, *26*, 340–351.
- [23] M. Altun, P. J. Galardy, R. Shringarpure, T. Hideshima, R. LeBlanc, K. C. Anderson, H. L. Ploegh, B. M. Kessler, *Cancer Res.* **2005**, *65*, 7896–7901.
- [24] M. Britton, M. M. Lucas, S. L. Downey, M. Screen, A. A. Pletnev, M. Verdoes, R. A. Tokhunts, O. Amir, A. L. Goddard, P. M. Pelphrey, *Chem. Biol.* **2009**, *16*, 1278–1289.
- [25] P. Maher, *Bio Protoc.* **2014**, *4*, e1028.
- [26] J. Adams, *Nat. Rev. Cancer* **2004**, *4*, 349–360.
- [27] S. H. Kaufmann, S. Desnoyers, Y. Ottaviano, N. E. Davidson, G. G. Poirier, *Cancer Res.* **1993**, *53*, 3976–3985.
- [28] S. H. Hong, J. Kim, J.-M. Kim, S.-Y. Lee, D.-S. Shin, K.-H. Son, D. C. Han, Y. K. Sung, B.-M. Kwon, *Biochem. Pharmacol.* **2007**, *74*, 557–565.
- [29] B. Fabre, I. Livneh, T. Ziv, A. Ciechanover, *Biochem. Biophys. Res. Commun.* **2019**, *517*, 188–192.
- [30] F. Blanchard, M. E. Rusiniak, K. Sharma, X. Sun, I. Todorov, M. M. Castellano, C. Gutierrez, H. Baumann, W. C. Burhans, *Mol. Biol. Cell* **2002**, *13*, 1536–1549.
- [31] M. Matondo, M. Marcellin, K. Chaoui, M.-P. Bousquet-Dubouch, A. Gonzalez-de-Peredo, B. Monsarrat, O. Burlet-Schiltz, *PROTEOMICS* **2017**, *17*, 1600089.
- [32] P. Mertins, J. W. Qiao, J. Patel, N. D. Udeshi, K. R. Clauser, D. R. Mani, M. W. Burgess, M. A. Gillette, J. D. Jaffe, S. A. Carr, *Nat. Methods* **2013**, *10*, 634–637.
- [33] Y. Tatsumi, S. Ohta, H. Kimura, T. Tsurimoto, C. Obuse, *J. Biol. Chem.* **2003**, *278*, 41528–41534.
- [34] E. H. J. Yew, N. S. Cheung, M. S. Choy, R. Z. Qi, A. Y.-W. Lee, Z. F. Peng, A. J. Melendez, J. Manikandan, E. S.-C. Koay, L.-L. Chiu, W. L. Ng, M. Whiteman, J. Kandiah, B. Halliwell, *J. Neurochem.* **2005**, *94*, 943–956.

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- [35] K. U. Hong, Y. S. Park, Y.-S. Seong, D. Kang, C.-D. Bae, J. Park, *Mol. Cell. Biol.* **2007**, *27*, 3667–3681.
- [36] R. Kwan, K. Looi, M. B. Omary, *Exp. Cell Res.* **2015**, *335*, 12–22.
- [37] H. Chen, P. Mohan, J. Jiang, O. Nemirovsky, D. He, M. C. Fleisch, D. Niederacher, L. M. Pilarski, C. J. Lim, C. A. Maxwell, *Cell Cycle* **2014**, *13*, 2248–2261.
- [38] P. Liu, B. Xu, J. Li, H. Lu, *FEBS Lett.* **2009**, *583*, 401–406.
- [39] K. K. Starheim, T. Holien, K. Misund, I. Johansson, K. A. Baranowska, A.-M. Sponaas, H. Hella, G. Buene, A. Waage, A. Sundan, G. Bjørkøy, *Blood Cancer J.* **2016**, *6*, e446.
- [40] S. P. Shah, A. K. Nooka, D. L. Jaye, N. J. Bahlis, S. Lonial, L. H. Boise, *Oncotarget* **2016**, *7*, 59727–59741.
- [41] J. B. Hedges, K. S. Ryan, *Chem. Rev.* **2019**, DOI:10.1021/acs.chemrev.9b00408.



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Concise Chemoenzymatic Total Synthesis and Identification of Cellular Targets of Cepafungin I*Alexander Amatuni, Anton Shuster, Alexander Adibekian*, Hans Renata***Contribution from the Department of Chemistry, The Scripps Research Institute, 130 Scripps Way, Jupiter, FL 33458***SUPPLEMENTARY MATERIAL****Table of Contents**

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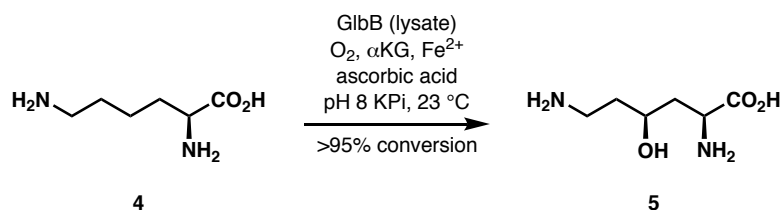
General materials and methods

Unless otherwise noted, all chemicals and reagents for chemical reactions were purchased at the highest commercial quality and used without further purification. Reactions were monitored by thin layer chromatography (TLC) and liquid chromatography/mass spectrometry (LC/MS). TLC was performed with 0.25 mm E. Merck silica plates (60F-254) using short-wave UV light as the visualizing agent, and ninhydrin or KMnO₄ and heat as developing agents. Sonication was performed using a Qsonica Q500 sonicator. LC/MS was performed with an Agilent 1260 Infinity System equipped with Poroshell 120 EC-C18 column (3.0 x 50 mm, 2.7 μm). HRMS(ESI-TOF) was performed with an Agilent 1260 Infinity System equipped with Poroshell 120 EC-C18 column (4.6 x 5.0 mm, 2.7 μm) and an Agilent G6230B TOF LC/MS. Preparative HPLC was performed on an Agilent 1260 Infinity II system equipped with a Dr. Maisch Reprosil 100 C18 column (10 x 250 mm, 5 μm), or on an Agilent 1260 Infinity system equipped with a Varian Dynamax C18 column (21.4 x 250 mm, 10 μm). NMR spectra were recorded on a Bruker AVANCE AV400 (400 MHz and 100 MHz) or Bruker AVANCE AV600 (600 MHz and 151 MHz) and calibrated using residual non-deuterated solvent. Specific rotations were measured on Autopol IV polarimeter (Rudolph Research Analytical). DMEM/High glucose media (with L-Glutamine and sodium pyruvate), RPMI 1640 media (with L-Glutamine), phosphate buffered saline (PBS), MEM Non-Essential Amino Acids, Penicillin Streptomycin (Pen/Strep), opti-MEM and Trypsin-EDTA were obtained from Life Technologies. Protein concentration was determined using the Bradford assay (Bio-Rad). Expression plasmids for PSMB2-Myc-DDK and PSMB5-Myc-DDK were obtained from Origene. Plasmids were prepared using the QIAprep Spin Miniprep Kit (Qiagen). Primary antibodies were purchased from Cell Signaling Technology Inc. unless otherwise noted and secondary antibodies were acquired from Jackson ImmunoResearch Laboratories Inc.

Bacterial strain construction

pET-28a(+)-GlbB expression vector was obtained from Genscript as described previously.^{S1} *E. coli* BL21(DE3) harboring pET-28a(+)-GlbB and pGro7 was constructed by transforming electrocompetent *E. coli* BL21(DE3) with the appropriate plasmids.

Chemoenzymatic synthesis of cepafungin I



Enzymatic hydroxylation of L-lysine:

200 mL of TB media containing 25 µg/mL chloramphenicol and 50 µg/mL kanamycin was inoculated with 1 mL of an overnight culture of *E. coli* BL21(DE3) cells harboring pET-28a(+)-GlbB and pGro7. The culture was shaken at 250 rpm at 36 °C for approximately 2.5 hours or until an optical density of 0.6 was reached. The culture was then cooled on ice (20 minutes) and induced by adding IPTG and arabinose to a final concentration of 0.025 mM and 1 mg/mL, respectively. The culture was allowed to continue for another 20 hours at 23 °C and shaking at 250 rpm. Cells were harvested by centrifugation at 4200 rpm at 4 °C for 15 minutes, then resuspended in pH = 8 kPi buffer (150 mL) to an optical density of 25. The cells were lysed by sonication for 3 minutes (1 second on, 4 seconds off) at 0 °C and 50% amplitude. Cell debris was pelleted by centrifugation and the supernatant was diluted to 250 mL with pH = 8 kPi buffer into a 1L Erlenmeyer flask containing L-lysine (1.46 g, 10 mmol, 1 eq, 40 mM final concentration), α-ketoglutaric acid (2.83 g, 12.5 mmol, 1.25 eq, 50 mM final concentration), ascorbic acid (440 mg, 2.5 mmol, 0.25 eq, 10 mM final concentration) and FeSO₄•7H₂O (139 mg, 0.5 mmol, 0.05 eq, 2 mM final concentration). The mixture was shaken at 200 rpm at 23 °C overnight or until completion as judged by LC-MS.

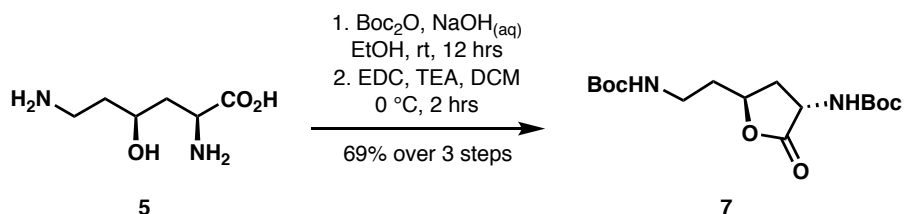
The reaction mixture was then acidified to pH = 2 with concentrated HCl and centrifuged at 4200 rpm at 4 °C for 15 minutes. The supernatant containing crude 4-hydroxylysine **5** was carried forward to the next step without further purification. For characterization purposes, the crude product was purified by ion exchange chromatography with Dowex 50WX8 resin.

^1H NMR (600 MHz, D_2O): δ 4.09 – 3.99 (m, 1H), 3.89 – 3.78 (m, 1H), 3.21 – 3.08 (m, 2H), 2.18 – 2.09 (m, 1H), 1.98 – 1.91 (m, 1H), 1.91 – 1.80 (m, 2H).

^{13}C NMR (151 MHz, D_2O with 1% TFA): δ 174.4, 67.7, 53.5, 37.1, 36.6, 34.0.

$[\alpha]_{\text{D}} = 3.7^\circ$ ($c = 0.5$, H_2O)

HRMS (ESI-TOF): calculated for $\text{C}_6\text{H}_{16}\text{N}_2\text{O}_3^+$ ($[\text{M}+\text{H}]^+$) 163.1083, found 163.1078



Boc protection and lactonization of crude 4-hydroxylysine 5:

The above supernatant was concentrated to ~33 mL then basified to pH 11 with 2 M NaOH. Boc_2O (8.73 g, 40 mmol, 4 eq) in 17 mL ethanol was added and the mixture was allowed to stir at room temperature. The mixture was re-basified to pH 11 after 3.5 hours and allowed to continue stirring overnight or until completion as indicated by LC-MS. Ethanol was removed *in vacuo* and the mixture was diluted with 50 mL ethyl acetate. The pH of the mixture was adjusted to 2 with 6 M HCl and the aqueous layer was separated and further extracted with ethyl acetate (3 x 50 mL). The combined organic layers were washed with brine, dried over Na_2SO_4 and concentrated *in vacuo* to provide 4.29 g crude di-Boc-4-hydroxylysine that was used without further purification.

The crude Boc-protected hydroxylysine (4.29 g) was dissolved in 50 mL anhydrous DCM, cooled to 0 °C, then treated with EDC·HCl (1.92 g, 10 mmol, 1 eq) followed by triethylamine (1.39 mL, 10 mmol, 1 eq). The reaction was stirred under argon at 0 °C for 2 hours or until completion as indicated by TLC. The reaction was concentrated to dryness. The resulting residue was dissolved in 100 mL ethyl acetate and washed with water (3 x 20 mL) and brine, then dried over Na_2SO_4 . Purification by silica flash chromatography (step gradient 35-40-50% ethyl acetate in hexanes) provided pure lactone 7 (2.39 g, 69%).

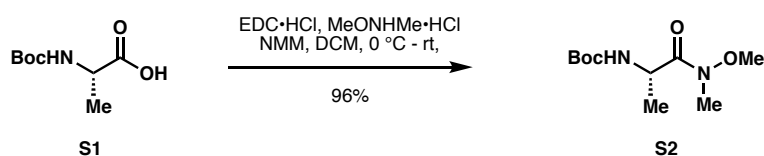
Note: the above 3-step sequence can be scaled up to 6.90 grams of L-lysine (47.2 mmol) to provide 9.53 grams of lactone 7 (59% yield).

^1H NMR (400 MHz, DMSO): δ 7.45 (d, J = 8.3 Hz, 1H), 6.89 (t, J = 5.7 Hz, 1H), 4.62 – 4.48 (m, 1H), 4.28 (q, J = 9.1 Hz, 1H), 3.07 – 2.90 (m, 2H), 2.32 – 2.09 (m, 2H), 1.82 – 1.60 (m, 2H), 1.38 (s, 9H), 1.37 (s, 9H).

^{13}C NMR (101 MHz, DMSO): δ 175.2, 155.6, 155.1, 78.6, 77.6, 75.4, 48.5, 36.4, 35.1, 32.5, 28.2, 28.1.

$[\alpha]_{\text{D}}^{20}$ = 26.7° (c = 0.5, CHCl_3)

HRMS (ESI-TOF): calculated for $\text{C}_{16}\text{H}_{29}\text{N}_2\text{O}_6^+$ ($[\text{M}+\text{H}]^+$) 345.2026, found 345.2026



Synthesis of Weinreb amide S2:

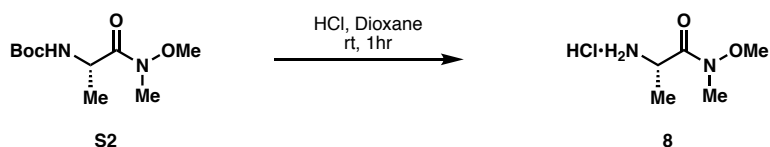
Boc-L-alanine (**S1**, 9.10 g, 48.1 mmol, 1.0 eq), *N,O*-dimethylhydroxylamine hydrochloride (5.16 g, 52.9 mmol, 1.1 eq) and *N*-methylmorpholine (5.82 mL, 52.9 mmol, 1.1 eq) were dissolved in 120 mL anhydrous DCM. The mixture was cooled to 0 °C, and EDC·HCl (9.22 g, 48.1 mmol, 1.0 eq) was added portionwise. The reaction was stirred at 0 °C for two hours, and then at room temperature overnight. Upon complete consumption of **S1** by TLC, the reaction was diluted with 75 mL water and the pH of the mixture was adjusted to 2 with 1 M HCl. The layers were separated, and the aqueous phase extracted twice with 20 mL DCM. The combined organic layers were washed with 30 mL water, saturated NaHCO_3 , brine, then dried over Na_2SO_4 and concentrated *in vacuo* to provide pure **S2** as a crystalline white solid (10.7 g, 96% yield).

^1H NMR (600 MHz, MeOD): δ 4.60 – 4.53 (m, 1H), 3.81 (s, 3H), 3.20 (s, 3H), 1.44 (s, 9H), 1.26 (d, J = 7.1 Hz, 3H).

^{13}C NMR (151 MHz, MeOD): δ 175.7, 157.6, 80.4, 62.0, 48.0, 32.4, 28.7, 17.4.

$[\alpha]_{\text{D}}^{22}$ = -26.74° (c 2.45, MeOH)

HRMS (ESI-TOF): calculated for $\text{C}_{10}\text{H}_{20}\text{N}_2\text{O}_4\text{Na}^+$ ($[\text{M}+\text{Na}]^+$) 255.1315, found 255.1315



Deprotection of Weinreb amide **S2**:

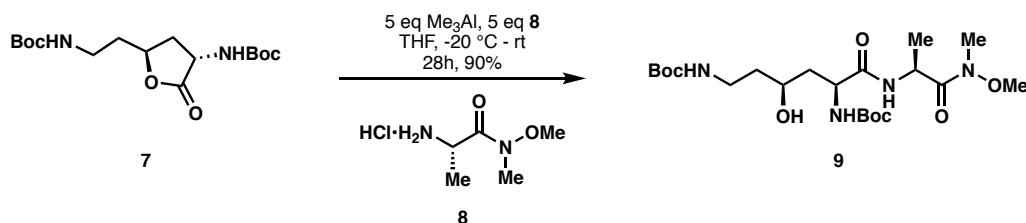
Boc-L-alanine amide **S2** (7.00 g, 29.4 mmol, 1 eq) was dissolved in 49 mL of 4 M HCl in dioxane at room temperature. Upon complete consumption of **S2** by TLC, the reaction was concentrated to dryness, then evaporated twice from 50 mL 1:1 methanol:toluene to provide **8** as a white solid (5.72 g, quantitative).

¹H NMR (600 MHz, MeOD): δ 4.35 (q, $J = 7.0$ Hz, 1H), 3.81 (s, 3H), 3.25 (s, 3H), 1.50 (d, $J = 7.0$ Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 170.9, 62.4, 48.7, 32.5, 16.3.

$[\alpha]_D^{24} = -27.71^\circ$ (c 2.23, MeOH)

HRMS (ESI-TOF): calculated for $C_5H_{13}N_2O_2^+$ ($[M+H]^+$) 133.0972, found 133.0974



Synthesis of dipeptide **9**:

Amine hydrochloride **8** (5.71g, 33.9 mmol, 5 eq) was set stirring (undissolved) in 85 mL anhydrous THF. The mixture was cooled to $-20^\circ C$, then a 2 M solution of trimethylaluminum in anhydrous toluene was added dropwise (16.8 mL, 4.95 eq). The reaction was stirred at $-20^\circ C$ for 30 minutes under argon to provide a clear, light yellow solution. To this mixture was added lactone **7** in 17 mL anhydrous THF (2.33 g, 6.77 mmol, 1 eq) dropwise at $-20^\circ C$. The reaction was stirred to room temperature overnight, until completion by TLC. After 28 hours, the reaction was cooled to $0^\circ C$ and quenched by the careful addition of 20 mL 2 M $NaHSO_4$ solution dropwise. The pH of the mixture was adjusted to 1 with 50 mL 1 M HCl, then concentrated *in vacuo* to remove most of the organic solvent. The remaining aqueous mixture was extracted with ethyl acetate (5 x 50

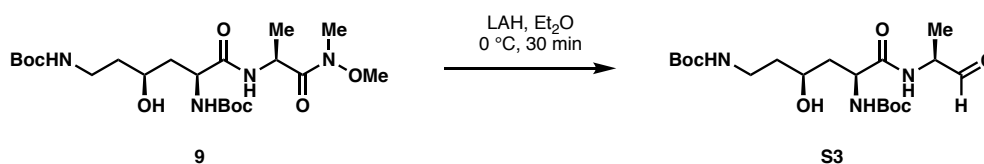
mL). The combined organic layers were then washed with water, saturated NaHCO₃, water, brine and finally dried over Na₂SO₄. Concentration *in vacuo* provided 3.15 g of crude dipeptide **9** that was further purified by silica flash chromatography (60:30:10 hexanes:ethyl acetate:methanol) to provide pure **9** as a white solid (2.90 g, 90 %).

¹H NMR (400 MHz, MeOD): δ 6.52 (s, 1H), 4.86 – 4.77 (m, 1H), 4.17 (t, *J* = 7.3 Hz, 1H), 3.82 (s, 3H), 3.80 – 3.73 (m, 1H), 3.21 (s, 3H), 3.19 – 3.13 (m, 2H), 1.90 – 1.75 (m, 1H), 1.72 – 1.61 (m, 2H), 1.60 – 1.49 (m, 1H), 1.44 (s, 9H), 1.43 (s, 9H), 1.34 (d, *J* = 7.1 Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 174.6, 174.5, 158.6, 157.6, 80.6, 80.0, 67.2, 62.1, 53.5, 47.1, 40.8, 38.4, 38.1, 32.5, 28.8, 28.7, 17.1.

$[\alpha]_D^{24} = -28.81^\circ$ (*c* 1.01, MeOH)

HRMS (ESI-TOF): calculated for C₂₁H₄₁N₄O₈⁺ ([M+H]⁺) 477.2919, found 477.2917

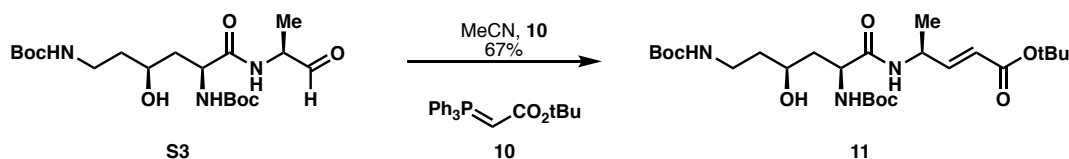


Reduction of Weinreb amide **9**:

In a procedure adapted from Fehrentz et al.,^{S4} dipeptide **9** (100 mg, 0.210 mmol, 1 eq) was dissolved in 2.1 mL anhydrous diethyl ether and cooled to 0 °C. A solution of lithium aluminum hydride (1.05 M in Et₂O, 0.50 mL, 2.5 eq) was then added dropwise at 0 °C. Upon complete addition, the reaction was stirred for 30 minutes at 0 °C then quenched with 2 mL 2M NaHSO₄. The layers were separated and the aqueous phase was extracted with Et₂O (2 x 2 mL). The combined organic layers were washed with saturated NaHCO₃ and brine, then dried over Na₂SO₄. Concentration *in vacuo* provided aldehyde **S3** as a white foam, which was used without further purification. A sample of the material was purified by silica flash chromatography (9:0.9:0.1 ethyl acetate:dichloromethane:triethylamine) to aid characterization by ¹H NMR.

¹H NMR (400 MHz, CDCl₃): δ 9.53 (d, *J* = 2.4 Hz, 1H), 7.23 – 6.99 (m, 1H), 5.82 – 5.55 (m, 1H), 4.91 – 4.73 (m, 1H), 4.50 – 4.36 (m, 1H), 4.35 – 4.18 (m, 2H), 3.86 – 3.68 (m, 1H), 3.55 – 3.36 (m, 1H), 3.18 – 3.00 (m, 1H), 2.03 – 1.91 (m, 1H), 1.85 – 1.71 (m, 1H), 1.63 – 1.53 (m, 2H), 1.45 – 1.41 (m, 18H), 1.35 (d, *J* = 7.3 Hz, 2H).

HRMS (ESI-TOF): calculated for C₁₉H₃₆N₃O₇⁺ ([M+H]⁺) 418.2548, found 418.2548



Wittig olefination of aldehyde S3:

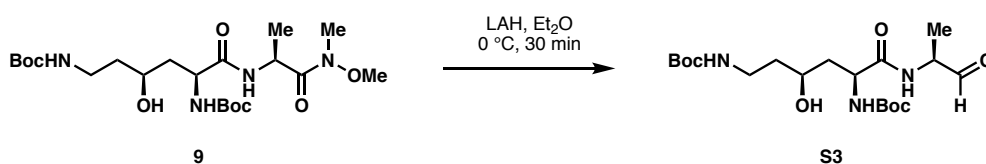
Ylide **10** (106 mg, 0.281 mmol, 1.25 eq) was dissolved in 0.5 mL anhydrous acetonitrile, then a solution of aldehyde **S3** (94 mg) in 3 mL acetonitrile was added dropwise at room temperature. The reaction was refluxed for 2 hours at 60 °C, then concentrated to dryness *in vacuo*. Purification by silica flash chromatography (step gradient 70:29.5:0.5 to 70:27:3 dichloromethane:ethyl acetate:methanol) provided **11** as an off-white solid (73 mg, 67%).

¹H NMR (600 MHz, MeOD): δ 6.78 (dd, $J = 15.7, 5.0$ Hz, 1H), 5.84 (dd, $J = 15.7, 1.8$ Hz, 1H), 4.59 (qdd, $J = 7.0, 4.9, 1.7$ Hz, 1H), 4.16 – 4.03 (m, 1H), 3.73 – 3.62 (m, 1H), 3.16 (t, $J = 6.9$ Hz, 2H), 1.89 – 1.77 (m, 1H), 1.75 – 1.64 (m, 2H), 1.58 – 1.51 (m, 1H), 1.47 (s, 9H), 1.45 (s, 9H), 1.43 (s, 9H), 1.28 (d, $J = 7.0$ Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 174.4, 167.4, 158.7, 157.7, 149.1, 122.9, 81.7, 80.7, 80.0, 67.7, 54.4, 47.0, 40.7, 38.4, 38.1, 28.8, 28.8, 28.4, 19.9.

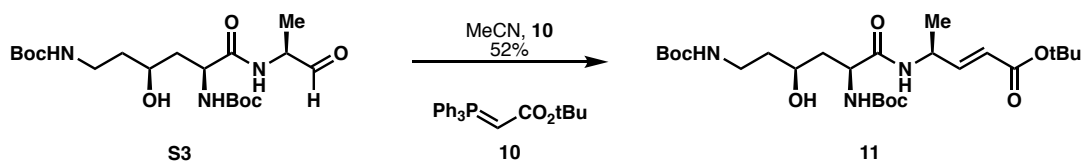
$[\alpha]_{\text{D}}^{24} = -23.47^\circ$ (c 0.72)

HRMS (ESI-TOF): calculated for $\text{C}_{25}\text{H}_{46}\text{N}_3\text{O}_8^+$ ($[\text{M}+\text{H}]^+$) 516.3279, found 516.3299



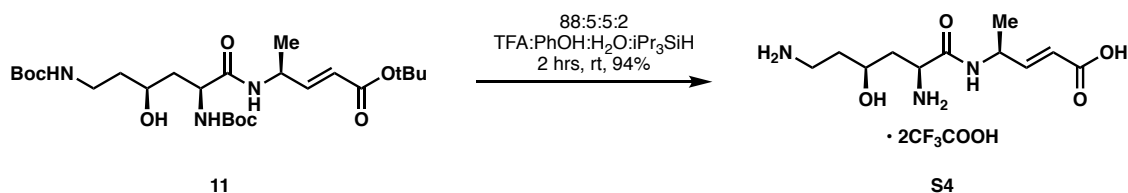
Reduction of Weinreb amide 9 (gram scale):

Dipeptide **9** (2.84 g, 5.96 mmol, 1 eq) was dissolved in 60 mL anhydrous diethyl ether and cooled to 0 °C. A solution of lithium aluminum hydride (1 M in Et_2O , 14.9 mL, 2.5 eq) was then added dropwise at 0 °C. Upon complete addition, the reaction was stirred for 30 minutes at 0 °C then quenched with 30 mL 2 M NaHSO_4 . The layers were separated and the aqueous phase was extracted with Et_2O (4 x 25 mL). The combined organic layers were washed with water, saturated NaHCO_3 and brine, then dried over Na_2SO_4 . Concentration *in vacuo* provided aldehyde **S3** as a white foam that was used for the next step without further purification (2.15 g).



Wittig olefination of aldehyde S3 (gram scale):

Ylide **10** (2.42 g, 6.42 mmol, 1.25 eq) was dissolved in 63 mL anhydrous acetonitrile, then a solution of aldehyde **S3** (2.15 g) in 10 mL acetonitrile was added dropwise at room temperature. The reaction was stirred for 30 minutes or until completion by ¹H NMR or TLC, and then concentrated to dryness. Purification by silica flash chromatography (100% diethyl ether) provided **11** as an off-white solid (1.59 g, 52%).



Deprotection of dipeptide 11:

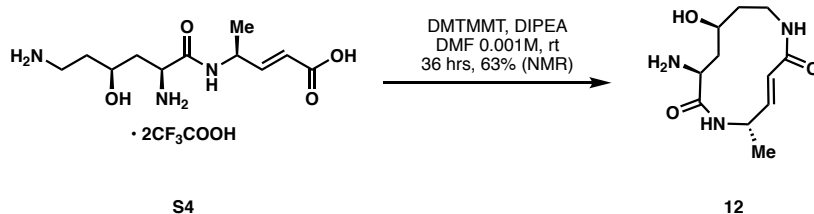
Dipeptide **11** (500 mg, 0.970 mmol, 1 eq) was dissolved in 24.2 mL of a freshly prepared solution of “Reagent B” (88:5:5:2 trifluoroacetic acid:phenol:water:triisopropylsilane). After stirring for 1 hour at room temperature, the reaction was diluted with 30 mL toluene and concentrated *in vacuo* to dryness, followed by an additional evaporation from 30 mL toluene. The residue was then dissolved in 2 mL methanol and added dropwise to 100 mL diethyl ether at 0 °C. The solids were collected by centrifugation at 4200 RPM for 10 minutes at 4 °C, then precipitated again into 50 mL diethyl ether at 0 °C from 1.5 mL methanol. The solids were collected by centrifugation as above, then dried from methanol to provide **S4** as an off-white solid (442 mg, 94 %).

¹H NMR (600 MHz, MeOD): δ 6.82 (dd, *J* = 15.7, 5.4 Hz, 1H), 5.89 (dd, *J* = 15.7, 1.6 Hz, 1H), 4.67 – 4.61 (m, 1H), 4.04 – 3.97 (m, 1H), 3.96 – 3.87 (m, 1H), 3.13 – 3.01 (m, 2H), 2.06 – 2.00 (m, 1H), 1.94 – 1.84 (m, 2H), 1.84 – 1.74 (m, 1H), 1.33 (d, *J* = 7.0 Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 170.3, 169.4, 148.9, 122.9, 68.3, 53.6, 47.4, 39.2, 37.8, 36.0, 19.7.

$$[\alpha]_D^{24} = -1.811^\circ \text{ (} c \text{ 4.03, MeOH)}$$

HRMS (ESI-TOF): calculated for $C_{11}H_{22}N_3O_4^+$ ($[M+H]^+$) 260.1605, found 260.1605



Macrolactamization of **S4**:

Linear macrocycle precursor **S4** (366 mg, 0.751 mmol, 1 eq) was dissolved in 750 mL anhydrous DMF. The solution was treated with diisopropylethylamine (0.523 mL, 3.00 mmol, 4 eq), followed by solid 4-(4,6-dimethoxy-1,3,5-triazin-2-yl)-4-methyl-morpholinium tetrafluoroborate (DMTMMT) (369 mg, 1.13 mmol, 1.50 eq) at room temperature. The reaction was stirred under argon for 36 hours, then quenched with 20 mL water and concentrated *in vacuo* to dryness. The residue was dissolved in 3 mL methanol and precipitated into 50 mL diethyl ether with rapid stirring. The solids were collected by centrifugation at 4200 RPM for 15 minutes at 4 °C to yield crude **12** as a tan solid (540 mg, 63% from **S4**, 59% from **11**). Yield was determined by ^1H NMR analysis of a 7.4 mg crude sample with 4-toluenesulfonamide (7.8 mg, 0.0465 mmol) added as internal standard.

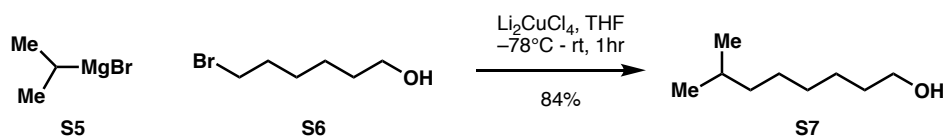
^1H NMR (400 MHz, MeOD): 4-toluenesulfonamide: δ 7.82 – 7.72 (m, 2H), 7.40 – 7.27 (m, 2H), 2.42 (s, 3H). Compound **12**: 6.63 (dd, $J = 16.0, 6.1$ Hz, 1H), 6.38 (dd, $J = 16.0, 1.1$ Hz, 1H), 4.73 – 4.64 (m, 1H), 3.83 – 3.76 (m, 1H), 2.27 – 2.10 (m, 1H), 2.01 – 1.92 (m, 1H), 1.92 – 1.79 (m, 0H), 1.75 – 1.64 (m, 2H).

HRMS (ESI-TOF): calculated for $C_{11}H_{20}N_3O_3^+$ ($[M+H]^+$) 242.1499, found 242.1495

Table S1. Macrolactamization optimization. General reaction conditions followed those reported above. NMR yield was determined with 4-toluenesulfonamide as internal standard.

Entry	Reagent(s)	Equiv.	NMR yield of 12 (%)
1	CDI	1.0 – 2.0	N.R.*
2	CITU	1.1	N.R.*
3	T3P	1.1	1.7
4	EDC/HOBt	1.1 (ea.)	3.5
5	EDC/Pfp-OH	1.1 (ea.)	3.7
6	EDC/Oxyrna	1.1 (ea.)	5.9
7	HATU	2.0	23
8	FDPP	2.0	27
9	HBTU	1.1	28
10	FDPP	1.1	29
11	PyAOP	1.1	30
12	HATU (40 °C)	1.1	32
13	DMTMMT	1.1	33 – 46
14	DMTMMT (40 °C)	1.1	41
15	HATU	1.1	42
16	DMTMMT	2.0	40-55
17	DMTMMT	1.5	55-63

*No product was detected by ¹H NMR analysis.



Synthesis of branched alcohol S7:

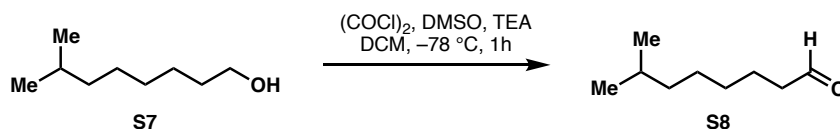
Following a procedure adapted from Melaugh et al.,^{S2} lithium chloride (6.66 g, 157 mmol, 2.05 eq) was flame-dried in a 250 mL round-bottom flask under high vacuum. Solid copper(II) chloride (10.3 g, 76.6 mmol, 1 eq) was added under argon. The combined reagents were then dissolved in 105 mL anhydrous THF to provide a dark red solution of Li_2CuCl_4 .

A flame-dried 3-neck 1L flask fitted with a reflux condenser was charged with magnesium turnings (12.9 g, 531 mmol, 1.18 eq with respect to 2-bromopropane) and 200 mL anhydrous THF. With rapid stirring, 2-bromopropane (42.3 mL, 451 mmol, 6.5 eq with respect to **15**) was added dropwise until refluxing began, at which point the flask was lowered into a water bath. Upon complete addition, the water bath was removed and the reaction was allowed to stir under argon for 30 minutes to produce a dark gray suspension of **S5**. The mixture was cooled to $-78\text{ }^{\circ}\text{C}$, and bromoalcohol **S6** (12.6 g, 69.6 mmol, 1 eq) was added in 10 mL dry THF, followed by the above solution of Li_2CuCl_4 ($\sim 0.7\text{ M}$ in THF, 105 mL, 1.1 eq with respect to **S6**). Upon complete addition, the reaction was removed from its cooling bath and allowed to warm to room temperature. Reaction progress was monitored by TLC until completion at 1 hour. The reaction was then carefully quenched at $0\text{ }^{\circ}\text{C}$ with 50 mL saturated NH_4Cl solution, filtered through a sintered glass funnel, and the filtrate was concentrated *in vacuo* to remove most of the THF. The mixture was diluted with 100 mL ethyl acetate and 100 mL water. The layers were separated, and the aqueous phase was extracted with ethyl acetate (3 x 200 mL). The combined organic layers were washed with 50 mL each of saturated aqueous NaHCO_3 and brine, then dried over Na_2SO_4 . Purification by silica flash chromatography (90:10 hexanes:ethyl acetate) provided pure **16** as a colorless liquid (8.38 g, 84%).

$^1\text{H NMR}$ (600 MHz, CDCl_3): δ 3.63 (t, $J = 6.7\text{ Hz}$, 2H), 1.60 – 1.45 (m, 3H), 1.38 – 1.31 (m, 2H), 1.31 – 1.22 (m, 4H), 1.20 – 1.10 (m, 2H), 0.85 (d, $J = 6.7\text{ Hz}$, 6H).

$^{13}\text{C NMR}$ (151 MHz, CDCl_3): δ 63.2, 39.1, 32.9, 29.8, 28.1, 27.5, 25.9, 22.8.

HRMS (ESI-TOF): calculated for $\text{C}_{11}\text{H}_{24}\text{NO}^+$ ($[\text{M}+\text{MeCN}+\text{H}]^+$) 186.1852, found 186.1852



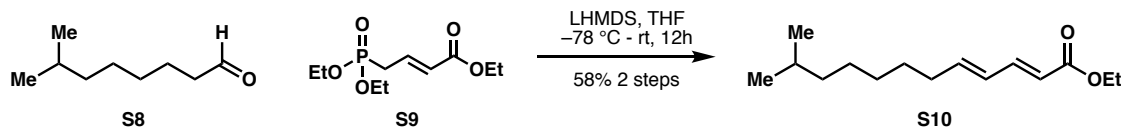
Oxidation of branched alcohol S8:

Oxalyl chloride (893 μL , 10.4 mmol, 1.5 eq) was dissolved in 8 mL anhydrous DCM at $-78\text{ }^{\circ}\text{C}$. An anhydrous solution of DMSO (1.48 mL, 20.8 mmol, 3 eq) in 3 mL DCM was added dropwise and the resulting mixture was stirred at $-78\text{ }^{\circ}\text{C}$ for 15 minutes. A solution of branched alcohol **S7** (1.00 g, 6.93 mmol, 1 eq) in 6 mL anhydrous DCM was then added dropwise over 10

minutes. The mixture was stirred at $-78\text{ }^{\circ}\text{C}$ for 1 hour, and treated with triethylamine (4.83 mL, 34.7 mmol, 5 eq) dropwise. The resulting thick slurry was diluted with 10 mL DCM to aid stirring, and reaction progress was monitored by TLC until completion at 1 hour. The reaction was quenched at $-78\text{ }^{\circ}\text{C}$ with 20 mL water and allowed to warm to room temperature. The layers were separated, and the aqueous layer was extracted with DCM (3 x 10 mL). The combined organic layers were washed with water (twice) and brine, then dried over Na_2SO_4 . Concentration *in vacuo* provided **S8** as a pale yellow oil, which was used without further purification (1.19 g).

^1H NMR (400 MHz, CDCl_3): δ 9.75 (t, $J = 1.9$ Hz, 1H), 2.41 (td, $J = 7.3, 1.9$ Hz, 2H), 1.66 – 1.58 (m, 2H), 1.56 – 1.44 (m, 1H), 1.34 – 1.24 (m, 4H), 1.20 – 1.10 (m, 2H), 0.85 (d, $J = 6.6$ Hz, 6H).

HRMS (ESI-TOF): calculated for $\text{C}_9\text{H}_{19}\text{O}^+$ ($[\text{M}+\text{H}]^+$) 143.1430, found 143.1431



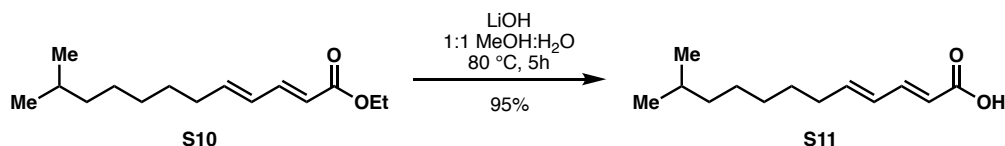
Synthesis of diene ester **S10**:

In a procedure adapted from Imker et al.,^{S5} Phosphonate **S9** (2.60 g, 10.4 mmol, 1.5 eq) in 20 mL anhydrous THF was cooled to $-78\text{ }^{\circ}\text{C}$. A solution of lithium hexamethyldisilazide (1 M THF, 9.91 mL, 1.4 eq) was then added dropwise and allowed to stir for an additional 1 hour at $-78\text{ }^{\circ}\text{C}$. Crude aldehyde **S8** (1.19 g) in 5 mL THF was added dropwise at $-78\text{ }^{\circ}\text{C}$, and the mixture was allowed to stir to room temperature overnight. Upon completion by TLC, the reaction was cooled to $0\text{ }^{\circ}\text{C}$ and quenched with 20 mL saturated NH_4Cl . The layers were separated, and the aqueous layer was extracted with ethyl acetate (3 x 30 mL). The combined organic layers were washed with 20 mL brine and dried over Na_2SO_4 . Purification by silica flash chromatography (97:3 hexanes:ethyl acetate) provided **S10** as a yellow oil (957 mg, 58% from **S7**).

^1H NMR (600 MHz, CDCl_3): δ 7.26 (dd, $J = 18.1, 15.4$ Hz, 1H), 6.20 – 6.07 (m, 2H), 5.78 (d, $J = 15.4$ Hz, 1H), 4.19 (q, $J = 7.2$ Hz, 2H), 2.16 (td, $J = 7.5, 6.1$ Hz, 2H), 1.55 – 1.48 (m, 1H), 1.46 – 1.38 (m, 2H), 1.29 (t, $J = 7.1$ Hz, 3H), 1.30 – 1.24 (m, 4H), 1.18 – 1.12 (m, 2H), 0.86 (d, $J = 6.6$ Hz, 6H).

^{13}C NMR (151 MHz, CDCl_3): δ 167.5, 145.3, 144.9, 128.5, 119.3, 60.3, 39.0, 33.1, 29.6, 28.9, 28.1, 27.3, 22.8, 14.5.

HRMS (ESI-TOF): Calculated for $\text{C}_{15}\text{H}_{27}\text{O}_2^+$ ($[\text{M}+\text{H}]^+$) 239.2006, found 239.2004



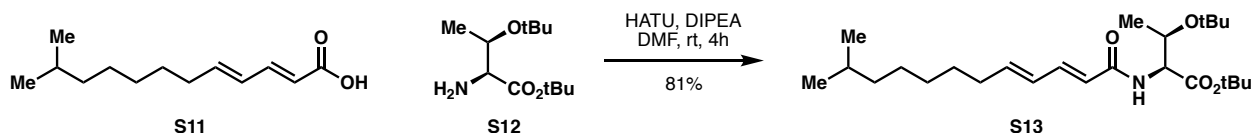
Hydrolysis of ester **S10**:

Ester **S10** (450 mg, 1.89 mmol, 1 eq) was dissolved in 9.5 mL methanol. With rapid stirring, a solution of lithium hydroxide (226 mg, 9.44 mmol, 5 eq) in 9.5 mL water was added. The reaction was refluxed at 80 °C for 5 hours or until completion by TLC. Methanol was evaporated *in vacuo*, then the mixture was adjusted to pH 1 with 1 M HCl and diluted with 20 mL DCM. The layers were separated, and the aqueous layer was extracted with DCM (3 x 20 mL). The combined organic layers were washed with 10 mL of brine then dried over Na₂SO₄. Concentration *in vacuo* provided pure **S11** as a waxy white solid (379 mg, 95%).

¹H NMR (600 MHz, CDCl₃): δ 7.38 – 7.31 (m, 1H), 6.24 – 6.14 (m, 2H), 5.78 (d, *J* = 15.3 Hz, 1H), 2.18 (td, *J* = 7.4, 5.5 Hz, 2H), 1.56 – 1.48 (m, 1H), 1.46 – 1.40 (m, 2H), 1.32 – 1.26 (m, 4H), 1.19 – 1.12 (m, 2H), 0.86 (d, *J* = 6.6 Hz, 6H).

¹³C NMR (151 MHz, CDCl₃): δ 172.8, 147.7, 146.5, 128.3, 118.3, 39.0, 33.2, 29.6, 28.8, 28.1, 27.3, 22.8.

HRMS (ESI-TOF): calculated for C₁₃H₂₃O₂⁺ ([M+H]⁺) 211.1693, found 211.1695



Synthesis of amide **S13**:

Fatty acid **S11** (125 mg, 0.594 mmol, 1 eq) was combined with amine **S12** (206 mg, 0.892 mmol, 1.5 eq) in 3 mL anhydrous DMF. Diisopropylethylamine was added (0.311 mL, 1.78 mmol, 3 eq), followed by HATU (237 mg, 0.624 mmol, 1.05 eq). The reaction was stirred at room temperature under argon for 4 hours or until completion by LCMS. The reaction was then quenched with 0.3 mL water and concentrated *in vacuo*. The residue was dissolved in 50 mL ethyl acetate and washed with 1M HCl (twice), water, NaHCO₃ and brine, then dried over Na₂SO₄.

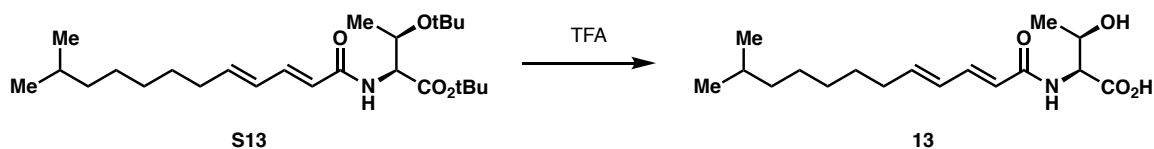
Concentration *in vacuo* followed by silica flash chromatography (90:10 hexanes:ethyl acetate) provided **S13** as a colorless oil (203 mg, 81%).

¹H NMR (600 MHz, CDCl₃): δ 7.21 (dd, *J* = 15.0, 10.6 Hz, 1H), 6.19 – 6.11 (m, 2H), 6.06 (dt, *J* = 15.1, 6.8 Hz, 1H), 5.87 (d, *J* = 15.1 Hz, 1H), 4.49 (dd, *J* = 9.2, 2.2 Hz, 1H), 4.21 (qd, *J* = 6.3, 2.2 Hz, 1H), 2.17 – 2.11 (m, 2H), 1.55 – 1.47 (m, 1H), 1.45 (s, 9H), 1.43 – 1.38 (m, 2H), 1.30 – 1.23 (m, 4H), 1.17 (s, 9H), 1.16 (d, *J* = 6.3 Hz, 3H), 1.15 – 1.12 (m, 2H), 0.86 (d, *J* = 6.6 Hz, 6H).

¹³C NMR (151 MHz, CDCl₃): δ 170.2, 166.6, 143.6, 141.9, 128.4, 121.6, 82.0, 73.9, 67.6, 58.4, 39.0, 33.1, 29.5, 29.0, 28.9, 28.3, 28.1, 27.3, 22.8, 21.0.

$[\alpha]_{\text{D}}^{24} = 2.836^{\circ}$ (*c* 2.01, MeOH)

HRMS (ESI-TOF): calculated for C₂₅H₄₆NO₄⁺ ([M+H]⁺) 424.3421, found 424.3423



Deprotection of tail fragment S13:

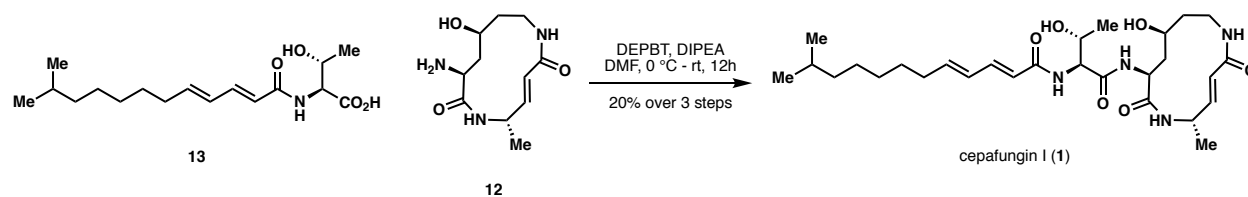
Amide **S13** (170 mg, 0.401 mmol, 1 eq) was dissolved in 4 mL trifluoroacetic acid at 0 °C, then stirred at room temperature for 1 hour. The reaction was then diluted with 10 mL toluene and concentrated *in vacuo* to dryness. The residue was evaporated twice more from 10 mL toluene to provide **13** as a colorless resin (138 mg, quant.).

¹H NMR (600 MHz, CDCl₃): δ 7.22 (dd, *J* = 15.0, 9.5 Hz, 1H), 7.04 (d, *J* = 8.4 Hz, 1H), 6.18 – 6.07 (m, 2H), 5.93 (d, *J* = 15.1 Hz, 1H), 4.67 – 4.59 (m, 1H), 4.53 – 4.43 (m, 1H), 2.21 – 2.09 (m, 2H), 1.55 – 1.47 (m, 1H), 1.46 – 1.37 (m, 2H), 1.30 – 1.24 (m, 4H), 1.21 (d, *J* = 6.3 Hz, 3H), 1.18 – 1.12 (m, 2H), 0.86 (d, *J* = 6.6 Hz, 6H).

¹³C NMR (151 MHz, CDCl₃): δ 173.6, 168.6, 145.3, 143.7, 128.2, 120.3, 67.8, 57.8, 39.1, 33.3, 29.7, 29.0, 28.1, 27.3, 22.8, 19.3.

$[\alpha]_{\text{D}}^{24} = 6.203^{\circ}$ (*c* 2.66, MeOH)

HRMS (ESI-TOF): calculated for C₁₇H₃₀NO₄⁺ ([M+H]⁺) 312.2169, found 312.2170



Coupling of tail fragment to glidobamine:

Acid **13** (38 mg, 0.122 mmol, 2 eq) and crude glidobamine **12** (75 mg, ~0.0610 mmol as judged by ^1H NMR analysis, 1 eq) were dissolved in 1.5 mL anhydrous DMF and cooled to 0 °C. To the mixture was added diisopropylethylamine (64 μL , 0.366 mmol, 6 eq), followed by solid DEPBT (37 mg, 0.122 mmol, 2 eq). The reaction was warmed to room temperature and stirred overnight, and the reaction progress was monitored by LCMS. After 12 hours, the reaction was cooled to 0 °C and quenched with 0.5 mL water, then concentrated *in vacuo* to dryness. The residue was precipitated into 50 mL diethyl ether at 0 °C from 0.9 mL methanol, and the resulting solids were collected by centrifugation at 4200 RPM at 4 °C for 15 minutes. The solids were dissolved in methanol, filtered through a 0.2 μm PTFE membrane filter, then purified by reversed-phase HPLC (gradient 30–60% acetonitrile in water over 35 minutes, 0.1% formic acid added) to provide 10.9 mg of cepafungin I (**1**) as a fluffy white powder after lyophilization (33%, 20% from **11**).

^1H NMR (600 MHz, DMSO): δ 8.79 – 8.53 (m, 1H), 7.99 – 7.91 (m, 1H), 7.75 (d, $J = 7.7$ Hz, 1H), 7.46 – 7.36 (m, 1H), 7.00 (dd, $J = 15.1, 10.8$ Hz, 1H), 6.40 (d, $J = 14.4$ Hz, 1H), 6.22 – 6.04 (m, 4H), 5.03 – 4.80 (m, 1H), 4.80 – 4.56 (m, 1H), 4.46 – 4.30 (m, 2H), 4.28 (dd, $J = 8.9, 4.1$ Hz, 1H), 4.01 – 3.90 (m, 1H), 3.63 – 3.51 (m, 1H), 3.09 – 2.91 (m, 2H), 2.16 – 2.09 (m, 2H), 1.93 – 1.73 (m, 1H), 1.58 (d, $J = 11.1$ Hz, 1H), 1.53 – 1.46 (m, 1H), 1.46 – 1.41 (m, 1H), 1.41 – 1.34 (m, 3H), 1.29 – 1.18 (m, 7H), 1.16 – 1.11 (m, 2H), 1.00 (d, $J = 6.3$ Hz, 3H), 0.84 (d, $J = 6.6$ Hz, 6H).

^{13}C NMR (151 MHz, DMSO): δ 171.1, 169.4, 167.6, 165.4, 143.1, 142.1, 139.7, 128.6, 123.3, 123.1, 66.9, 66.7, 58.2, 51.2, 44.7, 42.5, 38.4, 32.3, 28.9, 28.4, 27.4, 26.6, 22.5, 19.9, 18.5.

$[\alpha]_{\text{D}}^{24} = -106.5^\circ$ (c 0.20, MeOH)

HRMS (ESI-TOF): calculated for $\text{C}_{28}\text{H}_{47}\text{N}_4\text{O}_6^+$ ($[\text{M}+\text{H}]^+$) 535.3490, found 535.3491

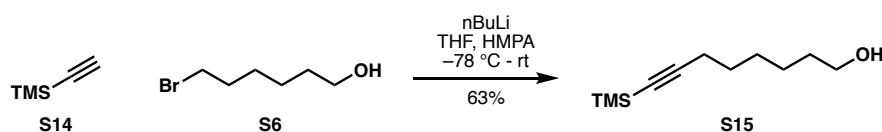
Table S2. Optimization of final fragment coupling between **12** and **13**.

Entry	Reagent(s)	Conditions	NMR yield 1 (%)
1	DEPBT	Standard*	28
2	DMTMMT	Standard*	14
3	HATU	Standard*	18
4	PyAOP	Standard*	26
5	DEPBT	2 eq. 13 and DEPBT, 6 eq. DIPEA	37
6	DEPBT	4 eq. 13 and DEPBT, 12 eq. DIPEA	36
7	DEPBT	6 eq. 13 and DEPBT, 18 eq. DIPEA	36
8	DEPBT	2 eq. 13 , 6 eq. DIPEA, 3 hr DEPBT addition	37

*Standard coupling procedure: 0.017 mmol (1 eq) each of carboxylic acid **13** and amine **12** were combined in anhydrous DMF. Diisopropylethylamine was added (3 eq), followed by the corresponding coupling reagent (1 eq) at 0 °C. The reaction was stirred to room temperature overnight or until completion as judged by LC-MS. Reactions were quenched with water, concentrated *in vacuo* and triturated with 15 mL diethyl ether. NMR yields were determined with 4-toluenesulfonamide as internal standard.

Synthesis of cepafungin analogs

Synthesis of cepafungin alkyne (**14**)



Synthesis of alkynyl alcohol **S15**:

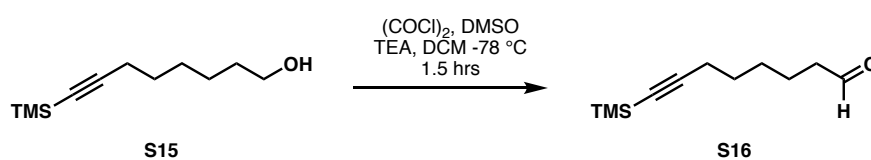
In a procedure adapted from Ye et al.,^{S3} trimethylsilylacetylene **S14** (2.95 g, 30.0 mmol, 2.72 eq) was dissolved in 21 mL anhydrous THF, cooled to -78 °C and treated with n-butyllithium (2.5 M in hexanes, 12.5 mL, 2.82 eq) dropwise. The mixture was stirred at -78 °C for 1 hour, then treated dropwise with a solution of bromoalcohol **S6** (2.00 g, 11.0 mmol, 1 eq) in 17 mL anhydrous THF, followed by 8.4 mL HMPA. The reaction was allowed to stir under argon at -78 °C to room temperature overnight or until completion by TLC analysis. The reaction was quenched at -20 °C with 20 mL saturated NH₄Cl, diluted with 20 mL ethyl acetate and the layers were separated. The aqueous layer was extracted with ethyl acetate (3 x 25 mL). The combined organic layers were

washed with 20 mL water, brine and dried over Na_2SO_4 . Concentration *in vacuo* followed by silica flash chromatography (85:15 hexanes:ethyl acetate) provided alkynyl alcohol **S15** as a colorless oil (1.37 g, 63%).

$^1\text{H NMR}$ (600 MHz, CDCl_3): δ 3.63 (t, $J = 6.6$ Hz, 2H), 2.21 (t, $J = 7.1$ Hz, 2H), 1.60 – 1.48 (m, 4H), 1.43 – 1.32 (m, 4H), 0.13 (s, 9H).

$^{13}\text{C NMR}$ (151 MHz, CDCl_3): δ 107.7, 84.5, 63.0, 32.7, 28.6, 28.6, 25.3, 19.9, 0.3.

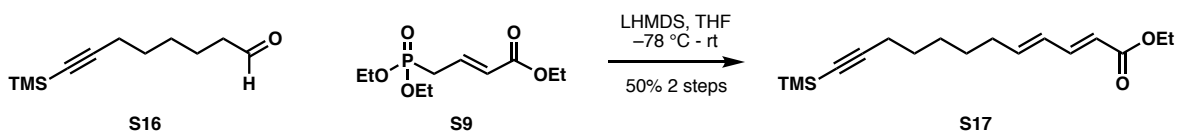
HRMS (ESI-TOF): calculated for $\text{C}_{11}\text{H}_{23}\text{OSi}^+$ ($[\text{M}+\text{H}]^+$) 198.1513, found 199.1517



Oxidation of alkynyl alcohol S15:

Oxalyl chloride (439 μL , 5.12 mmol, 1.5 eq) was dissolved in 4 mL anhydrous DCM at -78°C . An anhydrous solution of DMSO (727 μL , 10.2 mmol, 3 eq) in 1 mL DCM was added dropwise and the resulting mixture was stirred at -78°C for 15 minutes. A solution of alkynyl alcohol **S15** (677 mg, 3.41 mmol, 1 eq) in 4 mL anhydrous DCM was then added dropwise. The mixture was stirred at -78°C for 30 minutes, then treated with triethylamine (2.38 mL, 17.1 mmol, 5 eq) dropwise. Reaction progress was monitored by TLC until completion at 1.5 hours. The reaction was quenched at -78°C with 20 mL water and allowed to warm to room temperature. The layers were separated, and the aqueous layer was extracted with DCM (3 x 10 mL). The combined organic layers were washed with water (twice) and brine, then dried over Na_2SO_4 . Concentration *in vacuo* provided **S16** as a pale yellow oil which was used without further purification (975 mg).

$^1\text{H NMR}$ (600 MHz, CDCl_3): δ 9.76 (t, $J = 1.8$ Hz, 1H), 2.43 (td, $J = 7.4, 1.8$ Hz, 2H), 2.22 (t, $J = 7.1$ Hz, 2H), 1.64 (p, $J = 7.4$ Hz, 2H), 1.57 – 1.48 (m, 2H), 1.46 – 1.40 (m, 2H), 1.27 – 1.17 (m, 1H), 0.13 (s, 9H).

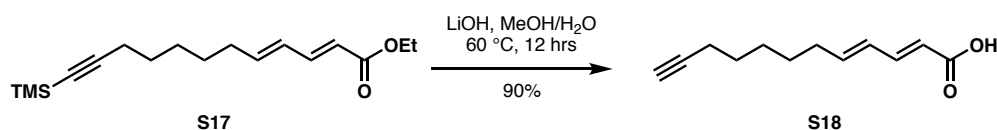


Synthesis of alkyne diene ester **34**:

Phosphonate **S9** (1.28 g, 5.12 mmol, 1.5 eq) in 17 mL anhydrous THF was cooled to -78 °C. A solution of lithium hexamethyldisilazide (1 M THF, 4.78 mL, 1.4 eq) was then added dropwise and allowed to stir for 30 minutes at -78 °C. Crude aldehyde **S16** (975 mg) in 2 mL THF was added dropwise at -78 °C, and the mixture was allowed to stir to room temperature overnight. Upon its completion as judged by TLC, the reaction was quenched with 20 mL saturated NH_4Cl at room temperature. After evaporation of THF *in vacuo*, the mixture was diluted with 30 mL water, 30 mL ethyl acetate and minimal brine to aid separation. The aqueous layer was extracted with ethyl acetate (3 x 40 mL). The combined organic layers were washed with 20 mL water and brine, then dried over Na_2SO_4 . Purification by silica flash chromatography (97:3 hexanes:ethyl acetate) provided **S17** as a yellow oil (498 mg, 50% from **S15**).

$^1\text{H NMR}$ (600 MHz, CDCl_3): δ 7.24 (dd, $J = 15.4, 10.5$ Hz, 1H), 6.21 – 6.04 (m, 2H), 5.77 (d, $J = 15.4$ Hz, 1H), 4.18 (q, $J = 7.1$ Hz, 2H), 2.21 (t, $J = 7.1$ Hz, 2H), 2.17 (q, $J = 7.4, 7.0$ Hz, 2H), 1.51 (p, $J = 7.3$ Hz, 2H), 1.47 – 1.36 (m, 4H), 1.28 (t, $J = 7.1$ Hz, 3H), 0.13 (s, 9H).

$^{13}\text{C NMR}$ (151 MHz, CDCl_3): δ 167.4, 145.1, 144.4, 128.6, 119.4, 107.5, 84.6, 60.3, 32.9, 28.5, 28.4, 28.3, 19.9, 14.4, 0.3.



Hydrolysis/desilylation of ester **34**:

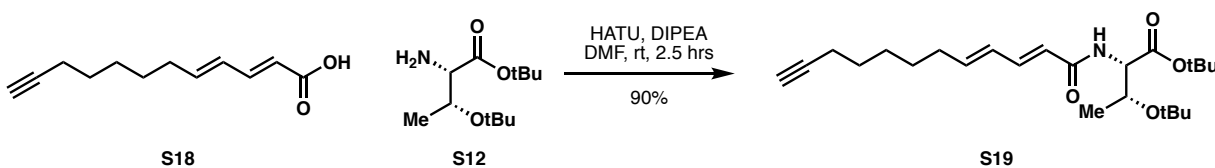
Ester **S17** (374 mg, 1.28 mmol, 1 eq) was dissolved in 6.4 mL methanol. With rapid stirring, a solution of lithium hydroxide (153 mg, 6.40 mmol, 5 eq) in 6.4 mL water was added. The reaction was heated at 60 °C overnight or until completion as judged by TLC. Methanol was evaporated *in vacuo*. The mixture was diluted with 10 mL water and the mixture was adjusted to pH 1 with 1 M HCl and diluted with 10 mL DCM. The layers were separated, and the aqueous layer was extracted

with DCM (3 x 10 mL). The combined organic layers were washed with 10 mL brine then dried over Na₂SO₄. Concentration *in vacuo* provided pure **S18** as a white solid (221 mg, 90%).

¹H NMR (400 MHz, CDCl₃): δ 7.34 (dd, *J* = 15.2, 9.5 Hz, 1H), 6.27 – 6.10 (m, 2H), 5.79 (d, *J* = 15.3 Hz, 1H), 2.23 – 2.16 (m, 4H), 1.95 (t, *J* = 2.6 Hz, 1H), 1.54 (p, *J* = 7.0 Hz, 2H), 1.49 – 1.39 (m, 4H).

¹³C NMR (101 MHz, CDCl₃): δ 172.5, 147.6, 146.0, 128.5, 118.4, 84.6, 68.5, 33.0, 28.4, 28.3, 28.2, 18.4.

HRMS (ESI-TOF): calculated for C₁₂H₁₅O₂⁻ ([M-H]⁻) 191.1077, found 191.1078



Synthesis of amide **S19**:

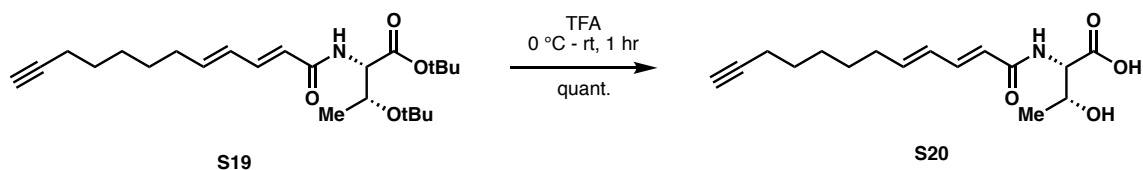
Alkynyl fatty acid **S18** (216 mg, 1.12 mmol, 1 eq) was combined with diisopropylethylamine (880 μL, 5.05 mmol, 4.5 eq) and HATU (427 mg, 1.12 mmol, 1 eq) in 5 mL anhydrous DMF and allowed to stir for 5 minutes. Amine **S12** (390 mg, 1.69 mmol, 1.5 eq) dissolved in 0.6 mL DMF was then added and the reaction was stirred under argon for 2.5 hours or until completion by TLC or LCMS. The reaction was then quenched at 0 °C with 20 mL saturated NH₄Cl, diluted with 15 mL ethyl acetate and the resulting layers were separated. The aqueous layer was extracted with ethyl acetate (4 x 15 mL). The combined organic layers were washed with water (2 x 10 mL) and 10 mL brine, then dried over Na₂SO₄. Concentration *in vacuo* followed by silica flash chromatography (85:15 hexanes:ethyl acetate) provided **S19** as a yellow oil (410 mg, 90%).

¹H NMR (600 MHz, CDCl₃): δ 7.19 (dd, *J* = 15.0, 10.8 Hz, 1H), 6.21 – 6.10 (m, 2H), 6.08 – 6.01 (m, 1H), 5.87 (d, *J* = 15.0 Hz, 1H), 4.48 (dd, *J* = 9.2, 2.1 Hz, 1H), 4.20 (qd, *J* = 6.3, 2.2 Hz, 1H), 2.16 (dtd, *J* = 14.1, 7.0, 1.9 Hz, 4H), 1.93 (t, *J* = 2.7 Hz, 1H), 1.55 – 1.49 (m, 2H), 1.44 (s, 9H), 1.43 – 1.38 (m, 4H), 1.16 (s, 9H), 1.15 (d, *J* = 6.3 Hz, 3H).

¹³C NMR (151 MHz, CDCl₃): δ 170.2, 166.6, 143.0, 141.8, 128.6, 121.8, 84.6, 82.0, 73.9, 68.4, 67.6, 58.4, 32.9, 28.8, 28.4, 28.4, 28.3, 28.2, 21.0, 18.4.

$[\alpha]_D^{23} = 5.000$ (c 0.680, MeOH)

HRMS (ESI-TOF): calculated for $C_{24}H_{39}NO_4Cl^-$ ($[M+Cl]^-$) 440.2573, found 440.2573



Deprotection of amide **S19**:

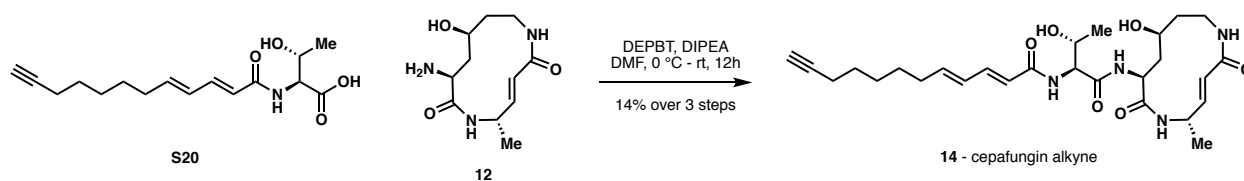
Alkynyl fatty acid amide **S19** (50 mg, 0.123 mmol, 1 eq) was dissolved in 1.2 mL trifluoroacetic acid at 0 °C, then stirred at room temperature for 1 hour. The reaction was then diluted with 10 mL toluene and concentrated *in vacuo* to dryness to provide **S20** as a pale yellow resin (50 mg, quant.).

^1H NMR (600 MHz, CDCl_3): δ 7.21 (dd, $J = 15.0, 10.1$ Hz, 1H), 7.05 (d, $J = 8.1$ Hz, 1H), 6.12 (dtd, $J = 21.8, 15.1, 8.4$ Hz, 2H), 5.94 (d, $J = 15.0$ Hz, 1H), 4.63 (d, $J = 8.5$ Hz, 1H), 4.46 (s, 1H), 2.21 – 2.13 (m, 4H), 1.95 (t, $J = 2.6$ Hz, 1H), 1.56 – 1.49 (m, 2H), 1.46 – 1.37 (m, 4H), 1.20 (d, $J = 6.3$ Hz, 3H).

^{13}C NMR (151 MHz, CDCl_3): δ 173.7, 168.3, 144.6, 143.4, 128.5, 120.6, 84.6, 68.5, 67.8, 57.8, 33.0, 28.4, 28.4, 28.4, 19.4, 18.5.

$[\alpha]_D^{23} = 8.318$ (c 2.14, MeOH)

HRMS (ESI-TOF): calculated for $C_{32}H_{45}N_2O_8^-$ ($[2M-H]^-$) 585.3181, found 585.3192



Coupling alkynyl tail fragment to glidobamine:

Acid **S20** (38 mg, 0.128 mmol, 2 eq) and crude glidobamine **12** (82 mg, ~0.0641 mmol as judged by ^1H NMR analysis, 1 eq) were dissolved in 3.2 mL anhydrous DMF and cooled to 0 °C. To the mixture was added diisopropylethylamine (34 μL , 0.192 mmol, 3 eq), followed by solid

DEPBT (38 mg, 0.128 mmol, 2 eq). The reaction was stirred to room temperature overnight, and reaction progress was monitored by LCMS. At 12 hours, the reaction was cooled to 0 °C and quenched with 0.5 mL water, then concentrated *in vacuo* to dryness. The residue was precipitated into 50 mL diethyl ether at 0 °C from 1.2 mL methanol, and the resulting solids were collected by centrifugation at 4200 RPM at 4 °C for 15 minutes. The solids were dissolved in methanol, filtered through a 0.2 µm PTFE membrane filter, then purified by reversed-phase HPLC (gradient 30–60% acetonitrile in water over 35 minutes, 0.1% formic acid added) to provide 8.1 mg of cepafungin alkyne (**14**) as a fluffy white powder after lyophilization (14% from **11**).

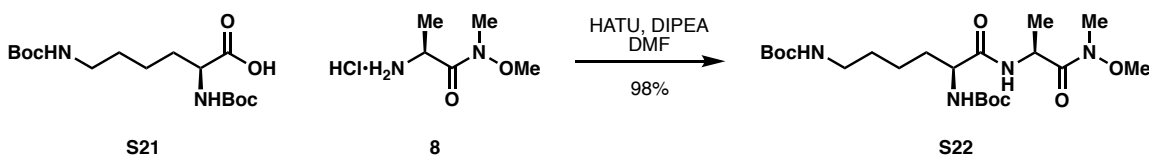
¹H NMR (600 MHz, DMSO): δ 8.66 (s, 1H), 7.97 – 7.83 (m, 1H), 7.74 (d, *J* = 7.8 Hz, 1H), 7.41 (t, *J* = 6.3 Hz, 1H), 7.00 (dd, *J* = 15.2, 10.8 Hz, 1H), 6.40 (d, *J* = 13.2 Hz, 1H), 6.24 – 6.03 (m, 4H), 4.87 (s, 1H), 4.67 (s, 1H), 4.50 – 4.30 (m, 2H), 4.28 (dd, *J* = 8.9, 4.1 Hz, 1H), 3.95 (s, 1H), 3.57 (s, 1H), 3.08 – 2.92 (m, 2H), 2.74 (t, *J* = 2.6 Hz, 1H), 2.19 – 2.06 (m, 4H), 1.85 (s, 1H), 1.58 (d, *J* = 13.5 Hz, 1H), 1.48 – 1.41 (m, 3H), 1.41 – 1.32 (m, 5H), 1.29 – 1.11 (m, 3H), 1.00 (d, *J* = 6.3 Hz, 3H).

¹³C NMR (151 MHz, DMSO): δ 171.0, 169.3, 167.6, 165.4, 143.1, 141.9, 139.7, 128.6, 123.3, 123.1, 84.5, 71.2, 67.0, 66.7, 58.1, 51.2, 44.7, 42.5, 32.1, 27.8, 27.8, 27.7, 19.9, 18.5, 17.6.

$[\alpha]_D^{23} = -74.231$ (*c* 0.260, MeOH)

HRMS (ESI-TOF): calculated for C₂₈H₄₁N₄O₈⁻ ([M+HCOOH-H]⁻) 561.2930, found 561.2936.

Synthesis of desoxycepafungin (**15**)



Synthesis of dipeptide **S22**:

Di-Boc lysine **S21** (2.38 g, 6.86 mmol, 1 eq) and amine hydrochloride **8** (1.45 g, 8.57 mmol, 1.25 eq) were combined in 34 mL anhydrous DMF. The mixture was treated with diisopropylethylamine (5.37 mL, 30.9 mmol, 4.5 eq) followed by HATU (2.61 g, 6.86 mmol, 1 eq) and allowed to stir at room temperature under argon for 1.5 hours or until completion by TLC. The reaction was then quenched at 0 °C with 5 mL saturated aqueous NH₄Cl and concentrated to dryness. The residue was diluted with 200 mL ethyl acetate and washed with 30 mL 1 M HCl,

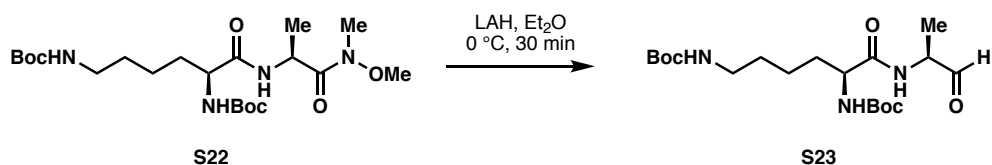
water, NaHCO₃ and brine. The combined aqueous layers were back-extracted twice with 30 mL ethyl acetate. The combined organic layers were then dried over Na₂SO₄, concentrated *in vacuo*, and purified by flash silica chromatography (55:40:5 hexanes:ethyl acetate:methanol) to provide **S22** as a colorless foam (3.10 g, 98%).

¹H NMR (600 MHz, MeOD): δ 4.85 – 4.78 (m, 1H), 4.05 – 3.91 (m, 1H), 3.82 (s, 3H), 3.20 (s, 3H), 3.04 (h, *J* = 6.8 Hz, 2H), 1.80 – 1.66 (m, 1H), 1.63 – 1.52 (m, 1H), 1.52 – 1.45 (m, 3H), 1.44 (s, 9H), 1.43 (s, 9H), 1.42 – 1.36 (m, 2H), 1.32 (d, *J* = 7.0 Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 174.8, 174.6, 158.6, 157.9, 80.6, 79.8, 62.1, 55.7, 46.9, 41.0, 33.0, 32.4, 30.6, 28.8, 28.7, 24.0, 17.3.

$[\alpha]_D^{23} = -20.000$ (*c* 1.45, MeOH)

HRMS (ESI-TOF): calculated for C₂₂H₄₁N₄O₉⁻ ([M+HCOOH-H]⁻) 505.2879, found 505.2880

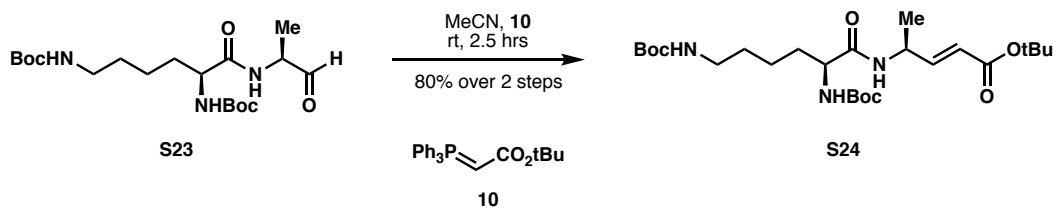


Reduction of Weinreb amide S22:

Dipeptide **S22** (1.00 g, 2.17 mmol, 1 eq) was dissolved in 22 mL anhydrous diethyl ether and cooled to 0 °C. A solution of lithium aluminum hydride (1 M in Et₂O, 8.14 mL, 3.75 eq) was then added dropwise at 0 °C. Upon complete addition, the reaction was stirred for 30 minutes at 0 °C then quenched with 16 mL 2 M NaHSO₄. The layers were separated and the aqueous phase was extracted with Et₂O (3 x 25 mL). The combined organic layers were washed with water, saturated NaHCO₃ and brine, then dried over Na₂SO₄. Concentration *in vacuo* provided aldehyde **S23** as a white foam that was used for the next step without further purification (0.892 g).

¹H NMR (600 MHz, CDCl₃): δ 9.44 (s, 1H), 6.84 (d, *J* = 6.3 Hz, 1H), 5.17 (d, *J* = 7.5 Hz, 1H), 4.65 – 4.53 (m, 1H), 4.41 – 4.32 (m, 1H), 4.07 – 3.98 (m, 1H), 3.06 – 2.94 (m, 2H), 1.81 – 1.67 (m, 1H), 1.63 – 1.48 (m, 1H), 1.47 – 1.37 (m, 4H), 1.34 (s, 9H), 1.34 (s, 9H), 1.26 (d, *J* = 7.4 Hz, 3H).

HRMS (ESI-TOF): calculated for C₁₉H₃₄N₃O₆⁻ ([M-H]⁻) 400.2453, found 400.2457



Wittig olefination of aldehyde S23:

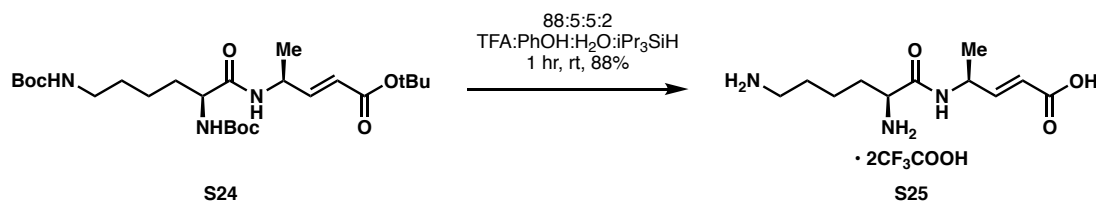
Ylide **10** (1.02 g, 2.71 mmol, 1.25 eq) was dissolved in 21 mL anhydrous acetonitrile, then a solution of crude aldehyde **S23** (0.892 g) in 10 mL acetonitrile was added dropwise at room temperature. The reaction was stirred for 30 minutes or until completion by ^1H NMR or TLC, and then concentrated to dryness. Purification by silica flash chromatography (60:40 hexanes:ethyl acetate) provided **S24** as a white foam (0.863 g, 80% from **S22**).

^1H NMR (600 MHz, MeOD): δ 6.77 (dd, $J = 15.7, 5.0$ Hz, 1H), 5.80 (dd, $J = 15.7, 1.8$ Hz, 1H), 4.59 (qdd, $J = 6.9, 4.9, 1.7$ Hz, 1H), 4.03 – 3.84 (m, 1H), 3.03 (td, $J = 6.8, 2.8$ Hz, 2H), 1.78 – 1.66 (m, 1H), 1.66 – 1.56 (m, 1H), 1.54 – 1.48 (m, 2H), 1.47 (s, 9H), 1.45 (s, 9H), 1.43 (s, 9H), 1.40 – 1.31 (m, 2H), 1.28 (d, $J = 7.0$ Hz, 3H).

^{13}C NMR (151 MHz, MeOD): δ 174.6, 167.3, 158.6, 157.8, 149.2, 122.8, 81.7, 80.6, 79.8, 56.3, 46.9, 41.0, 33.1, 30.6, 28.8, 28.8, 28.4, 24.2, 19.9.

$[\alpha]_{\text{D}}^{23} = -17.603$ (c 1.46, MeOH)

HRMS (ESI-TOF): calculated for $\text{C}_{26}\text{H}_{46}\text{N}_3\text{O}_9^-$ ($[\text{M}+\text{HCOOH}-\text{H}]^-$) 544.3240, found 544.3246



Deprotection of dipeptide S24:

Dipeptide **S24** (431 mg, 0.863 mmol, 1 eq) was dissolved in 22 mL of a freshly prepared solution of “Reagent B” (88:5:5:2 trifluoroacetic acid:phenol:water:triisopropylsilane). After stirring for 1 hour at room temperature, the reaction was diluted with 30 mL toluene and concentrated *in vacuo* to dryness, followed by an additional evaporation from 30 mL toluene. The residue was then dissolved in 2 mL methanol and added dropwise to 100 mL diethyl ether at 0 °C. The solids were collected by centrifugation at 4200 RPM for 10 minutes at 4 °C, then precipitated

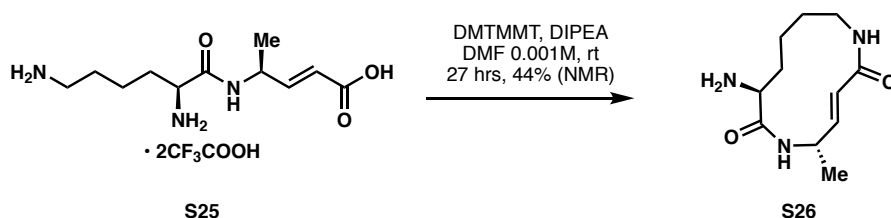
again into 50 mL diethyl ether at 0 °C from 1.5 mL methanol. The solids were collected by centrifugation as above, then dried from methanol to provide **S25** as an off-white solid (356 mg, 88%).

¹H NMR (600 MHz, MeOD): δ 6.83 (dd, *J* = 15.7, 5.4 Hz, 1H), 5.86 (dd, *J* = 15.7, 1.6 Hz, 1H), 4.69 – 4.59 (m, 1H), 3.87 (t, *J* = 6.4 Hz, 1H), 2.98 – 2.89 (m, 2H), 1.99 – 1.82 (m, 2H), 1.76 – 1.66 (m, 2H), 1.54 – 1.42 (m, 2H), 1.33 (d, *J* = 7.0 Hz, 3H).

¹³C NMR (151 MHz, MeOD): δ 170.1, 169.3, 149.0, 122.7, 54.2, 47.4, 40.3, 32.1, 28.2, 22.9, 19.7.

$[\alpha]_D^{23} = -13.585$ (*c* 0.530, MeOH)

HRMS (ESI-TOF): calculated for free base C₁₁H₂₀N₃O₃⁻ ([M-H]⁻) 242.2521, found 242.1511

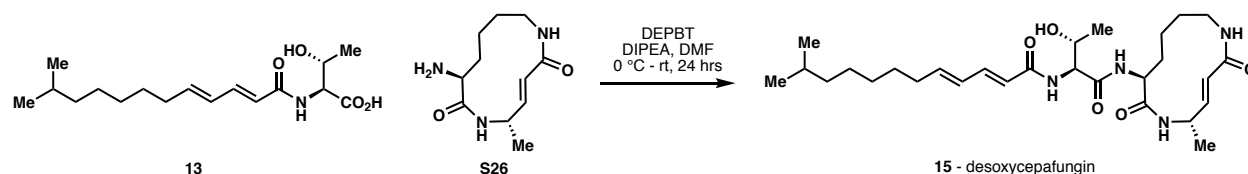


Macrolactamization of **S25**:

Linear macrocycle precursor **S25** (200 mg, 0.424 mmol, 1 eq) was dissolved in 424 mL anhydrous DMF. The solution was treated with diisopropylethylamine (296 μL, 1.70 mmol, 4 eq), followed by solid 4-(4,6-dimethoxy-1,3,5-triazin-2-yl)-4-methyl-morpholinium tetrafluoroborate (DMTMMT) (209 mg, 0.637 mmol, 1.5 eq) at room temperature. The reaction was stirred under argon for 27 hours, then quenched with 10 mL water and concentrated *in vacuo* to dryness. The residue was dissolved in 2 mL methanol and precipitated into 50 mL diethyl ether with rapid stirring. The solids were collected by centrifugation at 4200 RPM for 15 minutes at 4 °C to yield crude **S26** as a tan solid (276 mg, 44% from **S25**, 39% from **S24**). Yield was determined by ¹H NMR analysis of a 6.2 mg crude sample with 4-toluenesulfonamide (7.7 mg, 0.0450 mmol) added as internal standard.

¹H NMR (400 MHz, MeOD): 4-toluenesulfonamide: δ 7.82 – 7.72 (m, 2H), 7.40 – 7.30 (m, 2H), 2.42 (s, 3H). Compound **S26**: 7.03 (dd, *J* = 15.4, 4.9 Hz, 1H), 6.35 (dd, *J* = 15.5, 1.4 Hz, 1H), 4.66 – 4.58 (m, 1H), 4.16 (t, *J* = 3.7 Hz, 1H), 3.58 – 3.44 (m, 2H), 2.36 – 2.24 (m, 1H), 1.98 – 1.77 (m, 2H), 1.77 – 1.62 (m, 2H).

HRMS (ESI-TOF): calculated for $C_{11}H_{18}N_3O_2^-$ ($[M-H]^-$) 224.1404, found 224.1406



Coupling of tail fragment to desoxyglidobamine:

Acid **13** (42 mg, 0.134 mmol, 2 eq) and crude desoxyglidobamine **S26** (100 mg, ~0.0670 mmol as judged by 1H NMR analysis, 1 eq) were dissolved in 3.4 mL anhydrous DMF and cooled to 0 °C. To the mixture was added diisopropylethylamine (35 μ L, 0.201 mmol, 3 eq), followed by solid DEPBT (40 mg, 0.134 mmol, 2 eq). The reaction was warmed to room temperature and stirred overnight, and the reaction progress was monitored by LCMS. At 24 hours, the reaction was cooled to 0 °C and quenched with 2 mL saturated NH_4Cl . The mixture was extracted with ethyl acetate (4 x 4 mL), then n-butanol (3 x 4 mL). The combined organic layers were washed with brine, dried over Na_2SO_4 , and concentrated *in vacuo*. The residue was filtered through a 0.2 μ m PTFE membrane filter in methanol, then purified by reversed-phase HPLC (gradient 30–60% acetonitrile in water over 35 minutes, 0.1% formic acid added) to provide 7.9 mg of desoxycepa fungin I (**15**) as a fluffy white powder after lyophilization (23%, 9% from **S24**).

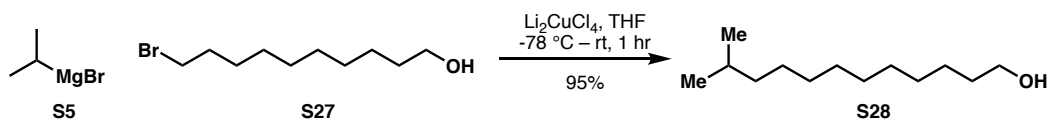
1H NMR (600 MHz, DMSO): δ 8.44 (d, $J = 7.9$ Hz, 1H), 7.99 (d, $J = 8.5$ Hz, 1H), 7.62 (d, $J = 7.2$ Hz, 1H), 7.35 (dd, $J = 8.0, 6.1$ Hz, 1H), 7.00 (dd, $J = 15.1, 10.8$ Hz, 1H), 6.78 (dd, $J = 15.3, 4.7$ Hz, 1H), 6.23 (dd, $J = 15.4, 1.4$ Hz, 1H), 6.21 – 6.15 (m, 2H), 6.09 (dt, $J = 14.8, 6.9$ Hz, 1H), 4.54 – 4.48 (m, 1H), 4.44 – 4.36 (m, 1H), 4.32 (dd, $J = 8.5, 3.9$ Hz, 1H), 4.02 – 3.96 (m, 1H), 3.32 – 3.23 (m, 1H), 2.98 – 2.91 (m, 1H), 2.13 (q, $J = 7.2$ Hz, 2H), 2.10 – 2.03 (m, 1H), 1.74 – 1.64 (m, 1H), 1.50 (hept, $J = 6.7$ Hz, 1H), 1.46 – 1.41 (m, 1H), 1.41 – 1.35 (m, 2H), 1.35 – 1.29 (m, 1H), 1.29 – 1.22 (m, 5H), 1.20 (d, $J = 7.0$ Hz, 3H), 1.17 – 1.11 (m, 2H), 1.02 (d, $J = 6.3$ Hz, 3H), 0.98 – 0.90 (m, 1H), 0.85 (d, $J = 6.6$ Hz, 6H).

^{13}C NMR (151 MHz, DMSO): δ 170.5, 169.4, 165.8, 165.5, 146.7, 142.1, 139.8, 128.6, 122.9, 118.4, 66.6, 58.1, 51.5, 45.6, 38.4, 37.9, 32.2, 30.2, 29.6, 28.8, 28.4, 27.4, 26.6, 22.5, 19.6, 18.3, 17.1.

$[\alpha]_D^{23} = -14.375$ ($c = 0.160$, MeOH)

HRMS (ESI-TOF): calculated for $C_{28}H_{47}N_4O_5^+$ ($[M+H]^+$) 519.3541, found 519.3564

Synthesis of cepafungin analog with saturated lipid tail (16)



Synthesis of branched alcohol S28:

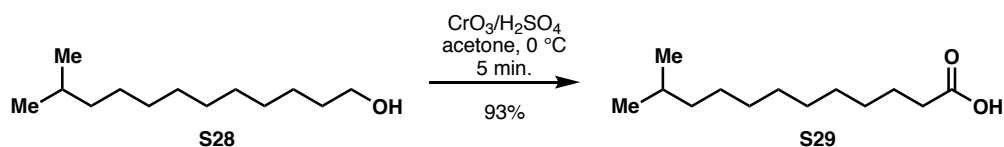
Following a procedure adapted from Melaugh et al.,² lithium chloride (1.61 g, 42.4 mmol, 2.05 eq) was flame-dried in a 250 mL round-bottom flask under high vacuum. Solid copper(II) chloride (2.50 g, 18.6 mmol, 1 eq) was added under argon. The combined reagents were then dissolved in 25 mL anhydrous THF to provide a dark red solution of Li_2CuCl_4 .

A flame-dried 3-neck 500 mL flask fitted with a reflux condenser was charged with magnesium turnings (3.14 g, 129 mmol, 1.18 eq with respect to 2-bromopropane) and 50 mL anhydrous THF. With rapid stirring, 2-bromopropane (10.3 mL, 110 mmol, 6.5 eq with respect to **S27**) was added dropwise until refluxing began, at which point the flask was lowered into a water bath. Upon complete addition, the water bath was removed and the reaction was allowed to stir under argon for 30 minutes to produce a dark gray suspension of **S5**. The mixture was cooled to -78°C , and bromoalcohol **S27** (4.00 g, 16.9 mmol, 1 eq) was added in 4.2 mL dry THF, followed by the above solution of Li_2CuCl_4 (1.5 M in THF, 25.4 mL, 1.1 eq with respect to **S27**). Upon complete addition, the reaction was removed from its cooling bath and allowed to warm to room temperature. Reaction progress was monitored by TLC until completion at 1 hour. The reaction was then carefully quenched at 0°C with 50 mL saturated NH_4Cl solution, filtered through a sintered glass funnel, and the filtrate concentrated *in vacuo* to remove most of the THF. The mixture was diluted with 100 mL ethyl acetate and 100 mL 1M HCl. The layers were separated, and the aqueous phase was extracted with ethyl acetate (3 x 50 mL). The combined organic layers were washed with 50 mL each of water, saturated aqueous NaHCO_3 and brine, then dried over Na_2SO_4 . Purification by silica flash chromatography (90:10 hexanes:ethyl acetate) provided pure **S28** as a colorless liquid (3.22 g, 95%).

^1H NMR (600 MHz, CDCl_3): δ 3.63 (t, $J = 6.7$ Hz, 2H), 1.59 – 1.54 (m, 2H), 1.53 – 1.47 (m, 1H), 1.36 – 1.22 (m, 14H), 1.19 – 1.10 (m, 2H), 0.85 (d, $J = 6.7$ Hz, 6H).

^{13}C NMR (151 MHz, CDCl_3): δ 63.2, 39.2, 32.9, 30.1, 29.8, 29.8, 29.7, 29.6, 28.1, 27.6, 25.9, 22.8.

HRMS (ESI-TOF): calculated for $\text{C}_{14}\text{H}_{32}\text{O}_1\text{N}_1^+$ ($[\text{M}+\text{CH}_3\text{CN}+\text{H}]^+$) 242.2478, found 242.2475



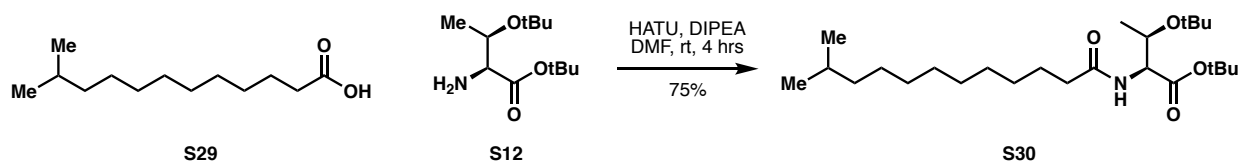
Oxidation of branched alcohol **S28**:

Alcohol **S28** (1.60 g, 7.96 mmol, 1 eq) was dissolved in 50 mL acetone and cooled to 0 °C. A solution of Jones' reagent (6.52 mL, 19.9 mmol, 2.5 eq) was then added dropwise and allowed to stir at 0 °C. Upon completion by TLC in five minutes, the reaction was quenched with 3 mL isopropanol, filtered through a plug of celite and concentrated *in vacuo* to remove the organic solvent. The remaining aqueous mixture was diluted with 25 mL 1 M HCl and extracted with ethyl acetate (4 x 25 mL). The combined organic layers were washed with 25 mL water and brine, then dried over Na_2SO_4 and concentrated *in vacuo* to provide 1.58 g of pure **S29** (93%).

^1H NMR (600 MHz, CDCl_3): δ 2.34 (t, $J = 7.5$ Hz, 2H), 1.67 – 1.59 (m, 2H), 1.56 – 1.46 (m, 1H), 1.36 – 1.21 (m, 12H), 1.19 – 1.11 (m, 2H), 0.86 (d, $J = 6.6$ Hz, 6H).

^{13}C NMR (151 MHz, CDCl_3): δ 180.5, 39.3, 34.4, 30.1, 29.9, 29.7, 29.5, 29.3, 28.2, 27.6, 24.9, 22.9.

HRMS (ESI-TOF): calculated for $\text{C}_{13}\text{H}_{25}\text{O}_2^-$ ($[\text{M}-\text{H}]^-$) 213.1860, found 213.1861



Synthesis of fatty acid amide **S30**:

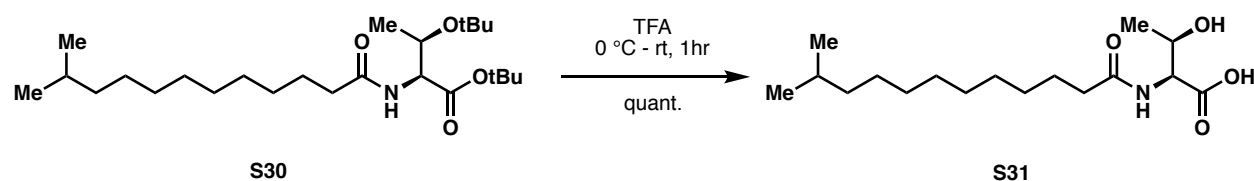
Fatty acid **S29** (636 mg, 2.97 mmol, 1 eq) was dissolved in 14 mL anhydrous DMF at 0 °C. Diisopropylethylamine was added (2.33 mL, 13.4 mmol, 4.5 eq), followed by HATU (1.13 g, 2.97 mmol, 1 eq). The mixture was stirred at 0 °C under argon for five minutes before adding **S12** (1.03 g, 4.45 mmol, 1.5 eq) in 1 mL DMF. The reaction was stirred to room temperature under

argon for 4 hours or until completion by LCMS. The reaction was then diluted at 0 °C with 50 mL saturated NH₄Cl and ethyl acetate. The pH of the mixture was adjusted to 7 with 1 M HCl, and the aqueous layer was extracted with ethyl acetate (3 x 50 mL). The combined organic layers were washed with 30 mL 1M HCl, water, NaHCO₃ and brine, then dried over Na₂SO₄. Concentration *in vacuo* followed by silica flash chromatography (85:15 hexanes:ethyl acetate) provided **S30** as a colorless oil (955 mg, 75%).

¹H NMR (600 MHz, CDCl₃): δ 6.12 (d, *J* = 9.2 Hz, 1H), 4.39 (dd, *J* = 9.2, 2.1 Hz, 1H), 4.19 (qd, *J* = 6.2, 2.1 Hz, 1H), 2.26 (d, *J* = 7.5 Hz, 2H), 1.69 – 1.61 (m, 2H), 1.51 (dq, *J* = 13.3, 6.6 Hz, 1H), 1.45 (s, 9H), 1.38 – 1.21 (m, 14H), 1.16 (s, 9H), 1.15 (d, *J* = 6.3 Hz, 3H), 0.85 (d, *J* = 6.6 Hz, 6H).
¹³C NMR (151 MHz, CDCl₃): δ 173.5, 170.3, 81.9, 73.9, 67.4, 58.3, 39.2, 36.9, 30.0, 29.8, 29.6, 29.5, 29.4, 28.9, 28.3, 28.1, 27.5, 25.8, 22.8, 21.1.

$[\alpha]_D^{23} = -4.402$ (*c* 2.09, MeOH)

HRMS (ESI-TOF): calculated for C₂₅H₅₀NO₄⁺ ([M+H]⁺) 428.3735, found 428.3748



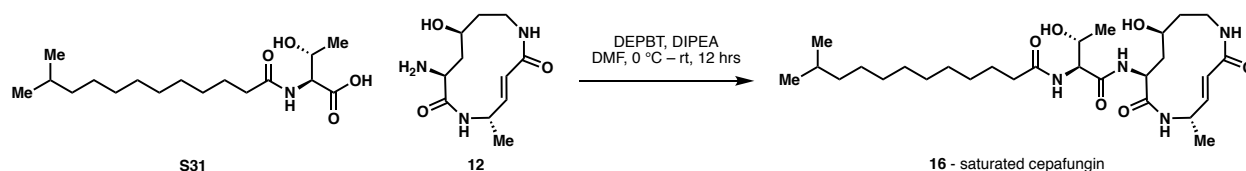
Deprotection of amide **S30**:

Fatty acid amide **S30** (100 mg, 0.234 mmol, 1 eq) was dissolved in 2.3 mL trifluoroacetic acid at 0 °C, then stirred at room temperature for 1 hour. The solution was then diluted with 10 mL toluene and concentrated *in vacuo* to dryness, followed by an additional evaporation from 10 mL toluene to provide **S31** as a colorless oil (91 mg, quantitative).

¹H NMR (600 MHz, CDCl₃): δ 6.99 (s, 1H), 4.76 – 4.10 (m, 2H), 2.28 (s, 2H), 1.62 (s, 2H), 1.53 – 1.46 (m, 1H), 1.35 – 1.22 (m, 14H), 1.19 (s, 1H), 1.17 – 1.11 (m, 2H), 0.86 (d, *J* = 6.6 Hz, 6H).
¹³C NMR (151 MHz, CDCl₃): δ 175.5, 39.2, 36.6, 32.0, 30.1, 29.9, 29.8, 29.6, 29.5, 28.1, 27.6, 26.3, 26.0, 22.8, 19.5, 14.3.

$[\alpha]_D^{23} = 4.643$ (*c* 1.40, MeOH)

HRMS (ESI-TOF): calculated for C₁₇H₃₂NO₄⁻ ([M-H]⁻) 314.2337, found 314.2339



Coupling of saturated tail fragment to glidobamine:

Acid **S31** (33 mg, 0.104 mmol, 2 eq) and crude glidobamine **12** (62 mg, ~0.0521 mmol as judged by $^1\text{H NMR}$ analysis, 1 eq) were dissolved in 2.6 mL anhydrous DMF and cooled to 0 °C. To the mixture was added diisopropylethylamine (27 μL , 0.156 mmol, 3 eq), followed by solid DEPBT (31 mg, 0.104 mmol, 2 eq). The reaction was stirred to room temperature overnight, and reaction progress was monitored by LCMS. At 12 hours, the reaction was cooled to 0 °C and quenched with 0.5 mL water, then concentrated *in vacuo* to dryness. The residue was precipitated into 50 mL diethyl ether at 0 °C from 0.75 mL methanol, and the resulting solids were collected by centrifugation at 4200 RPM at 4 °C for 15 minutes. The solids were dissolved in methanol, filtered through a 0.2 μm PTFE membrane filter, then purified by reversed-phase HPLC (gradient 30–100% acetonitrile in water over 20 minutes, 0.1% formic acid added) to provide 9.6 mg of **16** as a fluffy white powder after lyophilization (34%, 20% from **11**).

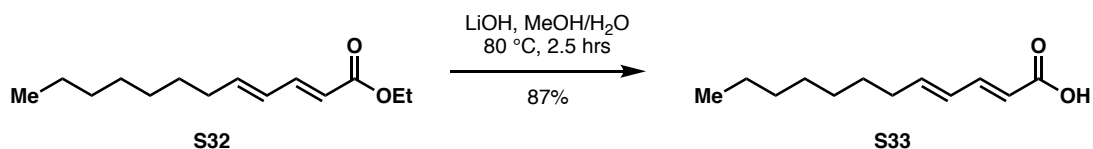
$^1\text{H NMR}$ (600 MHz, DMSO): δ 8.66 (s, 1H), 7.67 (dd, $J = 28.3, 8.3$ Hz, 2H), 7.41 (t, $J = 6.3$ Hz, 1H), 6.40 (d, $J = 15.9$ Hz, 1H), 6.18 (dd, $J = 15.8, 1.2$ Hz, 1H), 4.85 – 4.74 (m, 1H), 4.73 – 4.60 (m, 1H), 4.48 – 4.25 (m, 2H), 4.18 (dd, $J = 8.8, 3.9$ Hz, 1H), 3.99 – 3.88 (m, 1H), 3.63 – 3.50 (m, 1H), 3.09 – 2.91 (m, 2H), 2.24 – 2.09 (m, 2H), 1.92 – 1.74 (m, 1H), 1.64 – 1.54 (m, 1H), 1.54 – 1.41 (m, 4H), 1.41 – 1.33 (m, 1H), 1.27 – 1.18 (m, 15H), 1.17 – 1.10 (m, 2H), 0.99 (d, $J = 6.3$ Hz, 3H), 0.84 (d, $J = 6.6$ Hz, 6H).

$^{13}\text{C NMR}$ (151 MHz, DMSO): δ 172.5, 171.0, 169.4, 167.6, 142.7, 123.5, 67.0, 66.6, 57.9, 51.2, 44.7, 42.5, 38.5, 35.2, 29.3, 29.1, 29.0, 28.8, 28.6, 27.4, 26.8, 25.4, 22.5, 19.9, 18.5.

$[\alpha]_{\text{D}}^{23} = -76.842$ (c 0.190, MeOH)

HRMS (ESI-TOF): calculated for $\text{C}_{28}\text{H}_{49}\text{N}_4\text{O}_6^-$ ($[\text{M}-\text{H}]^-$) 537.3657, found 537.3657

Synthesis of glidobactin A (2)



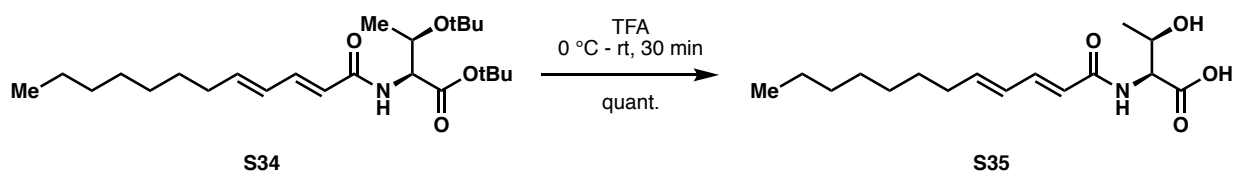
Hydrolysis of diene ester **S32**:

Ester **S32**^{S5} (1.00 g, 4.458 mmol, 1 eq) was dissolved in 22.5 mL methanol. With rapid stirring, a solution of lithium hydroxide (534 mg, 22.3 mmol, 5 eq) in 22.5 mL water was added. The reaction was heated at 80 °C for 2.5 hours or until completion as judged by TLC. Methanol was evaporated *in vacuo*. The mixture was adjusted to pH 1 with 1 M HCl and diluted with 50 mL DCM. The layers were separated, and the aqueous layer was extracted with DCM (3 x 20 mL). The combined organic layers were washed with 20 mL brine then dried over Na₂SO₄. Concentration *in vacuo* provided pure **S33** as a waxy white solid (764 mg, 87%).

¹H NMR (600 MHz, CDCl₃): δ 7.39 – 7.29 (m, 1H), 6.25 – 6.11 (m, 2H), 5.78 (d, *J* = 15.3 Hz, 1H), 2.24 – 2.10 (m, 2H), 1.47 – 1.39 (m, 2H), 1.33 – 1.22 (m, 8H), 0.88 (t, *J* = 7.0 Hz, 3H).

¹³C NMR (151 MHz, CDCl₃): δ 173.0, 147.7, 146.4, 128.4, 118.4, 33.2, 31.9, 29.3, 29.2, 28.8, 22.8, 14.2.

HRMS (ESI-TOF): calculated for C₁₂H₁₉O₂⁻ ([M-H]⁻) 195.1391, found 195.1392



Deprotection of amide **S34**:

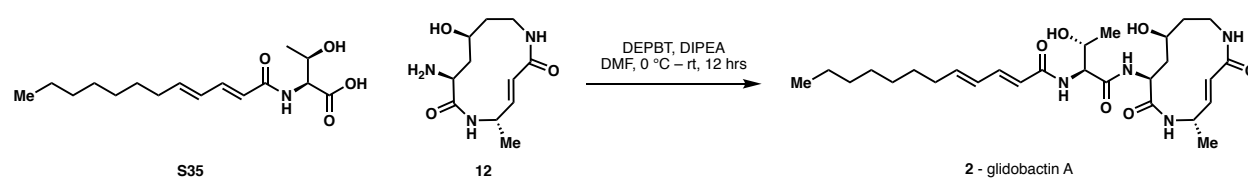
Amide **S34** was prepared in a similar fashion to **S13**. Amide **S34** (100 mg, 0.244 mmol, 1 eq) was dissolved in 2.4 mL trifluoroacetic acid at 0 °C, then stirred at room temperature for 30 minutes. The solution was then diluted with 8 mL toluene and concentrated *in vacuo* to dryness, followed by two additional evaporations from 8 mL toluene to provide pure **S35** as a colorless resin (92 mg, quantitative).

¹H NMR (400 MHz, CDCl₃): δ 7.25 – 7.15 (m, 1H), 7.08 (d, *J* = 8.4 Hz, 1H), 6.21 – 6.03 (m, 2H), 5.92 (d, *J* = 15.0 Hz, 1H), 4.65 (d, *J* = 8.0 Hz, 1H), 4.55 – 4.37 (m, 1H), 2.20 – 2.07 (m, 2H), 1.45 – 1.35 (m, 2H), 1.33 – 1.24 (m, 8H), 1.21 (d, *J* = 6.3 Hz, 3H), 0.88 (t, *J* = 6.9 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃): δ 173.8, 168.4, 145.1, 143.5, 128.3, 120.4, 67.9, 57.8, 33.3, 31.9, 29.4, 29.3, 29.0, 22.8, 19.4, 14.2.

[α]_D²³ = 13.472 (*c* 0.720, MeOH)

HRMS (ESI-TOF): calculated for C₁₆H₂₆NO₄⁻ ([M-H]⁻) 296.1867, found 296.1870



Coupling of glidobactin A tail fragment to glidobamine:

Acid **S38** (60 mg, 0.223 mmol, 2 eq) and crude glidobamine **12** (129 mg, ~0.111 mmol as judged by ¹H NMR analysis, 1 eq) were dissolved in 5.6 mL anhydrous DMF and cooled to 0 °C. To the mixture was added diisopropylethylamine (116 μL, 0.668 mmol, 6 eq), followed by solid DEPBT (67 mg, 0.223 mmol, 2 eq). The reaction was warmed to room temperature and stirred overnight, and reaction progress was monitored by LCMS. At 12 hours, the reaction was cooled to 0 °C and quenched with 1 mL water, then concentrated *in vacuo* to dryness. The residue was precipitated into 50 mL diethyl ether at 0 °C from 0.75 mL methanol, and the resulting solids were collected by centrifugation at 4200 RPM at 4 °C for 15 minutes. The solids were dissolved in methanol, filtered through a 0.2 μm PTFE membrane filter, then purified by reversed-phase HPLC (32% acetonitrile in water) to provide 25 mg of glidobactin A (**17**) as a fluffy white powder after lyophilization (43%, 25% from **11**).

¹H NMR (600 MHz, DMSO): δ 8.66 (s, 1H), 7.91 (d, *J* = 8.8 Hz, 1H), 7.74 (d, *J* = 7.9 Hz, 1H), 7.41 (t, *J* = 6.5 Hz, 1H), 7.00 (dd, *J* = 15.1, 10.8 Hz, 1H), 6.40 (d, *J* = 13.9 Hz, 1H), 6.23 – 6.05 (m, 4H), 4.88 (s, 1H), 4.67 (s, 1H), 4.46 – 4.30 (m, 2H), 3.95 (s, 1H), 3.57 (s, 1H), 3.10 – 2.90 (m, 2H), 2.18 – 2.07 (m, 2H), 1.84 (s, 1H), 1.63 – 1.52 (m, 1H), 1.50 – 1.41 (m, 1H), 1.41 – 1.33 (m, 3H), 1.30 – 1.22 (m, 8H), 1.22 – 1.16 (m, 2H), 1.00 (d, *J* = 6.3 Hz, 3H), 0.86 (t, *J* = 6.8 Hz, 3H).

¹³C NMR (151 MHz, DMSO): δ 171.0, 169.4, 167.6, 165.4, 143.1, 142.1, 139.7, 128.6, 123.3, 123.1, 66.9, 66.7, 58.1, 51.2, 44.7, 42.5, 32.2, 31.2, 28.5, 28.5, 28.4, 22.1, 19.9, 18.5, 14.0.

$[\alpha]_D^{22}$ = -91.957 (c = 0.460, MeOH)

HRMS (ESI-TOF): calculated for C₂₇H₄₃N₄O₆⁻ ([M-H]⁻) 519.3188, found 519.3180

Chemoproteomics Experimental Procedures

Cell culture and lysate preparation

RPMI 8226 and MM1.R cells were maintained in RPMI-1640 media. HEK293T cells were maintained in DMEM. All media were supplemented with 10% fetal calf serum (FCS), non-essential amino acids and penicillin/streptomycin. Cells were grown at 37 °C under 5% CO₂ atmosphere. Cells were allowed to grow to confluence, harvested by pipeting, then washed 2 times in PBS by brief centrifugation at 300 x g at 4 °C and resuspended in PBS. Cells were lysed by needle sonication to obtain cell lysates and protein concentration was determined using the Bradford assay.

Cell toxicity assays

RPMI 8226 (20,000 cells/well) or MM1.R (20,000 cells/well) cells were seeded in a 96-well plate in cell culture media supplemented with indicated concentrations of either **1** or bortezomib (BTZ) (1,000x stock in DMSO) and cultured for either 24 or 48 hours. Toxicity was determined using the WST-1 assay (Roche) according to the protocol of the manufacturer. EC₅₀ values were calculated with GraphPad Prism (V7.02).

Preparation of proteomes for SDS-PAGE activity-based probe profiling experiments

Proteins in full cell lysate (2 mg/mL, 25 μ L) were treated with indicated concentrations of **14** (1 μ L of 25x stock in DMSO) or DMSO for one hour at r.t. Click chemistry was then initiated by the addition of TAMRA alkyne (Click Chemistry Tools, 25x stock in DMSO), tris(2-carboxyethyl)phosphine hydrochloride (TCEP, Alfa Aesar, 1 mM, fresh 50x stock in water), tris[(1-benzyl-1*H*-1,2,3-triazol-4-yl)methyl]amine (TBTA, Sigma-Aldrich, 100 μ M, 16x stock in DMSO:*t*BuOH 1:4), and copper(II) sulfate (1 mM, 50x stock in water) to the lysate and incubated in the dark for one hour at r.t. SDS-PAGE reducing loading buffer (4x) was added and proteins were separated using an 11% SDS-PAGE gel. Gels were visualized using a Sapphire Biomolecular Imager (Azure Biosystems), then stained using Coomassie Brilliant Blue (CBB). Images were quantified with ImageJ.

Gel-based in situ competitive experiments

RPMI 8226 cells were seeded in a 6-well plate (1,000,000 cells/well) in cell culture media supplemented with indicated concentrations of **1** (1'000x stock in DMSO) or DMSO and cultured for 6 hours. Cells were then collected and lysed as described above. Lysates (2 mg/mL, 25 μ L) were treated with **14** (10 μ M; 1 μ L of 25x stock in DMSO) for one hour at r.t. Click chemistry, reducing SDS-PAGE and visualization were performed as described above.

In situ competitive 14 pulldown experiment for mass spectrometry

RPMI 8226 cells were seeded in 14 cm Petri dishes and cultured as previously described until they reached confluence. Cell culture media was then removed and the cells were incubated in fresh media with either **1** (100 nM; 25 μ L of 1000x stock in DMSO) or DMSO for 6 hours. Cells were washed two times with PBS and harvested by centrifugation, resuspended in PBS and lysed as described above. The protein concentration of the lysate was determined using the Bradford assay. Lysates (2.32 mg/mL, 645 μ L) were treated with **14** (10 μ M; 6.51 μ L of 100x stock in DMSO) for one hour at r.t. and subjected to click chemistry using biotin azide (30 μ M, 50x stock in DMSO), tris(2-carboxyethyl)phosphine hydrochloride (TCEP) (1 mM, 50x fresh stock in water), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (TBTA) (100 μ M, 16x stock in DMSO:tBuOH 1:4), and copper(II) sulfate (1 mM, 50x stock in water) for one hour at r.t. Protein was precipitated by adding methanol/chloroform/water (4:1:3 v/v) to the reaction mixture and the turbid mixture was centrifuged for five minutes at 14,000 x g at 4 °C yielding a protein layer between the aqueous and organic layers. The protein layer was isolated, dried and solubilized in 2 % SDS in PBS via sonication. The proteome was centrifuged at 4,700 x g for five minutes and the supernatant was transferred to a new tube. PBS was added to give a final SDS concentration of 0.2 %. Streptavidin agarose beads (150 μ L, ProteoChem) were added and the mixture was rotated overnight at r.t. Beads were washed with 1 % SDS in PBS (1x 10 mL), PBS (3x 10 mL), and water (3x 10 mL). Beads were resuspended in 6 M urea in PBS (500 μ L), reduced with 10 mM neutralized TCEP (200 mM fresh stock in water) for 30 minutes at r.t. and alkylated with 25 mM iodoacetamide (400 mM fresh stock in water) for 30 minutes at r.t. in the dark. Beads were pelleted by centrifugation (1'400 x g, 2 minutes) and resuspended in 150 μ L of 2 M urea in 50 mM NH_4HCO_3 , 1 mM CaCl_2 (100x stock in water) and trypsin (Thermo Scientific, 1.5 μ L of 0.5 $\mu\text{g}/\mu\text{L}$). The digestion was performed for 12 hours at 37 °C. Samples were acidified to a final concentration of 5 % acetic

acid, desalted over a self-packed C18 spin column and dried. Samples were analyzed by LC-MS/MS (described below) and the MS data was processed with MaxQuant (described below).

LC-MS/MS analysis

Peptides were resuspended in water with 0.1 % formic acid (FA) and analyzed using EASY-nLC 1200 nano-UHPLC coupled to a Q Exactive HF-X Quadrupole-Orbitrap mass spectrometer (Thermo Scientific). The chromatography column consisted of a 50 cm long, 75 μm i.d. microcapillary capped by a 5 μm tip and packed with ReproSil-Pur 120 C18-AQ 2.4 μm beads (Dr. Maisch GmbH). LC solvents were 0.1 % FA in H₂O (Buffer A) and 0.1 % FA in 90 % MeCN: 10 % H₂O (Buffer B). Peptides were eluted into the MS at a flow rate of 300 nL/min. over a 240 min. linear gradient (5-35 % Buffer B) at 65 °C. Data was acquired in data-dependent mode (top-20, NCE 28, R = 7,500) after full MS scan (R = 60,000, m/z 400-1,300). Dynamic exclusion was set to 10 s, peptide match to prefer and isotope exclusion was enabled.

MaxQuant analysis

The MS data was analyzed with MaxQuant^{S6} (V1.6.1.0) and searched against the human proteome (Uniprot) and a common list of contaminants (included in MaxQuant). The first peptide search tolerance was set at 20 ppm, 10 ppm was used for the main peptide search and fragment mass tolerance was set to 0.02 Da. The false discovery rate for peptides, proteins and sites identification was set to 1%. The minimum peptide length was set to 6 amino acids and peptide re-quantification and label-free quantification (MaxLFQ) were enabled. The ‘match between runs’ function was activated for the global changes in protein expression experiment. The minimal number of peptides per protein was set to two. Methionine oxidation was searched as a variable modification and carbamidomethylation of cysteines was searched as a fixed modification.

Transfection and Western blot

HEK293T cells were seeded (6,000,000 cells in 20 mL DMEM 10% FCS without Pen/Strep) in a 10 cm Petri dish and left overnight to attach. Cells were transfected using a mixture of 96 μg PEI MAX 40000 (Polysciences Inc.) and 24 μg DNA in 2 mL opti-MEM. After 24 hours, cells were harvested by scraping, washed two times with PBS and lysates were prepared and treated with 30 μM **14** as described above. Click chemistry, reducing SDS-PAGE and visualization were performed as described above. Proteins were transferred to a PVDF membrane using a Trans-Blot Turbo transfer system (Bio-Rad). Membrane was blocked with 5% milk in Tris-Buffered Saline

with 0.1 % Tween 20 (TBST) for one hour. Rabbit polyclonal antibody against DYKDDDDK (FLAG) (CST, #2368S, 1/1,000 in 5% milk in TBST) and α -tubulin (CST, #2144S, 1/1,000 in 5% milk in TBST) were added and incubated overnight at 4 °C. Membrane was washed three times for five minutes with TBST and incubated with Alexa Fluor 647-AffiniPure Donkey Anti-Rabbit IgG (H+L) (Jackson ImmunoResearch Inc., 711-605-152, 1/500 in 5 % milk in TBST) for one hour at r.t. Membrane was washed four times for five minutes with TBST and visualized with a Sapphire Biomolecular Imager (Azure Biosystems).

In situ β 5 proteasome activity inhibition assay

RPMI 8226 cells were seeded in a 6-well plate (1,000,000 cells/well) in cell culture media supplemented with indicated concentrations of **1**, **2**, **15** or **16** (1,000x stock in DMSO) or DMSO and cultured for 6 hours. Cells were then collected and lysed as described above. Lysates (1 mg/mL, 25 μ L) were dispensed into 100 μ L assay buffer (PBS (pH 7.4), MgCl₂ (1.5 mM), EDTA (1 mM), EGTA (1 mM), sucrose (250 mM) and freshly added DTT (5 mM), ATP (2 mM) and proteasome substrate Suc-LLVY-AMC (Enzo Life Sciences, 100 μ M, 1 μ L of 100x stock in DMSO)) in the wells of a black / clear bottom 96-well plate. The plate was incubated at 37 °C for two hours and fluorescence was read at A_{360ex}/A_{460em} using a Synergy H1 hybrid multi-mode microplate reader (Biotek). The protocol was modified from reference S7. IC₅₀ values were calculated with GraphPad Prism (V7.02).

Western Blot for mono- / polyubiquitinated conjugates and PARP-1

RPMI 8226 cells were seeded in a 6-well plate (1,000,000 cells/well) in cell culture media supplemented with indicated concentrations of **1** (1,000x stock in DMSO) or DMSO and cultured for 6 hours. Cells were then quickly washed twice in PBS and lysed using RIPA buffer (20 mM Tris, 150 mM NaCl, 2 mM EDTA, 0.1 % SDS, 1 % NP-40, 0.25 % deoxycholate, 1 mM PMSF) plus protease inhibitor cocktail (100x, RPI Corp., Cat.No. P50700-1) for five minutes on ice. Cells were quickly sonicated using a needle sonicator, the lysate was spun down in a tabletop centrifuge at 17000 x g for 10 minutes at 4 °C and the cleared lysate was transferred into a new microtube. Protein concentration was measured using the BCA protein assay (Thermo Fisher, Cat No. 23225). SDS-PAGE was performed as previously described and wet transfer to a PVDF membrane was done at 350 mA for one hour. Membrane was blocked with 5 % milk in TBST for one hour. Primary antibodies against respective proteins: PARP-1 (CST, #9532, 1:1,000 in 5 % BSA in TBST), mono- / polyubiquitinated conjugate antibody (Enzo Life Sciences, Prod. No. BML-

PW8805, 1:500 in 5 % milk in TBST), and α -tubulin antibody (CST, #2144S, 1:1,000 in 5 % milk in TBST)), were added and incubated overnight at 4 °C. Membrane was washed three times for five minutes with TBST and incubated for one hour at r.t. with Alexa Fluor 647-AffiniPure Donkey Anti-Rabbit IgG (Jackson ImmunoResearch Inc., 711-605-152) or Alexa Fluor 488-AffiniPure Donkey Anti-Mouse IgG (Jackson ImmunoResearch Inc., 715-545-150). Membrane was washed four times for five minutes with TBST and visualized with a Sapphire Biomolecular Imager (Azure Biosystems).

Global proteomic profiling of cells treated with 1 or bortezomib using Mass Spectrometry.

RPMI 8226 cells were seeded in a 6-well plate (1,000,000 cells/well) in cell culture media supplemented with **1** (100 nM, 1,000x stock in DMSO), bortezomib (BTZ, 2.5 nM, 1,000x stock in DMSO) or DMSO and cultured for 6 hours. Cells were then collected and lysed in PBS as described earlier and protein concentration was measured using the Bradford assay. Proteins (30 μ g) were then denatured in 6 M urea in 50 mM NH_4HCO_3 , reduced with 10 mM tris(2-carboxyethyl)phosphine hydrochloride (TCEP) for 30 minutes and alkylated with 25 mM iodoacetamide for 30 minutes in the dark. Samples were diluted to 2 M urea with 50 mM NH_4HCO_3 , and digested with trypsin (Thermo Scientific, 1.5 μ L of 0.5 μ g/ μ L) in the presence of 1 mM CaCl_2 (100 \times stock in water). The digestion was performed for 12 hours at 37 °C. Samples were acidified to a final concentration of 5% acetic acid, desalted over a self-packed C18 spin column, and dried. Samples were analyzed by LC-MS/MS (see above), and the MS data were processed with MaxQuant (see above).

Supplemental figures

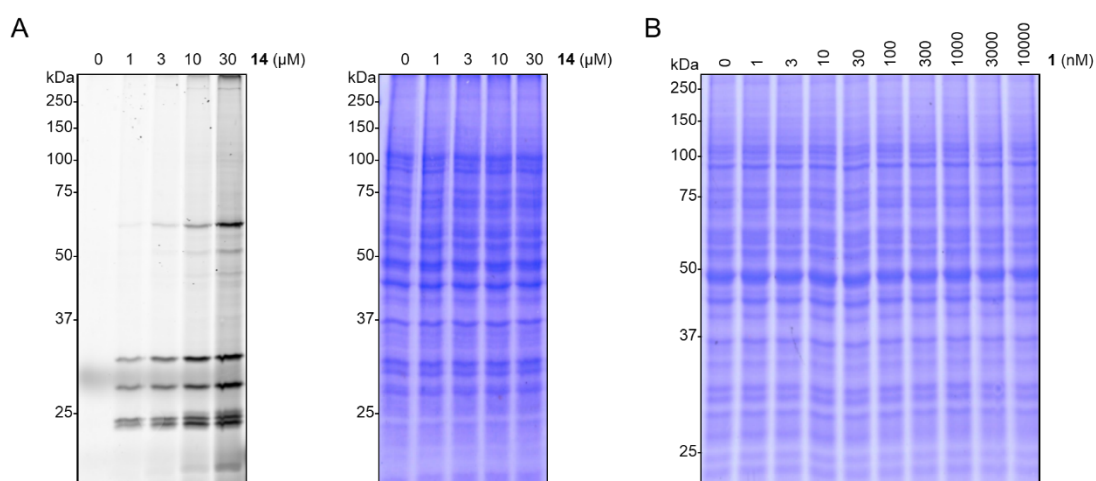


Figure S1. Probe **14** and compound **1** label proteins in a concentration-dependent manner. (A) Concentration-dependent labeling of RPMI 8226 lysates with the alkyne probe **14**. TAMRA fluorescence profile of **14** is shown on the left and the corresponding Coomassie stained gel is shown on the right. (B) Coomassie stained gel corresponding to the gel presented in Figure 3B.

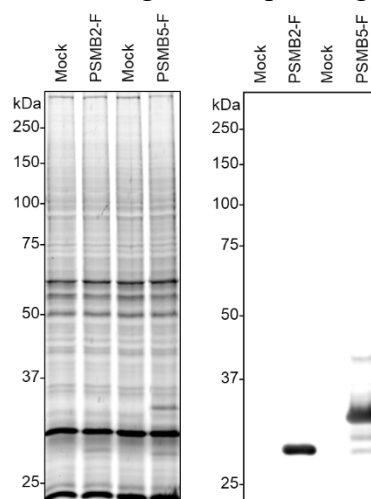


Figure S2. Labeling of mock and overexpressed PSMB2-F and PSMB5-F in HEK293T lysate with 30 μ M **14**. Full length **14** labeling fluorescence profile is shown on the left and the corresponding Western blotting profile of the same gel probed for FLAG is shown on the right. Full profiles were cropped and shown in Figure 4A.

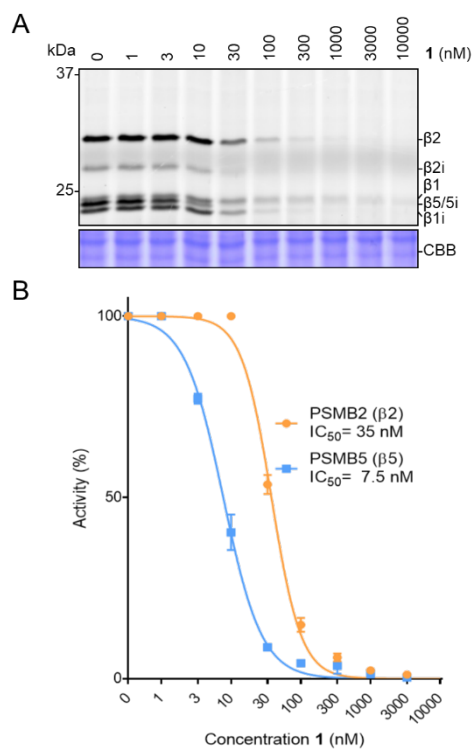


Figure S3. Measurement of *in situ* **1** IC₅₀ values for PSMB2 and PSMB5 using a competitive gel fluorescence assay. (A) Gel-based competitive *in situ* profiling of **1** targets. RPMI 8226 cells were treated with various concentrations of **1** for 6 h, lysed and treated with 10 μM **14**, followed by ‘click conjugation’ to TAMRA. Proteasome subunit band assignment was performed as previously described.^{S8} CBB staining profile is included to verify equal loading. (B) **1** IC₅₀ curves were obtained via quantification of the gel-based activity assay shown in (A).

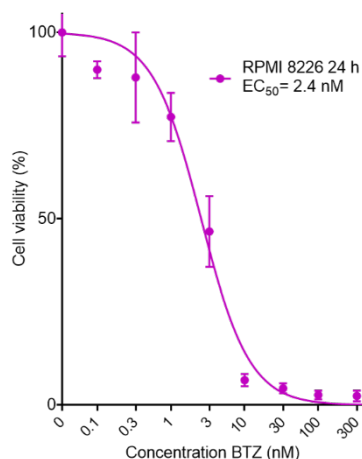


Figure S4. Cytotoxicity curve of RPMI 8226 cells treated with indicated concentrations of BTZ for 24 hours. Quantification was performed using the WST-1 assay (relative values \pm SD and EC_{50} s; $n = 3$).

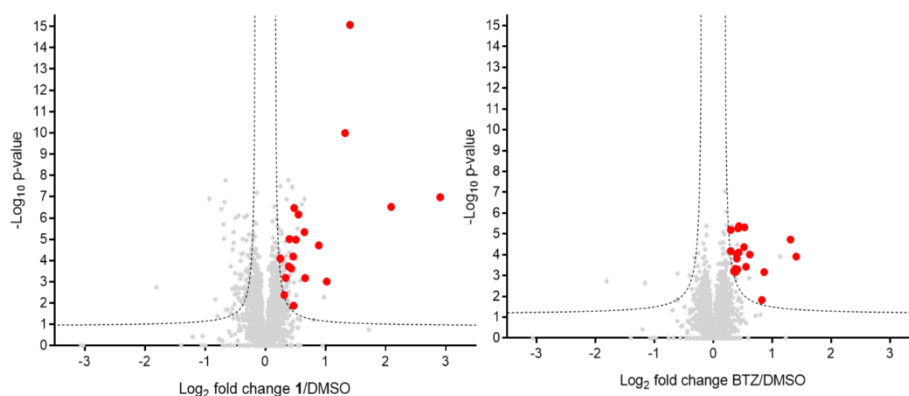


Figure S5. Volcano plots representing the global proteome profile of RPMI 8226 cells treated with 100 nM **1** vs DMSO or 2.5 nM BTZ versus DMSO. Data are represented as \log_2 fold change; dotted lines represent a false discovery rate of 5% and an S_0 of 0.01, indicating an adjusted p-value of 0.05. Colored dots represent proteins (19 in total) with significantly increased expression levels in response to treatment with both **1** and BTZ.

References

- S1.** Amatuni, A.; Renata, H. Identification of a Lysine 4-Hydroxylase from the Glidobactin Biosynthesis and Evaluation of Its Biocatalytic Potential. *Org. Biomol. Chem.* **2019**, *17* (7), 1736–1739.
- S2.** Melaugh, G.; Giri, N.; Davidson, C. E.; James, S. L.; Del Pópolo, M. G. Designing and Understanding Permanent Microporosity in Liquids. *Phys. Chem. Chem. Phys.* **2014**, *16* (20), 9422–9431.
- S3.** Ye, B.; Jiang, P.; Zhang, T.; Ding, Y.; Sun, Y.; Hao, X.; Li, L.; Wang, L.; Chen, Y. Total Synthesis of the Highly N -Methylated Peptide Jahanyne. *J. Org. Chem.* **2018**, *83* (12), 6741–6747.
- S4.** Fehrentz, J.-A.; Heitz, A.; Castro, B. Synthesis of Aldehydic Peptides Inhibiting Renin. *Int. J. Pept. Protein Res.* 1985, *26* (3), 236–241.
- S5.** Imker, H. J.; Krahn, D.; Clerc, J.; Kaiser, M.; Walsh, C. T. N-Acylation during Glidobactin Biosynthesis by the Tridomain Nonribosomal Peptide Synthetase Module GlbF. *Chem. Biol.* 2010, *17* (10), 1077–1083.
- S6.** Cox, J.; Mann, M. MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nat Biotechnol* **2008**, *26* (12), 1367–1372.
- S7.** Maher, P. Proteasome Assay in Cell Lysates. *Bio Protoc* **2014**, *4* (2), e1028.
- S8.** Kuhn, D. J.; Chen, Q.; Voorhees, P. M.; Strader, J. S.; Shenk, K. D.; Sun, C. M.; Demo, S. D.; Bennett, M. K.; van Leeuwen, F. W. B.; Chanan-Khan, A. A.; Orłowski, R. Z. Potent activity of carfilzomib, a novel, irreversible inhibitor of the ubiquitin-proteasome pathway, against preclinical models of multiple myeloma. *Blood* **2007**, *110* (9), 3281–3290.

Supplemental tables

Table S3. Full list of 14-enriched proteins from the LC-MS/MS-based competitive pulldown experiment with the corresponding LFQ ratios and SDs

Majority protein IDs	Protein names	Gene names	Average ratio LFQ intensity 1 100 nM/DMSO	SD
P28074	Proteasome subunit beta type-5	PSMB5	0.15	0.02
P40306	Proteasome subunit beta type-10	PSMB10	0.31	0.05
P28066	Proteasome subunit alpha type-5	PSMA5	0.41	0.05
P20618	Proteasome subunit beta type-1	PSMB1	0.47	0.11
P49721	Proteasome subunit beta type-2	PSMB2	0.47	0.08
O14818;H0Y586	Proteasome subunit alpha type-7	PSMA7	0.53	0.08
P25786;F5GX11;B4DEV8	Proteasome subunit alpha type-1;Proteasome subunit alpha type	PSMA1	0.53	0.07
P28070	Proteasome subunit beta type-4	PSMB4	0.56	0.12
A0A024RA52;P25787;C9JCK5	Proteasome subunit alpha type;Proteasome subunit alpha type-2	PSMA2	0.57	0.11
P25789;H0YN18;H0YMZ1;H0YL69;H0YMA1;H0YKT8;H0YMI6	Proteasome subunit alpha type-4;Proteasome subunit alpha type;Proteasome subunit beta type	PSMA4	0.58	0.05
X5D2R7;P28062;Q5JNW7;A0A140T998	Proteasome subunit beta type;Proteasome subunit beta type-8	PSM8;PSMB8	0.59	0.07
P49720	Proteasome subunit beta type-3	PSMB3	0.61	0.09
P25788;G3V4X5	Proteasome subunit alpha type-3	PSMA3	0.64	0.05
Q07812;K4JQN1	Apoptosis regulator BAX	BAX	0.65	0.03
O75531	Barrier-to-autointegration factor;Barrier-to-autointegration factor, N-terminally processed	BANF1	0.68	0.08
G3V5Z7;P60900;G3V295;G3V311	Proteasome subunit alpha type;Proteasome subunit alpha type-6	PSMA6	0.68	0.06
P27797;K7EJB9	Calreticulin	CALR	0.68	0.43
Q9BZE4	Nucleolar GTP-binding protein 1	GTPBP4	0.69	0.06
Q99436	Proteasome subunit beta type-7	PSMB7	0.71	0.08
P12277;H0YJG0	Creatine kinase B-type	CKB	0.71	0.22
A2ACR1;P28065;A0A0G2JJA7;A2ACR0	Proteasome subunit beta type;Proteasome subunit beta type-9	PSMB9	0.72	0.15
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed	FKBP4	0.73	0.14
P50395;Q5SX87	Rab GDP dissociation inhibitor beta	GDI2	0.73	0.11
P61289;B3KQ25;K7ESG5;K9J957;A0A087WTV2;K7EPX6;K7EKR3;K7ENH2	Proteasome activator complex subunit 3	PSME3	0.74	0.05
P61247;D6RAT0;D6RG13;E9PF15;D6RB09;H0Y8L7;H0Y9Y4;D6R9B6;D6RAS7	40S ribosomal protein S3a	RPS3A	0.74	0.35
O15371	Eukaryotic translation initiation factor 3 subunit D	EIF3D	0.74	0.42
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	0.74	0.02
M0QYS1;P40429;Q8J015	60S ribosomal protein L13a	RPL13A;RPL13a	0.74	0.04
Q5T8U5;O15260	Surfeit locus protein 4	SURF4	0.75	0.13
Q14997	Proteasome activator complex subunit 4	PSME4	0.75	0.02
P42126;Q96DC0	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1;DC1	0.76	0.04
F8VR84;Q9HB07;F8VQQ3	UPF0160 protein MYG1, mitochondrial	C12orf10	0.77	0.00
P48735;H0YL11	Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	0.77	0.27
H0YGX7;P52566;F5H2R5;F5H6Q0;F5H3P3	Rho GDP-dissociation inhibitor 2	ARHGDI2	0.78	0.02
P28072	Proteasome subunit beta type-6	PSMB6	0.78	0.20
P62258;K7EM20	14-3-3 protein epsilon	YWHAE	0.78	0.07
R4GMY8;E5RHG8;Q15369	Transcription elongation factor B polypeptide 1	TCEB1	0.79	0.10
P31939	Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide formyltransferase;IMP cyclohydrolase	ATIC	0.79	0.04
Q9Y2S7;B4DEM9	Polymerase delta-interacting protein 2	POLDIP2	0.79	0.18
B5MDF5;J3KQE5;P62826;F5H018;H0YFC6	GTP-binding nuclear protein Ran	RAN	0.80	0.08
E9PIR7;F8W809;A0A087WSW9;A0A182DW13;A0A087WSY9;Q16881;E2QRB9;E9PKD3	Thioredoxin reductase 1, cytoplasmic	TXNRD1	0.80	0.14

F8WAJ0;Q9H8H2	Probable ATP-dependent RNA helicase DDX31	DDX31	0.80	0.37
P62753;A2A3R5	40S ribosomal protein S6	RPS6	0.80	0.37
Q96KP4;J3QKT2	Cytosolic non-specific dipeptidase	CNDP2	0.81	0.06
C9JIT5;C9JU26;G3V325;P56134	ATP synthase subunit f, mitochondrial	ATP5J2-PTCD1;ATP5J2	0.81	0.05
P18669;P15259	Phosphoglycerate mutase 1;Phosphoglycerate mutase 2	PGAM1;PGAM2	0.81	0.05
P23284	Peptidyl-prolyl cis-trans isomerase B	PPIB	0.81	0.14
Q9UKX7	Nuclear pore complex protein Nup50	NUP50	0.82	0.37
Q14683;G8JLG1	Structural maintenance of chromosomes protein 1A;Structural maintenance of chromosomes protein	SMC1A	0.82	0.32
P31946	14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	YWHAB	0.82	0.06
P43490;A0A0C4DFS8	Nicotinamide phosphoribosyltransferase	NAMPT	0.83	0.14
P62937;F8WE65;C9J5S7	Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase A, N-terminally processed;Peptidyl-prolyl cis-trans isomerase	PPIA	0.83	0.13
P11387	DNA topoisomerase 1	TOP1	0.83	0.36
P50914;E7EPB3	60S ribosomal protein L14	RPL14	0.83	0.41
P62913;Q5VVC8;Q5VVC9	60S ribosomal protein L11	RPL11	0.84	0.39
P30046;B5MCS2;A6NHG4;J3KQ18	D-dopachrome decarboxylase;D-dopachrome decarboxylase-like protein	DDT;DDTL	0.84	0.16
P18077;C9K025;F8WBS5;F8WB72	60S ribosomal protein L35a	RPL35A	0.84	0.29
P29401;A0A0B4J1R6	Transketolase	TKT	0.84	0.06
Q8N163;G3V119;H0YB24	Cell cycle and apoptosis regulator protein 2	CCAR2	0.85	0.11
Q9UHB9	Signal recognition particle subunit SRP68	SRP68	0.85	0.14
P07195;A8MW50	L-lactate dehydrogenase B chain;L-lactate dehydrogenase	LDHB	0.85	0.05
P27824	Calnexin	CANX	0.85	0.23
P37802;X6RJP6	Transgelin-2	TAGLN2	0.86	0.10
C9J9K3;A0A0C4DG17;P08865;F8WD59	40S ribosomal protein SA	RPSA	0.86	0.18
J3KTF8;J3QQX2;P52565;J3KRE2;J3K S60;J3KRY1	Rho GDP-dissociation inhibitor 1	ARHGDI1A	0.86	0.06
Q15233;C9JYS8;H7C367	Non-POU domain-containing octamer-binding protein	NONO	0.86	0.21
A0A0B4J1W3;Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15	0.86	0.01
Q16543;K7EQA9;K7EKQ2	Hsp90 co-chaperone Cdc37;Hsp90 co-chaperone Cdc37, N-terminally processed	CDC37	0.86	0.07
Q9BRA2;I3L0K2;I3L3M7;I3L2R6	Thioredoxin domain-containing protein 17	TXNDC17	0.86	0.05
P60174	Triosephosphate isomerase	TPI1	0.86	0.02
P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	0.87	0.07
P26038	Moesin	MSN	0.87	0.12
P68133;P68032;P63267;P62736;A6NL76;F8WBG3;B8ZZJ2;C9JFL5;F6UVQ4;F6QUT6	Actin, alpha skeletal muscle;Actin, alpha cardiac muscle 1;Actin, gamma-enteric smooth muscle;Actin, aortic smooth muscle	ACTA1;ACTC1;ACTG2;ACTA2	0.87	0.13
P56537;B7ZBH1;A0A0U1RQV5	Eukaryotic translation initiation factor 6	EIF6	0.87	0.06
Q96RQ3;E9PHF7;F5GYT8;E9PG35;G5E9X5	Methylcrotonyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	0.87	0.21
E9PE20;P49458	Signal recognition particle 9 kDa protein	SRP9	0.87	0.03
P18124;A8MUD9	60S ribosomal protein L7	RPL7	0.88	0.18
Q96IX5	Up-regulated during skeletal muscle growth protein 5	USMG5	0.88	0.11
P61604;B8ZZ54;B8ZZL8	10 kDa heat shock protein, mitochondrial	HSPE1	0.88	0.15
P00558	Phosphoglycerate kinase 1	PGK1	0.88	0.05
P37837;F2Z393	Transaldolase	TALDO1	0.88	0.23
P55072	Transitional endoplasmic reticulum ATPase	VCP	0.88	0.03
A0A087WTT1;P11940;E7EQV3;E7ERJ7;H0YAR2	Polyadenylate-binding protein;Polyadenylate-binding protein 1	PABPC1	0.89	0.05
O43615;M0QXU7	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	0.89	0.20
J3KQ32;Q9NTK5;C9JTK6	Obg-like ATPase 1	OLA1	0.89	0.25
P61160;F5H6T1	Actin-related protein 2	ACTR2	0.89	0.12
A0A1W2PPH1;A0A1W2PQH3;P23368;A0A1W2PR68;A0A1W2PQT3;A0A1W2PQY8;A0A1W2PQ37;A0A1W2PQF8	NAD-dependent malic enzyme, mitochondrial	ME2	0.89	0.08
P04406;E7EUT5	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	0.89	0.06
P13796	Plastin-2	LCPI	0.89	0.11
Q9H0U4;E9PLD0;Q92928	Ras-related protein Rab-1B;Putative Ras-related protein Rab-1C	RAB1B;RAB1C	0.89	0.07
E7EQR4;P15311;P35241	Ezrin;Radixin	EZR;RDX	0.89	0.28
Q16531;F5GY55	DNA damage-binding protein 1	DDB1	0.89	0.10
Q99538;G3V2T4;G3V4E4	Legumain	LGMN	0.90	0.04
J3QR09;J3KTE4;P84098;J3QL15	Ribosomal protein L19;60S ribosomal protein L19	RPL19	0.90	0.12

G3V1D3;G3V180;Q9NY33;E9PQ14	Dipeptidyl peptidase 3	DPP3	0.90	0.18
A0A087WVM4;B7ZM99;Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	0.90	0.23
P68431	Histone H3.1	HIST1H3A	0.90	0.05
P28838;H0Y9Q1	Cytosol aminopeptidase	LAP3	0.90	0.36
P30050	60S ribosomal protein L12	RPL12	0.90	0.08
P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	0.90	0.13
A6NFX8;Q9UKK9;A6NCQ0;A6NJU6	ADP-sugar pyrophosphatase	NUDT5	0.90	0.10
P07900	Heat shock protein HSP 90-alpha	HSP90AA1	0.90	0.06
A0A087X1Z3;Q9UL46;H0YM70	Proteasome activator complex subunit 2	PSME2	0.90	0.05
H0YCY8;P53634	Dipeptidyl peptidase 1;Dipeptidyl peptidase 1 exclusion domain chain;Dipeptidyl peptidase 1 heavy chain;Dipeptidyl peptidase 1 light chain	CTSC	0.90	0.02
C9IZ01;Q96RP9;F8WAU4	Elongation factor G, mitochondrial	GFM1	0.90	0.11
Q14697;F5H6X6;E9PKU7	Neutral alpha-glucosidase AB	GANAB	0.90	0.10
C9JIF9;P13798;H7C393;H7C1U0	Acylamino-acid-releasing enzyme	APEH	0.90	0.09
Q16698;ESRJG7;E5RFV2	2,4-dienoyl-CoA reductase, mitochondrial	DECRI	0.91	0.10
P63104;E7EX29;B0AZS6;B7Z2E6;H0YB80;E7ESK7	14-3-3 protein zeta/delta	YWHAZ	0.91	0.06
P09874	Poly [ADP-ribose] polymerase 1	PARP1	0.91	0.26
Q16777;Q6F113	Histone H2A type 2-C;Histone H2A type 2-A	HIST2H2AC;HIST2H2AA3	0.91	0.11
A0A1B0GWJ0;A0A1B0GTJ7;A0A0A6YY92;P30566;A0A096LNY6;A0A096LNY5;A0A1B0GTG9;A0A1B0GWF8	Adenylosuccinate lyase	ADSL	0.91	0.10
P34932;A0A087WYC1;A0A087WTS8	Heat shock 70 kDa protein 4	HSPA4	0.91	0.10
O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14	0.91	0.19
E9PK01;A0A087X1X7;E9PRY8;P29692;E9PPR1;E9PL12;E9PQ49;E9PI39;E9PMW7;E9PIZ1;H0YCK7;E9PL71;E9PN91;E9PQZ1	Elongation factor 1-delta	EEF1D	0.91	0.09
P06576;H0YH81;F8W079	ATP synthase subunit beta, mitochondrial;ATP synthase subunit beta	ATP5B	0.91	0.09
P46777	60S ribosomal protein L5	RPL5	0.91	0.07
P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1	0.91	0.05
B9A041;P40925;B8ZZ51	Malate dehydrogenase, cytoplasmic	MDH1	0.91	0.06
O76021;J3QSV6;I3L3U9	Ribosomal L1 domain-containing protein 1	RSL1D1	0.91	0.45
B1AMS2;Q14141	Septin-6	SEPT6	0.91	0.11
P07954	Fumarate hydratase, mitochondrial	FH	0.91	0.10
Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	0.91	0.37
Q07021;I3L3Q7;I3L3B0	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	0.92	0.10
P26447	Protein S100-A4	S100A4	0.92	0.11
A0A140T9T7;Q03518	Antigen peptide transporter 1	TAP1	0.92	0.32
P00338	L-lactate dehydrogenase A chain	LDHA	0.92	0.03
Q9Y3U8;J3QSB5	60S ribosomal protein L36	RPL36	0.92	0.13
P62318	Small nuclear ribonucleoprotein Sm D3	SNRPD3	0.92	0.26
A6NLN1;P26599;A0A0U1RRM4	Polypyrimidine tract-binding protein 1	PTBP1	0.92	0.04
P16152;E9PQ63;A8MTM1	Carbonyl reductase [NADPH] 1	CBR1	0.92	0.09
P00966;Q5T6L6	Argininosuccinate synthase	ASS1	0.92	0.41
P35232;C9JW96;E9PCW0;C9JZ20;E7ESE2	Prohibitin	PHB	0.92	0.23
Q86X55;K7EQA8	Histone-arginine methyltransferase CARM1	CARM1	0.92	0.29
P78371;F5GWF6;F8VQ14	T-complex protein 1 subunit beta	CCT2	0.92	0.04
Q07065	Cytoskeleton-associated protein 4	CKAP4	0.93	0.08
Q9BVA1;Q13885	Tubulin beta-2B chain;Tubulin beta-2A chain	TUBB2B;TUBB2A	0.93	0.12
A0A087WTP3;Q92945;M0R0I5	Far upstream element-binding protein 2	KHSRP	0.93	0.08
P30040;F8VY02	Endoplasmic reticulum resident protein 29	ERP29	0.93	0.13
F5H1S8;Q14165;H0YG07;F5GX14	Malectin	MLEC	0.93	0.16
P14174	Macrophage migration inhibitory factor	MIF	0.94	0.18
Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6	0.94	0.07
P04080;A0A1W2PQG6	Cystatin-B	CSTB	0.94	0.07
O14929	Histone acetyltransferase type B catalytic subunit	HAT1	0.94	0.19
P16930;H0YLC7	Fumarylacetoacetase	FAH	0.94	0.15
A0A087X054;Q9Y4L1;E9PJ21;A0A087WWI4;K7EQK2	Hypoxia up-regulated protein 1	HYOU1	0.94	0.04
Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP	0.94	0.05

K7EMH1;K7ER17;P35268;K7EP65;K7EKS7;K7ELC4	60S ribosomal protein L22	RPL22	0.94	0.10
G3V1A4;E9PK25;P23528;E9PP50;E9PQB7;E9PLJ3;E9PS23	Cofilin-1	CFL1	0.94	0.07
P06733	Alpha-enolase	ENO1	0.94	0.08
A0A024QZX5;A0A087X1N8;P35237	Serpin B6	SERPINB6	0.94	0.13
P63261;P60709;I3L3I0;I3L1U9;I3L4N8	Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed;Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed	ACTG1;ACTB	0.94	0.08
P60842;J3KT12;J3KTB5;J3QS69;J3KSZ0;J3QL43	Eukaryotic initiation factor 4A-I	EIF4A1	0.94	0.19
P40926;G3XAL0	Malate dehydrogenase, mitochondrial;Malate dehydrogenase	MDH2	0.94	0.06
P00505	Aspartate aminotransferase, mitochondrial	GOT2	0.94	0.05
P51149;C9J592;C9J8S3;C9IZZ0;C9J4V0	Ras-related protein Rab-7a	RAB7A	0.95	0.08
H0Y8G5;Q14103;H0YA96;D6RAF8;D6RF44;D6RBQ9	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0.95	0.05
K7EP06;O43148	mRNA cap guanine-N7 methyltransferase	RNMT	0.95	0.11
Q06323	Proteasome activator complex subunit 1	PSME1	0.95	0.39
E7EVA0;P27816	Microtubule-associated protein;Microtubule-associated protein 4	MAP4	0.95	0.11
I3L0H8;F6QDS0;H3BQK0;Q9NUU7;Q9UMR2;H3BTB3;H3BMQ5;H3BN59;I3L352	ATP-dependent RNA helicase DDX19A;ATP-dependent RNA helicase DDX19B	DDX19A;DDX19B	0.95	0.31
H7C0A3;F8WCF6;P59998;F8WDD7;A0A0A6YYG9	Actin-related protein 2/3 complex subunit 4	ARPC4-TTLL3;ARPC4	0.95	0.07
A0A087WT44;P30519;I3L159;I3L1F5	Heme oxygenase 2	HMOX2	0.95	0.20
Q3LXA3;H0YCY6;I3L252	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);ATP-dependent dihydroxyacetone kinase;FAD-AMP lyase (cyclizing)	DAK;TKFC	0.95	0.08
D6RFH4;H3BUX2;J3KNF8;O43169	Cytochrome b5 type B	CYB5B	0.95	0.20
J3KTL2;Q07955;J3KSR8	Serine/arginine-rich splicing factor 1	SRSF1	0.95	0.13
P19623	Spermidine synthase	SRM	0.95	0.08
P61221;D6R9I9	ATP-binding cassette sub-family E member 1	ABCE1	0.95	0.06
O75400	Pre-mRNA-processing factor 40 homolog A	PRPF40A	0.95	0.00
Q96PZ0;E7EUH7	Pseudouridylate synthase 7 homolog	PUS7	0.95	0.03
P41250	Glycine--tRNA ligase	GARS	0.95	0.08
A0A0D9SE19;A0A0D9SFE1;E9PIH7;Q9H1K4;Q9H936;K4DIB6;K4DIB3;K4DIB8;K4DIA8;E9PS95;A0A0D9SFA8;K4DIB0;K4DIA2;A0A0D9SG84;E9PI74;E9PQ36	Mitochondrial glutamate carrier 2;Mitochondrial glutamate carrier 1	SLC25A22;SLC25A18	0.95	0.39
U3KQK0;Q99880;Q99879;Q99877;Q93079;Q5QNW6;P62807;P58876;P57053;O60814;Q96A08	Histone H2B;Histone H2B type 1-L;Histone H2B type 1-M;Histone H2B type 1-N;Histone H2B type 1-H;Histone H2B type 2-F;Histone H2B type 1-C/E/F/G/I;Histone H2B type 1-D;Histone H2B type F-S;Histone H2B type 1-K;Histone H2B type 1-A	HIST1H2BN;HIST1H2BL;HIST1H2BM;HIST1H2BH;HIST2H2BF;HIST1H2BC;HIST1H2BD;H2BFS;HIST1H2BK;HIST1H2BA	0.95	0.12
Q9NUQ9	Protein FAM49B	FAM49B	0.95	0.08
P05455;E7ERC4	Lupus La protein	SSB	0.95	0.17
P62191	26S protease regulatory subunit 4	PSMC1	0.95	0.05
Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	0.96	0.10
P49321;Q5T624;H0YDS9;H0YF33;E9PRH9	Nuclear autoantigenic sperm protein	NASP	0.96	0.07
G3V576;G3V4W0;B4DY08;B2R5W2;G3V4C1;G3V2Q1;P07910;G3V555;G3V575;G3V5X6;G3V3K6;G3V251;B4DSU6;G3V4M8;A0A0G2JPF8;A0A0G2JNQ3;P0DMR1;O60812;B7ZW38;B2RXXH8	Heterogeneous nuclear ribonucleoproteins C1/C2;Heterogeneous nuclear ribonucleoprotein C-like 4;Heterogeneous nuclear ribonucleoprotein C-like 1;Heterogeneous nuclear ribonucleoprotein C-like 3;Heterogeneous nuclear ribonucleoprotein C-like 2	HNRNPC;HNRNPCL4;HNRNPCL1;HNRNPCL3;HNRNPCL2	0.96	0.19
H3BQB1;P07741;H3BQF1;H3BQZ9	Adenine phosphoribosyltransferase	APRT	0.96	0.07
P61026	Ras-related protein Rab-10	RAB10	0.96	0.10
P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	0.96	0.11
P49588	Alanine--tRNA ligase, cytoplasmic	AARS	0.96	0.15
E9PCS2;Q16576	Histone-binding protein RBBP7	RBBP7	0.96	0.08
P14618;B4DNK4;H3BTN5;H3BQ34	Pyruvate kinase PKM;Pyruvate kinase	PKM	0.96	0.03
Q9UJU6;B4DDD6;H0Y5J4	Drebrin-like protein	DBNL	0.96	0.10
P62140	Serine/threonine-protein phosphatase PPI-beta catalytic subunit	PPP1CB	0.96	0.08

P53396	ATP-citrate synthase	ACLY	0.96	0.07
O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	0.96	0.04
P00492	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	0.96	0.12
A0A087WUK2;O14979	Heterogeneous nuclear ribonucleoprotein D-like	HNRNPDL	0.96	0.06
P08238	Heat shock protein HSP 90-beta	HSP90AB1	0.96	0.06
P62805	Histone H4	HIST1H4A	0.96	0.07
O15067	Phosphoribosylformylglycinamide synthase	PFAS	0.96	0.13
Q14166	Tubulin--tyrosine ligase-like protein 12	TTL12	0.97	0.09
P62857	40S ribosomal protein S28	RPS28	0.97	0.08
Q6ZT21	Transmembrane protein with metallophosphoesterase domain	TMPPE	0.97	0.05
B1ANR0;Q13310;H0Y5F5;H0YEU6	Polyadenylate-binding protein;Polyadenylate-binding protein 4	PABPC4	0.97	0.03
Q13547;Q5TEE2;Q92769;E5RFI6;E5RJ04;E5RGV4;E5RHE7;E5RHS2;E5RG37;E5RFP9;H3BM24	Histone deacetylase 1;Histone deacetylase 2	HDAC1;HDAC2	0.97	0.11
P30044	Peroxisome oxidin-5, mitochondrial	PRDX5	0.97	0.27
Q49AN9;F5H013;P62308;A8MWD9;C9JYQ0	Small nuclear ribonucleoprotein G;Putative small nuclear ribonucleoprotein G-like protein 15	SNRPG;SNRPGP15	0.97	0.01
Q04917	14-3-3 protein eta	YWHAH	0.97	0.07
P15121;E9PCX2;E9PEF9	Aldose reductase	AKR1B1	0.97	0.11
O75367;D6RCF2;B4DJC3	Core histone macro-H2A.1;Histone H2A	H2AFY	0.97	0.14
O43707	Alpha-actinin-4	ACTN4	0.97	0.26
O96008;K7EKG4;K7EJ57	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	0.97	0.12
P53004	Biliverdin reductase A	BLVRA	0.97	0.11
F6T1Q0;Q6L8Q7	2,5-phosphodiesterase 12	PDE12	0.97	0.04
Q6XQN6;G5E977;C9J8U2	Nicotinate phosphoribosyltransferase	NAPRT	0.97	0.10
B4DJV2;O75390;A0A0C4DGI3	Citrate synthase;Citrate synthase, mitochondrial	CS	0.97	0.24
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	0.97	0.08
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	0.97	0.09
P22626;A0A087WUI2	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0.97	0.11
Q9UNM6;A0A087WUL9;J3KNQ3;E9PL38	26S proteasome non-ATPase regulatory subunit 13	PSMD13	0.98	0.16
O95831	Apoptosis-inducing factor 1, mitochondrial	AIFM1	0.98	0.08
P11021	78 kDa glucose-regulated protein	HSPA5	0.98	0.02
Q9Y230;M0R0Y3	RuvB-like 2	RUVBL2	0.98	0.06
P49790	Nuclear pore complex protein Nup153	NUP153	0.98	0.15
P11142;E9PKE3;E9PN89;E9PNE6;A8K7Q2	Heat shock cognate 71 kDa protein	HSPA8	0.98	0.05
B1AK87;B1AK88;P47756;B1AK85	F-actin-capping protein subunit beta	CAPZB	0.98	0.08
A6NDG6	Phosphoglycolate phosphatase	PGP	0.98	0.20
O00299	Chloride intracellular channel protein 1	CLIC1	0.98	0.05
J3KQ96;E7ETY2;Q13428	Treacle protein	TCOF1	0.98	0.13
Q5JP53;P07437;Q5ST81	Tubulin beta chain	TUBB	0.98	0.11
Q5T7C4;P09429	High mobility group protein B1	HMGB1	0.98	0.16
P02751;H0Y7Z1	Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3	FN1	0.98	0.10
P24534	Elongation factor 1-beta	EEF1B2	0.98	0.04
P20073	Annexin A7	ANXA7	0.98	0.31
Q6IBS0;D6RG15	Twinfilin-2	TWF2	0.98	0.09
Q01813;B1APP6	ATP-dependent 6-phosphofructokinase, platelet type	PFKP	0.98	0.12
P04075;J3KPS3;H3BQN4;H3BUH7;H3BPS8	Fructose-bisphosphate aldolase A;Fructose-bisphosphate aldolase	ALDOA	0.98	0.07
P14625	Endoplasmic reticulum chaperone	HSP90B1	0.98	0.24
Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB	0.98	0.05
P13639	Elongation factor 2	EEF2	0.98	0.04
Q92598;A0A0A0MSM0	Heat shock protein 105 kDa	HSPH1	0.98	0.07
Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2	0.98	0.10
Q9Y383;A0A0A6YYJ8	Putative RNA-binding protein Luc7-like 2	LUC7L2	0.99	0.12
P00390	Glutathione reductase, mitochondrial	GSR	0.99	0.14
Q58FF8	Putative heat shock protein HSP 90-beta 2	HSP90AB2P	0.99	0.20
P46060	Ran GTPase-activating protein 1	RANGAP1	0.99	0.21
Q96C86	m7GpppX diphosphatase	DCPS	0.99	0.08
E9PLK3;P55786	Puromycin-sensitive aminopeptidase	NPEPPS	0.99	0.10
Q15306;F2Z3D5	Interferon regulatory factor 4	IRF4	0.99	0.10
P47914	60S ribosomal protein L29	RPL29	0.99	0.07
P12004	Proliferating cell nuclear antigen	PCNA	0.99	0.06

P67936	Tropomyosin alpha-4 chain	TPM4	0.99	0.11
Q9BY44;F8WAE5;C9IZE1	Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A, N-terminally processed	EIF2A	0.99	0.13
Q9UQ80	Proliferation-associated protein 2G4	PA2G4	0.99	0.46
Q9Y266	Nuclear migration protein nudC	NUDC	0.99	0.12
H0YK49;P13804;H0YL12;H0YNX6;H0YLU7;H0YKF0	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	0.99	0.09
F5H423;P84077;P61204;F5HOC7	ADP-ribosylation factor 1;ADP-ribosylation factor 3	ARF1;ARF3	0.99	0.08
E9PEX6;P09622	Dihydropolyl dehydrogenase;Dihydropolyl dehydrogenase, mitochondrial	DLD	0.99	0.15
P32119;A6NIW5	Peroxioredoxin-2	PRDX2	0.99	0.11
P07099	Epoxide hydrolase 1	EPHX1	0.99	0.21
P63244;J3KPE3;D6RHH4;H0YAF8;D6RAC2;H0Y8W2;D6RFX4;D6R9Z1;D6R9L0;D6REE5;D6RAU2;E9PD14;D6RBD0;D6RFZ9;H0YAM7	Guanine nucleotide-binding protein subunit beta-2-like 1;Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed	GNB2L1	0.99	0.25
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	0.99	0.07
B0YIY6;P48444	Coatmer subunit delta	ARCN1	0.99	0.09
P62851	40S ribosomal protein S25	RPS25	0.99	0.11
P07355;H0YN42;H0YMD0;H0YMU9;H0YKS4;A6NMY6;H0YMM1;H0YMS0	Annexin A2;Annexin;Putative annexin A2-like protein	ANXA2;ANXA2 P2	0.99	0.05
E9PKG1;H7C2I1;Q99873;A0A087X1W2;E9PNR9;E9PQ98;E9PIX6;H0YDE4	Protein arginine N-methyltransferase 1	PRMT1	1.00	0.19
O14828	Secretory carrier-associated membrane protein 3	SCAMP3	1.00	0.06
P19338;H7BY16	Nucleolin	NCL	1.00	0.14
P38117	Electron transfer flavoprotein subunit beta	ETFB	1.00	0.05
P14317;E7EVW7	Hematopoietic lineage cell-specific protein	HCLS1	1.00	0.13
Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1	1.00	0.07
Q99733;C9J6D1;E9PNW0;E9PJJ2;E9PS34;E9PNJ7;A8MXH2;E9PKT8;C9JZ17	Nucleosome assembly protein 1-like 4	NAP1L4	1.00	0.08
E9PPJ0;Q13435;H0YEX5	Splicing factor 3B subunit 2	SF3B2	1.00	0.09
P31146;H3BRY3	Coronin-1A;Coronin	CORO1A	1.00	0.06
P50991	T-complex protein 1 subunit delta	CCT4	1.00	0.07
P31153	S-adenosylmethionine synthase isoform type-2	MAT2A	1.00	0.05
Q32Q12;P22392;J3KPD9;E7ERL0;O60361	Nucleoside diphosphate kinase;Nucleoside diphosphate kinase B;Putative nucleoside diphosphate kinase	NME1-NME2;NME1;NME2P1	1.00	0.12
Q04446;E9PGM4	1,4-alpha-glucan-branching enzyme	GBE1	1.00	0.10
E9PEB5;Q96AE4	Far upstream element-binding protein 1	FUBP1	1.00	0.08
Q5RKV6	Exosome complex component MTR3	EXOSC6	1.00	0.05
P62424;Q5T8U3	60S ribosomal protein L7a	RPL7A	1.00	0.20
P61088;Q5JXB2;F8VZ29;F8VSD4;F8VV71	Ubiquitin-conjugating enzyme E2 N;Putative ubiquitin-conjugating enzyme E2 N-like	UBE2N;UBE2NL	1.00	0.23
P31947	14-3-3 protein sigma	SFN	1.00	0.12
Q14566	DNA replication licensing factor MCM6	MCM6	1.00	0.06
Q9Y310	tRNA-splicing ligase RtcB homolog	RTCB	1.00	0.09
P07737;K7EJ44	Profilin-1	PFN1	1.00	0.10
P13489;E9PMJ3;E9PLZ3;E9PIM9	Ribonuclease inhibitor	RNH1	1.01	0.01
Q13185;C9JMM0;B8ZZ43;S4R2Y4	Chromobox protein homolog 3	CBX3	1.01	0.08
P00367;P49448	Glutamate dehydrogenase 1, mitochondrial;Glutamate dehydrogenase 2, mitochondrial	GLUD1;GLUD2	1.01	0.05
P22695;H3BRG4;H3BSJ9	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	1.01	0.14
Q9BU23	Lipase maturation factor 2	LMF2	1.01	0.25
P68371;P04350	Tubulin beta-4B chain;Tubulin beta-4A chain	TUBB4B;TUBB4A	1.01	0.09
P62906	60S ribosomal protein L10a	RPL10A	1.01	0.13
O15145;C9JZD1	Actin-related protein 2/3 complex subunit 3	ARPC3	1.01	0.06
P62195;J3QQM1;J3QSA9;J3QLH6;J3KRP2	26S protease regulatory subunit 8	PSMC5	1.01	0.11
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	1.01	0.33
Q06830;A0A0A0MSI0	Peroxioredoxin-1	PRDX1	1.01	0.13
P61981	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	YWHAG	1.01	0.14
P52209;K7EMN2;K7EM49;K7EPF6	6-phosphogluconate dehydrogenase, decarboxylating	PGD	1.01	0.07
A0A087WW66;Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1	1.01	0.10
P51571;A6NLM8	Translocon-associated protein subunit delta	SSR4	1.01	0.34

P30153;B3KQV6;C9J9C1	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	1.01	0.12
J3QLE5;P63162;P14678	Small nuclear ribonucleoprotein-associated protein N;Small nuclear ribonucleoprotein-associated proteins B and B	SNRPN;SNRPB	1.01	0.05
P14866;M0QXS5	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	1.01	0.27
Q16629;A0A0B4J1Z1;C9JAB2	Serine/arginine-rich splicing factor 7	SRSF7	1.01	0.07
Q9HB71	Calcyclin-binding protein	CACYBP	1.01	0.08
H0YHC3;F8W020;F8W118;F8VY35;F8VV59;B7Z9C2;F8W0J6;F5H4R6;H0YIV4;P55209;H0YH88;F8W543;F8VRJ2;F8VXI6;F8VUX1;F8VVV5	Nucleosome assembly protein 1-like 1	NAP1L1	1.01	0.11
O60506;B7Z645;F6UXX1	Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	1.01	0.10
P23526	Adenosylhomocysteinase	AHCY	1.01	0.08
P49736;H0Y8E6	DNA replication licensing factor MCM2	MCM2	1.01	0.14
Q99714;Q5H928	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	1.01	0.04
Q9UIG0	Tyrosine-protein kinase BAZ1B	BAZ1B	1.01	0.03
Q15393	Splicing factor 3B subunit 3	SF3B3	1.01	0.08
P25398	40S ribosomal protein S12	RPS12	1.01	0.33
P63173;J3KT73;J3QL01	60S ribosomal protein L38	RPL38	1.01	0.15
O15143	Actin-related protein 2/3 complex subunit 1B	ARPC1B	1.02	0.16
P07858	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	CTSB	1.02	0.12
P27348;E9PG15	14-3-3 protein theta	YWHAQ	1.02	0.11
P61313;E7EQV9;E7ENU7;E7EX53	60S ribosomal protein L15;Ribosomal protein L15	RPL15	1.02	0.12
Q8TB45	DEP domain-containing mTOR-interacting protein	DEPTOR	1.02	0.12
P06748	Nucleophosmin	NPM1	1.02	0.09
Q9NUB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	ACSS1	1.02	0.09
P16403;P10412;P16402	Histone H1.2;Histone H1.4;Histone H1.3	HIST1H1C;HIST1H1E;HIST1H1D	1.02	0.21
P61978;Q5T6W2	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	1.02	0.18
P55084;B5MD38;C9JEY0;C9JE81;F5GZQ3	Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase	HADHB	1.02	0.20
A0A0B4J2A4;P42765;K7EMEO	3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	1.02	0.15
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	1.02	0.26
A0A0A0MTS2;P06744;K7EQ48;A0A0J9YXP8;A0A0J9YH3;A0A0J9YX90	Glucose-6-phosphate isomerase	GPI	1.02	0.11
A0A087WUT6;O60841	Eukaryotic translation initiation factor 5B	EIF5B	1.02	0.23
P48643;E7ENZ3;B7ZAR1;E9PCA1	T-complex protein 1 subunit epsilon	CCT5	1.02	0.07
O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	1.02	0.11
H7C3I1;F6VDH7;Q3KNR6;P50502;Q8IZP2;Q8NF14	Hsc70-interacting protein;Putative protein FAM10A4;Putative protein FAM10A5	ST13;ST13P4;ST13P5	1.02	0.07
I3L397;I3L504;P63241;Q6IS14;F8WCJ1;C9J7B5;C9J4W5;Q9GVZ4	Eukaryotic translation initiation factor 5A;Eukaryotic translation initiation factor 5A-1;Eukaryotic translation initiation factor 5A-1-like;Eukaryotic translation initiation factor 5A-2	EIF5A;EIF5AL1;EIF5A2	1.03	0.17
O43776	Asparagine--tRNA ligase, cytoplasmic	NARS	1.03	0.12
A0A087X0X3;P52272	Heterogeneous nuclear ribonucleoprotein M	HNRNPM	1.03	0.33
E5RIW3;E5RJD8;O75347;E5RHG6	Tubulin-specific chaperone A	TBCA	1.03	0.22
P05165;A0A1B0GU58;A0A1B0GW14;A0A1B0GUX9;A0A1B0GWA1	Propionyl-CoA carboxylase alpha chain, mitochondrial	PCCA	1.03	0.17
P31948	Stress-induced-phosphoprotein 1	STIP1	1.03	0.08
P30085;Q5T0D2	UMP-CMP kinase	CMPK1	1.03	0.00
F2Z2V0;B0QZ18;Q99829;H0Y524;E7ENH5;A6PVH9	Copine-1	CPNE1	1.03	0.12
P10809	60 kDa heat shock protein, mitochondrial	HSPD1	1.03	0.08
Q14974;J3KTM9	Importin subunit beta-1	KPNB1	1.03	0.10
Q15046	Lysine--tRNA ligase	KARS	1.03	0.08
P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	1.03	0.42
P52907	F-actin-capping protein subunit alpha-1	CAPZA1	1.03	0.06
O95347	Structural maintenance of chromosomes protein 2	SMC2	1.03	0.17
P33993	DNA replication licensing factor MCM7	MCM7	1.03	0.13
Q15717;M0QZR9	ELAV-like protein 1	ELAVL1	1.03	0.39
O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	1.03	0.24
Q15181	Inorganic pyrophosphatase	PPA1	1.03	0.07
P34897;H0YIZ0;G3V2Y4	Serine hydroxymethyltransferase, mitochondrial;Serine hydroxymethyltransferase	SHMT2	1.03	0.05

P23246	Splicing factor, proline- and glutamine-rich	SFPQ	1.03	0.26
E9PGT1;Q15631;H7C1D4	Translin	TSN	1.03	0.08
Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2	1.03	0.08
Q15424	Scaffold attachment factor B1	SAFB	1.03	0.06
A2A274;Q99798	Aconitate hydratase, mitochondrial	ACO2	1.03	0.10
G3V3M6;P27695;G3V5Q1;G3V3C7;G3V5D9;A0A0C4DGK8	DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, mitochondrial	APEX1	1.03	0.45
Q86VP6;A0A0C4DGH5	Cullin-associated NEDD8-dissociated protein 1	CAND1	1.03	0.06
E7EWK3;Q9H2U1	ATP-dependent RNA helicase DHX36	DHX36	1.03	0.15
Q96124	Far upstream element-binding protein 3	FUBP3	1.03	0.07
P62995;H7BXF3	Transformer-2 protein homolog beta	TRA2B	1.03	0.23
A6NKB8;Q9H4A4	Aminopeptidase B	RNPEP	1.04	0.13
P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1	1.04	0.10
P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	1.04	0.16
Q13263;M0R0K9	Transcription intermediary factor 1-beta	TRIM28	1.04	0.19
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	1.04	0.26
P78417;Q5TA02;Q5TA01	Glutathione S-transferase omega-1	GSTO1	1.04	0.25
J3QT28;O43684	Mitotic checkpoint protein BUB3	BUB3	1.04	0.09
F8W1R7;J3KND3;G8JLA2;G3V1V0;B7Z64;P60660;F8VFP3;G3V1Y7;F8VZU9;F8W180	Myosin light polypeptide 6	MYL6	1.04	0.19
F5GYN4;J3KR44;F5GYJ8;Q96FW1;F5H6Q1;F5H3F0	Ubiquitin thioesterase OTUB1	OTUB1	1.04	0.10
O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12	1.04	0.39
P84103;A0A087X2D0	Serine/arginine-rich splicing factor 3	SRSF3	1.04	0.07
Q02878	60S ribosomal protein L6	RPL6	1.04	0.31
B4DLN1			1.04	0.09
O75396	Vesicle-trafficking protein SEC22b	SEC22B	1.04	0.28
Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	1.04	0.12
P30501	HLA class I histocompatibility antigen, Cw-2 alpha chain	HLA-C	1.04	0.09
P35998;A0A1W2PQS1	26S protease regulatory subunit 7	PSMC2	1.04	0.20
P46940;H0YLE8;A0A0J9YXZ5	Ras GTPase-activating-like protein IQGAP1	IQGAP1	1.04	0.03
P26641	Elongation factor 1-gamma	EEF1G	1.04	0.11
Q9Y490	Talin-1	TLN1	1.04	0.18
Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	1.04	0.11
P11413;E7EU18	Glucose-6-phosphate 1-dehydrogenase	G6PD	1.04	0.11
Q12906	Interleukin enhancer-binding factor 3	ILF3	1.04	0.05
P32942;K7ERN2	Intercellular adhesion molecule 3	ICAM3	1.04	0.27
Q5VTE0;P68104;A0A087WV01;A0A087WVQ9	Putative elongation factor 1-alpha-like 3;Elongation factor 1-alpha 1;Elongation factor 1-alpha	EEF1A1P5;EEF1A1	1.04	0.05
E7ES33;E7EPK1;Q16181;G3V1Q4	Septin-7	SEPT7	1.04	0.18
P13667	Protein disulfide-isomerase A4	PDIA4	1.04	0.04
P04183;K7ERV3;K7ES52;K7ERJ1	Thymidine kinase, cytosolic;Thymidine kinase	TK1	1.05	0.03
P30041	Peroxisome oxidoreductin-6	PRDX6	1.05	0.29
A0A096LP16;A0A096LNH5;H7C2G3;A0A0B4J2H4;H7C1F6;A0A0B4J2D5;P30042;A0A096LNJ1;A0A096LP73;F2Z2Q0;A0A096LP12	ES1 protein homolog, mitochondrial	C21orf33	1.05	0.14
B4DXW1;P61158	Actin-related protein 3	ACTR3	1.05	0.26
B0QY89;Q9Y262;B0QY90	Eukaryotic translation initiation factor 3 subunit L	EIF3L	1.05	0.39
P50990	T-complex protein 1 subunit theta	CCT8	1.05	0.04
P00403	Cytochrome c oxidase subunit 2	MT-CO2	1.05	0.16
Q8WU39	Marginal zone B- and B1-cell-specific protein	MZB1	1.05	0.15
H0Y109;Q9H8H3;F8VQX6	Methyltransferase-like protein 7A	METTL7A	1.05	0.12
P30101	Protein disulfide-isomerase A3	PDIA3	1.05	0.06
H0YKD8;P46779;H0YMF4;H0YLP6	60S ribosomal protein L28	RPL28	1.05	0.20
Q10713	Mitochondrial-processing peptidase subunit alpha	PMPCA	1.05	0.17
P0DN79;P35520	Cystathionine beta-synthase	CBS	1.05	0.14
P17987;E7EQR6;F5H282;E7ERF2	T-complex protein 1 subunit alpha	TCP1	1.05	0.05
P43246;E9PHA6	DNA mismatch repair protein Msh2	MSH2	1.05	0.11
J3QQ67;Q07020;H0YHA7;G3V203;F8VYV2;F8VUA6;A0A075B7A0	60S ribosomal protein L18	RPL18	1.05	0.16
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	1.05	0.08
Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	1.05	0.13

B4E3S0;Q9ULV4	Coronin;Coronin-1C	CORO1C	1.05	0.26
O43390;B4DT28	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	1.05	0.32
Q99832	T-complex protein 1 subunit eta	CCT7	1.05	0.06
C915N1;Q9BTE6;L7N2F4	Alanyl-tRNA editing protein Aarsd1	PTGES3L-AARS D1;AARS D1	1.05	0.06
P46063	ATP-dependent DNA helicase Q1	RECQL	1.05	0.12
Q9Y320	Thioredoxin-related transmembrane protein 2	TMX2	1.06	0.10
F8W6I7;P09651;F8VZ49;Q32P51;F8V TQ5	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed;Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1;HNR NPA1L2	1.06	0.08
P78347	General transcription factor II-1	GTF2I	1.06	0.18
P51659;E7ER27;E7EWE5;G5E9S2;E7 ET17	Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2	HSD17B4	1.06	0.09
P62917;E9PKZ0;E9PKU4;G3V1A1;E9 PP36	60S ribosomal protein L8	RPL8	1.06	0.07
P07237;H7BZ94;H0Y3Z3	Protein disulfide-isomerase	P4HB	1.06	0.10
E9PLL6;P46776;E9PJD9	60S ribosomal protein L27a	RPL27A	1.06	0.25
O43396;K7ER96	Thioredoxin-like protein 1	TXNL1	1.06	0.34
Q15645	Pachytene checkpoint protein 2 homolog	TRIP13	1.06	0.08
P35606	Coatmer subunit beta	COPB2	1.06	0.10
Q15084	Protein disulfide-isomerase A6	PDIA6	1.06	0.08
Q14684	Ribosomal RNA processing protein 1 homolog B	RRP1B	1.06	0.15
P26196	Probable ATP-dependent RNA helicase DDX6	DDX6	1.06	0.05
P42167;G5E972	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin	TMPO	1.06	0.04
Q13148;A0A087WX29;B1AKP7;G3V 162;A0A087X260;A0A087WYY0;K7E JM5;K7EN94;A0A087WXQ5;A0A087 WV68	TAR DNA-binding protein 43	TARDBP	1.06	0.15
O43772;C9JPE1	Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	1.07	0.13
P33241;E9PBD8;E7EMG9	Lymphocyte-specific protein 1	LSP1	1.07	0.07
A0A0C4DGS1;P39656;U3KQ84	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST	1.07	0.20
P15170;H3BR35;Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	GSPT1;GSPT2	1.07	0.09
O75439;G3V0E4	Mitochondrial-processing peptidase subunit beta	PMPCB	1.07	0.09
P25205;J3KQ69	DNA replication licensing factor MCM3	MCM3	1.07	0.05
P08240	Signal recognition particle receptor subunit alpha	SRPR	1.07	0.46
O15127	Secretory carrier-associated membrane protein 2	SCAMP2	1.07	0.12
P35249;C9JZI1;C9J8M3;C9JTT7	Replication factor C subunit 4	RFC4	1.07	0.16
Q96TA1	Niban-like protein 1	FAM129B	1.07	0.16
P13010	X-ray repair cross-complementing protein 5	XRCC5	1.07	0.08
P38646	Stress-70 protein, mitochondrial	HSPA9	1.07	0.03
P41091;Q2VIR3;F8W810	Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation initiation factor 2 subunit 3-like protein	EIF2S3;EIF2S3L	1.07	0.07
H0YN26;P39687;H7BZ09	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	1.07	0.14
Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	1.07	0.13
E9PC15;Q53H12;E9PG39;A0A0G2JL G5	Acylglycerol kinase, mitochondrial	AGK	1.07	0.26
F5H5D3;Q9BQE3;A0A1W2PQM2;F8 VVB9	Tubulin alpha-1C chain	TUBA1C;TUBA 1B	1.07	0.11
A0A0J9YYL3;A0A0J9YXJ8;A0A0J9Y VP6;A0A0J9YXX5;Q9UHX1;A0A0J9 YVR6;E9PQ56;A0A0J9YWM1;H0YE M1;E9PMU7;E9PN18;H0YCP8	Poly(U)-binding-splicing factor PUF60	PUF60	1.07	0.33
A0A0D9SF54;A0A0D9SGF6;Q13813	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	1.07	0.34
P62316;K7ERG4	Small nuclear ribonucleoprotein Sm D2	SNRPD2	1.07	0.13
Q9Y2X3	Nucleolar protein 58	NOP58	1.07	0.09
O15355	Protein phosphatase 1G	PPM1G	1.07	0.48
P62266;D6RD47	40S ribosomal protein S23	RPS23	1.07	0.33
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	1.07	0.11
P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase	ALDH18A1	1.07	0.05
O00170;E9PMH2	AH receptor-interacting protein	AIP	1.07	0.19
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2	HSDL2	1.07	0.20
O60547	GDP-mannose 4,6 dehydratase	GMDS	1.08	0.07

Q96GW9	Methionine--tRNA ligase, mitochondrial	MARS2	1.08	0.33
D6R9P3;D6RD18;D6RBZ0;Q99729	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	1.08	0.09
Q96AG4	Leucine-rich repeat-containing protein 59	LRRCS59	1.08	0.16
Q5JTH9	RRP12-like protein	RRP12	1.08	0.42
Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA	1.08	0.23
Q13423;E9PCX7	NAD(P) transhydrogenase, mitochondrial	NNT	1.08	0.10
A0A0G2J1W1;P0DMV9;P0DMV8;V9GZ37	Heat shock 70 kDa protein 1B;Heat shock 70 kDa protein 1A	HSPA1B;HSPA1A	1.08	0.03
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	1.08	0.16
P49915	GMP synthase [glutamine-hydrolyzing]	GMPS	1.08	0.15
J3KTA4;P17844	Probable ATP-dependent RNA helicase DDX5	DDX5	1.08	0.08
P26373;J3QSB4	60S ribosomal protein L13	RPL13	1.08	0.11
Q13162;H7C3T4	Peroxisomal protein 4	PRDX4	1.08	0.15
G8JLD5;O00429;F8VZ52	Dynamin-1-like protein	DNM1L	1.08	0.22
Q8NBY1;B4E0Y9;Q9P289;H0Y630;B4DR80;Q9Y6E0;C9JDH9;C9JCC0;C9J232;Q5JV98;H7C279;O00506	Serine/threonine-protein kinase 26;Serine/threonine-protein kinase 24;Serine/threonine-protein kinase 24 36 kDa subunit;Serine/threonine-protein kinase 24 12 kDa subunit;Serine/threonine-protein kinase 25	STK26;STK24;S TK25	1.08	0.13
P11586;F5H2F4	C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methylenetetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally processed	MTHFD1	1.08	0.32
J9JIE6;Q9UM00;J3QQY2;J3KS45	Transmembrane and coiled-coil domain-containing protein 1	TMCO1	1.08	0.11
Q9Y5B9	FACT complex subunit SPT16	SUPT16H	1.08	0.10
P23396;E9PL09;E9PPU1;F2Z2S8;H0Y CJ7;H0YEU2;E9PQ96;E9PJH4;H0YF3 2;E9PK82	40S ribosomal protein S3	RPS3	1.08	0.08
E5KJL9;O60313	Dynamin-like 120 kDa protein, mitochondrial;Dynamin-like 120 kDa protein, form S1	OPA1	1.08	0.49
P50402;Q5HY57	Emerin	EMD	1.08	0.11
A0A024R4E5;Q00341;H0Y394	Vigilin	HDLBP	1.08	0.45
F8W914;Q9NQC3;H7C106	Reticulon;Reticulon-4	RTN4	1.08	0.17
Q14152	Eukaryotic translation initiation factor 3 subunit A	EIF3A	1.08	0.06
P14868	Aspartate--tRNA ligase, cytoplasmic	DARS	1.08	0.08
P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine ligase;Phosphoribosylformylglycinamide cyclo- ligase;Phosphoribosylglycinamide formyltransferase	GART	1.09	0.09
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	1.09	0.04
P12956;B1AHC9	X-ray repair cross-complementing protein 6	XRCC6	1.09	0.06
Q13155;A8MU58;F8W950	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	1.09	0.22
Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	1.09	0.03
A0A1X7SBZ2;A0A1W2PQ51;Q92841	Probable ATP-dependent RNA helicase DDX17	DDX17	1.09	0.14
P16188;P16189;A0A140T975;A0A140 T941;A0A1W2PQS8;Q9GJ45;A0A1W 2P539;A0A140T9Z6;B0UXQ0;P30512 ;P30459;P10314;Q5SRN7;A0A1W2PS 24;Q5SRN5;P13746;P04439;P30456	HLA class I histocompatibility antigen, A-30 alpha chain;HLA class I histocompatibility antigen, A-31 alpha chain;HLA class I histocompatibility antigen, A-29 alpha chain;HLA class I histocompatibility antigen, A-74 alpha chain;HLA class I histocompatibility antigen, A-32 alpha chain;HLA class I histocompatibility antigen, A-11 alpha chain;HLA class I histocompatibility antigen, A-3 alpha chain;HLA class I histocompatibility antigen, A-43 alpha chain	HLA-A	1.09	0.05
P50995	Annexin A11	ANXA11	1.09	0.21
Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	1.09	0.30
P40939	Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase	HADHA	1.09	0.06
P48449;C9J315;A0A0G2JQD0	Lanosterol synthase	LSS	1.09	0.14
Q9BX59	Tapasin-related protein	TAPBP1	1.09	0.16
Q12931;I3L0K7	Heat shock protein 75 kDa, mitochondrial	TRAP1	1.09	0.14
P02545;Q3BDU5;Q5TC18	Prelamin-A/C;Lamin-A/C	LMNA	1.09	0.08
P62854;Q5JNZ5	40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1	RPS26;RPS26P1 1	1.09	0.48
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	STT3B	1.09	0.10
E9PCY5;Q02880	DNA topoisomerase 2;DNA topoisomerase 2-beta	TOP2B	1.09	0.10
Q92922	SWI/SNF complex subunit SMARCC1	SMARCC1	1.09	0.34
O75947;F5H608	ATP synthase subunit d, mitochondrial	ATP5H	1.09	0.17
M0R0F0;P46782;M0R0R2;M0QZ2N H3BLU7;O43488	40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed Aflatoxin B1 aldehyde reductase member 2	RPSS AKR7A2	1.09 1.09	0.39 0.48

P49368;B4DUR8	T-complex protein 1 subunit gamma	CCT3	1.09	0.06
O95881	Thioredoxin domain-containing protein 12	TXNDC12	1.09	0.11
P10515;H0YDD4;E9PEJ4	Dihydropolyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	1.09	0.08
Q92973	Transportin-1	TNPO1	1.09	0.08
Q9H568	Actin-like protein 8	ACTL8	1.09	0.09
Q8TEX9;H0YN14;H0YN07;H0YMR4	Importin-4	IPO4	1.09	0.27
Q9Y277;E5RJN6;E5RHZ6;E5RFP6	Voltage-dependent anion-selective channel protein 3	VDAC3	1.10	0.18
P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	1.10	0.11
P08243;F8WEJ5	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	1.10	0.22
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2	1.10	0.24
P20700;E9PBF6;A0A0D9SFE5;A0A0D9SFY5	Lamin-B1	LMNB1	1.10	0.22
P31949	Protein S100-A11;Protein S100-A11, N-terminally processed	S100A11	1.10	0.14
A0A024QZP7;P06493;E5RIU6;A0A087WZZ9	Cyclin-dependent kinase 1	CDC2;CDK1	1.10	0.12
P43686	26S protease regulatory subunit 6B	PSMC4	1.10	0.46
Q9H9B4;D6RDG7;S4R2X2;D6RFI0	Sideroflexin-1	SFXN1	1.10	0.19
O00567	Nucleolar protein 56	NOP56	1.10	0.14
Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18	1.10	0.29
Q14137	Ribosome biogenesis protein BOP1	BOP1	1.10	0.14
A0A024R4M0;P46781;B5MCT8;C9JM19	40S ribosomal protein S9	RPS9	1.10	0.41
Q7KZF4	Staphylococcal nuclease domain-containing protein 1	SND1	1.10	0.25
Q13232;H3BPR2	Nucleoside diphosphate kinase 3;Nucleoside diphosphate kinase	NME3	1.10	0.19
O00148;K7EQN7	ATP-dependent RNA helicase DDX39A	DDX39A	1.10	0.15
I3L0N3;P46459	Vesicle-fusing ATPase	NSF	1.10	0.44
P33992;B1AHB1	DNA replication licensing factor MCM5;DNA helicase	MCM5	1.10	0.04
Q08211	ATP-dependent RNA helicase A	DHX9	1.10	0.10
P22234;E9PBS1;D6RF62	Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase	PAICS	1.10	0.07
P05023;M0R116;A0A0A0MT26;P13637	Sodium/potassium-transporting ATPase subunit alpha-1;Sodium/potassium-transporting ATPase subunit alpha-3	ATP1A1;ATP1A3	1.10	0.08
G5EA31;P53992	Protein transport protein Sec24C	SEC24C	1.10	0.19
Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	1.10	0.06
P35579	Myosin-9	MYH9	1.10	0.16
Q5HY54;Q60FE5;P21333;A0A087WY3	Filamin-A	FLNA	1.11	0.11
P47897;A0A1B0GVU9;B4DDN1	Glutamine--tRNA ligase	QARS	1.11	0.11
G8JLB6;P31943;E9PCY7;D6RBM0;H0YB39;E5RGV0;E7EN40;D6RIU0	Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed	HNRNPH1	1.11	0.26
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	1.11	0.10
P52597	Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed	HNRNPF	1.11	0.17
P12236;P12235;V9GYG0	ADP/ATP translocase 3;ADP/ATP translocase 3, N-terminally processed;ADP/ATP translocase 1	SLC25A6;SLC25A4	1.11	0.13
E9PD53;Q9NTJ3	Structural maintenance of chromosomes protein;Structural maintenance of chromosomes protein 4	SMC4	1.11	0.18
Q5TDF0;Q9BSD7	Cancer-related nucleoside-triphosphatase	NTPCR	1.11	0.13
Q8WWM7;H3BUF6;H3BSK9	Ataxin-2-like protein	ATXN2L	1.11	0.25
F5GXX5;P61803;F5H895;A0A0B4J239	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	1.11	0.10
P63167;F8VXL2;F8VRV5	Dynein light chain 1, cytoplasmic	DYNLL1	1.11	0.19
Q96JJ7	Protein disulfide-isomerase TMX3	TMX3	1.11	0.21
A0A0A6YYL4;P57737	Coronin;Coronin-7	CORO7-PAM16;CORO7	1.11	0.08
J3KN36;A0A0G2JN29;A0A087X117;Q15155;P69849;Q5JPE7;A0A0G2JP90;A0A087WW46	Nodal modulator 1;Nodal modulator 3;Nodal modulator 2	NOMO3;NOMO1;NOMO2	1.11	0.10
Q13501;E7EMC7	Sequestosome-1	SQSTM1	1.11	0.19
A0A0D9SFB3;A0A0D9SG12;A0A0D9SF53;O00571;O15523	ATP-dependent RNA helicase DDX3X;ATP-dependent RNA helicase DDX3Y	DDX3X;DDX3Y	1.11	0.25
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	1.11	0.05
P63000	Ras-related C3 botulinum toxin substrate 1	RAC1	1.11	0.12
P11498;E9PS68	Pyruvate carboxylase, mitochondrial	PC	1.11	0.31

P04792	Heat shock protein beta-1	HSPB1	1.11	0.27
H0YNNW5;P33316;A0A0C4DGL3;H0YKC5;H0YMM5;H0YJN9;H0YK10	Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	1.11	0.10
O94826	Mitochondrial import receptor subunit TOM70	TOMM70A	1.11	0.26
B9A067;Q16891;C9J406;H7C463	MICOS complex subunit MIC60	IMMT	1.11	0.11
B4DXZ6;P51114;E7EU85;E9PFF5	Fragile X mental retardation syndrome-related protein 1	FXR1	1.11	0.16
P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	1.11	0.06
Q8N2K0;I3L294	Monoacylglycerol lipase ABHD12	ABHD12	1.11	0.18
P36542	ATP synthase subunit gamma, mitochondrial	ATP5C1	1.11	0.18
P30086	Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimulating peptide	PEBP1	1.11	0.06
P40227	T-complex protein 1 subunit zeta	CCT6A	1.12	0.09
H0YL72;P50213;H0YM64;H0YKD0;H0YL16;H0YMU3	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	1.12	0.04
P04843;B7Z4L4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	1.12	0.04
A0A087WVV2;A0A0A0MRV0;Q9P2E9;F8W7S5;A0A087WU26	Ribosome-binding protein 1	RRBP1	1.12	0.10
Q8WUX1;C9JU1;C9JMY2;C9JHH7;C9JWG4;C9JNK4	Sodium-coupled neutral amino acid transporter 5	SLC38A5	1.12	0.11
P26640;A0A140T936	Valine--tRNA ligase	VAR5	1.12	0.19
Q9Y265;E7ETR0;H7C4G5	RuvB-like 1	RUVBL1	1.12	0.11
P05388;F8VWS0;F8VU65;F8VPE8;G3V210;F8VQY6;F8VRK7;F8VW21;Q8NHW5;F8VWV4	60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-like	RPLP0;RPLP0P6	1.12	0.18
Q8TCT9;A0A075B6F6	Minor histocompatibility antigen H13	HM13	1.12	0.14
Q8TEQ6	Gem-associated protein 5	GEMIN5	1.12	0.14
Q16666	Gamma-interferon-inducible protein 16	IFI16	1.12	0.18
P02786;G3V0E5	Transferrin receptor protein 1;Transferrin receptor protein 1, serum form	TFRC	1.12	0.05
P62241;Q5JR95	40S ribosomal protein S8	RPS8	1.12	0.04
Q9Y678	Coatmer subunit gamma-1	COPG1	1.12	0.06
Q9UMS4	Pre-mRNA-processing factor 19	PRPF19	1.12	0.10
B7ZC38;Q9NR46;B7ZC39;F8WFB9	Endophilin-B2	SH3GLB2	1.12	0.21
P33991	DNA replication licensing factor MCM4	MCM4	1.12	0.15
P22087;M0R0P1;M0R299;M0QXL5;M0R2Q4;M0R2U2;M0R1H0;M0R2B0	rRNA 2-O-methyltransferase fibrillar	FBL	1.12	0.18
Q00765	Receptor expression-enhancing protein 5	REEP5	1.13	0.24
P35659;B4DFG0;D6RDA2;D6R9L5	Protein DEK	DEK	1.13	0.43
Q12788;J3KNP2	Transducin beta-like protein 3	TBL3	1.13	0.12
Q15365	Poly(rC)-binding protein 1	PCBP1	1.13	0.08
G3V153;Q14444;E9PLA9	Caprin-1	CAPRIN1	1.13	0.09
A0A024RCR6;A0A0G2JK23;P46379;A0A0G2JL47;F6S6P2;X6REW1;A0A0G2JMI1	Large proline-rich protein BAG6	BAT3;BAG6	1.13	0.08
P45880;A0A0A0MR02;Q5JSD2;Q5JSD1	Voltage-dependent anion-selective channel protein 2	VDAC2	1.13	0.14
A0A087X211;P62333;H0YJC0	26S protease regulatory subunit 10B	PSMC6	1.13	0.42
P49327;A0A0U1RQF0	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-carrier-protein] hydrolase	FASN	1.13	0.12
Q9H0S4	Probable ATP-dependent RNA helicase DDX47	DDX47	1.13	0.24
Q9P258	Protein RCC2	RCC2	1.13	0.08
Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I	1.13	0.39
Q15061	WD repeat-containing protein 43	WDR43	1.13	0.17
F8VY04;F8W1A4;P54819;G3V213;F8VZG5;F8VPP1	Adenylylase 2, mitochondrial;Adenylylase 2, mitochondrial;Adenylylase 2, mitochondrial, N-terminally processed	AK2	1.13	0.09
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	1.13	0.18
A0A087WU53;Q9H0U3	Magnesium transporter protein 1	MAGT1	1.13	0.07
F5GWX5;A0A0C4DGG9;Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	1.13	0.19
P27635;X1WI28	60S ribosomal protein L10	RPL10	1.13	0.25
Q14739;C9JXK0	Lamin-B receptor	LBR	1.13	0.39
Q9ULW0	Targeting protein for Xklp2	TPX2	1.13	0.05
P42677;Q5T4L4	40S ribosomal protein S27	RPS27	1.13	0.34
P62888;E5R199;A0A0C4DH44	60S ribosomal protein L30	RPL30	1.13	0.12
P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	1.14	0.09

P68366	Tubulin alpha-4A chain	TUBA4A	1.14	0.13
F8W8R3;A0A087WWF6;P49005;C9IZD2;C9J8Z7;C9JLE1;C9JHC7	DNA polymerase delta subunit 2	POLD2	1.14	0.03
B4DY09;Q12905;X6R6Z1	Interleukin enhancer-binding factor 2	ILF2	1.14	0.06
P62249;M0R210;M0R3H0;M0R1M5	40S ribosomal protein S16	RPS16	1.14	0.05
O75131;A0A087WYQ3	Copine-3	CPNE3	1.14	0.07
P20839;C9J381;C9K0R9	Inosine-5-monophosphate dehydrogenase 1;Inosine-5-monophosphate dehydrogenase	IMPDH1	1.14	0.08
P16615;H7C5W9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	1.14	0.21
O75821;K7ENA8;K7ER90;K7EL20	Eukaryotic translation initiation factor 3 subunit G	EIF3G	1.14	0.17
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	1.14	0.02
H0Y8C6;O00410	Importin-5	IPO5	1.14	0.25
P53618	Coatamer subunit beta	COPB1	1.14	0.09
Q93009;H3BND8	Ubiquitin carboxyl-terminal hydrolase 7;Ubiquitin carboxyl-terminal hydrolase	USP7	1.14	0.15
Q04760	Lactoylglutathione lyase	GLO1	1.14	0.19
A0A0R4J2E8;A8MXP9;P43243;D6RE M6;D6R991	Matrin-3	MATR3	1.14	0.10
C9J050;C9JEJ2;P49585;H7C1T3;Q9Y5K3	Choline-phosphate cytidyltransferase A;Choline-phosphate cytidyltransferase B	PCYT1A;PCYT1 B	1.14	0.12
Q9BW27;J3KT10;J3QL54	Nuclear pore complex protein Nup85	NUP85	1.15	0.19
E9PF19;Q9Y4P3;Q96E41	Transducin beta-like protein 2	TBL2	1.15	0.16
P52292;J3QLL0;J3KS65	Importin subunit alpha-1	KPNA2	1.15	0.06
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	1.15	0.30
P09543	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	1.15	0.25
F1T0B3;A0A087X2G1;Q92499	ATP-dependent RNA helicase DDX1	DDX1	1.15	0.09
Q9HCU5;B5MC98	Prolactin regulatory element-binding protein	PREB	1.15	0.12
Q8NE71;H0YGW7	ATP-binding cassette sub-family F member 1	ABCF1	1.15	0.05
Q06203;D6RCC8	Amidophosphoribosyltransferase	PPAT	1.15	0.24
P49411	Elongation factor Tu, mitochondrial	TUFM	1.15	0.17
Q9UG63	ATP-binding cassette sub-family F member 2	ABCF2	1.15	0.47
P62263;H0YB22;E5RH77	40S ribosomal protein S14	RPS14	1.15	0.45
O15042;E7ET15	U2 snRNP-associated SURP motif-containing protein	U2SURP	1.15	0.01
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	1.15	0.35
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A	1.15	0.07
Q14318;U3KQ64;A0A0A0MTJ1	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	1.16	0.28
Q14534;E7EVQ6;H0YBN7	Squalene monooxygenase	SQLE	1.16	0.10
A0A087WYT3;Q15185;B4DDC6	Prostaglandin E synthase 3	PTGES3	1.16	0.18
D6RAA6;P57088	Transmembrane protein 33	TMEM33	1.16	0.19
P60468	Protein transport protein Sec61 subunit beta	SEC61B	1.16	0.10
O14980	Exportin-1	XPO1	1.16	0.13
P56182	Ribosomal RNA processing protein 1 homolog A	RRP1	1.16	0.17
Q9UHD8;K7EL40	Septin-9	SEPT9	1.16	0.10
Q15366;F8VZX2;H3BRU6;F8W0G4	Poly(rC)-binding protein 2	PCBP2	1.16	0.16
O75223;B8ZZK2;M0QZK8	Gamma-glutamylcyclotransferase	GGCT	1.16	0.18
Q53EL6;Q5VZS7	Programmed cell death protein 4	PDCD4	1.16	0.26
Q9P2J5	Leucine--tRNA ligase, cytoplasmic	LARS	1.16	0.35
F8VPD4;P27708	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase	CAD	1.16	0.11
Q00325	Phosphate carrier protein, mitochondrial	SLC25A3	1.16	0.02
P08574	Cytochrome c1, heme protein, mitochondrial	CYC1	1.16	0.17
P36578;H3BM89	60S ribosomal protein L4	RPL4	1.17	0.31
P39748;I3L3E9	Flap endonuclease 1	FEN1	1.17	0.49
C9JXB8;C9JNW5;P83731	60S ribosomal protein L24	RPL24	1.17	0.26
P49257	Protein ERGIC-53	LMAN1	1.17	0.33
K7EJE8;K7EKE6;P36776	Lon protease homolog, mitochondrial	LONP1	1.17	0.04
P56192	Methionine--tRNA ligase, cytoplasmic	MARS	1.17	0.26

A6NEM2;P51610	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-terminal chain 3;HCF N-terminal chain 4;HCF N-terminal chain 5;HCF N-terminal chain 6;HCF C-terminal chain 1;HCF C-terminal chain 2;HCF C-terminal chain 3;HCF C-terminal chain 4;HCF C-terminal chain 5;HCF C-terminal chain 6	HCFC1	1.17	0.28
Q9NR30	Nucleolar RNA helicase 2	DDX21	1.17	0.16
P39023;G5E9G0;H7C422;B5MCW2;H7C3M2	60S ribosomal protein L3	RPL3	1.17	0.59
A0A087WUZ3;Q01082;F8W6C1	Spectrin beta chain, non-erythrocytic 1	SPTBN1	1.17	0.24
Q9BZX2	Uridine-cytidine kinase 2	UCK2	1.17	0.25
Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	1.17	0.14
Q9H1C4;E9PNE5	Protein unc-93 homolog B1	UNC93B1	1.17	0.10
Q9NRG9;F8VZ44;H3BU82	Aladin	AAAS	1.17	0.06
J3KR24;P41252;A0A0A0MSX9	Isoleucine--tRNA ligase, cytoplasmic	IARS	1.17	0.23
Q6P2E9	Enhancer of mRNA-decapping protein 4	EDC4	1.17	0.29
P55060	Exportin-2	CSEIL	1.17	0.19
P53621	Coatamer subunit alpha;Xenin;Proxenin	COPA	1.17	0.14
A0A087WUC6;Q15005;E9PL01;E9P168;E9PRB9	Signal peptidase complex subunit 2	SPCS2	1.17	0.14
O75533	Splicing factor 3B subunit 1	SF3B1	1.17	0.15
Q8NCA5;E9PH82	Protein FAM98A	FAM98A	1.17	0.44
H0Y4R1;P12268	Inosine-5-monophosphate dehydrogenase 2	IMPDH2	1.17	0.27
P14635;E9PC90	G2/mitotic-specific cyclin-B1	CCNB1	1.17	0.31
P62829;C9JD32;J3KT29;B9ZVP7	60S ribosomal protein L23	RPL23	1.17	0.21
P05141	ADP/ATP translocase 2;ADP/ATP translocase 2, N-terminally processed	SLC25A5	1.18	0.15
A0A0U1RQH7;G3XAC6;Q14498;H0Y4X3;A0A0U1RQW2	RNA-binding protein 39	RBM39	1.18	0.22
P49207	60S ribosomal protein L34	RPL34	1.18	0.24
Q12907;D6RBV2;D6RIU4;D6RDX1	Vesicular integral-membrane protein VIP36	LMAN2	1.18	0.16
P21796;C9JI87	Voltage-dependent anion-selective channel protein 1	VDAC1	1.18	0.25
A0A1W2PPS1;Q00839;A0A1X7SBS1;A0A1W2PP35;Q5RI18;A0A1W2PQL0;A0A1W2PP34;A0A1W2PPL4;A0A1W2PPH7;A0A1W2PRZ7;A0A1W2PQ74;A0A1W2PQD4	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1.18	0.07
P43007	Neutral amino acid transporter A	SLC1A4	1.18	0.15
F5GZS6;J3KPF3;P08195	4F2 cell-surface antigen heavy chain	SLC3A2	1.18	0.08
Q9Y6G9;E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	1.18	0.47
Q99613;B5ME19	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C;EIF3CL	1.19	0.11
P51148;F8VVK3;K7ERI8;K7ERQ8	Ras-related protein Rab-5C	RAB5C	1.19	0.13
Q9BSJ8	Extended synaptotagmin-1	ESYT1	1.19	0.14
P48047;H7C0C1	ATP synthase subunit O, mitochondrial	ATP5O	1.19	0.59
E7EX73;E9PGM1;E7EUU4;Q04637	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	1.19	0.09
Q08945	FACT complex subunit SSRP1	SSRP1	1.19	0.10
Q8N1F7;H3BVG0;H3BM93	Nuclear pore complex protein Nup93	NUP93	1.19	0.17
P35250	Replication factor C subunit 2	RFC2	1.19	0.14
Q6NUQ4;H7C085	Transmembrane protein 214	TMEM214	1.19	0.15
Q9HAV4	Exportin-5	XPO5	1.19	0.33
P15924	Desmoplakin	DSP	1.19	0.22
Q5QNZ2;P24539	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	1.19	0.26
O60832;C9IYT0;H7C0M1	H/ACA ribonucleoprotein complex subunit 4	DKC1	1.20	0.17
A0A1W2PNX8;Q9H3U1	Protein unc-45 homolog A	UNC45A	1.20	0.08
P07814;V9GYZ6	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	1.20	0.23
Q13576;F5H7S7;E7EWC2;D6R939	Ras GTPase-activating-like protein IQGAP2	IQGAP2	1.20	0.10
P09972;J3KSV6;J3QKP5;A8MVZ9;K7EKH5;C9J8F3	Fructose-bisphosphate aldolase C;Fructose-bisphosphate aldolase	ALDOC	1.20	0.13
P15880;H0YEN5;E9PQD7;E9PMM9	40S ribosomal protein S2	RPS2	1.21	0.49
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	1.21	0.12
Q9BTX1	Nucleoporin NDC1	NDC1	1.21	0.23
E9PDR0;P05166;C9JQS9;E7EX59;E7EUY3;E7ETT1;E7ETT4;E9PEC3;F8WB19	Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB	1.21	0.21
O94776	Metastasis-associated protein MTA2	MTA2	1.21	0.42

Q9NZL4;K7EL16	Hsp70-binding protein 1	HSPBP1	1.21	0.36
O95197	Reticulon-3	RTN3	1.22	0.16
O96011	Peroxisomal membrane protein 11B	PEX11B	1.22	0.26
Q10589	Bone marrow stromal antigen 2	BST2	1.22	0.08
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	1.22	0.12
P40938	Replication factor C subunit 3	RFC3	1.22	0.06
J3KPT4;Q9H4I3	TraB domain-containing protein	TRABD	1.22	0.28
P51858	Hepatoma-derived growth factor	HDGF	1.23	0.22
Q9BT22;K7EID2	Chitobiosyldiphosphodolichol beta-mannosyltransferase	ALG1	1.23	0.19
Q9BW19	Kinesin-like protein KIFC1	KIFC1	1.23	0.39
P52701;A0A087WWJ1	DNA mismatch repair protein Msh6	MSH6	1.23	0.14
Q9BTE3	Mini-chromosome maintenance complex-binding protein	MCMBP	1.23	0.46
P17812	CTP synthase 1	CTPS1	1.23	0.25
Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP	1.23	0.29
E7ETZ4;Q9Y6E2;E9PFD4;B5MCE7;Q75MG1;B5MCH7	Basic leucine zipper and W2 domain-containing protein 2	BZW2	1.23	0.49
A0A087WVQ6;Q00610	Clathrin heavy chain;Clathrin heavy chain 1	CLTC	1.23	0.11
Q9NZ01	Very-long-chain enoyl-CoA reductase	TECR	1.23	0.23
Q9UBM7;E9PM00;E9PJ54	7-dehydrocholesterol reductase	DHCR7	1.23	0.42
Q9Y5M8;H7C4H2	Signal recognition particle receptor subunit beta	SRPRB	1.23	0.08
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	1.24	0.32
P11388	DNA topoisomerase 2-alpha	TOP2A	1.24	0.13
P26010;F5H6T4	Integrin beta-7;Integrin beta	ITGB7	1.24	0.17
P0DOY3;P0DOY2;P0CF74;A0A0B4J231;A0M8Q6;P0CG04;B9A064	Ig lambda-6 chain C region;Ig lambda-7 chain C region;Ig lambda-1 chain C regions;Immunoglobulin lambda-like polypeptide 5	IGLC6;IGLL5;IGLC7;IGLC1	1.25	0.39
P31689	DnaJ homolog subfamily A member 1	DNAJ1	1.25	0.14
B5MCF9;O00541;B3KXD6	Pescadillo homolog	PES1	1.26	0.36
A0A0A0MTB8;Q8NI36	WD repeat-containing protein 36	WDR36	1.26	0.10
E9PNM1;A0A1W2PQ47;P37268	Squalene synthase	FDFT1	1.26	0.26
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	1.26	0.28
A0A0U1RRM1;Q8WXI9;A0A0U1RR30	Transcriptional repressor p66-beta	GATAD2B	1.27	0.08
E9PIF2;Q13206	Probable ATP-dependent RNA helicase DDX10	DDX10	1.27	0.09
Q9BQG0;I3L1L3	Myb-binding protein 1A	MYBBP1A	1.27	0.27
Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10	1.27	0.05
Q14008	Cytoskeleton-associated protein 5	CKAP5	1.28	0.37
E7EQN5;P98171;E9PCM6;A0A0B4J1X7	Rho GTPase-activating protein 4	ARHGAP4	1.28	0.23
Q96HE7	ERO1-like protein alpha	ERO1L	1.28	0.24
P10599	Thioredoxin	TXN	1.28	0.10
Q9Y6C9;E9PIE4	Mitochondrial carrier homolog 2	MTCH2	1.28	0.26
Q9NV11;F8W7R3;H3BP78	Fanconi anemia group I protein	FANCI	1.28	0.24
Q14690	Protein RRP5 homolog	PDCD11	1.29	0.16
K7EMQ8;J3QKS7;B4DGM3;Q969G3;H7C048	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	1.29	0.42
Q9NYK5;C9JG87	39S ribosomal protein L39, mitochondrial	MRPL39	1.29	0.43
P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	1.29	0.28
O60763	General vesicular transport factor p115	USO1	1.29	0.13
Q9HD20	Manganese-transporting ATPase 13A1	ATP13A1	1.29	0.09
P48651	Phosphatidylserine synthase 1	PTDSS1	1.30	0.14
Q9BVP2	Guanine nucleotide-binding protein-like 3	GNL3	1.30	0.20
Q1KMD3;H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2;HNRNPUL2-BSCL2	1.30	0.12
H7C3A1;Q9BXP5	Serrate RNA effector molecule homolog	SRRT	1.30	0.49
P49238	CX3C chemokine receptor 1	CX3CR1	1.31	0.13
P46778;G3V1B3;M0R181	60S ribosomal protein L21	RPL21	1.31	0.42
Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	UTP6	1.32	0.22
P55265;H0YCK3	Double-stranded RNA-specific adenosine deaminase	ADAR	1.32	0.15
P0DN76;Q01081	Splicing factor U2AF 35 kDa subunit	U2AF1	1.32	0.40
Q03701	CCAAT/enhancer-binding protein zeta	CEBPZ	1.32	0.52
P28907;H0Y950	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1	CD38	1.33	0.25
Q9NUQ8	ATP-binding cassette sub-family F member 3	ABCF3	1.33	0.30
Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	1.33	0.26
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	1.35	0.21
O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11	1.35	0.33
B1AHD1;P55769	NHP2-like protein 1;NHP2-like protein 1, N-terminally processed	NHP2L1	1.37	0.23

Q92616	Translational activator GCN1	GCN1L1	1.37	0.31
P49792	E3 SUMO-protein ligase RanBP2	RANBP2	1.38	0.21
B4DR61;P61619;F8W776;Q8TC24;Q9H9S3	Protein transport protein Sec61 subunit alpha isoform 1;Protein transport protein Sec61 subunit alpha isoform 2	SEC61A1;SEC61A2	1.39	0.26
Q6P2Q9;I3L0J9	Pre-mRNA-processing-splicing factor 8	PRPF8	1.39	0.36
P62979;J3QS39;J3QTR3;F5H6Q2;F5GYU3;F5H2Z3;F5H265;B4DV12;F5H388;F5H747;F5GXXK7;J3QKN0;Q5PY61;Q96C32;P62987;P0CG47;P0CG48;M0R1V7;Q49A90;M0R1M6;M0R2S1	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Ubiquitin-60S ribosomal protein L40;Ubiquitin;60S ribosomal protein L40;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin	RPS27A;UBB;UBC;UBA52	1.40	0.13
V9GYM8;Q92974	Rho guanine nucleotide exchange factor 2	ARHGEF2	1.41	0.33
A0A087WXM6;J3QQT2;J3KRX5;A0A0A6YYL6;P18621;J3KRB3;A0A087WWH0;J3QS96;J3QLC8;A0A0A0MR F8;A0A087WY81	60S ribosomal protein L17	RPL17;RPL17-C18orf32	1.43	0.40
D6RD17;P01591;C9JA05;D6RHJ6	Immunoglobulin J chain	JCHAIN;IGJ	1.44	0.20
M0R117;Q02543;M0R3D6;M0R1A7;M0R0P7	60S ribosomal protein L18a	RPL18A	1.45	0.16
P62701	40S ribosomal protein S4, X isoform	RPS4X	1.49	0.37
O94906	Pre-mRNA-processing factor 6	PRPF6	1.49	0.23
Q9Y5K5;Q5LJA5;Q5LJA9;Q5LJB0;H0Y6Y4;H0Y4E0	Ubiquitin carboxyl-terminal hydrolase isozyme L5;Ubiquitin carboxyl-terminal hydrolase	UCHL5	1.66	0.05

Table S4. Full list of proteins identified in the LC-MS/MS-based global proteomics experiment with the corresponding 1/DMSO and BTZ/DMSO ratios and the p-values

Majority protein IDs	Protein names	Gene names	-LOG(P-value) 1/DMSO	Difference 1/DMSO	-LOG(P-value) BTZ/DMSO	Difference BTZ/DMSO
Q9NRG9;F8VZ44;H3BU82	Aladin	AAAS	0.740701379	0.112125397	0.023081923	0.004932086
Q86V21	Acetoacetyl-CoA synthetase	AACS	0.01647608	0.005587578	0.036989888	-0.009498596
Q6PD74	Alpha- and gamma-adaptin-binding protein p34	AAGAB	1.219752795	0.134010315	0.868405902	0.095850627
C9JG97;C9JEH3;Q13685;H7C0 R2;C9JTS3	Angio-associated migratory cell protein	AAMP	3.507189426	0.468536059	2.065693977	0.309325536
A2A2Q9;Q9Y312	Protein AAR2 homolog	AAR2	0.01799938	0.007062467	0.50547297	0.131598663
P49588	Alanine--tRNA ligase, cytoplasmic	AARS	1.616778134	0.08425045	1.663003901	0.084717751
Q5JTZ9	Alanine--tRNA ligase, mitochondrial	AARS2	0.732578691	0.086998304	0.052338701	0.008609136
Q9BTE6;C9J5N1	Alanyl-tRNA editing protein Aarsd1	AARSD1;PTGES3L- AARSD1	0.013111719	-0.001521428	0.748523797	-0.054401716
Q9NRN7;E9PLW6	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT	0.61365474	-0.076082548	0.256025042	-0.036196073
Q9NY61	Protein AATF	AATF	0.699631454	0.081151962	1.164804173	-0.134879112
Q9NRK6	ATP-binding cassette sub-family B member 10, mitochondrial	ABCB10	0.871525317	0.203327688	0.15807824	-0.036422984
O75027;B4DGL8;A0A087WW6 5	ATP-binding cassette sub-family B member 7, mitochondrial	ABCB7	0.656632986	0.073694865	0.071608879	0.01193587
Q9NUT2	ATP-binding cassette sub-family B member 8, mitochondrial	ABCB8	0.889893725	0.215771039	0.435536625	0.131882985
O15439	Multidrug resistance-associated protein 4	ABCC4	0.155579327	-0.051941554	0.656527283	-0.198279953
P28288	ATP-binding cassette sub-family D member 3	ABCD3	1.927273745	0.138257662	0.024255786	-0.001982053
P61221;D6R9I9	ATP-binding cassette sub-family E member 1	ABCE1	2.36025055	-0.091574987	0.41953501	-0.023593267
Q8NE71;H0YGW7	ATP-binding cassette sub-family F member 1	ABCF1	0.293609365	-0.02039814	0.120030344	0.009642919
Q9UG63	ATP-binding cassette sub-family F member 2	ABCF2	0.406416755	0.055211385	0.568019737	0.073165258
Q9NUQ8	ATP-binding cassette sub-family F member 3	ABCF3	0.911232519	0.082228025	0.999313049	0.082656542
Q9UNQ0	ATP-binding cassette sub-family G member 2	ABCG2	0.193029986	-0.05191466	0.819538818	-0.149905332
Q9NUJ1	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	ABHD10	0.353122643	0.095905622	0.66074696	0.132658958
Q8NFV4	Alpha/beta hydrolase domain-containing protein 11	ABHD11	0.494346272	0.064129512	2.66989459	-0.123833974
Q8N2K0	Monoacylglycerol lipase ABHD12	ABHD12	0.120270851	0.01124986	0.364495164	-0.032961528
Q96IU4;F8W9U3;B4DQI4	Alpha/beta hydrolase domain-containing protein 14B	ABHD14B	2.025746173	-0.207283974	0.920524891	-0.070040703
A0A0G2JJD3;O95870;A0A0G2J I89	Abhydrolase domain-containing protein 16A	ABHD16A	0.626185566	0.065216064	0.303407055	-0.067022006
P08910	Abhydrolase domain-containing protein 2	ABHD2	0	NaN	0	NaN
J3KTE1;Q8WU67	Phospholipase ABHD3	ABHD3	3.927057085	0.322288831	0.256653531	0.049373945
B6VEX4;A0A0A0MRT6;Q8IZP 0	Abl interactor 1	ABI1	0.402114037	0.045502981	0.150975233	0.025828044
Q9ULW3	Activator of basal transcription 1	ABT1	0.423680033	0.095344861	1.06821882	-0.202794393
P09110;C9JDE9;H7C131	3-ketoacyl-CoA thiolase, peroxisomal	ACAA1	2.143745649	0.219548543	0.746443046	0.076205571
A0A0B4J2A4;P42765;K7EMEO	3-ketoacyl-CoA thiolase, mitochondrial	ACAA2	4.147407714	0.180546125	0.877575075	0.042394002
Q13085;Q59FY4	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA	0.610380672	-0.051144282	2.278745695	-0.122849147
F8W1I9;Q6JQN1	Acyl-CoA dehydrogenase family member 10	ACAD10	0.386403188	-0.079139392	0.434022882	-0.08876578
Q9H845;H0Y8Z9	Acyl-CoA dehydrogenase family member 9, mitochondrial	ACAD9	2.116283965	0.087186178	0.113055734	-0.00772508
B7Z9I1;Q5T4U5;P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	0.379548507	0.043895086	0.052303583	-0.009812355
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL	2.797176106	0.088994026	0.233085493	0.012531916

A0A087X1H5;Q15057;A0A0U1RQT1	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	ACAP2	0.184619382	-0.086675644	0.431251312	-0.098744869
P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1	4.606639224	0.18592453	0.582380643	-0.03068765
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	1.129658757	-0.116367022	0.087504832	-0.015112559
Q9H3P7	Golgi resident protein GCP60	ACBD3	0.061326883	0.011280696	0.029901673	0.005721728
Q9BR61	Acyl-CoA-binding domain-containing protein 6	ACBD6	0.162102402	0.029332479	0.327298363	-0.066373507
A0A0C4DGT6;Q96AP0;R4GNJ5	Adrenocortical dysplasia protein homolog 5	ACD	0.997236786	0.211865743	0.270790125	0.141669591
E7EQT4;S4R3H4;Q9UKV3;G3V3B0	Apoptotic chromatin condensation inducer in the nucleus	ACIN1	0.642700613	-0.065039635	0.24452896	0.024569511
P53396	ATP-citrate synthase	ACLY	2.586945219	-0.099928538	1.535177954	-0.063512484
Q99798;A2A274	Aconitate hydratase, mitochondrial	ACO2	3.079187178	0.124943415	0.252857593	0.012322426
Q9NPF3	Acyl-coenzyme A thioesterase 13;Acyl-coenzyme A thioesterase 13, N-terminally processed	ACOT13	0.547005593	0.082631429	0.70154541	0.07260259
O00154;K7EKP8	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	1.314732044	-0.098095576	0.974517869	-0.079589526
E9PJN0;O14734;Q9BR14;E9PMC4;E9PIS4;H7C5A7;H0Y698	Acyl-coenzyme A thioesterase 8	ACOT8	0.688304267	0.165577571	0.3309382	0.119470596
Q9Y305;H7C5Q2	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	0.912772945	0.072067579	0.031026544	0.004374186
Q15067	Peroxisomal acyl-coenzyme A oxidase 1	ACOX1	0.376977237	-0.055135409	0.30176706	-0.037376722
P24666;G5E9R5	Low molecular weight phosphotyrosine protein phosphatase	ACPI	2.499395422	-0.131744385	1.030699083	-0.071869214
P15309	Prostatic acid phosphatase;PAPF39	ACPP	0	NaN	0	NaN
E7EPM6;P33121;B7Z3Z9;D6RE R0	Long-chain-fatty-acid--CoA ligase 1	ACSL1	0.27641639	-0.109424146	0.015902544	-0.005313555
O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3	0.091747784	-0.014583906	0.519936236	-0.078455925
O60488	Long-chain-fatty-acid--CoA ligase 4	ACSL4	0.07252278	0.007008235	0.79767864	-0.054131826
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5	ACSL5	0	0.106654167	0.269571536	0.181055546
C9J8C7;E7ERD7;Q9UKU0;C9JT10;C9JPA5;C9J411;C9JK59;C9J3Z0	Long-chain-fatty-acid--CoA ligase 6	ACSL6	0	NaN	0	0.169200897
Q9NUB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	ACSS1	0.745862807	0.082205455	1.036911351	-0.096629779
Q9NR19;C9J7L5	Acetyl-coenzyme A synthetase, cytoplasmic	ACSS2	0.560862074	-0.101221848	0.576552125	-0.13295002
P68133;P68032;P63267;P62736;A6NL76	Actin, alpha skeletal muscle;Actin, alpha cardiac muscle 1;Actin, gamma-enteric smooth muscle;Actin, aortic smooth muscle	ACTA1;ACTC1;ACTG2;ACTA2	0.982805836	0.413607915	0.838905121	0.38793246
P60709;P63261;I3L3I0;I3L1U9	Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed;Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed	ACTB;ACTG1	0.029764918	-0.00292333	0.581825295	0.034582774
O96019;H7C5S0	Actin-like protein 6A	ACTL6A	0.722474741	0.067202886	1.038209956	0.073441505
Q9H568	Actin-like protein 8	ACTL8	1.126067906	0.19215711	0.4110514	0.084125837
O43707;F5GX52	Alpha-actinin-4	ACTN4	2.229103565	-0.111174266	0.338651044	0.028240204
G3V5Y4;G3V2Q5;F6S9Y6		ACTR10	0	0.549077988	0.878425423	-0.319660187
P61163;R4GMT0;A0A1B0GV53	Alpha-centractin	ACTR1A	0.879742612	-0.079171499	0.582645103	-0.063183149
P42025	Beta-centractin	ACTR1B	1.890447336	-0.194183985	1.23471156	-0.140581449
P61160;F5H6T1	Actin-related protein 2	ACTR2	0.026336685	-0.005772591	0.147414918	0.024240176
P61158;B4DXW1	Actin-related protein 3	ACTR3	0.607171332	-0.056412379	0.466867022	-0.037344297
Q9H9F9	Actin-related protein 5	ACTR5	0	-0.182547887	0.175309129	0.185750167
A0A1B0GU86;A0A1B0GW23;Q03154;A0A1B0GVA5;A0A1B0GV31;C9JMV9;F8WC59;C9JYZ0	Aminoacylase-1	ACY1;ABHD14A-ACY1	0.226757558	-0.06099542	1.120104178	-0.261113167
G3V2U7;P07311	Acylphosphatase;Acylphosphatase-1	ACYP1	0.080898888	0.023625755	0.137859692	-0.03359127
P00813;F5GW14;F5GXW0	Adenosine deaminase	ADA	0.658789777	-0.099727313	0.344087082	-0.047608693
O14672	Disintegrin and metalloproteinase domain-containing protein 10	ADAM10	0.65585033	-0.04650116	1.062249936	-0.070075035
Q13444	Disintegrin and metalloproteinase domain-containing protein 15	ADAM15	1.543785851	0.334253947	0.908094524	0.224195798
P55265;H0YCK3	Double-stranded RNA-specific adenosine deaminase	ADAR	1.559924748	0.097853661	0.087869575	-0.008827209

Q8NI60	Atypical kinase ADCK3, mitochondrial	ADCK3	0.917587617	-0.141277313	1.072419519	-0.218475342
E7EV99;E7ENY0;P35611;A0A0 A0MSR2;H0Y9H2 P35612	Alpha-adducin	ADD1	0.033211542	-0.007505417	0.599066418	0.08231163
	Beta-adducin	ADD2	0.133228195	-0.029177984	0.483491304	0.106266975
P11766;H0YAG8	Alcohol dehydrogenase class-3	ADH5	2.635672014	-0.21602122	0.887457917	-0.103581746
Q9BV57	1,2-dihydroxy-3-keto-5- methylthiopentene dioxygenase	ADI1	1.231471714	0.175786336	0.97786643	0.144576073
P55263	Adenosine kinase	ADK	0.097819038	0.012993495	0.07533685	-0.010958989
Q9H2P0	Activity-dependent neuroprotector homeobox protein	ADNP	0.242250878	0.027046522	0.110628399	-0.012753487
Q9BRR6;H3BRS6	ADP-dependent glucokinase	ADPGK	1.534288253	0.148866653	0.45450711	0.058999379
Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3	ADPRHL2	0	NaN	0.303393213	0.084529559
P25098;E9PRV7	Beta-adrenergic receptor kinase 1	ADRBK1	0.59692375	-0.12836647	1.430322935	-0.16705958
Q16186;A0A087WX59	Proteasomal ubiquitin receptor ADRM1	ADRM1	2.089763411	-0.094560623	0.396970513	0.046552976
A0A1B0GWJ0;A0A1B0GTJ7;P 30566;A0A1B0GTG9;A0A1B0 GWF8 P30520	Adenylosuccinate lyase	ADSL	2.807240628	-0.188419978	1.305632531	-0.101045926
Q9Y4W6	Adenylosuccinate synthetase isozyme 2	ADSS	3.064350959	-0.231233915	0.963820988	-0.110589663
Q9Y4W6	AFG3-like protein 2	AFG3L2	3.191610666	0.134651502	0.021876125	-0.001715342
F8VVT9;J3KNM6;Q99490	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	AGAP2	0.525054835	0.10338281	0.448856433	0.098079681
Q53H12;E9PC15;E9PG39;A0A0 G2JLG5 Q9BSE5	Acylglycerol kinase, mitochondrial	AGK	2.393495954	0.189176242	0.241706539	-0.031974475
	Agmatinase, mitochondrial	AGMAT	0.002277063	0.000669607	0.666691169	-0.128989792
Q9UKV8	Protein argonaute-2	AGO2	0.357860069	-0.146959941	0.636962369	-0.139137586
Q99943	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	AGPAT1	0.244312985	0.085725466	0.402775813	-0.174269676
O15120	1-acyl-sn-glycerol-3-phosphate acyltransferase beta	AGPAT2	0	-0.256785393	0	NaN
Q9NUQ2	1-acyl-sn-glycerol-3-phosphate acyltransferase epsilon	AGPAT5	0.145247766	0.060243607	0.637333297	-0.363004208
Q53EU6	Glycerol-3-phosphate acyltransferase 3	AGPAT9	0.260275484	0.079943657	0.372182129	0.080100695
O00116;A0A1B0GWA2	Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS	3.924719236	0.15547657	1.586581325	0.073961576
Q8WYP5	Protein ELYS	AHCTF1	0.004293324	-0.000896772	0.019779323	0.005071004
P23526	Adenylosuccinate synthetase	AHCY	1.263543239	-0.112174352	0.02742243	-0.00349617
O43865	Putative adenylosuccinate synthetase 2	AHCYL1	0.161914479	0.028426488	0.135986942	0.022357623
Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK	4.490015326	-0.229257584	0.214557115	-0.016541799
O95433;H0YJG7	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1	0.012699578	-0.001347224	0.880827755	0.056839943
Q5JUP3;Q9BQI0	Allograft inflammatory factor 1-like	AIF1L	0.364711505	0.104523913	1.797827445	0.420845922
O95831;E9PMA0	Apoptosis-inducing factor 1, mitochondrial	AIFM1	2.982696714	0.1061306	0.28021977	0.019257228
Q9BRQ8	Apoptosis-inducing factor 2	AIFM2	1.593936271	0.297718366	0.54443094	0.125006994
Q12904	Aminoacyl tRNA synthase complex- interacting multifunctional protein 1;Endothelial monocyte-activating polypeptide 2	AIMP1	0.257428004	0.02117761	0.142069729	0.013409932
Q13155;A8MU58;F8W950	Aminoacyl tRNA synthase complex- interacting multifunctional protein 2	AIMP2	0.866680846	-0.088042895	0.320080027	-0.034901301
O00170;E9PMH2	AH receptor-interacting protein	AIP	0.090427243	0.012635549	0.038897427	0.00498263
Q5T9B7;P00568;H0YID2;H0Y4 J6 F8W1A4;P54819;F8VZG5;F8V Y04;G3V213	Adenylosuccinate kinase isoenzyme 1	AK1	0.555803132	0.103360748	0.400640806	0.069846471
	Adenylosuccinate kinase 2, mitochondrial;Adenylosuccinate kinase 2, mitochondrial;Adenylosuccinate kinase 2, mitochondrial, N-terminally processed	AK2	2.458767211	-0.171694438	0.52656303	-0.053048452
Q9UIJ7	GTP:AMP phosphotransferase AK3, mitochondrial	AK3	0.19864497	-0.098574193	0.573696223	-0.264629237
Q9Y3D8;A0A087WVD7;D6RD H4 Q9UKA4	Adenylosuccinate kinase isoenzyme 6	AK6;TAF9	2.117435863	-0.233214696	0.284997464	-0.0503184
O43823	A-kinase anchor protein 11	AKAP11	0.581749386	-0.080571969	0.611381037	-0.106931019
	A-kinase anchor protein 8	AKAP8	0.794219861	-0.176065922	0.255498503	-0.059890429
Q9ULX6	A-kinase anchor protein 8-like	AKAP8L	0	-0.270549774	0	-0.258090973
P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1	0.959541258	-0.079649289	1.179061075	-0.098489443

P15121;E9PCX2	Aldose reductase	AKR1B1	1.654540999	-0.082718531	0.218456154	0.011812528
P52895;B4DK69;S4R3P0;H0Y804	Aldo-keto reductase family 1 member C2	AKR1C2;AKR1C1	1.260945616	0.135140101	0.54774267	0.074046135
A0A0A0MSS8;P42330;S4R3Z2	Aldo-keto reductase family 1 member C3	AKR1C3	0.739093135	0.048915863	2.318027315	0.105412801
P51857	3-oxo-5-beta-steroid 4-dehydrogenase	AKR1D1	1.194992431	0.08935976	1.613592937	0.205613454
O43488;H3BLU7	Aflatoxin B1 aldehyde reductase member 2	AKR7A2	0.491578236	-0.071176211	0.359737515	-0.05485185
Q8IZ83;F5H4B6	Aldehyde dehydrogenase family 16 member A1	ALDH16A1	1.788329087	-0.138105075	0.350865862	-0.038682302
P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase	ALDH18A1	0.46470044	0.036508878	0.875099474	-0.046270688
P30837	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	0.622886555	-0.183590571	0.951722452	-0.253474236
P51648;J3QRD1;I3L1M4	Fatty aldehyde dehydrogenase	ALDH3A2	0.061296038	-0.015942574	0.015328615	-0.004122098
P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1	0.11798977	-0.009556452	1.511135625	-0.072781563
P04075;J3KPS3;H3BQN4;H3BPS8;H3BUH7;H3BR04	Fructose-bisphosphate aldolase A;Fructose-bisphosphate aldolase	ALDOA	5.125163981	-0.170412064	2.523313513	0.053367615
P09972;A8MVZ9	Fructose-bisphosphate aldolase C;Fructose-bisphosphate aldolase	ALDOC	1.671309614	-0.086592992	0.135267289	0.014134407
Q9BT22;K7EID2	Chitobiosylidiphosphodolichol beta-mannosyltransferase	ALG1	1.640935386	-0.172780355	0.501086354	-0.104850769
Q9H553	Alpha-1,3/1,6-mannosyltransferase ALG2	ALG2	0.184189472	-0.057465235	0.490010891	-0.127208074
H7C0X4;Q92685;F8WF93;H7BZZ2;F8WE30;C9J7S5	Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase	ALG3	0.029485946	0.013964208	0.852751196	-0.209871292
Q9Y673	Dolichyl-phosphate beta-glucosyltransferase	ALG5	1.336499244	0.301449585	0.850864904	0.216734028
A2A2G4;Q9Y672;S4R350	Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase	ALG6	0	0.433148575	0	0.298564529
H0YDD3;Q9BVK2;H0YDQ1;H0YD42;E9PKA5;E9PK79;H0YE0;E9PP96	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	ALG8	0.129730466	-0.041326777	0.055143934	-0.008691883
A0A087WZ62;H0YCW6;Q9H6U8	Alpha-1,2-mannosyltransferase ALG9	ALG9	0.392682218	0.059753736	0.103317019	-0.023570697
Q6P6C2	RNA demethylase ALKBH5	ALKBH5	0.008204347	0.001507123	0.594068101	0.076352119
E9PB61;Q86V81	THO complex subunit 4	ALYREF	2.060817786	-0.395675977	0.485467549	-0.106622696
H0Y360;Q01433	AMP deaminase 2	AMPD2	0	NaN	0	-0.089176178
Q9H1A4;H0Y564	Anaphase-promoting complex subunit 1	ANAPC1	0.006532827	0.001612027	0.002203338	0.000562986
Q9UJX5;D6RFM7;D6RAP6	Anaphase-promoting complex subunit 4	ANAPC4	0.698987673	-0.106543223	0.300022614	-0.053229014
F5H0F9;Q9UJX4	Anaphase-promoting complex subunit 5	ANAPC5	0.604914729	0.171644847	0.08691483	-0.026866277
Q9UJX3	Anaphase-promoting complex subunit 7	ANAPC7	0.018890301	0.002215703	1.316469583	-0.117302895
Q9P2R3	Rabankyrin-5	ANKFY1	0.002456879	-0.000796445	0.117849805	0.039678574
H0YM23;O75179;E9PDP5;Q8IWZ3;A0A1W2PQ15	Ankyrin repeat domain-containing protein 17;Ankyrin repeat and KH domain-containing protein 1	ANKRD17;ANKHD1	0.684891086	0.08630689	1.625490689	0.153333982
O15084;B4DIW9	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	ANKRD28	0.226188226	0.064614296	0.073212421	-0.024823507
Q53RE8	Ankyrin repeat domain-containing protein 39	ANKRD39	0	0.020832062	0	0.094200134
Q8N8A2;H7C209	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B	ANKRD44	0.091521205	-0.017354965	0.421991587	-0.078870138
Q9H8Y5;B8ZZS4	Ankyrin repeat and zinc finger domain-containing protein 1	ANKZF1	0.842328565	0.209419092	0.187025817	0.053864956
P39687;H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A	1.442408916	-0.077518781	0.989184373	-0.039829254
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B	0.15875142	-0.02629439	0.0222366	-0.004492442
Q9BTT0;Q5TB19;E9PLC4	Acidic leucine-rich nuclear phosphoprotein 32 family member E	ANP32E	0.178423868	0.040583293	0.090778918	-0.0212183
P50995	Annexin A11	ANXA11	0.681395228	0.131461461	0.046409014	0.011144002
P07355;H0YN42;H0YMD0;H0YMU9;A6NMY6;H0YMS0	Annexin A2;Annexin;Putative annexin A2-like protein	ANXA2;ANXA2P2	0.766307703	-0.076827367	3.275213593	0.216618538
P09525;Q6P452	Annexin A4;Annexin	ANXA4	1.116916542	-0.202360471	0.527780316	-0.093158404
P08758;D6RBL5;D6RBE9	Annexin A5;Annexin	ANXA5	1.309412766	-0.075714747	0.482725296	-0.044505755
P20073	Annexin A7	ANXA7	1.105333578	0.091203372	2.892965068	0.146001816

Q10567;C9J1E7	AP-1 complex subunit beta-1	AP1B1	1.457637121	-0.13731575	0.486237911	-0.053107897
O43747	AP-1 complex subunit gamma-1	AP1G1	0.040383152	0.003077189	0.287514174	0.019861857
Q9BXS5;E7ENJ6;K7EJL1	AP-1 complex subunit mu-1	AP1M1	0.688986485	-0.046769142	0.882584579	-0.056416194
P61966;H7C1E4	AP-1 complex subunit sigma-1A	AP1S1	0.408889854	-0.065782102	0.244992312	-0.047819646
P56377;H7BZG6;H0Y673;F6SF B5;A6NH01 O95782	AP-1 complex subunit sigma-2	AP1S2	0.471501591	-0.095757484	0.119822168	-0.038332621
O94973;A0A0G2JS82;A0A0G2J QM1	AP-2 complex subunit alpha-2	AP2A2	1.460977209	-0.232197762	1.561400965	-0.210983594
P63010;A0A087X253;A0A087 WU93;A0A087WZQ6;A0A087 WYD1	AP-2 complex subunit beta	AP2B1	0.097992188	0.006572088	0.618573839	0.029775937
A0A087WY71;Q96CW1;E9PF W3;C9JJ47	AP-2 complex subunit mu	AP2M1	2.656519711	0.255102475	1.769529784	0.171738942
M0R0N4;M0QY22;P53680;M0 QZ21;X6R390	AP-2 complex subunit sigma	AP2S1	0.099149543	-0.020085716	0.710218906	0.101519203
O00203	AP-3 complex subunit beta-1	AP3B1	1.551165884	0.070523898	0.062800387	-0.005893707
O14617	AP-3 complex subunit delta-1	AP3D1	3.241881707	-0.113925934	2.159822897	-0.085844994
Q9Y2T2	AP-3 complex subunit mu-1	AP3M1	0.126247281	0.013789495	0.192374319	-0.02356561
Q92572	AP-3 complex subunit sigma-1	AP3S1	0.162149041	-0.048639933	0.035495761	-0.012493451
Q9NUS5	AP-5 complex subunit sigma-1	AP5S1	0	NaN	0	NaN
Q7Z5R6	Amyloid beta A4 precursor protein- binding family B member 1-interacting protein	APBB1IP	1.509800025	-0.226968129	0.755649643	-0.142827352
C9JIF9;P13798	Acylamino-acid-releasing enzyme	APEH	4.11228506	-0.205856641	1.567236963	-0.102172852
P27695;G3V3M6;G3V5Q1;G3V 3C7;A0A0C4DGK8;G3V5D9;G 3V5M0;G3V359	DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, mitochondrial	APEX1	0.161478907	-0.020555814	0.288976642	0.034154574
G3V1C3;Q9BZZ5;H0YER7	Apoptosis inhibitor 5	API5	1.80747064	-0.11493206	0.024127538	0.003177007
Q9HDC9;H0Y512	Adipocyte plasma membrane-associated protein	APMAP	1.193328785	0.091592471	0.211414974	0.021480878
Q8NCW5	NAD(P)H-hydrate epimerase	APOA1BP	0.538587246	-0.077493668	0.015804871	0.003200849
B0QYD3;Q9UH17	DNA dC->dU-editing enzyme APOBEC- 3B	APOBEC3B	4.190785225	0.250196139	1.229383587	0.081795692
Q9NRW3	DNA dC->dU-editing enzyme APOBEC- 3C	APOBEC3C	0.31094426	-0.038777987	0.044456278	0.009567579
J3KQL8;Q9BQE5	Apolipoprotein L2	APOL2	0	0.154690552	0	0.246884155
H7C1U8;Q9BUR5;A0A0J9YW W6	Apolipoprotein O	APOO	4.123692669	0.208873749	2.859276828	0.162601153
A0A087WUX8;A0A087WYF7; Q6UXV4	MICOS complex subunit MIC27	APOOL	0.479291999	0.068288803	0.153137026	-0.035271645
A0A0A0MRG2;E9PG40;P05067 ;H7C0V9	Amyloid beta A4 protein;N-APP;Soluble APP-alpha;Soluble APP-beta;C99;Beta- amyloid protein 42;Beta-amyloid protein 40;C83;P3(42);P3(40);C80;Gamma- secretase C-terminal fragment 59;Gamma-secretase C-terminal fragment 57;Gamma-secretase C-terminal fragment 50;C31	APP	0.541859435	-0.309240341	0.059674511	-0.028943698
P07741;H3BQZ9;H3BQB1	Adenine phosphoribosyltransferase	APRT	0.812602864	-0.065003395	0.773192995	-0.066312472
O60306	Intron-binding protein aquarius	AQR	0.095134394	-0.017031352	0.714790349	-0.085455577
Q96II5;P10398	Serine/threonine-protein kinase A-Raf	ARAF	0.743320976	-0.160392761	0.813191729	-0.152019119
P48444;B0YIW6	Coatomer subunit delta	ARCN1	0.178090849	-0.020419121	0.414530857	0.042601903
P84077;P61204;F5H423	ADP-ribosylation factor 1;ADP- ribosylation factor 3	ARF1;ARF3	0.123863688	-0.022084554	0.148991424	0.021050453
P18085;C9JPM4;C9JAK5	ADP-ribosylation factor 4	ARF4	1.1691702	0.146425883	1.401356305	0.169041316
P84085;C9J1Z8	ADP-ribosylation factor 5	ARF5	0.559383628	-0.075936317	0.038588484	-0.00936985
P62330	ADP-ribosylation factor 6	ARF6	0.206233152	0.02345562	0.567616774	0.078722
A0A0D9SF70;G5E9L0;Q8N6H7 ;E9PQP3;H0YDN9	ADP-ribosylation factor GTPase- activating protein 2	ARFGAP2	0.004301581	-0.000819206	0.297774971	0.044289271
Q9NP61;H0Y6A0	ADP-ribosylation factor GTPase- activating protein 3	ARFGAP3	0.262216391	-0.176412837	0.603836407	-0.307675616
Q9Y6D5	Brefeldin A-inhibited guanine nucleotide- exchange protein 2	ARFGEF2	0.270119159	-0.038949649	0.217016002	-0.041749636
Q07960;H0YE29	Rho GTPase-activating protein 1	ARHGAP1	0.069658131	-0.004997889	0.58169723	-0.031638781
E7EQN5;P98171;A0A0B4J1X7	Rho GTPase-activating protein 4	ARHGAP4	0.282216758	0.018725395	0.802608972	-0.051952044
P52565;J3KTF8;J3QX2;J3KR E2;J3KRY1	Rho GDP-dissociation inhibitor 1	ARHGDI1	0.285204243	-0.024929682	0.149243155	0.017992973

P52566;F5H3P3;H0YGX7;F5H6 Q0;F5H2R5 M0QZR4;Q92888;M0QYC1	Rho GDP-dissociation inhibitor 2	ARHGDI1B	0.685473604	-0.065234502	1.605234208	0.169671059
V9GYM8;Q92974	Rho guanine nucleotide exchange factor 1	ARHGEF1	0.631833911	0.04945151	0.866535091	-0.090154648
B1ALK7;E7EUY6	Rho guanine nucleotide exchange factor 2	ARHGEF2	0.612150298	0.029659271	0.004246678	-0.000162443
O14497;H0Y488;A0A1B0GTU5	AT-rich interactive domain-containing protein 1A	ARID1A	0.431105504	-0.046714783	1.041209052	0.089278539
Q68CP9;F8W108;F8WCU9;F8V WP4 Q9Y4X5	AT-rich interactive domain-containing protein 2	ARID2	0.183210707	-0.03271389	0.612365999	-0.092317263
O95376	E3 ubiquitin-protein ligase ARIH1	ARIH1	2.475164685	-0.172197342	0.459762459	0.064595858
P40616;F8VYN9;B4DZG7	E3 ubiquitin-protein ligase ARIH2	ARIH2	0.392965812	0.086129189	0.354772831	0.061027209
P36404;V9GYD0	ADP-ribosylation factor-like protein 1	ARL1	1.249814516	-0.153723399	0.347626664	-0.063286463
H3BU49;Q9Y2Y0	ADP-ribosylation factor-like protein 2	ARL2;ARL2-SNX15	1.314269358	0.104681651	0.678957182	0.10675621
P36405	ADP-ribosylation factor-like protein 2-binding protein	ARL2BP	0.388285853	-0.193450928	0.158794012	0.143226306
O75915	ADP-ribosylation factor-like protein 3	ARL3	0.641766987	-0.14168485	1.039130379	-0.149958293
Q9NVJ2	PRA1 family protein 3	ARL6IP5	0.677941099	0.082744916	0.336689865	0.060826302
Q9NVT9;E5RJ86	ADP-ribosylation factor-like protein 8B	ARL8B	2.990235522	0.193995158	0.735883484	0.068012873
Q8N2F6;A0A0J9YWR7;A0A0J 9YXE4;H7C2M7;C9J5N7	Armadillo repeat-containing protein 1	ARMC1	0.849964789	0.195686722	0.60285455	0.154647255
Q6NXE6;B4E1N1;F5GVV0;F5 H4P3	Armadillo repeat-containing protein 10	ARMC10	0.513113445	0.221853256	0.298862412	-0.076956431
G5E9V7;G5E9V6;B7Z637;Q8IU R7;C9J8P8;C9JAA7;C9JBY2;C9 J2I1	Armadillo repeat-containing protein 6	ARMC6	0.50267138	-0.045354843	0.651440294	-0.050442696
Q9UH62	Armadillo repeat-containing protein 8	ARMC8	0.417954235	0.098114649	0.488184257	0.149053733
Q9H993;F5GZY1	Armadillo repeat-containing X-linked protein 3	ARMCX3	1.941345292	0.203595479	1.535361551	0.143806458
A0A1W2PNV4;O15143	Protein-glutamate O-methyltransferase	ARMT1	0.061990889	0.007084529	0.107529282	-0.023732503
O15144	Actin-related protein 2/3 complex subunit 1B	ARPC1B	1.324874642	0.115185738	1.942022567	0.17701149
O15145;C9JZD1	Actin-related protein 2/3 complex subunit 2	ARPC2	1.639316374	-0.080616633	0.781021616	-0.036795298
F8WCF6;P59998;H7C0A3;R4G N08;F8WDD7;A0A0A6YYG9 O15511;B1ALC0	Actin-related protein 2/3 complex subunit 3	ARPC3	0.348894284	0.036391576	0.240511806	0.031445821
Q9BPX5	Actin-related protein 2/3 complex subunit 4	ARPC4-TTLL3;ARPC4	0.97117593	-0.108694394	1.069083523	-0.119104703
H3BMD8;P56211;H3BQ52;H3B TD3	Actin-related protein 2/3 complex subunit 5	ARPC5	1.660310078	-0.189876874	0.07576921	0.014526049
H0YCB3;Q8N9N2;H0YER2;H0 YE76 Q9H1I8;B1AH59	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L	0.249722836	-0.031375249	0.988319983	0.088782628
Q8N3C0	cAMP-regulated phosphoprotein 19	ARPP19	1.895718718	-0.242760658	2.15402654	0.28322506
Q9Y294	Activating signal cointegrator 1 complex subunit 1	ASCC1	0.070567881	0.047835986	0.706369172	0.192802111
Q9NVP2;K7ES22	Activating signal cointegrator 1 complex subunit 2	ASCC2	0.044566198	0.011955897	0.054308206	0.015312831
Q9NR48	Activating signal cointegrator 1 complex subunit 3	ASCC3	0.21269097	-0.031402588	0.851199905	-0.080625216
F5H8F7;Q9UBL3;H0YBF6	Histone chaperone ASF1A	ASF1A	1.694103774	-0.139107704	1.767572262	0.123347282
P04424;F8W943	Histone chaperone ASF1B	ASF1B	0.131090289	-0.022470792	0.075631409	0.013362567
O95671	Histone-lysine N-methyltransferase ASH1L	ASH1L	0.472598972	-0.568090757	0.250516391	-0.437609673
A0A087WXS7;O43681	Set1/Ash2 histone methyltransferase complex subunit ASH2	ASH2L	0.080980083	0.031820234	0.538700184	-0.195362155
P08243;F8WEJ5	Argininosuccinate lyase	ASL	0.085631531	-0.021700859	0.399741235	-0.117141406
Q8IZT6	N-acetylserotonin O-methyltransferase-like protein	ASMTL	1.15259743	-0.088081042	0.554747205	0.059015592
Q9BZE9;J3QR12;J3QL04	ATPase ASNA1	ASNA1	0.888414764	-0.076966604	2.279144682	-0.155867259
P00966;Q5T6L6;Q5T6L5	Asparagine synthetase [glutamine-hydrolyzing]	ASNS	3.462639363	0.112503688	4.04505289	0.163396517
Q9NVM9	Abnormal spindle-like microcephaly-associated protein	ASPM	0.43052942	0.117125575	0.038348292	-0.012703578
Q8NBU5	Tether containing UBX domain for GLUT4	ASPSCR1	0.751539491	-0.081849098	1.510798336	-0.127808571
Q6PL18	Argininosuccinate synthase	ASS1	1.185675472	-0.03528436	0.505512052	0.027656237
Q9NT62	Protein asunder homolog	ASUN	1.61539497	-0.096147855	0.083626607	-0.008973122
	ATPase family AAA domain-containing protein 1	ATAD1	0.386103832	0.078887622	0.181149694	0.042127291
	ATPase family AAA domain-containing protein 2	ATAD2	0.280401059	0.039293607	1.596621158	-0.165271568
	Ubiquitin-like-conjugating enzyme ATG3	ATG3	2.715933246	-0.224579493	0.746040675	-0.067210515

H7C2A6;Q9Y4P1;C9JIK8	Cysteine protease ATG4B	ATG4B	1.05569514	-0.172695351	1.058694985	-0.174399376
O95352	Ubiquitin-like modifier-activating enzyme ATG7	ATG7	0.80834745	0.191476504	0.76789219	0.231163979
P31939	Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide formyltransferase;IMP cyclohydrolase	ATIC	4.338658777	-0.163941383	2.610323578	-0.079253515
Q8NHH9;B5MCN0	Atlastin-2	ATL2	0.700009482	-0.100177765	0.15077428	-0.03934892
Q6DD88;F5H6I7	Atlastin-3	ATL3	0.190001623	0.020131747	0.585701001	-0.057506879
Q13315	Serine-protein kinase ATM	ATM	0.053906393	0.015276273	0.196035463	-0.052872976
E5RGN3;E5RIM7;O00244	Copper transport protein ATOX1	ATOX1	0.023705633	0.005036354	0.093888158	0.030639013
Q9HD20	Manganese-transporting ATPase 13A1	ATP13A1	0.166093477	0.013897896	2.62910244	-0.11911869
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1	0.310104136	0.026071231	0.284413594	0.030400912
P54709	Sodium/potassium-transporting ATPase subunit beta-3	ATP1B3	3.924425877	-0.183691343	2.996781732	-0.124768575
P16615;H7C5W9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2	1.57969498	0.082446734	0.496460999	0.027702332
Q93084	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	ATP2A3	0.0674216	-0.0540905	0.235262258	0.10727946
P20020;E7ERY9	Plasma membrane calcium-transporting ATPase 1;Calcium-transporting ATPase	ATP2B1	0	-0.006753922	0	-0.064493179
P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4	0.919557777	-0.094742139	0.811327271	-0.077554385
B4E2Q0;P98194;H0Y9V7	Calcium-transporting ATPase;Calcium-transporting ATPase type 2C member 1	ATP2C1	0.622904784	0.156980197	0.050964344	-0.014838537
P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1	2.510387589	0.115708033	0.322524538	-0.02411588
P06576;H0YH81;F8W079	ATP synthase subunit beta, mitochondrial;ATP synthase subunit beta	ATP5B	2.922896297	0.11223793	0.42601389	-0.016369502
P36542	ATP synthase subunit gamma, mitochondrial	ATP5C1	1.176870289	0.086177826	0.498264017	-0.057580948
P30049	ATP synthase subunit delta, mitochondrial	ATP5D	1.511286868	-0.157756488	1.550007506	-0.130981763
Q5VTU8;P56381	ATP synthase subunit epsilon-like protein, mitochondrial;ATP synthase subunit epsilon, mitochondrial	ATP5EP2;ATP5E	0.491939269	-0.098747253	0.248714952	0.03067023
P24539;Q5QNZ2	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1	2.776751623	0.100209554	0.632276319	0.042715708
O75947	ATP synthase subunit d, mitochondrial	ATP5H	1.837576023	0.249690692	0.419780306	0.079967499
P56385	ATP synthase subunit e, mitochondrial	ATP5I	0.032587937	0.006331762	0.055657061	0.007927895
P18859;A8MUH2	ATP synthase-coupling factor 6, mitochondrial	ATP5J	0.151617503	-0.033814748	1.135116906	-0.148939133
G3V325;C9JJT5;C9JU26;P56134;O75127	ATP synthase subunit f, mitochondrial;Pentatricopeptide repeat-containing protein 1, mitochondrial	ATP5J2-PTCD1;ATP5J2;PTCD1	0.32800868	-0.064829826	1.115264231	-0.167999903
E9PN17;O75964	ATP synthase subunit g, mitochondrial	ATP5L	0.216970657	-0.034543037	0.27579571	-0.041897456
P48047	ATP synthase subunit O, mitochondrial	ATP5O	0.720263918	0.056642214	1.255911017	-0.086970647
Q15904;A0A0C4DGX8;A6QRJ1	V-type proton ATPase subunit S1	ATP6AP1	1.025904246	-0.227643967	0.434100648	-0.132316589
A0A1B0GWJ8;H7C3E1;A0A1B0GTB0;A0A1B0GVB9;A0A1B0GVW0;A0A1C7CYW4;O75787;A0A1B0GTU8;A0A1B0GUT7;A0A1B0GVC7;B7Z119;A0A1B0GU12;B7Z413;A0A1B0GW13;A0A1B0GV60	Renin receptor	ATP6AP2	0.462579889	0.062889099	0.408260764	0.067403158
Q93050;B7Z641;B7Z2A9	V-type proton ATPase 116 kDa subunit a isoform 1;V-type proton ATPase subunit a	ATP6V0A1	0.857979831	0.122791926	0.742504193	-0.096815745
Q9Y487;Q8TBM3	V-type proton ATPase 116 kDa subunit a isoform 2;V-type proton ATPase subunit a	ATP6V0A2	0	NaN	0	NaN
F5GYQ1;P61421;J3QL14;R4GN72	V-type proton ATPase subunit d 1	ATP6V0D1	0.480467723	0.050575892	0.303035879	0.042551676
Q8N8Y2	V-type proton ATPase subunit d 2	ATP6V0D2	0.064410775	0.024203014	0.044810696	-0.018917847
P38606	V-type proton ATPase catalytic subunit A	ATP6V1A	2.811719762	0.09109656	7.046561664	0.203897794
P21281;H0YC04	V-type proton ATPase subunit B, brain isoform	ATP6V1B2	0.652641895	-0.05358537	0.285552152	-0.032685598
P21283;E7EV59	V-type proton ATPase subunit C 1	ATP6V1C1	1.660036761	-0.203420639	0.657166414	-0.08416907
H0YJS0;G3V559;G3V2S6;Q9Y5K8;H0YJ55	V-type proton ATPase subunit D	ATP6V1D	0.42468071	0.096006076	0.051018389	0.019171715
P36543;C9J8H1;Q96A05	V-type proton ATPase subunit E 1;V-type proton ATPase subunit E 2	ATP6V1E1;ATP6V1E2	0.045232187	0.022490501	0.038760648	0.015283585

Q16864	V-type proton ATPase subunit F	ATP6V1F	0.580523792	0.250642395	1.160547754	0.473978043
O75348	V-type proton ATPase subunit G 1	ATP6V1G1	0.534619946	0.123744965	0.391834636	-0.097871335
G3V126;Q9UI12	V-type proton ATPase subunit H	ATP6V1H	0.021589747	0.006689707	0.959382797	0.155205409
Q04656	Copper-transporting ATPase 1	ATP7A	0.3564366	0.046772957	0.37212173	0.060863813
H0YD21;I3L448;Q5TC12;H0YE W4;A8MRA7	ATP synthase mitochondrial F1 complex assembly factor 1	ATPAF1	0	-0.129971186	0	-0.103167534
Q8N5M1;C9J2Q2	ATP synthase mitochondrial F1 complex assembly factor 2	ATPAF2	0.107169534	0.100757599	0.008612039	-0.00958697
Q9UII2	ATPase inhibitor, mitochondrial	ATPIF1	0.380842061	0.177237193	0.161609717	-0.085349083
P46100	Transcriptional regulator ATRX	ATRX	0.033084019	0.016745758	0.07945222	0.030754471
Q9UBB4;A0A1W2PQD2	Ataxin-10	ATXN10	1.069647595	0.09054184	2.073838386	0.118078868
Q8WWM7;H3BUF6;H3BSK9	Ataxin-2-like protein	ATXN2L	0.239798638	0.020642916	0.569379445	0.043523788
Q96GX2	Putative ataxin-7-like protein 3B	ATXN7L3B	0.123800763	-0.02788496	0.116379091	0.050084114
Q9Y679	Ancient ubiquitous protein 1	AUP1	0.687876202	0.060407003	0.873751251	-0.067270597
O14965;Q5QPD4;A3KFJ0	Aurora kinase A	AURKA	1.42141512	0.277199109	0.822298749	0.157423973
Q96GD4;J3QLN8;J3QR41;J3KT D6;J3KT86	Aurora kinase B	AURKB	0.653932729	0.079814593	0.525816215	0.066109975
P61769;H0YLF3;F5H6I0	Beta-2-microglobulin;Beta-2- microglobulin form pl 5.3	B2M	4.330911479	-0.366888046	0.498323429	0.088616689
G3V150;O94766;E9PNA1	Galactosylgalactosylxylosylprotein 3- beta-glucuronosyltransferase 3	B3GAT3	0.61506134	0.045812289	0.802052784	-0.085021019
O60512	Beta-1,4-galactosyltransferase 3;N- acetylglucosaminylglycopeptide beta-1,4- galactosyltransferase;Beta-N- acetylglucosaminyl-glycolipid beta-1,4- galactosyltransferase	B4GALT3	0.704664051	0.190144221	1.108278263	0.274479675
J3QTA2;Q99933	BAG family molecular chaperone regulator 1	BAG1	0.301711213	0.088069407	0.993189024	0.204517365
O95816	BAG family molecular chaperone regulator 2	BAG2	0.012508084	0.001913071	0.051423924	0.006304741
O95817	BAG family molecular chaperone regulator 3	BAG3	6.973294833	2.906472524	3.915059682	1.407524427
Q9UL15	BAG family molecular chaperone regulator 5	BAG5	1.03971581	-0.183707555	0.024452047	-0.009559631
I3L2M4;I3L4C2;Q9UQB8;I3L1 13;I3L526;I3L0Y9;I3L125;I3L0 M4;I3L327;I3L1C8;B4DWA1 O75531	Brain-specific angiogenesis inhibitor 1- associated protein 2	BAIAP2	0	-0.085762024	0	-0.107364655
P80723	Barrier-to-autointegration factor;Barrier- to-autointegration factor, N-terminally processed	BANF1	0.575023365	0.084502538	0.690170038	0.104779879
A0A024RCR6;A0A0G2JK23;P4 6379;A0A0G2JL47;X6REW1;A 0A0G2JMJ1;F6S6P2 Q07812;K4JQN1	Brain acid soluble protein 1	BASP1	0.122102002	-0.024814606	0.49203537	0.112207413
A0A024RCR6;A0A0G2JK23;P4 6379;A0A0G2JL47;X6REW1;A 0A0G2JMJ1;F6S6P2 Q07812;K4JQN1	Large proline-rich protein BAG6	BAT3;BAG6	1.565885482	0.071750959	1.385054885	0.069080671
Q9UIG0	Apoptosis regulator BAX	BAX	0	-0.706906319	0	-0.756276131
Q9UIG0	Tyrosine-protein kinase BAZ1B	BAZ1B	0.573792045	0.038798332	0.859904873	-0.057898204
J3KPG5;F8VU39;Q9UIF9;A0A0 C4DG19	Bromodomain adjacent to zinc finger domain protein 2A	BAZZA	0.996587672	0.151391347	0.155067351	0.03030014
P51572;C9JSP1;C9JQ75;C9J0M 4;C9JMD7 O75934	B-cell receptor-associated protein 31	BCAP31	0.373162638	0.056902568	2.454897707	0.279174169
B3KSI3;O15382;M0QZ10;M0Q XF9;M0QZP4	Pre-mRNA-splicing factor SPF27	BCAS2	0.022753402	0.004329681	0.014446895	-0.003065427
Q9P287	Branched-chain-amino-acid aminotransferase;Branched-chain-amino- acid aminotransferase, mitochondrial	BCAT2	1.070148259	0.083975792	0.387615842	-0.052038193
F5H5P2;P12694;F5GXU9	BRCA2 and CDKN1A-interacting protein	BCCIP	0.290553972	0.027229309	0.646099682	-0.067492485
Q5QP56;Q9H1R6;Q5TE64;Q07 817;Q5QP59	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	BCKDHA	0.132687948	0.043904305	0.291353567	-0.070580482
A0A087WX97;Q9BXX5;A0A08 7WTL4	Bel-2-like protein 1	BCL2L1	0	NaN	0	NaN
E9PK91;Q9NYF8;A0A1W2PQ4 3;E9PK09;E9PQN2;E9PKI6 Q9Y276	Bel-2-like protein 13	BCL2L13	0.046422286	0.020525932	0.243423223	0.11349233
Q02338;E9PCG9;C9K0G7;C9J M78;C9JQ90;A0A0G2JRX6 H7C1N3;O15155;C9JTT8;Q68D U7	Bel-2-associated transcription factor 1	BCLAF1	0.043088903	-0.005902608	0.009523146	-0.001705805
Q7RTS1	Mitochondrial chaperone BCS1	BCS1L	1.541362923	0.154700915	0.401737288	0.110470772
Q8TD16	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	BDH1	0.717354083	0.051411947	1.24844605	-0.125962257
	BET1 homolog	BET1;DKFZp781C0 425	0.213813377	0.094085375	0.358965342	0.17163976
	Class A basic helix-loop-helix protein 15	BHLHA15	4.057662308	0.514053663	1.750368152	0.164656321
	Protein bicaudal D homolog 2	BICD2	0.295828581	-0.24359417	0.438786732	-0.22989254

P55957	BH3-interacting domain death agonist;BH3-interacting domain death agonist p15;BH3-interacting domain death agonist p13;BH3-interacting domain death agonist p11	BID	0.125968194	0.02431043	0.705408888	0.085187594
K7EMW2;A0A0B4J1S3;H3BLT4;O15392	Baculoviral IAP repeat-containing protein 5	BIRC5	0.65115012	0.097451846	1.646902737	0.2081604
Q9NR09	Baculoviral IAP repeat-containing protein 6	BIRC6	0.079621311	0.027640661	0.053825338	0.022390048
E9PJX5;P51451	Non-specific protein-tyrosine kinase;Tyrosine-protein kinase Blk	BLK	0.825995999	0.137647629	1.484398936	-0.167056402
Q13867;K7ESE8;K7ES02;J3KS D8	Bleomycin hydrolase	BLMH	2.891007853	-0.201618195	0.683029888	-0.058990161
Q8WV28;Q2MD59	B-cell linker protein	BLNK;BASH	0	NaN	0	-0.156208992
P78537;G8JLQ3;A0A087WSV2;F8W036;F8VP73	Biogenesis of lysosome-related organelles complex 1 subunit 1	BLOC1S1	0.138073472	0.035515785	0.259757709	-0.051564852
P53004	Biliverdin reductase A	BLVRA	2.440126137	-0.110853831	3.129903492	-0.137135506
P30043;M0R192;M0QZL1	Flavin reductase (NADPH)	BLVRB	3.357265956	0.123312632	1.538005363	0.113069534
Q14692	Ribosome biogenesis protein BMS1 homolog	BMS1	0.538752106	0.035211881	0.577011666	-0.03779157
H7C096;J3KN59;Q12982;Q86WG3	BCL2/adenovirus E1B 19 kDa protein-interacting protein 2;Caytaxin	BNIP2;ATCAY	0.118775657	-0.101121902	0.2851915	-0.197956149
A0A087WZT3;Q9H3K6;H3BV85;H3BTW0;A0A0B4J295;H3BVE0	BolA-like protein 2	BOLA2;BOLA2B	0.329036601	0.049405734	1.929334292	0.140692075
Q14137	Ribosome biogenesis protein BOP1	BOP1	0.625783043	0.049390157	0.161677153	-0.019958814
O95861;A6NF51	3(2),5-bisphosphate nucleotidase 1	BPNT1	0.508104725	-0.035531998	0.233748572	-0.014994621
F5GXF5;E7ETD6;Q12830	Nucleosome-remodeling factor subunit BPTF	BPTF	0	0.277724266	0	-0.032320976
Q6PJG6	BRCA1-associated ATM activator 1	BRAT1	0.373831855	-0.063192685	0.691638903	-0.100038528
A0A087WZR3;H9KVA9;A0A0D9SF50;P46736;X6RJS7	Lys-63-specific deubiquitinase BRCC36	BRCC3	0.556459998	-0.131726583	0.490553052	-0.124416351
H0Y6K2;A0A140T9E9;A0A0G2JK44;P25440;A0A0G2JHN8;A0A140T9I1;U3KQA6;A0A0G2JHL0;A0A140T9F7;A0A140T9V2	Bromodomain-containing protein 2	BRD2	0.181880399	0.052925746	0.015089741	0.005394936
O60885;M0QZD9	Bromodomain-containing protein 4	BRD4	0.290017732	-0.035427411	0.094353469	-0.009929657
Q9NP11	Bromodomain-containing protein 7	BRD7	0.225695201	-0.109185537	0.582515511	0.160600026
Q9NXR7;F8W733	BRCA1-A complex subunit BRE	BRE	0.319140141	-0.099859238	0.138835699	0.043944359
Q8WY22	BRI3-binding protein	BRI3BP	0	NaN	1.725316063	0.47868983
Q8TDN6	Ribosome biogenesis protein BRX1 homolog	BRX1	0.716312579	0.061623255	0.03902131	0.004195531
Q8WUW1	Protein BRICK1	BRK1	1.444970155	-0.156274796	0.506097028	-0.319095294
Q5VW32;F5GXQ0	BRO1 domain-containing protein BROX	BROX	1.594773242	-0.181191127	1.021743128	-0.140401204
Q5TI65;A0A087WVZ0;Q9Y5U8	Mitochondrial pyruvate carrier 1	BRP44L;MPC1	0.507650851	0.38333931	0.519476653	0.36163826
J3KQ12;Q96G97;H0YF20;H7C2D5;F8W7Q8;E9PIU3;H7BXM1	Seipin	BSCL2	2.839953438	0.256439686	1.378180781	0.236725966
Q9NW68;F8W6C6;E9PNA9;E9PS77	BSD domain-containing protein 1	BSDC1	0.443879246	0.37480545	0.15442649	0.220783615
P35613;A0A087X2B5;A0A087WUV8;I3L192	Basigin	BSG	0.845047552	0.058693568	2.408670232	0.119032542
Q10589	Bone marrow stromal antigen 2	BST2	0.05017687	-0.015365283	0.532506478	0.113864263
A0A0A0MTH9;O14981	TATA-binding protein-associated factor 172	BTAF1	1.089552951	-0.177178446	0.71399052	-0.179571533
P20290	Transcription factor BTF3	BTF3	1.161887757	-0.090635935	0.492203822	0.054856618
Q96K17;E9PL10	Transcription factor BTF3 homolog 4;Transcription factor BTF3	BTF3L4	2.250987829	-0.283320109	0.324918112	-0.042471568
Q06187;Q5JY90;U3NG26	Tyrosine-protein kinase BTK;Non-specific protein-tyrosine kinase	BTK	0.220809125	0.025886536	0.043364354	-0.007040024
O43683	Mitotic checkpoint serine/threonine-protein kinase BUB1	BUB1	2.1340883	0.2772487	0.727967496	0.127951622
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta	BUB1B	1.677243181	0.245406723	2.601047661	0.298477618
J3QT28;O43684;J3QSX4	Mitotic checkpoint protein BUB3	BUB3	1.785564466	0.137265523	2.151754995	0.157801946
P41223;C9JCD9	Protein BUD31 homolog	BUD31	1.281066841	0.105923971	1.192246091	0.118252436
Q13895	Bystin	BYSL	0.329535279	0.0230697	0.459791464	-0.033327421

O95153	Peripheral-type benzodiazepine receptor-associated protein 1	BZRAP1	0	-3.02603817	0	-3.061934471
Q7L1Q6;C9IZ80	Basic leucine zipper and W2 domain-containing protein 1	BZW1	0.509535271	-0.054015477	0.200799448	-0.024501483
E7ETZ4;Q9Y6E2;B5MCH7;Q75MG1;B5MCE7;E9PFD4	Basic leucine zipper and W2 domain-containing protein 2	BZW2	2.011399569	-0.10653019	0.370553679	-0.036982218
A0A087WYP2;Q8IZQ5;H0YE28	Selenoprotein H	C11orf31;SELH	0.849473626	-0.165727615	2.335852373	-0.285921097
A0A087WT99;Q9H0W9;E9PQS1;E9PPB5;E9PJU8	Ester hydrolase C11orf54	C11orf54	0.317233813	-0.034974416	0.303353067	0.046827634
Q9H3H3	UPF0696 protein C11orf68	C11orf68	0.469571621	-0.094848315	0.423223342	-0.068243027
A0A0B4J220;E9PRG8	Uncharacterized protein C11orf98	C11orf98	0.23593826	-0.047914187	0.082822224	-0.026655197
Q9HB07;F8VQQ3;F8VR84	UPF0160 protein MYG1, mitochondrial	C12orf10	0.352104871	-0.033474286	1.431940398	0.085353533
Q99622;U3KQ85;F5GXW5;U3KQ07	Protein C10	C12orf57	2.769196704	0.357471148	1.565976232	0.214715958
Q9Y224;G3V4C6	UPF0568 protein C14orf166	C14orf166	1.246396055	-0.056555748	0.130182857	-0.012024562
H3BR29;H3BSM7;Q96GQ5	RUS1 family protein C16orf58	C16orf58	1.702412985	0.294687271	1.065495803	0.177291552
F8W038;Q8IXM2;F8W1H0;H0YIS7	Chromatin complexes subunit BAP18	C17orf49;BAP18;R	0.55170371	0.072835604	0.286515986	-0.052300771
J3KTF4;J3QRG5;J3KSJ5;Q9BQ	Uncharacterized protein C17orf62	NASEK-C17orf49	1.143252034	0.153809547	0.020430816	0.004025141
A9J3QKS6;J3QLB7	Uncharacterized protein C18orf8	C17orf62	0.693099346	-0.4461085	0.129675601	-0.115118663
K7ENL9;Q96DM3;A0A087WZD4	Uncharacterized protein C18orf8	C18orf8	0.693099346	-0.4461085	0.129675601	-0.115118663
K7EK56;Q9UFG5	UPF0449 protein C19orf25	C19orf25	0	-0.512834549	0	-0.388994217
Q9BQ61	Uncharacterized protein C19orf43	C19orf43	0.060389199	0.017598788	1.335452892	0.150328954
Q9BSF4	Uncharacterized protein C19orf52	C19orf52	0.253724206	0.060649872	0.4277546	0.094032288
Q6ZSJ8	Uncharacterized protein C1orf122	C1orf122	0.537144411	0.072154236	0.352811097	0.090995979
Q9NWW4	UPF0587 protein C1orf123	C1orf123	4.12880258	-0.255374273	2.505183286	-0.235861142
Q07021;I3L3Q7;I3L3B0	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP	0.324178978	0.027984937	0.345750713	-0.030580203
Q9GZN8;H7BYU9	UPF0687 protein C20orf27	C20orf27	2.633049917	-0.30059274	1.65067078	-0.294985644
A0A0B4J2D5;P30042;H7C1F6;A0A0B4J2H4	ES1 protein homolog, mitochondrial	C21orf33	3.327290833	0.154387156	0.056086531	0.004463832
Q8WWC4;H7C0V0	Uncharacterized protein C2orf47, mitochondrial	C2orf47	0.491044465	0.091122055	0.191253873	0.032012812
C9J4K0;Q9BVC5	Ashwin	C2orf49	2.263227979	-0.350167274	0.185017986	0.049837748
Q49AR2	UPF0489 protein C5orf22	C5orf22	0.00505849	-0.001351674	0.556451647	-0.094699224
A0A0C4DGW6;A6NDU8	UPF0600 protein C5orf51	C5orf51	0.508734608	0.129841042	0	-0.008904266
C9JQV0;Q9BRJ6;H7C0T1;H7C2R9	Uncharacterized protein C7orf50	C7orf50	0.587586873	0.07519563	0.331933924	0.050866445
Q9H7E9	UPF0488 protein C8orf33	C8orf33	0.14131735	-0.024336974	0.012893207	-0.005120277
H0YF29;Q6P1X6	UPF0598 protein C8orf82	C8orf82	0.122752148	0.052162488	0.823288501	-0.196525892
Q5T280	Putative methyltransferase C9orf114	C9orf114	0.092599707	0.01782608	0.592584343	-0.084261576
Q9BUH6	Protein PAXX	C9orf142	0.557706867	-0.115014712	0.019687407	-0.005651792
Q9NZ63	Uncharacterized protein C9orf78	C9orf78	0.407017875	-0.102658272	0.059832627	0.014691989
A0A087X0K1;Q9Y376	Calcium-binding protein 39	CAB39	0.62368208	-0.189435959	0.215186195	0.077218056
Q9HB71	Calceyin-binding protein	CACYBP	0.201911788	0.024329503	1.570918599	0.117990176
P27708;F8VDP4	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase	CAD	2.764497787	-0.066420237	5.383839937	-0.112619082
P0DP25;P0DP24;P0DP23;E7ETZ0;H0Y7A7;E7EMB3;G3V361;Q96HY3		CALM1;CALM2	2.018095199	-0.17364343	0.054074884	0.009682655
P27482	Calmodulin-like protein 3	CALML3	0.828701329	-0.167311986	0.286032025	-0.082332293
P27797;K7EJB9	Calreticulin	CALR	1.373523015	0.191095988	1.129050531	0.174996058
O43852;H0Y875	Calumenin	CALU	0.498509545	0.043750445	0.132768206	-0.01818943
Q86VP6;A0A0C4DGH5	Cullin-associated NEDD8-dissociated protein 1	CAND1	4.593671278	-0.219173431	3.676746127	-0.122133891
P27824	Calnexin	CANX	3.383843246	0.189424515	1.024351395	0.079575857
Q01518	Adenylyl cyclase-associated protein 1	CAP1	0.887107813	-0.072745959	0.514413437	0.039230982
P07384	Calpain-I catalytic subunit	CAPN1	1.251713331	-0.121478081	0.042522846	0.00530529
A0A0C4DQG5;P04632;A0A075B7C0;K7ELJ7;U3KQE2;K7EIV0;K7EKD8;U3KPR7;K7EM73	Calpain small subunit 1	CAPNS1	2.922105046	0.255795161	2.668740034	0.243486404

Q14444;G3V153;E9PLA9	Caprin-1	CAPRIN1	5.050782258	-0.206204096	2.748439658	-0.091766357
P52907	F-actin-capping protein subunit alpha-1	CAPZA1	2.683555187	-0.148326874	0.477309392	-0.043512026
P47755;F8W9N7;A0A0D9SET8	F-actin-capping protein subunit alpha-2	CAPZA2	2.715879898	-0.179802895	1.329513901	-0.096857707
B1AK87;B1AK88;P47756;B1AK85	F-actin-capping protein subunit beta	CAPZB	0.502110329	-0.053367933	0.3718291	0.044274648
Q9Y2V2;H3BSW7;H3BUY4;H3BPY5;H3BNU9	Calcium-regulated heat stable protein 1	CARHSP1	0.190259784	0.020646731	0.113237709	-0.012935003
Q86X55;K7EQA8	Histone-arginine methyltransferase CARM1	CARM1	2.78428936	-0.128344218	1.547777357	-0.071597735
B4DKY1;P49589	Cysteine-tRNA ligase, cytoplasmic	CARS	0.087612953	-0.010084788	0.061663545	-0.007862727
O15234;J3KSY7	Protein CASC3	CASC3	3.518740965	0.482998212	1.139096543	0.207777659
P29466;B4DVD8;G3V169;H0YEC7	Caspase-1;Caspase-1 subunit p20;Caspase-1 subunit p10;Caspase	CASP1	0.057520023	-0.015461286	1.165566954	-0.161339188
Q92851	Caspase-10;Caspase-10 subunit p23/17;Caspase-10 subunit p12	CASP10	0.096209822	0.026593526	0.364832564	-0.089614868
P42575	Caspase-2;Caspase-2 subunit p18;Caspase-2 subunit p13;Caspase-2 subunit p12	CASP2	0.06357292	-0.035687129	0.28682266	-0.083134651
P42574;A8MVM1	Caspase-3;Caspase-3 subunit p17;Caspase-3 subunit p12	CASP3	0.204489174	-0.050831477	0.265281532	-0.071179708
P55212	Caspase-6;Caspase-6 subunit p18;Caspase-6 subunit p11	CASP6	0.00305061	-0.001235962	0.423025671	-0.121440252
Q14790;A0A0A0MS31;E7ETB7;E7EQ06	Caspase-8;Caspase-8 subunit p18;Caspase-8 subunit p10	CASP8	0.773053414	0.072901408	0.001193761	0.000138919
E7ES10;E9PCH5;B7Z574;A0A0C4DGB5;P20810;E7EYV3;E9PDE4;E7EQ12;E7EQA0;H0Y7F0;A0A0A0MR45;H0YD33;H0Y9H6	Calpastatin	CAST	3.158085288	-0.274537404	0.43906265	-0.07446607
P04040	Catalase	CAT	0.952071069	-0.065995852	1.50317136	-0.085855484
Q13951	Core-binding factor subunit beta	CBFB	0.479977435	0.040150642	0.12398834	-0.014532089
P16152;E9PQ63;A8MTM1	Carbonyl reductase [NADPH] 1	CBR1	1.117793933	-0.04861927	0.404437291	0.023548444
O75828	Carbonyl reductase [NADPH] 3	CBR3	0.30436064	0.019307137	3.076884247	0.111670494
P0DN79;P35520	Cystathionine beta-synthase	CBS	0.840742067	-0.046326319	0.122534581	0.010974248
A0A0A6YYH9;Q9BRT8;Q8IUF1;Q5RIA9;Q5JTY5;Q4V339;A0A087X140;A0A087WWG3;A0A0B4J2F1;Q5RIB0;H0Y5V3;C9J3G2;A0A0A0MRU4;Q5RIB5;Q5JTY2;A0A087WTC0;Q6NVZ8;F8WEG4;A0A0B4J2E3;A0A087WZQ3;F8WEU0;E7EUZ7;A0A087WYD2;F2Z2T4	COBW domain-containing protein 1;COBW domain-containing protein 2;COBW domain-containing protein 5;COBW domain-containing protein 3;COBW domain-containing protein 6	CBWD5;CBWD1;CBWD2;CBWD3;CBWD6;CBWD7	0.010391237	-0.00213782	1.225259719	-0.197644234
J3KS05;P83916;B5MD17;K7ELA4;C9JWS9	Chromobox protein homolog 1	CBX1	0.093941993	0.027073542	0.398513756	0.101401647
Q13185;S4R2Y4	Chromobox protein homolog 3	CBX3	1.087893848	0.079258601	1.438495352	0.089886983
P45973	Chromobox protein homolog 5	CBX5	2.217532436	0.220600128	1.002037282	0.119955063
Q6P1N0;K7EMP1	Coiled-coil and C2 domain-containing protein 1A	CC2D1A	0.230784897	-0.11459748	0.146689169	-0.065100829
Q8IX12;A0A0C4DGG8;F5H2E6;F5H3E1;F5H1H2	Cell division cycle and apoptosis regulator protein 1	CCAR1	0.391041395	-0.062735558	1.894599634	-0.193746249
Q8N163;H0YB24;G3V119	Cell cycle and apoptosis regulator protein 2	CCAR2	2.128278348	-0.055255572	0.495502872	-0.019731839
B8ZZ99;Q96NT0;F8WCZ3	Coiled-coil domain-containing protein 115	CCDC115	0	0.206178665	0	0.07196331
J3KR35;Q8WUD4;C9JUN5;S4R331	Coiled-coil domain-containing protein 12	CCDC12	1.172283016	-0.366316414	0.356067737	0.089234098
Q96CT7	Coiled-coil domain-containing protein 124	CCDC124	2.525230561	-0.137265523	0.672633524	0.034684817
Q96JG6;H0Y7Q2	Coiled-coil domain-containing protein 132	CCDC132	0.621755115	0.216564655	0.053097752	0.030209732
Q9H6E4;B0QY51	Coiled-coil domain-containing protein 134	CCDC134	2.23730816	0.286046664	1.084242211	0.15822347
A6NNP5;E9PBZ7	Coiled-coil domain-containing protein 169	CCDC169	0	NaN	0	NaN
E9PFB9;J3KP97;Q5T9S5;Q5T9S2	Coiled-coil domain-containing protein 18	CCDC18	0	NaN	0	NaN
O60826	Coiled-coil domain-containing protein 22	CCDC22	0.861587435	0.218631109	0.030888157	-0.015289942
Q86WV7;Q96MW1;K7ER24	Coiled-coil domain-containing protein 43	CCDC43	0.156482457	-0.115492185	0.000852193	-0.000777562
Q96A33	Coiled-coil domain-containing protein 47	CCDC47	1.085507673	0.096824328	0.464817641	0.051235835
Q96ER9	Coiled-coil domain-containing protein 51	CCDC51	1.330275701	0.179357211	0.122735636	0.025467873
C9JQ41;H7C525;Q4VC31	Coiled-coil domain-containing protein 58	CCDC58	0.213957695	0.247022947	0.21585763	0.258588155

Q16204	Coiled-coil domain-containing protein 6	CCDC6	0.047266649	0.013818105	0.339038924	-0.083209356
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	1.547542484	0.14411672	0.651104484	0.091431936
E9PPJ7;J3KN19;E9PKQ5;Q9GZ T6;H0YF06	Coiled-coil domain-containing protein 90B, mitochondrial	CCDC90B	0.275428708	-0.039393425	0.670580196	-0.072283109
M0R2S3;Q9BW85	Coiled-coil domain-containing protein 94	CCDC94	0.521602332	0.173839728	0.158164559	0.078869502
Q96F63	Coiled-coil domain-containing protein 97	CCDC97	1.079997905	0.208684921	0.474230027	0.104059219
P14635;E9PC90	G2/mitotic-specific cyclin-B1	CCNB1	6.465236477	0.48062102	5.322516704	0.528767586
O95067;H1UBN3;H0YMP3	G2/mitotic-specific cyclin-B2	CCNB2;CCNB2V	2.836184641	0.353001912	1.789739288	0.205547015
P30279	G1/S-specific cyclin-D2	CCND2	1.321534676	-0.129178047	2.131476729	-0.17742602
H3BR23;O95273	Cyclin-D1-binding protein 1	CCNDBP1	0	0.059044838	0	0.097048759
O75909;G3V2Q3;G3V5E1	Cyclin-K	CCNK	1.45608728	-0.227537791	1.147854513	-0.198360125
Q9UK58	Cyclin-L1	CCNL1	0.025943831	0.016259702	0.103508242	0.049436506
O60563	Cyclin-T1	CCNT1	0	-0.31295681	0	NaN
J3KNF4;O14618;E9PP76	Copper chaperone for superoxide dismutase;Superoxide dismutase [Cu-Zn]	CCS	1.159023429	-0.137030602	0.335613051	-0.047970772
P78371;F5GW6;F8VQ14	T-complex protein 1 subunit beta	CCT2	2.191967837	-0.091282527	0.424407509	-0.018904368
P49368;B4DUR8	T-complex protein 1 subunit gamma	CCT3	0.180495743	-0.011922518	0.20199084	0.014960289
P50991	T-complex protein 1 subunit delta	CCT4	2.265527772	-0.102315585	0.380670795	-0.024784724
P48643;B7ZAR1;E9PCA1;E7E NZ3	T-complex protein 1 subunit epsilon	CCT5	1.681749251	-0.082585653	0.119459889	0.011309624
P40227	T-complex protein 1 subunit zeta	CCT6A	0.759186253	-0.027555148	1.172047219	0.043938955
Q99832	T-complex protein 1 subunit eta	CCT7	3.278917342	-0.079910596	0.012804118	-0.000723203
P50990	T-complex protein 1 subunit theta	CCT8	0.271720155	0.015827179	1.368402122	0.066257477
P86791;P86790	Vacuolar fusion protein CCZ1 homolog;Vacuolar fusion protein CCZ1 homolog B	CCZ1;CCZ1B	0.388355572	0.159442202	0.313058786	-0.138929685
Q6YHK3	CD109 antigen	CD109	4.948844528	-0.31371816	1.379796527	-0.098611514
P10747	T-cell-specific surface glycoprotein CD28	CD28	0.071197541	0.022345861	0.14527863	0.040251732
Q9Y5K6	CD2-associated protein	CD2AP	1.633693934	-0.145675023	1.085498343	-0.079527219
O95400	CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2	0.797499197	-0.148207601	0.331523253	-0.053214963
Q9NPF0	CD320 antigen	CD320	0.362750815	-0.14165465	0.284608518	-0.134549967
P28907;H0Y950	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1	CD38	0.613947188	0.082401911	0.375674947	0.062728564
O15446	DNA-directed RNA polymerase I subunit RPA34	CD3EAP	0.882061443	-0.09936746	1.738316463	-0.129728317
Q08722	Leukocyte surface antigen CD47	CD47	0.682554342	-0.222124481	0.32592923	0.081225491
E9PNW4;E9PR17;P13987	CD59 glycoprotein	CD59	2.103749003	-0.415266991	2.32585988	-0.131059011
E7EQJ3;H0YBZ8;E7ESL3;H0Y BZ2;P04233;E7ER71	HLA class II histocompatibility antigen gamma chain	CD74	0.096031623	0.026342392	0.218674087	0.069382985
E9PD41;P10966	T-cell surface glycoprotein CD8 beta chain	CD8B	0.674394012	-0.247217496	1.507146898	-0.116209666
A6NNI4;G8JLH6;P21926	Tetraspanin;CD9 antigen	CD9	3.407535577	-0.500142415	1.049661673	-0.117090225
P48960	CD97 antigen;CD97 antigen subunit alpha;CD97 antigen subunit beta	CD97	1.082273284	-0.145614624	0.177590196	-0.045916239
O75794;X6RA30;X6RKY7;X6R F82	Cell division cycle protein 123 homolog	CDC123	2.180036172	0.219298999	4.471957528	0.409383456
Q13042;Q5T8C6	Cell division cycle protein 16 homolog	CDC16	0.090540705	-0.040566444	0.643888315	0.195937284
Q12834	Cell division cycle protein 20 homolog	CDC20	2.039992627	0.382324219	1.248538282	0.252169037
Q9UJX2	Cell division cycle protein 23 homolog	CDC23	3.232111961	0.332218329	1.662538872	0.306875324
G5EA36;P30260	Cell division cycle protein 27 homolog	CDC27	0.013009527	-0.004119873	0.137749224	0.032755852
U3KQ77;U3KPV8;P49427;U3K QP9;Q712K3	Ubiquitin-conjugating enzyme E2 R1;Ubiquitin-conjugating enzyme E2 R2	CDC34;UBE2R2	0	0.111560822	0	-0.002219518
Q16543;K7EQA9;K7EKQ2	Hsp90 co-chaperone Cdc37;Hsp90 co- chaperone Cdc37, N-terminally processed	CDC37	0.52395548	-0.072361628	0.532204623	0.073055267
P60953;Q5JYX0	Cell division control protein 42 homolog	CDC42	3.827922494	-0.220048269	0.7099539	-0.059304873
Q99459	Cell division cycle 5-like protein	CDC5L	2.617566426	-0.184333801	0.269192305	-0.023819606

Q99741	Cell division control protein 6 homolog	CDC6	3.176230712	0.662789853	3.417873661	0.55525322
Q6P1J9;A0A1B0GUB2	Parafibromin	CDC73	2.054101855	0.170778592	0.125401439	-0.014777819
E9PEI0;Q69YH5	Cell division cycle-associated protein 2	CDCA2	0	0.04082346	0	NaN
B5MBX0;Q96FF9	Sororin	CDCA5	1.578123893	0.201816241	0.922238494	0.135314941
Q53HL2	Borealin	CDCA8	2.79504082	0.23353831	1.450463837	0.138731639
B3KY94;O14735	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	CDIPT	0.093550067	-0.049000931	0.356680608	-0.12876358
P06493;A0A024QZP7;A0A087WZZ9;E5RIU6	Cyclin-dependent kinase 1	CDK1;CDC2	1.40070466	-0.097310066	1.045030499	-0.070885022
A0A0D9SER5;J3QR29;A0A0D9SEI3;B7ZVY7;A0A0D9SEN2;J3QR44;P21127;Q5QPR4;Q5QPR3;Q9UQ88	Cyclin-dependent kinase 11B;Cyclin-dependent kinase 11A	CDK11B;CDC2L1;CDK11A	1.095521059	0.113599459	0.325358812	-0.037039121
G3V5T9;P24941;E7ESI2	Cyclin-dependent kinase 2	CDK2	0.855205627	-0.04936854	0.157429141	0.015126228
P11802;F8VYH9;F8VTV8;F8VWX7;F8W1L8	Cyclin-dependent kinase 4	CDK4	0.781913381	-0.096253077	0.144843762	-0.020116488
Q00535	Cyclin-dependent-like kinase 5	CDK5	1.247012703	-0.110275586	0.697437263	-0.097718875
B1AMJ5;A0A0A0MRG9;Q96SN8;Q5JTU8	CDK5 regulatory subunit-associated protein 2	CDK5RAP2	0	NaN	0	NaN
Q96JB5;J3QQY1;J3QS62	CDK5 regulatory subunit-associated protein 3	CDK5RAP3	0.644035871	0.082562764	0.323919899	0.051964442
Q00534	Cyclin-dependent kinase 6	CDK6	0.010644036	-0.001502991	0.135403474	0.012653669
D6R9G1;P50613;D6REC6;D6RAD4	Cyclin-dependent kinase 7	CDK7	0.921171462	-0.066839536	1.515876692	0.142555555
P50750	Cyclin-dependent kinase 9	CDK9	0.24275845	0.044943174	0.848164632	0.151073456
Q5VV42	Threonylcarbamoyladenine tRNA methyltransferase	CDKAL1	0.287423676	-0.066905022	0.909291115	0.215154966
E7ES52;P46527	Cyclin-dependent kinase inhibitor 1B	CDKN1B	0.4362845	-0.06514136	1.18553668	-0.199467341
Q9NXV6	CDKN2A-interacting protein	CDKN2AIP	1.502284564	-0.307499568	0.13281118	-0.056173325
Q9UKY7;H0Y8K3	Protein CDV3 homolog	CDV3	0.601967277	-0.050736745	1.676162503	0.08856837
Q9Y232;C9JQG7	Chromodomain Y-like protein	CDYL	0.119774408	-0.018434207	0.029303033	0.007575989
Q03701	CCAAT/enhancer-binding protein zeta	CEBPZ	0.155758857	0.013553937	1.219417799	-0.068620364
Q9BXW7	Cat eye syndrome critical region protein 5	CECR5	0.153213729	0.033167203	3.006385204	-0.400149345
G5EA30;Q92879;E9PQK4;E9PSH0;E9PKU1	CUGBP Elav-like family member 1	CELF1	0.347738318	-0.066598574	0.152013723	-0.032499631
V9GYD9;Q5VZZ6;A0A0J9YX66;A0A1B0GU44;E9PC62;A0A1B0GUN8;A0A0J9YXJ0;O95319	CUGBP Elav-like family member 2	CELF2	0.414260322	0.078831991	0.136160473	-0.035216331
P49454	Centromere protein F	CENPF	1.77798469	0.374514898	0.66386361	0.170014381
B3KVZ3;Q9H3R5;H0Y9E6	Centromere protein H	CENPH	0.918811942	0.12948068	0.279908706	0.05423514
B1AHQ6;Q9NSP4	Centromere protein M	CENPM	0.098958293	0.032268206	0.359686297	0.092389743
Q9UPV0	Centrosomal protein of 164 kDa	CEP164	0.292159595	0.127786318	0.513973535	-0.066480637
Q96G23;Q5SZE1;H0YNU7;Q5SZE2;Q5SZE3;H0YKH6;H0YLQ6;Q5SZE4	Ceramide synthase 2	CERS2	1.377353508	-0.257171949	1.345514724	-0.189391136
P41208	Centrin-2	CETN2	1.586381523	0.22600174	3.000004321	0.351104736
Q9Y6A4	Cilia- and flagella-associated protein 20	CFAP20	0.061506367	-0.018137614	0.275057875	0.060583115
E9PK25;P23528;G3V1A4;E9PP50;E9PQB7;E9PLJ3;E9PS23	Cofilin-1	CFL1	2.111980742	-0.108200709	0.75357875	-0.036174774
Q8WUX2	Putative glutathione-specific gamma-glutamylcyclotransferase 2	CHAC2	1.012532609	-0.123004278	0.544136379	-0.05967617
Q13111	Chromatin assembly factor 1 subunit A	CHAF1A	0.035363277	0.008705775	0.952024432	-0.15693601
Q13112	Chromatin assembly factor 1 subunit B	CHAF1B	0.053170266	-0.016574542	0.086314784	0.026746496
Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1	0	-1.057534218	0	-1.399188995
Q9Y6H1;Q5T1J5	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2;Putative coiled-coil-helix-coiled-coil-helix domain-containing protein CHCHD2P9, mitochondrial	CHCHD2;CHCHD2P9	6.900532111	-0.932108879	0.67773213	-0.108827273
C9JRZ6;Q9NX63;F8WAR4	MICOS complex subunit MIC19	CHCHD3	1.238111335	0.100992203	0.817563778	0.074168205
J3QTA6;Q9BRQ6;J3QTB2;H0Y922	MICOS complex subunit MIC25	CHCHD6	0.270473585	0.146863461	0.02567995	0.024506569
O14646	Chromodomain-helicase-DNA-binding protein 1	CHD1	0.777836685	-0.148122152	0.877916385	-0.167686462
Q86WJ1;A0A0A0MSH9;A0A087WTM4;A0A0A0MRH8	Chromodomain-helicase-DNA-binding protein 1-like	CHD1L	0.103293717	0.019511859	1.36230383	-0.178046544

F5GWX5;A0A0C4DGG9;Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4	1.008171777	0.032273293	0.312794368	0.016126633
J3KN87;E7EPP6;O14757;E9PPA5	Serine/threonine-protein kinase Chk1	CHEK1	1.383768129	0.261466662	0.005980068	0.00371329
O96017;H7C0V7;C9JFD7;H0Y820;B7ZBF7	Serine/threonine-protein kinase Chk2	CHEK2	0	-0.147321701	0.08207878	-0.06307888
Q81WX8;J3QK89	Calcium homeostasis endoplasmic reticulum protein	CHERP	0.298113691	-0.028682709	0.785516816	-0.068574588
Q9BWS9	Chitinase domain-containing protein 1	CHID1	0.763704508	0.179986954	0.051686362	-0.009589513
P35790	Choline kinase alpha	CHKA	1.841321658	0.251171303	0.844666562	0.174024773
Q7LBR1	Charged multivesicular body protein 1b	CHMP1B	0.091531088	-0.059318542	0.389710767	0.126681328
O43633;M0R1T5;M0R1L7	Charged multivesicular body protein 2a	CHMP2A	0.209235931	-0.033269246	0.168908676	0.042937279
Q9BY43;E9PQI5;E9PQ80;E9PSI1	Charged multivesicular body protein 4a	CHMP4A	1.583664395	-0.195221265	0.077111167	-0.013612429
Q9H444	Charged multivesicular body protein 4b	CHMP4B	2.64410454	-0.335076332	0.506695246	-0.135346731
Q9NZZ3	Charged multivesicular body protein 5	CHMP5	2.232093609	-0.44828275	0.484664948	0.126923625
Q8WUX9;E5RJI3;E5RIU9	Charged multivesicular body protein 7	CHMP7	0.026418577	-0.01442585	0.672656019	-0.240043259
Q9UHD1;E9PHZ2	Cysteine and histidine-rich domain-containing protein 1	CHORDC1	0.548546059	-0.036221822	0.608723993	0.034573555
Q99653;H0YKE7;F5GX29;H0YNG9	Calcineurin B homologous protein 1	CHP1	0.51352881	0.090171178	0.603593124	0.088747978
Q9NRG0;E5RGS9	Chromatin accessibility complex protein 1	CHRAC1	1.168605475	-0.141909281	1.488777242	-0.183649699
Q9NRB3	Carbohydrate sulfotransferase 12	CHST12	1.729546848	-0.304739157	0.680718054	-0.200704416
E7EXA6;Q8WVB6;A0A0D9SF58	Chromosome transmission fidelity protein 18 homolog	CHTF18	0.943561969	0.073389689	0.520860364	-0.063442548
H0YAV5;P0CG13;J3KSJ7;H3BPP1	Chromosome transmission fidelity protein 8 homolog	CHTF8	0	-0.013998032	0	0.105644226
X6R700;Q9Y3Y2;A0A087X1B7	Chromatin target of PRMT1 protein	CHTOP	1.701276492	0.404335976	1.428329521	0.354641596
O76071	Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1	0.872566009	0.107856115	0.689922954	0.111797969
Q6F181;H3BV90;H3BT65;H3BUG4	Anamorsin	CIAPIN1	4.422831361	-0.19555823	2.073510526	-0.120953242
Q99828	Calcium and integrin-binding protein 1	CIB1	0.392556728	0.080725352	1.049810067	0.11773777
Q14011;K7EMY9;K7EPM4;K7EQR7;D6W5Y5;K7ENX8;K7ELV6;K7EJV5;K7ELT6;K7EJV1;K7ER40	Cold-inducible RNA-binding protein	CIRBP	2.747972332	-0.18164285	0.85354203	-0.058021863
Q969X6;H3BSH7;A0A0J9YW M9	Cirhin	CIRH1A	0.385676477	-0.037223498	0.231407714	-0.026441892
Q9NZ45	CDGSH iron-sulfur domain-containing protein 1	CISD1	1.670986717	0.148571332	1.972312889	0.131706556
Q8N5K1;D6RCF4	CDGSH iron-sulfur domain-containing protein 2	CISD2	0.012457468	0.003785451	0.189020519	-0.048563957
Q8WWK9	Cytoskeleton-associated protein 2	CKAP2	3.72015589	0.386566162	4.029294123	0.398850441
Q07065	Cytoskeleton-associated protein 4	CKAP4	0.742225121	0.111951192	0.271595629	-0.051774979
Q14008	Cytoskeleton-associated protein 5	CKAP5	1.457163766	-0.066087405	0.010672784	0.000896454
P12277	Creatine kinase B-type	CKB	1.932957415	-0.094126066	0.626122375	-0.043572108
Q9BZU3;P61024;Q5T179	Cyclin-dependent kinases regulatory subunit;Cyclin-dependent kinases regulatory subunit 1	CKS1B	3.009232103	1.021012942	1.830262004	0.82419014
Q7Z460;F8WA11;H0Y5T1	CLIP-associating protein 1	CLASP1	0.883641687	-0.084738413	0.168743593	-0.022765477
E3W994;A0A0U1RQI6;E7ERI8;E7EW49;J3KR49;O75122	CLIP-associating protein 2	CLASP2	0.050658531	0.012826602	0.459844794	0.085811297
Q96S66	Chloride channel CLIC-like protein 1	CLCC1	0.410310035	-0.106288846	1.173162012	0.193771998
P51798;H0Y2M6	H(+)/Cl(-) exchange transporter 7	CLCN7	0.779581659	0.128705343	0.581619532	0.096960386
O00299	Chloride intracellular channel protein 1	CLIC1	0.72715595	-0.040142377	0.062368285	-0.005638758
O15247	Chloride intracellular channel protein 2	CLIC2	2.728443608	0.167118073	1.906755306	0.120840073
Q9Y696	Chloride intracellular channel protein 4	CLIC4	0.135757576	-0.016166369	0.421795661	0.046474457
Q96NY7	Chloride intracellular channel protein 6	CLIC6	0	-0.283229828	0	0.460957527
Q14677	Clathrin interactor 1	CLINT1	0.041306416	-0.007394155	0.333025365	0.042238553
P49761;H3BRE4	Dual specificity protein kinase CLK3	CLK3	1.135644733	-0.16651233	1.241225434	-0.205720743
Q9NWW5;A0A1B0GUD2;H3BUT1;H3BTY4;A0A0S2Z5D0;H3BUV4;A0A1BOGTU6	Ceroid-lipofuscinosis neuronal protein 6	CLN6	0.924018587	0.175695101	0.144311186	0.030384382
P54105;E9PMI6;J3KN38;E9PJF4	Methylosome subunit pICln	CLNS1A	0.287901237	0.056284269	0.04089374	-0.007892609

E9PL17;Q92989	Polyribonucleotide 5-hydroxyl-kinase Clp1	CLP1	0.286051138	0.051312955	0.358493298	-0.075424512
H0YGM0;Q9H078;F5GX99;F5H392;F5H7A5	Caseinolytic peptidase B protein homolog	CLPB	0.149800814	-0.036076864	0.17200656	0.050912539
Q16740;M0R208	ATP-dependent Clp protease proteolytic subunit, mitochondrial;ATP-dependent Clp protease proteolytic subunit	CLPP	1.219079364	0.167208354	0.497842909	0.105421702
O96005	Cleft lip and palate transmembrane protein 1	CLPTM1	0.557506956	0.127888997	0.12823692	0.041323026
Q96KA5;G5E9Z2	Cleft lip and palate transmembrane protein 1-like protein	CLPTM1L	0.679449436	0.095328649	0.267769897	0.042047501
O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX	1.277931857	-0.081252098	2.001588304	-0.115727425
F8WF69;P09496	Clathrin light chain A	CLTA	0.493548665	0.129489517	1.334960512	0.292168617
P09497	Clathrin light chain B	CLTB	0.800984812	0.129533577	1.109102336	0.250079155
A0A087WVQ6;Q00610	Clathrin heavy chain;Clathrin heavy chain 1	CLTC	4.619999029	0.116370519	1.135582553	0.034172058
P10909;E7ERK6;HOYLK8	Clusterin;Clusterin beta chain;Clusterin alpha chain	CLU	0.434628278	0.193447749	0.565229034	0.213917732
K7EIG1;O75153	Clustered mitochondria protein homolog	CLUH	1.44286119	-0.091812134	0.798986013	-0.061189651
Q8NFW8	N-acylneuraminate cytidyltransferase	CMA5	0.678487684	0.052442233	0.99135722	0.053044001
P30085;Q5T0D2	UMP-CMP kinase	CMPK1	0.94105847	-0.052839597	0.002125621	0.000213623
Q9BQ75;C9J384	Protein CMSS1	CMSS1	0.494836478	0.100729307	0.550461914	-0.104076385
Q8N1G2	Cap-specific mRNA (nucleoside-2-O-)-methyltransferase 1	CMTR1	0.279661636	-0.053976695	0.082881757	0.037715912
P62633	Cellular nucleic acid-binding protein	CNBP	1.194826991	-0.204515457	0.313217432	-0.035272598
Q96KP4	Cytosolic non-specific dipeptidase	CNDP2	0.689317201	-0.059534391	0.427523531	-0.041902224
P29973	cGMP-gated cation channel alpha-1	CNGA1	0.055815137	-0.011322117	0.068073486	0.010342026
A0A087X271;B4DDF4;B4DUT8;Q99439;K7ES69;H3BV16;A0A087X1X5	Calponin;Calponin-2	CNN2	0.347135776	0.074785233	0.994291479	0.166971525
AS5YKK6	CCR4-NOT transcription complex subunit 1	CNOT1	1.691096607	0.144105911	1.180105945	0.095972697
Q9H9A5;H7C1X9;E9PCN5	CCR4-NOT transcription complex subunit 10	CNOT10	0.154540696	0.087456703	0.032350507	-0.011207581
Q9UKZ1	CCR4-NOT transcription complex subunit 11	CNOT11	0.205939769	-0.05651474	0.47421253	-0.103057543
F8VV52;Q9NZN8;H0Y111;HOYH84;F8VRS8;F8W145	CCR4-NOT transcription complex subunit 2	CNOT2	0.318326481	-0.045126247	0.233654794	-0.064541658
H0Y5X7;H7C3F5;O75175	CCR4-NOT transcription complex subunit 3	CNOT3	0.433136778	-0.08347257	0.133930097	0.030228615
Q9UIV1;H0YBT3;H0YAV9	CCR4-NOT transcription complex subunit 7	CNOT7	0.049313733	-0.009212176	0.009263528	0.001476924
P09543	2,3-cyclic-nucleotide 3-phosphodiesterase	CNP	1.092260533	0.120793978	0.201401567	0.035099983
Q9Y2B0	Protein canopy homolog 2	CNPY2	0.434479043	0.052932421	0.175342838	-0.016641935
Q9BT09	Protein canopy homolog 3	CNPY3	0.175759114	0.044840813	0.181393972	0.041486104
Q9Y2R0;K7EPV0	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	COA3	0.484877064	-0.146100521	0.07374685	-0.022815863
X6R5Z6;Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog	COA6	0	-0.425388336	0.528998576	-0.168905258
Q96BR5	Cytochrome c oxidase assembly factor 7	COA7	1.336349149	-0.198321978	0.252986119	-0.049172084
Q13057	Bifunctional coenzyme A synthase;Phosphopantetheine adenylyltransferase;Dephospho-CoA kinase	COASY	1.344513621	0.064393361	1.206548799	0.060122808
H7C1N2;O75128;A0A0J9YWK3;H7C2C4;J3KR05	Protein cordon-bleu	COBL	1.224041245	0.12685585	1.28749809	0.191836039
A0A087WV10;E9PBL8;Q8WTW3	Conserved oligomeric Golgi complex subunit 1	COG1	0.404498076	0.087227503	0	0.43863678
B7Z2Y2;Q14746	Conserved oligomeric Golgi complex subunit 2	COG2	0	NaN	0	NaN
A0A0A0MS45;J3KN11;Q9H9E3;J3QLW1;E9PRT5;H3BSD2;H3BMV9	Conserved oligomeric Golgi complex subunit 4	COG4	0.536469612	0.336510849	1.170670812	0.39046224
Q9UP83	Conserved oligomeric Golgi complex subunit 5	COG5	0.17962138	0.051428477	0.37408979	0.068175634
P83436	Conserved oligomeric Golgi complex subunit 7	COG7	0.08711377	0.02613163	0.428851641	0.089425405
P38432	Coilin	COIL	0.19942619	-0.047378222	0.078416363	-0.022164345
Q9Y5P4;H0Y9J1;A0A0A0MRE4	Collagen type IV alpha-3-binding protein	COL4A3BP	0	NaN	0.543395986	0.252429008
Q8NBJ5	Procollagen galactosyltransferase 1	COLGALT1	0.749368749	0.056831042	0.544162838	-0.038428624
Q8N668	COMM domain-containing protein 1	COMMD1	0.311731676	0.084355036	0.548464419	0.123504003

Q86X83;F8WBW1	COMM domain-containing protein 2	COMMD2	2.143047327	-0.214179357	2.346344001	-0.206832886
H0Y4E5		COMMD3	0.383679499	-0.055254364	1.054642915	-0.203247643
R4GMX3;R4GMW6;H0Y6Z9		COMMD3- BM11;COMMD3	1.232696494	-0.097042084	2.027026427	-0.110234896
A0A0B4J287;Q9H0A8;H3BM91	COMM domain-containing protein 4	COMMD4	0.236979426	0.098725637	0.043325831	0.023031235
E9PJ95;Q9P000	COMM domain-containing protein 9	COMMD9	0.046780574	0.02406613	0.475262066	0.177705606
P21964;E7EMS6;E7EUU8	Catechol O-methyltransferase	COMT	0.932490124	-0.097282092	1.36216482	-0.190683047
Q86VU5;R4GNF4	Catechol O-methyltransferase domain- containing protein 1	COMTD1	0.162334906	0.039746602	0.094083207	0.027513186
P53621	Coatomer subunit alpha;Xenin;Proxenin	COPA	1.339123131	0.061729431	0.987172751	0.053697268
P53618;E9PP73	Coatomer subunit beta	COPB1	1.839822634	-0.066179911	1.164243975	-0.063671112
P35606	Coatomer subunit beta	COPB2	2.87932088	0.114267349	3.204224023	0.124655088
O14579;M0QXB4;M0R061	Coatomer subunit epsilon	COPE	2.680025051	0.174900373	2.342839693	0.191348076
Q9Y678	Coatomer subunit gamma-1	COPG1	1.127835394	0.042441686	0.197255213	-0.016474724
Q9UBF2	Coatomer subunit gamma-2	COPG2	0.847668606	-0.160181681	0.995239871	-0.212755203
P61201;B4DIH5	COP9 signalosome complex subunit 2	COPS2	0.068194826	-0.01194636	0.133117059	0.019957542
Q9UNS2;H7C3P9	COP9 signalosome complex subunit 3	COPS3	0.339979352	0.044313749	0.446771196	0.054262161
Q9BT78;D6RFN0;D6RAX7;D6 RD63	COP9 signalosome complex subunit 4	COPS4	0.489976716	-0.049312274	0.094565956	-0.006830851
Q92905;E5RHH5	COP9 signalosome complex subunit 5	COPS5	0.096957135	-0.017187754	0.030183257	0.006732623
E7EM64;Q7L5N1	COP9 signalosome complex subunit 6	COPS6	0.206356592	-0.015503565	0.268717212	-0.030375481
Q9UBW8;F5H7C6;F5GYF7;F5 H248;F5H4U8	COP9 signalosome complex subunit 7a	COPS7A	0.717182542	-0.081819852	0.161248072	-0.025638898
A0A087X1P5;J3KQ34;Q9H9Q2 ;J3QT95;J3QT73;J3KQ41	COP9 signalosome complex subunit 7b	COPS7B	0.570549125	-0.149208514	0.044178384	-0.013513565
E9PGT6;Q99627;H7C3S9	COP9 signalosome complex subunit 8	COPS8	0.338802376	-0.054062843	0.250373074	0.051524162
F8VVA7;P61923;F8VXB1;F8W 156;F8W651;F8VXR1;F8VYZ4; F8VUC5	Coatomer subunit zeta-1	COPZ1	0.306247799	-0.041592598	0.508249585	-0.056841214
F8VXX6;Q5HYK3;F8VP53	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	COQ5	0.145643835	-0.09554863	0	-0.388837814
O75208;H3BSJ5;H3BNT2;H3B PC6;H3BRC0	Ubiquinone biosynthesis protein COQ9, mitochondrial	COQ9	0.596971562	0.121802966	0.374652431	-0.088712692
P31146;H3BRY3	Coronin-1A;Coronin	CORO1A	1.532170722	-0.09869194	0.314675414	-0.028794607
Q9ULV4;B4E3S0	Coronin-1C;Coronin	CORO1C	0.463846609	0.060115178	0.912715464	0.10363706
A0A0A6YYL4;P57737	Coronin;Coronin-7	CORO7- PAM16;CORO7	0.074974877	0.005653381	1.320397913	-0.082891464
Q14061;H7C4E5	Cytochrome c oxidase copper chaperone	COX17	2.732869482	-0.500445684	0.326761124	0.100988579
Q5RI15	Cytochrome c oxidase protein 20 homolog	COX20	0.123923218	-0.030166626	0.283442088	-0.068864187
P13073;H3BN72;H3BNV9;H3B PG0;Q86WV2	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1	1.946116387	0.141308784	0.337470545	0.048463504
P20674;H3BRM5;H3BV69;H3B NX8	Cytochrome c oxidase subunit 5A, mitochondrial	COX5A	0.084457664	0.011432648	0.199509716	-0.032819748
P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	0.707620815	0.049748421	0.701966454	-0.06493028
P12074;H0YIV9	Cytochrome c oxidase subunit 6A1, mitochondrial	COX6A1	0.477643117	0.150649707	0.96686351	0.256810824
P14854	Cytochrome c oxidase subunit 6B1	COX6B1	0.586361563	0.14146169	0.896311643	0.238792737
P09669	Cytochrome c oxidase subunit 6C	COX6C	0.596400629	0.077287038	0.259306605	-0.036298116
D6RIE3;D6RGV5;H0UI06;P144 06;D6R9C3	Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2	0.071275419	0.013649813	1.112952258	-0.124713834
O14548;E5RJZ1;H0YBD2	Cytochrome c oxidase subunit 7A-related protein, mitochondrial	COX7A2L	0	NaN	0.118724497	-0.063149134
P15954;D6R9Z7	Cytochrome c oxidase subunit 7C, mitochondrial	COX7C	0.732224624	0.085484982	1.34123709	0.144879436
B0QZ18;Q99829;F2Z2V0;A6PV H9;E7ENH5;Q5JX56;Q5JX58;Q 5JX59;Q5JX60;Q5JX44;Q5JX55 O75131;A0A087WYQ3	Copine-1	CPNE1	1.528918445	-0.064706484	3.529459858	-0.149985631
P36551	Copine-3	CPNE3	1.315281746	-0.055114428	0.424497091	-0.023955345
P36551	Oxygen-dependent coproporphyrinogen- III oxidase, mitochondrial	CPOX	0.846479198	-0.065728188	0.134493417	0.015249888
Q9BRF8	Serine/threonine-protein phosphatase CPPED1	CPPED1	1.285965726	-0.201951281	1.379402094	-0.200256284
Q10570	Cleavage and polyadenylation specificity factor subunit 1	CPSF1	2.217377008	-0.107692401	1.657244474	-0.093805631

Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	CPSF2	1.910074089	-0.13517348	1.085488976	-0.072082202
Q9UKF6;G5E9W3	Cleavage and polyadenylation specificity factor subunit 3	CPSF3	2.159255893	0.104640961	0.272493456	0.025286039
O95639;C9K0K2;B7Z7B0;C9JEV9	Cleavage and polyadenylation specificity factor subunit 4	CPSF4	0.874509859	-0.042354139	0.696241735	0.061732101
F8WJN3;Q16630	Cleavage and polyadenylation specificity factor subunit 6	CPSF6	0.213299011	-0.034879684	0.135332659	-0.013813019
Q8N684;F5H669	Cleavage and polyadenylation specificity factor subunit 7	CPSF7	0.336632839	-0.052742004	0.044598123	-0.008179029
P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A	2.451960481	0.186952273	0.4345578	0.049114863
P23786;A0A1B0GTB8;A0A1B0GWC0;A0A1B0GVF3;A0A1B0GV75	Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2	1.858006463	0.113669078	0.456755101	-0.038428307
Q5TA50;J3KST3	Ceramide-1-phosphate transfer protein	CPTP	0	0.396642685	0	0.356507619
P78560;F8VV49;F5H7C2;F8VY5	Death domain-containing protein CRADD	CRADD	0.169434238	-0.071915309	0.06777901	-0.035059929
A6PWM2;Q6UXH1	Cysteine-rich with EGF-like domain protein 2	CRELD2	0.50436835	0.095523357	0.62473546	0.120728811
P50238;K4DIB9;H3BRQ4	Cysteine-rich protein 1	CRIP1	1.021939364	-0.133514722	0.010062443	0.0018905
P46108;I3L297	Adapter molecule crk	CRK	1.704152648	-0.146370888	1.003747944	-0.098837852
P46109	Crk-like protein	CRKL	0.482751103	0.127919896	0.219540636	-0.062366486
Q8IUI8	Cytokine receptor-like factor 3	CRLF3	0.515053449	0.109907468	0.718289443	0.147622108
E9PD68;Q14194;H0YBT4	Dihydropyrimidinase-related protein 1	CRMP1;DPYSL3	0.540961155	-0.506144524	0.027782459	-0.072193146
Q5JY65;Q9BZJ0	Crooked neck-like protein 1	CRNKL1	1.428426082	0.117792447	0.420734164	0.038537979
B1AKD8;Q5TZA2	Rootletin	CROCC	1.003576443	-0.132647419	0.725466105	-0.087300142
C9JP16;O75718	Cartilage-associated protein	CRTAP	0.082535125	-0.037858009	0.685900064	0.142242241
P53674	Beta-crystallin B1	CRYBB1	1.016858576	-0.070105235	0.369401571	-0.051901499
Q08257;A6NP24;C9JH92	Quinone oxidoreductase	CRYZ	0.60002126	-0.080758413	0.55517734	0.075605075
O95825;C9JQD0;C9K0F7;C9JAL0;H7C3I5;A6NND8;A6NHJ8;A6NMA8	Quinone oxidoreductase-like protein 1	CRYZL1	0.131866971	0.086868286	0.067574265	-0.038063049
B4DJV2;O75390;A0A0C4DGI3	Citrate synthase;Citrate synthase, mitochondrial	CS	3.400440223	0.19765536	0.533463247	0.042515755
O75534;E9PLT0	Cold shock domain-containing protein E1	CSDE1	0.199999333	0.012629827	1.79177154	0.081852913
P55060	Exportin-2	CSEIL	2.100872612	-0.052365621	2.057429015	-0.039031982
P41240	Tyrosine-protein kinase CSK	CSK	0.829614672	-0.032218297	0.837738078	-0.036205928
P48729;D6REM4;Q8N752;E7ETM0	Casein kinase I isoform alpha;Casein kinase I isoform alpha-like	CSNK1A1;CSNK1A1L	0.347999326	-0.05936559	0.884112676	-0.131814957
E7EU96;P68400;Q8NEV1	Casein kinase II subunit alpha;Casein kinase II subunit alpha 3	CSNK2A1;CSNK2A3	0.220890441	-0.027989388	0.664457248	-0.057311058
P19784;H3BSA1;H3BV19	Casein kinase II subunit alpha	CSNK2A2	0.978095023	-0.126710256	0.633895109	-0.099493663
Q5SRQ6;P67870;Q5SRQ3;N0E472;A0A0G2JM12	Casein kinase II subunit beta	CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	0.042522651	0.006442706	0.061487068	0.009668032
P21291;E9PS42;E9PND2;E9PP21	Cysteine and glycine-rich protein 1	CSRP1	2.837282877	-0.169167201	0.86049251	-0.054966291
P04080	Cystatin-B	CSTB	1.194729982	-0.098999659	0.119686265	-0.018258413
Q05048;A0A0A0MSZ9	Cleavage stimulation factor subunit 1	CSTF1	0.21452381	0.03043143	0.473845896	0.064099312
P33240;E9PID8;E7EWR4	Cleavage stimulation factor subunit 2	CSTF2	0.233306316	-0.022713343	0.038567966	-0.005399386
Q12996	Cleavage stimulation factor subunit 3	CSTF3	1.272017163	-0.220018387	0.345238967	-0.088752111
Q13363;D6RAX2;E7ESU7;E7EPF8;E9PGB1	C-terminal-binding protein 1	CTBP1	0.891257077	-0.081574758	0.608374655	-0.070194562
P49711	Transcriptional repressor CTCF	CTCF	0.075395318	0.015553157	0.046234778	-0.008772532
A0A0J9YWB6;Q9Y5B0;A0A0J9YWJ4;K7EJD2;A0A0A0MR03	RNA polymerase II subunit A C-terminal domain phosphatase	CTDP1	0.044177723	0.008657455	0.510052325	-0.090204875
P35221;G3XAM7	Catenin alpha-1	CTNNA1	4.890333502	0.334606489	3.136386923	0.19603761
P26232;A0A0A0MTJ6;A0A0A0MRI5	Catenin alpha-2	CTNNA2	2.964919832	0.474168078	1.660201589	0.317695554
Q9UBT7;Q5JTQ9;Q5JTQ6	Alpha-catenin	CTNNA1	0.315715837	0.148127556	0.181158162	0.177091599
A0A087WUB9;Q8WYA6	Beta-catenin-like protein 1	CTNBL1	1.428038727	-0.109802246	0.833837948	-0.071109772
P17812	CTP synthase 1	CTPS1	1.948044597	-0.060016632	0.649121471	-0.032080015

Q6PD62	RNA polymerase-associated protein CTR9 homolog	CTR9	1.072713266	0.080746969	0.034381364	0.006410917
X6R5C5;X6R8A1;P10619	Carboxypeptidase;Lysosomal protective protein;Lysosomal protective protein 32 kDa chain;Lysosomal protective protein 20 kDa chain	CTSA	2.250034087	-0.307300568	0.373866025	-0.074321111
P07858	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	CTSB	0.027014151	-0.004217148	0.46595403	0.05351003
P53634	Dipeptidyl peptidase 1;Dipeptidyl peptidase 1 exclusion domain chain;Dipeptidyl peptidase 1 heavy chain;Dipeptidyl peptidase 1 light chain	CTSC	0.237792657	0.034424146	0.53892482	-0.070462863
A0A1B0GW44;A0A1B0GVD5;A0A1B0GWE8;P07339;H7C469;A0A1B0GVP3;A0A1B0GV23;A0A1B0GU92;A0A1B0GU03;C9JH19;H7C1V0 P25774;U3KQE7;U3KPS4	Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain	CTSD	1.993590567	-0.153647423	2.611847385	0.216879209
Q9UBR2	Cathepsin S	CTSS	2.177648364	-0.123030345	0.199305891	-0.017317136
Q13616;A0A0C4DGX4	Cathepsin Z	CTSZ	1.527221248	-0.312387466	1.207955647	-0.159397761
Q5T2B5;A0A0A0MTN0;Q13617	Cullin-1	CUL1	3.117585371	-0.072206497	0.766061947	-0.039837519
Q13618	Cullin-2	CUL2	1.044202342	-0.152991486	0.016603174	0.002928289
Q13619;A0A0A0MR50	Cullin-3	CUL3	0.667097466	-0.118283908	0.839401706	-0.093804359
K4DI93;Q13620	Cullin-4A	CUL4A	0.008200219	-0.002718925	0.159428997	0.040866852
Q93034	Cullin-4B	CUL4B	2.935159421	-0.221239408	2.946872605	-0.156145096
O60888;C9IZG4	Cullin-5	CUL5	0.273656009	0.100361697	0.000187667	-8.31E-05
P39880	Protein CutA	CUTA	0.252914767	0.054127057	0.578562461	0.117630005
B7WP74;Q9HCG8	Homeobox protein cut-like 1	CUX1	0.050755437	-0.021981875	0.104965254	0.03289636
Q6UX04;D6REK3	Pre-mRNA-splicing factor CWC22 homolog	CWC22	0.330796497	0.0767711	1.411239604	-0.219648361
Q69YN2	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	CWC27	2.438311016	-0.098320643	0.587525633	-0.048899333
Q9P0U4	CWF19-like protein 1	CWF19L1	1.245053102	-0.12292544	0.4059235	-0.061083794
D6RFH4;H3BUX2;J3KNF8;O43169	CXXC-type zinc finger protein 1	CXXC1	0.644849201	0.159399033	0.335388479	0.17549324
Q9UHQ9;H7C0R7	Cytochrome b5 type B	CYB5B	1.287089081	0.159126282	0.083185883	-0.022113482
P00387;B1AHF3	NADH-cytochrome b5 reductase 1	CYB5R1	1.213900843	0.23876826	1.323166247	0.245350202
P13498	NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bound form;NADH-cytochrome b5 reductase 3 soluble form	CYB5R3	1.031589463	0.098580678	0.080267981	-0.013605754
P04839	Cytochrome b-245 light chain	CYBA	5.337417248	0.649502436	3.815927298	0.400110881
P08574	Cytochrome b-245 heavy chain	CYBB	0.264716613	0.040139516	0.316529184	-0.045168877
C9JFR7;P99999	Cytochrome c1, heme protein, mitochondrial	CYC1	0.847443632	0.107853572	0.087790874	0.011041005
Q7L576;A0A0G2JR96;A0A0G2JQT1	Cytochrome c	CYCS	0.220952423	-0.039313316	0.148237356	-0.026357969
E7EVJ5;Q96F07;H7C229;E7EW33	Cytoplasmic FMR1-interacting protein 1	CYFIP1	1.019109357	-0.187810898	0.385708612	-0.08398819
Q9HBI6;F8W978;A0A0A0MQR0;A0A0A0MR49;Q08477;Q9HCS2	Cytoplasmic FMR1-interacting protein 2	CYFIP2	0.876980624	-0.064813296	0.034652503	-0.003989538
A0A0C4DFL7;Q16850	Phylloquinone omega-hydroxylase CYP4F11;Docosahexaenoic acid omega-hydroxylase CYP4F3;Cytochrome P450 4F12	CYP4F11;CYP4F2;CYP4F12;CYP4F3	0.612614559	0.134877205	0.717047386	0.088396072
Q15438;K7ENQ8;K7ERV8;K7ENH6;K7EKA2 F5GXX5;P61803	Lanosterol 14-alpha demethylase	CYP51A1	2.14713924	0.237217267	0.119533474	-0.016585986
E7ET49;Q8NCG7	Cytohesin-1	CYTH1	1.00748082	0.108316422	0.192905133	-0.032103221
Q3LXA3;H0YCY6	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	DAD1	0.658354783	0.099514008	0.455424967	0.078265508
P51398;V9GZ03;V9GYL9;V9GYA7	Sn1-specific diacylglycerol lipase beta	DAGLB	0.293326985	0.199798584	0.451793313	0.374655724
J3KKN3;Q9UN19	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);ATP-dependent dihydroxyacetone kinase;FAD-AMP lyase (cyclizing)	DAK;TKFC	1.425495946	-0.077532768	0.222378011	-0.014445623
P14868	28S ribosomal protein S29, mitochondrial	DAP3	2.117166042	-0.222511609	1.361740514	-0.148018519
	Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide	DAPP1	4.367018966	0.40241909	0.496809619	0.049985568
	Aspartate--tRNA ligase, cytoplasmic	DARS	0.599295629	0.040467262	0.061784695	-0.005723317

Q6PI48	Aspartate--tRNA ligase, mitochondrial	DARS2	0.610754995	0.05011495	1.466644372	-0.10370032
Q9UER7	Death domain-associated protein 6	DAXX	0.140879889	-0.057735443	0.097158973	-0.044129372
K7EQ55;K7EK33;Q96EP5;K7E Q02	DAZ-associated protein 1	DAZAP1	0.705794923	0.069176038	0.347322536	0.039626122
A0A0A0MTI5;B8ZWD1;P0710 8	Acyl-CoA-binding protein	DBI	0.878268836	-0.116746585	0.397757813	-0.061864535
Q9UJU6;B4DDD6;H0Y5J4	Drebrin-like protein	DBNL	1.35459293	0.099835078	1.785150256	0.138368607
Q9UK59	Lariat debranching enzyme	DBR1	1.056289404	-0.12459151	1.025241252	-0.165327072
P11182;Q5VV7	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	DBT	0.131091405	0.018918037	1.460829206	-0.14160951
A0A087WT20;Q9NV06;B3KM E9	DDB1- and CUL4-associated factor 13	DCAF13	0.460548568	0.056051254	0.321126142	0.055368106
P61962;A0A087WWI6	DDB1- and CUL4-associated factor 7	DCAF7	1.541261012	0.136879603	0.287476122	0.054790815
G3V3G9;Q5TAQ9;V9GY54	DDB1- and CUL4-associated factor 8	DCAF8	0.396241709	0.069232623	0.160241101	0.038285573
Q9NPI6	mRNA-decapping enzyme 1A	DCP1A	0.02053058	0.004989306	0.54703699	-0.144984881
Q96C86	m7GpppX diphosphatase	DCPS	0.732490715	-0.044261932	2.905887727	-0.136956533
E7EX90;Q14203	Dynactin subunit 1	DCTN1	2.086956924	0.186988195	1.461902046	0.134428342
Q13561;F8W1I6;F8VW18;H0YI 98	Dynactin subunit 2	DCTN2	1.463137307	-0.128974597	1.274117953	0.113723119
X6RCK5;O75935;X6RA56;A0A 0A0MRV8;X6RLR1	Dynactin subunit 3	DCTN3	0.736919675	-0.153753217	0.263706538	0.055851682
Q9UJW0	Dynactin subunit 4	DCTN4	1.752717412	0.244139099	0.634002984	0.169107819
Q9H773	dCTP pyrophosphatase 1	DCTPP1	1.491185026	-0.143321037	0.368749535	0.0495224
C9JVE2;Q96GG9;C9J8R4;C9JR U6;C9J0B2;C9JUW4	DCN1-like protein;DCN1-like protein 1	DCUN1D1	2.460736987	-0.23943011	0.492711978	-0.111447652
Q9BTE7;E9PM04;H0YCN4	DCN1-like protein 5;DCN1-like protein	DCUN1D5	0.710720325	0.150183678	0.173161921	0.049929937
Q7Z4W1;J3KS22;J3QS36;J3QS 45;J3KSZ5;J3QL34;J3KRZ4	L-xylulose reductase	DCXR	1.707651798	0.096144358	1.905073734	0.102565447
Q9BW61	DET1- and DDB1-associated protein 1	DDA1	0.8907023	0.09016552	2.506278806	0.156157494
Q16531;F5GY55	DNA damage-binding protein 1	DDB1	0.090865139	-0.007428487	0.109515016	0.009061495
Q5TDH0	Protein DDI1 homolog 2	DDI2	1.901608118	-0.139293671	4.076050358	-0.252301216
A0A0C4DGS1;P39656	Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase 48 kDa subunit	DDOST	0.965380663	0.087206523	0.237490952	-0.020963351
Q96HY6;A0A0A0MRX2	DDR GK domain-containing protein 1	DDR GK1	4.457322283	0.232808113	2.826032449	0.172818184
P30046;B5MC82;A6NHG4;J3K Q18	D-dopachrome decarboxylase;D- dopachrome decarboxylase-like protein	DDT;DDTL	1.509447757	-0.113317172	0.192958088	-0.022659938
Q92499;F1T0B3;A0A087X2G1	ATP-dependent RNA helicase DDX1	DDX1	0.363313958	0.016844432	0.865051915	0.034859975
Q13206;E9PIF2	Probable ATP-dependent RNA helicase DDX10	DDX10	1.715030164	0.150740306	0.285197934	-0.044111888
Q92771;A8MPP1;Q96FC9	Putative ATP-dependent RNA helicase DDX12;Putative ATP-dependent RNA helicase DDX11-like protein 8;Probable ATP-dependent RNA helicase DDX11	DDX12P;DDX11L8; DDX11	0.68303286	-0.174415906	1.333500925	-0.222708384
A0A1X7SBZ2;A0A1W2PQ51;Q 92841	Probable ATP-dependent RNA helicase DDX17	DDX17	1.201908404	-0.058928808	0.437454998	-0.030640602
Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18	1.285283402	0.063007037	0.118482345	-0.008857727
Q9NUU7;I3L0H8	ATP-dependent RNA helicase DDX19A	DDX19A	0.579910155	0.050322215	0.262189211	0.026316643
H3BQK0;Q9UMR2	ATP-dependent RNA helicase DDX19B	DDX19B	0.397076016	0.081482251	0.091492355	-0.020676931
Q9UHI6	Probable ATP-dependent RNA helicase DDX20	DDX20	1.037138669	-0.123436928	2.468991206	-0.153960546
Q9NR30	Nucleolar RNA helicase 2	DDX21	0.098848027	-0.008189201	0.620436359	-0.037801743
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23	DDX23	0.26737423	-0.03988711	0.681580628	-0.101338387
G3V529;Q9GZR7;F5GYL3;A0 A1W2PRR2;A0A087WXU8	ATP-dependent RNA helicase DDX24	DDX24	1.724173559	0.092802366	3.062372281	0.161598523
B7Z6D5;Q96GQ7	Probable ATP-dependent RNA helicase DDX27	DDX27	1.021246625	0.095295906	0.035430097	0.004011472
Q9NUL7	Probable ATP-dependent RNA helicase DDX28	DDX28	0.002057697	0.000552177	0.24568294	-0.036885579
F8WAJ0;Q9H8H2	Probable ATP-dependent RNA helicase DDX31	DDX31	0.723073334	0.116770744	0.752618391	-0.094320933
O00148;K7EQN7	ATP-dependent RNA helicase DDX39A	DDX39A	0.153062192	-0.009679794	0.755429775	-0.034791629
Q13838;A0A0G2JZ9;Q5STU3; A0A140T9X3;F6WLT2;F6S4E6 ;A0A0A0MT12;F6TRA5	Spliceosome RNA helicase DDX39B	DDX39B	0.090842354	0.01252683	0.030013541	0.005075455
A0A0D9SFB3;A0A0D9SG12;A 0A0D9SF53;O00571	ATP-dependent RNA helicase DDX3X	DDX3X	0.025332536	-0.001756668	0.691395495	-0.035840352

O15523	ATP-dependent RNA helicase DDX3Y	DDX3Y	0.120679945	-0.079418182	1.821963471	-0.609232108
J3KNN5;Q9UJV9	Probable ATP-dependent RNA helicase DDX41	DDX41	0.239231073	0.035568555	0.910941507	-0.15314134
Q86XP3;A0A0A0MSJ0	ATP-dependent RNA helicase DDX42	DDX42	0.937980161	-0.075435956	0.945242028	-0.065543175
A0A0C4DG89;Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46	0.002630765	0.000269572	0.336411543	-0.037609736
Q9H0S4	Probable ATP-dependent RNA helicase DDX47	DDX47	0.050645082	0.006388028	0.559491947	-0.05224673
Q9Y6V7	Probable ATP-dependent RNA helicase DDX49	DDX49	0.369468365	0.064916611	0.045869923	-0.008926074
J3KTA4;P17844	Probable ATP-dependent RNA helicase DDX5	DDX5	0.992967752	-0.059335073	0.847978837	-0.056517283
Q9BQ39;A0A087WVC1	ATP-dependent RNA helicase DDX50	DDX50	0.161455222	-0.034631093	0.348653086	-0.070370674
Q8N8A6	ATP-dependent RNA helicase DDX51	DDX51	0.928241222	-0.137457848	2.24421187	-0.196543376
Q9Y2R4	Probable ATP-dependent RNA helicase DDX52	DDX52	1.325381499	0.125064532	0.03306964	-0.006285032
Q8TDD1	ATP-dependent RNA helicase DDX54	DDX54	0.912932066	0.074634552	0.052158846	-0.004510562
Q9NY93;H7C3E9;G3V0G3	Probable ATP-dependent RNA helicase DDX56	DDX56	2.12452868	0.145664215	0.657503721	0.067518234
P26196	Probable ATP-dependent RNA helicase DDX6	DDX6	2.45137093	-0.111522992	1.257604216	-0.059341749
Q16698;E5RJG7;E5RFV2;E5RJ D2	2,4-dienoyl-CoA reductase, mitochondrial	DEC1	1.800202581	0.128247579	0.337959824	-0.034642537
Q9H4E7	Differentially expressed in FDCP 6 homolog	DEF6	0.095391824	-0.013040066	0.111633101	0.018631935
P35659;B4DFG0;D6RDA2	Protein DEK	DEK	0.067852617	-0.006627401	0.477846123	-0.038862228
A0A0U1RR27;Q7Z401;H3BTW 5	C-myc promoter-binding protein	DENND4A	0.36786982	0.03723526	0.098196491	0.012880325
O43583;F8VVL1	Density-regulated protein	DENR	0.016131783	0.005860138	0.296253252	0.057911682
Q8TB45	DEP domain-containing mTOR-interacting protein	DEPTOR	3.492800795	0.241386731	0.899677782	0.060791651
Q9Y315;E9PPM8;G3V158;E9P ML7;E9PMH9	Deoxyribose-phosphate aldolase	DERA	1.680011722	-0.221439997	0.423434383	-0.122065544
B4E1G1;Q9BUN8;E5RGGY0	Derlin-1	DERL1	0.350440983	0.053707759	0.287380018	-0.100991567
O00273;K7ERT1	DNA fragmentation factor subunit alpha	DFFA	3.987965237	-0.404614766	0.388162796	-0.051720301
Q9UBM7;E9PM00	7-dehydrocholesterol reductase	DHCR7	1.306648016	0.130116145	0.338008035	0.050622622
P00374;B4DM58	Dihydrofolate reductase	DHFR	1.594010772	0.134253184	0.305882656	0.03608036
Q02127;I3NI32	Dihydroorotate dehydrogenase (quinone), mitochondrial	DHODH	0.485775393	0.058233579	1.012839996	-0.104500771
P49366;A0A087WZK0;Q5J8M5	Deoxyhypusine synthase	DHPS	0.069969968	0.013590495	0.364916312	0.05753835
Q96LJ7;H0YNC2	Dehydrogenase/reductase SDR family member 1	DHRS1	1.397497009	0.115381877	0.246138021	-0.029728572
Q9BTZ2	Dehydrogenase/reductase SDR family member 4	DHRS4	0.744296253	-0.219587803	0.165495858	-0.050903002
Q9Y394;A0A087X0Z7;H0YJ66	Dehydrogenase/reductase SDR family member 7	DHRS7	0.044138911	0.014352163	0.054735048	-0.03348128
J3KRS1;A0A0C4DGQ8;Q6IAN 0	Dehydrogenase/reductase SDR family member 7B	DHRS7B	0	NaN	0	NaN
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15	0.445557871	0.036365191	0.79576949	-0.060571988
O60231;A0A140T947	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	DHX16	0.611915316	-0.043146769	0.475618484	-0.04127566
A0A087WYN9;Q7Z478	ATP-dependent RNA helicase DHX29	DHX29	2.191006768	-0.140302022	1.239196512	-0.094499906
H7BXY3;Q7L2E3	Putative ATP-dependent RNA helicase DHX30	DHX30	3.179359764	-0.224339803	2.726906648	-0.153693517
Q9H6R0;I3L1L6	Putative ATP-dependent RNA helicase DHX33	DHX33	0.158545658	0.03427728	0.495845611	-0.082370758
Q9H2U1;E7EWK3	ATP-dependent RNA helicase DHX36	DHX36	0.1103881	-0.013960203	0.152835744	-0.017962138
F5H3Y4;Q8IY37	Probable ATP-dependent RNA helicase DHX37	DHX37	0.046508262	-0.01382033	0.062604579	-0.021720886
Q92620	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	DHX38	0.002567909	0.00031058	0.005547777	-0.000628471
Q6P158	Putative ATP-dependent RNA helicase DHX57	DHX57	0.13655018	-0.053825696	0.207423455	-0.072076162
F5H658;Q14562	ATP-dependent RNA helicase DHX8	DHX8	0.148321302	0.044081688	0.05916106	-0.015435537
Q08211	ATP-dependent RNA helicase A	DHX9	0.204155442	-0.006624222	0.874401336	-0.023605347
Q9NR28;A0A024RBT2;F5H796 ;F5GXT8	Diablo homolog, mitochondrial	DIABLO	1.042292664	-0.151461601	0.180101084	-0.024590174
A0A140T8Z0;A0A0G2JH68;O6 0610;H9KV28	Protein diaphanous homolog 1	DIAPH1	1.402940678	0.045693715	2.512788193	0.105664571
Q9UPY3	Endoribonuclease Dicer	DICER1	0.124400601	-0.065451304	0.259068268	-0.059472402

Q9BTC0	Death-inducer obliterator 1	DIDO1	2.137688987	-0.147145907	1.879305397	-0.206243515
Q68CQ4	Digestive organ expansion factor homolog	DIEXF	0.13937481	0.020017942	0.092809293	0.016064008
Q9UNQ2;A0A0C4DGB1;D6RC L3	Probable dimethyladenosine transferase	DIMT1	0.686423804	-0.103368759	1.913869597	-0.209984461
Q9Y2L1;G3V1J5;F2Z2C0	Exosome complex exonuclease RRP44	DIS3	0.116248923	0.015434583	0.622799599	-0.075951894
O60832;C9IYT0;H7C0M1	H/ACA ribonucleoprotein complex subunit 4	DKC1	0.939293296	0.07453378	0.023714605	-0.002809207
Q9UFM8;Q9Y639;H3BQ94	Neuroplastin	DKFZp566H1924;NPTN	0.555173843	-0.08904171	0.713311843	-0.078710874
P10515;E9PEJ4;H0YDD4	Dihydropolyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	1.953769876	0.092619896	0.137112844	-0.007146835
P09622;E9PEX6	Dihydropolyl dehydrogenase, mitochondrial;Dihydropolyl dehydrogenase	DLD	3.306789765	0.13435936	3.576480703	0.10972182
P36957	Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	DLST	1.107908132	0.10540549	0.42351026	-0.048935254
Q9NPF5;Q5TG40	DNA methyltransferase 1-associated protein 1	DMAPI	1.848584278	-0.1743234	0.401079621	-0.05351359
Q86Y56;H0Y650	Dynein assembly factor 5, axonemal	DNAAF5	0.893486139	0.078389168	0.362263663	-0.029737473
P31689	DnaJ homolog subfamily A member 1	DNAJA1	3.274449238	0.226881027	1.285484483	0.120228767
O60884	DnaJ homolog subfamily A member 2	DNAJA2	0.833467666	-0.052763303	0.02559844	0.003068606
Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3	0.054722005	-0.008467038	0.581106722	-0.038862864
P25685;M0R080	DnaJ homolog subfamily B member 1	DNAJB1	6.890014007	0.651388804	2.659260548	0.161671956
Q9UBS4;H7C2Y5	DnaJ homolog subfamily B member 11	DNAJB11	0.675180063	0.094306946	0.336075161	0.059244474
O75190;A0A0J9YX62;E9PH18;C9J2C4	DnaJ homolog subfamily B member 6	DNAJB6	1.214849555	0.194905599	0.959688902	0.146512349
Q96KC8	DnaJ homolog subfamily C member 1	DNAJC1	0.228877866	-0.063072205	0.021489772	0.006066322
Q8IXB1	DnaJ homolog subfamily C member 10	DNAJC10	1.546129571	0.09528923	0.076516187	0.00767231
Q9NVH1	DnaJ homolog subfamily C member 11	DNAJC11	3.856435522	0.278745969	0.192131916	0.029785474
O75165	DnaJ homolog subfamily C member 13	DNAJC13	0.561119933	0.174093056	0.091847766	-0.067505074
Q96DA6;F2Z3A7	Mitochondrial import inner membrane translocase subunit TIM14	DNAJC19	1.193586402	0.097035726	0.294487966	0.039494514
Q99543	DnaJ homolog subfamily C member 2;DnaJ homolog subfamily C member 2, N-terminally processed	DNAJC2	0.537695117	0.043178558	0.020789244	-0.002480507
Q13217	DnaJ homolog subfamily C member 3	DNAJC3	0.461500021	0.098378499	0.184138764	0.042910576
Q99615;K7EIH8;K7ESP1;K7EP P7	DnaJ homolog subfamily C member 7	DNAJC7	1.479246195	0.094485919	0.786120077	0.045982997
O75937	DnaJ homolog subfamily C member 8	DNAJC8	3.171567604	-0.233359337	4.551653991	-0.168572108
Q8WXX5	DnaJ homolog subfamily C member 9	DNAJC9	0.030252635	0.013948758	0.00715383	-0.003442764
G8JLD5;O00429	Dynamin-1-like protein	DNM1L	3.246096593	-0.133927027	2.70449646	-0.103478432
P50570	Dynamin-2	DNM2	1.561237347	0.051902453	0.583702634	-0.023153623
P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1	0.241458401	0.009569168	1.977758171	-0.056360881
E7ETB3;Q9ULA0;E7EMB6;C9J BE1;F8WAN0	Aspartyl aminopeptidase	DNPEP	1.293391915	-0.120911916	0.039658473	-0.005384763
H0Y8X4;O43598	2-deoxynucleoside 5-phosphate N-hydrolase 1	DNP1H	1.148641183	-0.121265093	0.384972764	-0.036725044
Q5QJE6;J3KP30	Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2	2.818357918	0.245861689	0.699668624	0.089783351
Q96BY6;F8WE73	Dedicator of cytokinesis protein 10	DOCK10	1.316512684	-0.220997334	1.986058435	-0.163902283
Q92608;E5RFJ0	Dedicator of cytokinesis protein 2	DOCK2	0.581849923	0.037864049	1.660824922	-0.08564504
Q9BU89	Deoxyhypusine hydroxylase	DOHH	0.664759363	0.104341189	0.015058199	0.003170013
Q9Y3R5	Protein dopey-2	DOPEY2	2.413149958	-0.483065287	1.535853211	-0.228643735
J3KMZ8;Q92785	Zinc finger protein ubi-d4	DPF2	1.906823464	-0.224077225	0.459477831	-0.087498347
I3L1H5;Q9BZG8;U3KQN3;I3L 3X9	Diphthamide biosynthesis protein 1	DPH1	0.246029575	-0.05445137	0.232324364	-0.090550423
Q9BQC3;H0YCR5	Diphthamide biosynthesis protein 2	DPH2	1.393949769	-0.218420029	1.08645191	-0.209403356
Q9H2P9	Diphthine synthase	DPH5	0.175506614	-0.090059598	0.089268475	-0.065139453

Q5QPK2;H0Y368;O60762;Q5Q PJ9	Dolichol-phosphate mannosyltransferase subunit 1	DPM1	0.510108256	0.026861191	1.451660775	-0.096270879
Q9P2X0	Dolichol-phosphate mannosyltransferase subunit 3	DPM3	0.077755451	0.028520266	0.274339334	0.073227247
G3V1D3;G3V180;Q9NY33	Dipeptidyl peptidase 3	DPP3	3.90017745	-0.212222417	1.096014579	-0.068328222
Q9UHL4	Dipeptidyl peptidase 2	DPP7	2.694998483	0.188172023	0.185928637	0.018760045
Q86TI2;M0R2A8	Dipeptidyl peptidase 9	DPP9	0.683388856	-0.227316538	0.485857078	-0.144692612
A0A1B0GW05;H7C3M5;Q2PZI 1	Probable C-mannosyltransferase DPY19L1	DPY19L1	0.583448931	0.138230006	0.344987095	-0.087836901
Q9C005	Protein dpy-30 homolog	DPY30	0.003666853	0.002537251	0.010797004	0.007173061
A0A1C7CYX9;Q16555	Dihydropyrimidinase-related protein 2	DPYSL2	0.360440192	-0.026020368	0.532444236	0.04790624
Q01658	Protein Dr1	DR1	1.949036935	-0.307613373	1.516233927	-0.237352689
E9PNC7;C9JCC6;Q14919;E9PQ X9	Dr1-associated corepressor	DRAP1	0.661444883	-0.08880806	0.287642203	-0.035826683
Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1	0.564975845	-0.037826856	0.02526482	-0.002431552
A8MZF9;P55039;J3QKW7	Developmentally-regulated GTP-binding protein 2	DRG2	2.624202906	-0.182451884	2.867703546	-0.196589788
Q9BVC3	Sister chromatid cohesion protein DCC1	DSCC1	0.587656714	-0.197698911	0.521884361	-0.176127434
Q14126	Desmoglein-2	DSG2	3.721292464	-0.571676254	0.016386538	-0.003328005
P15924	Desmoplakin	DSP	5.836715877	0.120516459	1.705440744	0.040627162
F8W9J4;Q03001;E9PHM6;F6Q M17	Dystonin	DST	0	NaN	0	NaN
P60981;F6RFD5	Destrin	DSTN	3.145119243	-0.108856201	0.018173219	0.001515706
Q8TEA8;A0A087WZV9	D-tyrosyl-tRNA(Tyr) deacylase 1;D- tyrosyl-tRNA(Tyr) deacylase	DTD1	0.298995251	-0.111490885	0.463611265	0.130343119
F5GZ90;Q9NZJ0	Denticleless protein homolog	DTL	1.135037271	0.270840327	1.900865488	0.447658984
P23919;H7C312;H7BZ20;G5E9 E9	Thymidylate kinase	DTYMK	0.223354317	0.040051142	0.061762643	0.011849085
H0YGW8;J3QLE4;Q6P1R4;J3Q KP9	tRNA-dihydrouridine(16/17) synthase [NAD(P)(+)]-like	DUS1L	0	-0.248588562	0	-0.323041916
Q96G46	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	DUS3L	0.584094791	-0.123239517	0.500721984	0.13525486
Q9NRW4;S4R459;S4R3A4	Dual specificity protein phosphatase 22	DUSP22	0.968029032	-0.14526844	0.33803944	0.105533918
Q9BVJ7	Dual specificity protein phosphatase 23	DUSP23	0	-0.15555954	0	-0.056686401
P33316;H0YNNW5;A0A0C4DGL 3;H0YKCS;H0YKI0;H0YMM5	Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT	3.175542863	-0.088817596	1.713744764	-0.052813212
Q7RTS9	Dymeclin	DYM	0.41898829	-0.086946805	0.076884438	-0.021736145
Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	4.24920823	0.102249781	4.568844641	0.119023641
Q13409;E7EQL5	Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	0.400146596	0.057456017	1.334320884	0.126683235
Q9Y6G9;E9PHI6	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1	1.420926315	-0.057730675	0.321567576	0.01775074
O43237;B4E2E0	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2	0.154885438	-0.03583463	0.208428702	0.037015279
P63167;F8VXL2;F8VRV5	Dynein light chain 1, cytoplasmic	DYNLL1	0.657882566	0.117419561	0.527472892	0.081266721
B1AKR6;Q9NP97	Dynein light chain roadblock-type 1	DYNLRB1	0.587191132	-0.06656456	0.365764913	-0.04602623
Q5VTU3;P63172	Dynein light chain Tctex-type 1	DYNLT1	0.411827339	-0.162100474	0.053413505	-0.020805041
A6NGJ0;P51808;F2Z328	Dynein light chain Tctex-type 3	DYNLT3	0.659503195	-0.058303515	0.112861716	-0.013333956
H3BTB7;Q5JPH6	Probable glutamate-tRNA ligase, mitochondrial	EARS2	0.078569398	0.014677684	0.801131621	-0.104769071
H7C2Q8;Q99848	Probable rRNA-processing protein EBP2	EBNA1BP2	0.116624844	-0.018304507	1.188950395	-0.125383377
Q15125;C9J719;C9JJ78	3-beta-hydroxysteroid-Delta(8),Delta(7)- isomerase	EBP	0.56302472	0.127831777	0.63304232	0.142100334
Q13011;M0R248	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	2.267606157	0.129665375	0.339150056	0.029872259
P30084	Enoyl-CoA hydratase, mitochondrial	ECHS1	0.815188729	0.130530993	0.220063816	-0.036180496
P42126;Q96DC0;H3BS70	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1;DCI	1.875211143	0.230998675	0.393295732	0.064561208
Q9BQ95;J3KTF5;K7EPL5;K7E N32	Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial	ECSIT	0.103967931	-0.041191737	0.168232905	-0.054712296
Q96F86	Enhancer of mRNA-decapping protein 3	EDC3	0.196579208	0.025942802	0.065298977	0.010000547
Q6P2E9	Enhancer of mRNA-decapping protein 4	EDC4	4.479587831	0.121879896	0.124553668	-0.007561048
Q9BZQ6	ER degradation-enhancing alpha- mannosidase-like protein 3	EDEM3	0.29439762	-0.065147718	0.48796743	-0.116325061

O60869	Endothelial differentiation-related factor 1	EDF1	0.040299573	-0.007919947	0.654264494	0.112618764
Q15075	Early endosome antigen 1	EEA1	2.59834014	-0.236129443	1.711119738	-0.175287565
P68104;Q5VTE0;A0A087WVQ9	Elongation factor 1-alpha 1;Putative elongation factor 1-alpha-like 3	EEF1A1;EEF1A1P5	1.046961842	-0.050113678	0.88689283	-0.046312332
Q05639	Elongation factor 1-alpha 2	EEF1A2	0.404314393	-0.141462326	0.147914435	-0.065436363
P24534	Elongation factor 1-beta	EEF1B2	1.15818446	-0.145754496	0.145381067	-0.028997739
E9PRY8;P29692;E9PQZ1;E9PK01;A0A087X1X7;H0YE72	Elongation factor 1-delta	EEF1D	3.017645692	-0.15709432	1.041020166	-0.050168037
O43324;H0YAL7;D6RBD7;C9J1V9	Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1;EEF1E1-BLOC1SS	0.327260791	0.060612361	0.043832216	0.010300001
P26641	Elongation factor 1-gamma	EEF1G	3.805396797	-0.142192205	0.727344799	-0.038352331
P13639	Elongation factor 2	EEF2	2.07484146	-0.087399165	0.205774542	-0.015220642
O00418;H3BRH4	Eukaryotic elongation factor 2 kinase	EEF2K	0.335426701	0.053587278	0.158598054	0.02611955
Q96G04;K7ES84;E9PQV7;E9PN63;Q8N7N1;P0C5J1	Protein-lysine N-methyltransferase EEF2KMT;Putative protein N-methyltransferase FAM86B1;Putative protein N-methyltransferase FAM86B2	EEF2KMT;FAM86B2;FAM86B1	1.526404539	-0.097709338	0.200384624	0.030598005
P57772;C9J8T0	Selenocysteine-specific elongation factor	EEFSEC	1.015391977	-0.110822996	1.438786511	-0.132151604
Q96C19	EF-hand domain-containing protein D2	EFHD2	1.468087877	-0.169571241	0.234639297	-0.037508011
Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1	EFTUD1	0.253177162	0.092471822	0.174073898	-0.058323797
Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2	2.172190794	0.065066655	0.250293113	0.015274048
Q9UHF1	Epidermal growth factor-like protein 7	EGFL7	0	0.315979004	0	0.302454758
Q8N3D4	EH domain-binding protein 1-like protein 1	EHBP1L1	0.660503957	-0.215741475	0.799952964	-0.247345924
A0A024R571;Q9H4M9;C9JC03;C9J2Z4	EH domain-containing protein 1	EHD1	1.160415225	-0.054283778	1.762281695	-0.08238856
Q9H223	EH domain-containing protein 4	EHD4	0.06663748	0.012891452	0.465463373	0.075307528
K7EM18;P41567	Eukaryotic translation initiation factor 1	EIF1	1.749292332	-0.159981092	0.094765752	0.015057246
E9PLI6;E9PS76;Q8N9N8;E9PS30;E9PNH5	Probable RNA-binding protein EIF1AD	EIF1AD	0.321626506	-0.040947596	0.282973071	0.048641841
P47813;X6GRAC9	Eukaryotic translation initiation factor 1A, X-chromosomal	EIF1AX	0.170704999	0.016768456	0.493378648	0.041996638
O14602;A6NJH9	Eukaryotic translation initiation factor 1A, Y-chromosomal	EIF1AY	0.630527017	0.14868927	0.346498715	0.192052523
O60739	Eukaryotic translation initiation factor 1b	EIF1B	0.209895658	-0.203543027	0.022758602	0.014936606
Q9BY44;F8WAE5;H7C5R5	Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A, N-terminally processed	EIF2A	0.138605004	0.017839114	0.25167857	0.027543386
P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	2.424047531	-0.129528999	3.10936533	-0.145928383
Q14232;F5H0D0	Translation initiation factor eIF-2B subunit alpha	EIF2B1	1.183161934	-0.093519211	0.362586293	0.029269218
P49770;H0YJH8;G3V5E5	Translation initiation factor eIF-2B subunit beta	EIF2B2	0.108087105	-0.021244367	0.058069004	-0.013284365
Q9NR50;H0Y580	Translation initiation factor eIF-2B subunit gamma	EIF2B3	0.897001855	-0.094113032	0.010123948	0.001516978
A0A087WTA5;E7ERK9;Q9UI10	Translation initiation factor eIF-2B subunit delta	EIF2B4	0.135517098	-0.029622714	0.036220305	-0.009240468
Q13144	Translation initiation factor eIF-2B subunit epsilon	EIF2B5	0.460947664	-0.056680997	0.503160043	-0.064282099
P41214;Q5SY38	Eukaryotic translation initiation factor 2D	EIF2D	0.98325934	-0.114716848	0.380109269	-0.058308601
P05198;G3V4T5;H0YJ54	Eukaryotic translation initiation factor 2 subunit 1	EIF2S1	0.074186114	0.005358378	0.399711226	0.038901965
P20042	Eukaryotic translation initiation factor 2 subunit 2	EIF2S2	0.426975415	0.038883845	1.528029387	0.091498693
P41091;Q2VIR3;F8W810	Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation initiation factor 2 subunit 3-like protein	EIF2S3;EIF2S3L	0.153370585	0.013816833	1.714312155	0.104654948
Q14152	Eukaryotic translation initiation factor 3 subunit A	EIF3A	0.30211421	0.017960231	0.475926728	0.029218674
P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B	0.251870014	-0.029788653	0.16725119	-0.019980748
Q99613;B5ME19	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation factor 3 subunit C-like protein	EIF3C;EIF3CL	4.113231448	0.269690196	2.266162104	0.172805786
O15371	Eukaryotic translation initiation factor 3 subunit D	EIF3D	0.084630085	0.013576508	0.453938607	0.06303978
P60228;E5RGA2	Eukaryotic translation initiation factor 3 subunit E	EIF3E	0.321643376	0.040575345	0.611722219	0.067454338

O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F	1.030149654	-0.108824094	0.22622033	-0.033065478
O75821;K7EL20;K7ENA8;K7ER90	Eukaryotic translation initiation factor 3 subunit G	EIF3G	5.275845059	-0.199462891	0.340550484	-0.021127065
A0A087WZK9;B3KS98;O15372;E5RJT0	Eukaryotic translation initiation factor 3 subunit H	EIF3H	2.479476985	-0.109274864	0.273340478	-0.016279221
Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I	0.141665253	0.015311241	0.375301646	0.038522272
O75822	Eukaryotic translation initiation factor 3 subunit J	EIF3J	2.569678148	-0.18846639	0.45189956	-0.022225062
Q9UBQ5;A0A087WVB9;K7ERF1;K7EQM4;K7EK53;K7ES31	Eukaryotic translation initiation factor 3 subunit K	EIF3K	2.561947719	-0.140105247	0.11574787	-0.014971097
B0QY89;Q9Y262;B0QY90	Eukaryotic translation initiation factor 3 subunit L	EIF3L	2.44086828	-0.102173805	0.21018016	-0.017279625
Q7L2H7;J3KNJ2;H0YQC8	Eukaryotic translation initiation factor 3 subunit M	EIF3M	3.231525783	-0.200592041	3.236260579	-0.146728516
P60842;J3KT12;J3QS69;J3KTB5;J3QL43;J3KKSZ0	Eukaryotic initiation factor 4A-I	EIF4A1	0.747270017	0.051855087	0.696550325	0.047061284
Q14240;E7EQG2	Eukaryotic initiation factor 4A-II; Eukaryotic initiation factor 4A-II, N-terminally processed	EIF4A2	0.126372552	-0.026067416	0.429299139	-0.354751905
P38919	Eukaryotic initiation factor 4A-III; Eukaryotic initiation factor 4A-III, N-terminally processed	EIF4A3	1.631155038	0.09014829	0.048118902	0.003642082
E7EX17;P23588	Eukaryotic translation initiation factor 4B	EIF4B	5.221455893	-0.270088514	1.679465902	-0.071309408
D6RBW1;P06730;H0Y8J7	Eukaryotic translation initiation factor 4E	EIF4E	0.434613049	0.090242068	0.586709199	0.127785047
E7EX73;E9PGM1;E7EUU4;Q04637	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	0.225871155	0.015373866	1.951599968	0.078542074
D3DQV9;P78344;H0Y3P2	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2	0.013914524	-0.00184377	1.53602004	-0.116883596
Q15056	Eukaryotic translation initiation factor 4H	EIF4H	6.109769772	-0.444331805	0.358126445	-0.028409004
P55010;H0YLZ1;H0YN40	Eukaryotic translation initiation factor 5	EIF5	1.159237214	0.095662753	3.57740992	0.18304189
I3L397;I3L504;P63241;Q6IS14;F8WCJ1;C9J7B5;C9J4W5;Q9GZV4	Eukaryotic translation initiation factor 5A; Eukaryotic translation initiation factor 5A-1; Eukaryotic translation initiation factor 5A-1-like; Eukaryotic translation initiation factor 5A-2	EIF5A;EIF5AL1;EIF5A2	0.45509731	0.033497492	0.145411464	0.010526021
A0A087WUT6;O60841	Eukaryotic translation initiation factor 5B	EIF5B	2.796787171	-0.072244008	1.837454228	-0.045415878
P56537	Eukaryotic translation initiation factor 6	EIF6	1.790803194	-0.111585617	0.304064571	0.030888557
Q9BQ52;G5E9D5;E7ES68	Zinc phosphodiesterase ELAC protein 2	ELAC2	0.673566759	-0.088908513	0.504260796	-0.066179593
Q15717;M0QZR9	ELAV-like protein 1	ELAVL1	0.95275396	-0.067855517	0.887133668	-0.065374692
A0A0U1RRL5;P32519	ETS-related transcription factor Elf-1	ELF1	0.723824776	0.146419207	0.326257093	-0.055195808
Q92556	Engulfment and cell motility protein 1	ELMO1	0.432895244	0.041227341	1.753629072	0.139908155
Q6IA86	Elongator complex protein 2	ELP2	0.291313305	-0.097770214	0.269079784	-0.058291594
Q9H9T3;B4DKA4	Elongator complex protein 3	ELP3	0.44354991	0.049338023	1.898632856	-0.137631734
A0A1W2PNY5;A0A1W2PQZ6;A0A1W2PRF0;A0A1W2PRJ0;A0A1W2PPP6;A0A1X7SBS0;A0A1W2PS93;A0A1W2PR08;A0A1W2PRF5;G5E9D4;Q96EB1;A0A1W2PNW2;A0A1W2PP47	Elongator complex protein 4	ELP4	1.135525453	-0.198854446	0.374690937	-0.072137833
Q8N766	ER membrane protein complex subunit 1	EMC1	1.455980643	0.109493574	0.069182355	-0.009574254
M0R2A0;Q5UCC4	ER membrane protein complex subunit 10	EMC10	1.021546328	0.171021843	0.554783194	-0.543956375
Q15006	ER membrane protein complex subunit 2	EMC2	0.192861361	0.033342997	0.122918782	-0.017172813
Q9P0I2;S4R3U9	ER membrane protein complex subunit 3	EMC3	0.747009629	0.204601288	0.868225284	0.209798336
Q9NPA0;H0YDT8;H0YDX2	ER membrane protein complex subunit 7	EMC7	0.169573207	-0.065682093	0.669878867	-0.147982279
P50402;Q5HY57	Emerin	EMD	1.315853227	-0.156933467	0.709236796	0.087650299
Q92979;V9GYP5;A0A087WWQ2;A0A087WVM7	Ribosomal RNA small subunit methyltransferase NEP1	EMG1	0.285998923	0.026116053	0.422422012	0.040493965
B7WPE2;Q32P44;H0Y3M3;G3V195;G3V1D0	Echinoderm microtubule-associated protein-like 3	EML3	0.066540789	-0.012886047	0.360168437	0.050225258
B5MBZ0;Q9HC35	Echinoderm microtubule-associated protein-like 4	EML4	2.40732187	-0.243048986	1.714842855	-0.174204191
Q14249	Endonuclease G, mitochondrial	ENDOG	0.923068328	-0.16618379	0.026506835	0.008008639
P06733	Alpha-enolase	ENO1	7.182021768	-0.137606303	0.641185452	0.009817123
P09104;F5H0C8	Gamma-enolase; Enolase	ENO2	0.569755219	-0.087121646	1.625321218	0.179434458
P13929;E5RGGZ4;K7EPM1;K7EKN2	Beta-enolase; Enolase	ENO3	0.895634997	-0.16504701	0.000160915	4.61E-05
Q9UHY7;A0A0C4DGY8;D6RA00	Enolase-phosphatase E1	ENOPH1	3.108951922	-0.317336718	1.482880941	-0.171748797

Q7L5Y1;J3QL81	Mitochondrial enolase superfamily member 1	ENOSF1	0.703494238	-0.195972125	0.565543943	-0.076096853
Q9NPA8;E5RHX8	Transcription and mRNA export factor ENY2	ENY2	0.019821992	0.012326241	0.223623	0.170594215
P11171;Q4VVB86	Protein 4.1	EPB41	0.066262166	-0.006772677	0.375277489	0.044131597
A0A0C4DH22;Q9H4G0;Q4VXN1;Q4VXN0	Band 4.1-like protein 1	EPB41L1	0.812658907	-0.124913534	1.18162667	-0.149114927
B5MCA4;P16422	Epithelial cell adhesion molecule	EPCAM	1.742948332	-0.54532369	0.692196256	-0.25281779
P07099	Epoxide hydrolase 1	EPHX1	1.582220204	0.076449076	0.610535201	-0.045391719
Q7L775	EPM2A-interacting protein 1	EPM2AIP1	0.208735876	-0.055472851	0.160340141	0.090058327
Q9Y6I3	Epsin-1	EPN1	2.234844662	-0.362328529	0.079271836	-0.029268583
P07814;V9GYZ6	Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase	EPRS	0.555033317	0.046518326	0.891681233	0.067651749
M0R165;Q9UBC2;M0R2S2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1	1.190636168	-0.197856585	0.408373857	-0.076132139
O75616	GTPase Era, mitochondrial	ERAL1	1.835805487	-0.216944695	1.474552826	-0.140348434
Q9NZ08	Endoplasmic reticulum aminopeptidase 1	ERAP1	1.383163173	0.053793271	1.241019923	-0.059383074
Q6P179;D6RGW0	Endoplasmic reticulum aminopeptidase 2	ERAP2	0.170975199	0.029356639	0.791517572	-0.079761187
B4DIP2;Q96RT1	Protein LAP2	ERBB2IP	1.604249369	-0.147918383	0.604719763	-0.101096153
Q2NKX8;B5MDQ0	DNA excision repair protein ERCC-6-like	ERCC6L	0.411466594	0.161385536	0.086357925	-0.031994502
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	ERGIC1	0.310831113	0.027847608	0.671824364	-0.051144918
A0A087WU02;Q96RQ1;HOYI58;HOYI50	Endoplasmic reticulum-Golgi intermediate compartment protein 2	ERGIC2	0.0963678	-0.028976758	0.512615468	-0.100964864
A0A1W2PPS8;H0Y621;H0Y5K5;Q9Y282;H0Y802;H0Y6Z0	Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3	0	NaN	0	NaN
P84090;G3V279	Enhancer of rudimentary homolog	ERH	1.344410893	0.177619298	0.994618407	0.184950829
H0Y4B0;O43414;F6QUN3;F6UGJ8	ERI1 exoribonuclease 3	ERI3	0.108840535	0.039562988	0.951313703	0.158827209
Q96DZ1	Endoplasmic reticulum lectin 1	ERLEC1	1.047934444	0.127898534	0.228573823	0.045969327
O75477;B0QZ43	Erlin-1	ERLIN1	0.487474869	0.182878494	0.251103818	0.118304825
E5RHW4;O94905;E5RJ09	Erlin-2	ERLIN2	0.933165686	0.102966309	0.29669228	0.039383888
Q7Z2K6;E7ER77;A0A0C4DGF0	Endoplasmic reticulum metalloproteinase 1	ERMP1	0.038409536	-0.015870094	0.103408136	0.039305687
Q96HE7	ERO1-like protein alpha	ERO1L	0.364907383	0.023530642	0.880153046	-0.061537425
P30040;F8VY02	Endoplasmic reticulum resident protein 29	ERP29	0.136594493	0.008092562	0.681755206	-0.02442042
Q9BS26	Endoplasmic reticulum resident protein 44	ERP44	0.229551472	0.037009875	0.209573477	0.026381811
P10768;X6RA14;H7BZT7;U3KQT1	S-formylglutathione hydrolase	ESD	1.175535252	-0.134966532	0.442784247	-0.041261037
Q9H501;A0A087WX71	ESF1 homolog	ESF1	0.565346845	-0.04460303	0.036153528	-0.003970464
Q14674;H3BRX7	Separin	ESPL1	0	-0.081142426	0	NaN
Q6NXG1;H0YBR2;H0YBB3	Epithelial splicing regulatory protein 1	ESRP1	0.830901192	0.112013181	0.080489207	-0.012949308
H0YGT3;P11474	Steroid hormone receptor ERR1	ESRRA	2.372129385	-0.185700099	1.082356795	-0.167672157
Q9BSJ8	Extended synaptotagmin-1	ESYT1	0.567850735	0.033013662	0.439638419	-0.023592313
H7BX11;A0A087WXU3;A0FGR8	Extended synaptotagmin-2	ESYT2	0.597730425	-0.092131297	0.776026527	-0.131929715
B7Z7P8;P62495	Eukaryotic peptide chain release factor subunit 1	ETF1	3.731990301	-0.195091248	0.975164567	-0.06387043
P13804;H0YLU7;H0YK49;H0YNX6;H0YL12;H0YKF0	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	4.09699333	0.201607704	1.181711403	0.055169423
P38117;M0QY67	Electron transfer flavoprotein subunit beta	ETFB	2.378751058	0.130922	0.415977172	-0.037342389
H0YH69;Q9HBU6	Ethanolamine kinase 1	ETNK1	0.45188268	-0.119338036	0.334787233	-0.091229439
P41212	Transcription factor ETV6	ETV6	0.328473568	0.112096786	0.346199601	-0.126012802
A0A0D9SFL3;B0QYK0;C9JGE3;Q01844;H7BY36	RNA-binding protein EWS	EWSR1	0.980627667	0.158199628	0.369696182	0.078822772
Q9NVH0;C9JLF4	Exonuclease 3-5 domain-containing protein 2	EXD2	0.06681593	-0.027096748	0.847190948	-0.133428955
Q9NV70	Exocyst complex component 1	EXOC1	0.011504495	0.003610293	0.039870936	-0.013654073
Q96KP1	Exocyst complex component 2	EXOC2	0.096329105	-0.025111198	0.495615741	-0.115518888
O60645;D6RB59	Exocyst complex component 3	EXOC3	0.208556771	0.048960368	0.583905776	-0.100851695

Q96A65	Exocyst complex component 4	EXOC4	2.312162937	0.283180873	0.94135915	0.156528473
Q8IY16	Exocyst complex component 8	EXOC8	0.281237141	0.08293438	0.030028941	-0.00838693
B1AMU7;Q9Y3B2;R4GNH9;B1AMU4;R4GMQ7;B1AMU3	Exosome complex component CSL4	EXOSC1	0.575002059	0.061446508	0.089030954	0.01129818
Q01780	Exosome component 10	EXOSC10	0.555714532	-0.031996409	0.898764929	-0.058500608
Q13868;A3KFL2;A3KFL1;A3KFL5	Exosome complex component RRP4	EXOSC2	0.345659836	0.027123769	0.850708029	0.057987531
Q9NQT5	Exosome complex component RRP40	EXOSC3	0.250329812	-0.079111417	0.250901417	0.078087489
Q9NPD3;E9PI41	Exosome complex component RRP41	EXOSC4	1.56152445	0.153534571	0.898203809	0.110008876
Q9NQT4;M0R050	Exosome complex component RRP46	EXOSC5	0.344405673	-0.068973541	0.76426254	-0.116722107
Q5RKV6	Exosome complex component MTR3	EXOSC6	0.419097202	0.032254537	0.169517893	-0.015482903
Q15024	Exosome complex component RRP42	EXOSC7	0.12070602	0.020081838	0.523801987	0.062242826
Q96B26	Exosome complex component RRP43	EXOSC8	0.818360919	-0.063357035	0.046880154	-0.007995923
D6RIY6;Q06265;D6RA17;D6RAP4;D6R905	Exosome complex component RRP45	EXOSC9	0.971092831	-0.214351336	0.259104669	-0.082943916
B1APR7;Q99504	Eyes absent homolog;Eyes absent homolog 3	EYA3	0.081923195	0.026175817	0.20414558	-0.068320592
Q15910	Histone-lysine N-methyltransferase EZH2	EZH2	0.00286146	-0.00147028	0.861767896	-0.183864689
E7EQR4;P15311	Ezrin	EZR	1.116400605	-0.074229876	1.365696865	0.116891861
A0A087WY82;Q9Y624	Junctional adhesion molecule A	F11R	0.976837156	-0.119471232	0.348393669	-0.055340131
Q01469;I6L8B7	Fatty acid-binding protein, epidermal	FABP5	2.65844829	-0.21530501	0.199643443	-0.024445216
Q13158	FAS-associated death domain protein	FADD	3.756561171	0.237745921	2.067058783	0.183666229
O95864	Fatty acid desaturase 2	FADS2	0.055841518	0.008631388	2.180925104	-0.210291545
Q96CS3	FAS-associated factor 2	FAF2	2.289564032	0.208335559	0.200005	0.029707591
P16930	Fumarylacetoacetase	FAH	0.223784657	-0.02682209	0.366907497	0.042681058
Q6P587	Acylpyruvase FAHD1, mitochondrial	FAHD1	0.006172547	0.001455625	0.729147962	-0.105157216
Q96GK7;Q6P2I3;C9JGM0	Fumarylacetoacetate hydrolase domain-containing protein 2A;Fumarylacetoacetate hydrolase domain-containing protein 2B	FAHD2A;FAHD2B	0.060567312	-0.008620262	1.333729282	-0.110737801
C9J6N5;C9JQ40;C9JW51;A0A1C7CYX8;Q9H098;C9J3Q3;X6RET8;C9JP05	Protein FAM107B	FAM107B	1.613766782	0.229018847	1.957448946	0.255125999
Q6SJ93;E9PS27	Protein FAM111B	FAM111B	0.330798975	0.042117977	0.484871674	-0.123242474
Q9NRY5;E7ESJ7	Protein FAM114A2	FAM114A2	0.229559542	-0.045072079	0.83555481	-0.093291283
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	0.552622957	-0.055777868	0.513210085	-0.050974528
Q96TA1	Niban-like protein 1	FAM129B	2.48429612	-0.21927611	0.558728104	-0.048639615
Q5W0V3	Protein FAM160B1	FAM160B1	0.700098513	0.154881954	0.241233582	0.041426818
F8W7Q4;Q96A26;E9PH05	Protein FAM162A	FAM162A	0.593851789	0.106877645	0.037493733	-0.008815765
Q15018	BRISC complex subunit Abro1	FAM175B	0.406010405	-0.100428009	0.782518243	-0.141974258
Q9GZU8;H3BQQ6;H3BTI2;H3BTP8;H3BSY6;H3BP64;H3BUL4;H3BMX9;H3BN22;Q6P4H7;H3BSF0;H3BU93	Protein FAM192A	FAM192A;NIP30	0.698147059	-0.115736008	0.089938441	0.021242778
Q9BUT9	Protein FAM195A	FAM195A	0.043575906	-0.009790738	0.319147458	0.054364522
Q9NSI2;C9JU7	Protein FAM207A	FAM207A	0.062859621	0.02550443	0.144286867	0.054959933
Q9UK61;A0A087X0F1	Protein FAM208A	FAM208A	1.186761813	-0.19158872	0.012837001	0.00463295
A0A087WYF6;E7ESD2;A0A0A0MR88;A0A096LPC5;Q9Y4E1;Q641Q2;F8W7U3;J3KP36	WASH complex subunit FAM21C;WASH complex subunit FAM21A	FAM21A;FAM21C	0.483962127	-0.10939153	0.302140409	-0.117410024
K7E1Y1;Q9Y421;K7ELZ8;K7ENN5	Protein FAM32A	FAM32A	0.37338486	0.439251073	1.06824027	0.718795013
C9JP35;C9JMN4;Q92520	Protein FAM3C	FAM3C	0.751597107	0.311365032	0.570382332	0.313257376
Q9NUQ9	Protein FAM49B	FAM49B	2.056844197	-0.131309509	0.105564965	-0.008151054
Q14320;B0S8I6	Protein FAM50A	FAM50A	2.609423699	-0.175997098	0.095189203	-0.017877579
Q658Y4;E7ER68	Protein FAM91A1	FAM91A1	0.132267959	-0.032978694	0.056907744	-0.015334447
Q9HSX1;H0YKV4	MIP18 family protein FAM96A	FAM96A	0.277728933	-0.072726568	0.245205379	-0.053665161
Q9Y3D0;H3BNV7;J3KS95	Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B	0.391678544	-0.066714478	0.163840899	0.029466248

E9PH82;Q8NCA5	Protein FAM98A	FAM98A	0.462273198	-0.063123067	0.638835708	-0.105887731
Q52LJ0	Protein FAM98B	FAM98B	0.410634418	0.061366081	0.249887168	0.043887138
Q9BXW9	Fanconi anemia group D2 protein	FANCD2	0.003913562	0.00080204	0.302903685	-0.050448736
Q9NV11;F8W7R3;H3BP78	Fanconi anemia group I protein	FANCI	1.012919092	0.035113017	2.074827167	-0.069045703
Q8VWX9;E9PNW8	Fatty acyl-CoA reductase 1	FAR1	1.986572135	0.27029705	0.029206955	0.00861009
O95363	Phenylalanine--tRNA ligase, mitochondrial	FARS2	0.064332685	-0.016251882	0.662071814	-0.12815698
K7ER00;Q9Y285;K7EPH2	Phenylalanine--tRNA ligase alpha subunit	FARSA	1.01211194	-0.070285797	0.88318743	-0.062397957
Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB	4.293778379	-0.140962601	4.271618293	-0.136737823
P49327;A0A0UIRQF0	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-carrier-protein] hydrolase	FASN	5.799028469	-0.185522079	3.167002757	-0.097433726
Q9NYY8	FAST kinase domain-containing protein 2	FASTKD2	1.260542575	-0.187169075	1.779054054	-0.221301715
Q7L8L6	FAST kinase domain-containing protein 5	FASTKD5	0.000779491	0.000208537	0.133354398	-0.032639503
E9PR30;P62861	40S ribosomal protein S30	FAU	3.127440235	-0.411387126	2.780796719	-0.284740766
P22087;M0QXL5;M0R2Q4;M0R299;M0R0P1;M0R2U2;M0R1H0;M0R2B0	rRNA 2-O-methyltransferase fibrillar	FBL	0.934977605	0.066058795	0.329825275	-0.041627248
Q8N531	F-box/LRR-repeat protein 6	FBXL6	0.384450843	-0.08321476	0.524617752	-0.116928101
H3BTH6;Q8NEZ5	F-box only protein 22	FBXO22	0.541644075	-0.128238678	0.553822932	-0.152858098
Q9Y3I1	F-box only protein 7	FBXO7	1.323343643	0.11052901	1.055777366	0.104907735
G3V5S9;G3V1S4;Q9Y324;G3V2M5	rRNA-processing protein FCF1 homolog	FCF1	0	-0.266690254	0	-0.400463104
P37268;E9PNM1;A0A1W2PQ47	Squalene synthase	FDFT1	6.877538081	0.354556402	3.428627597	0.222110113
P14324;A0A087WVN4;A0A087X1D8	Farnesyl pyrophosphate synthase	FDPS	1.596304106	-0.186114629	3.449839592	-0.260172208
P22570;A0A0C4DFN8;A0A0A0MSZ4;J3QQX3;A0A0A0MTR6;A0A0A0MT64;A0A0A0MTN9	NADPH:adenodoxin oxidoreductase, mitochondrial	FDXR	0.118591964	-0.020249685	0.905652839	-0.111442566
P22830;K7ELX4	Ferrocyclase, mitochondrial	FECH	0.430440692	0.064021428	0.157874881	0.032868385
Q9UK73	Protein fem-1 homolog B	FEM1B	0.473991994	0.086518606	1.130915271	0.13215065
P39748	Flap endonuclease 1	FEN1	0.38452955	0.045741081	0.033416509	-0.005470912
Q9BQL6;G3V1L6	Fermitin family homolog 1	FERMT1	0.340036616	0.054221471	0.580828559	-0.126540502
Q5JSP0	FYVE, RhoGEF and PH domain-containing protein 3	FGD3	0.73001564	0.132154465	0.012189881	-0.004634221
A0A087WV25;O95684	FGFR1 oncogene partner	FGFR1OP	0.155772226	-0.049550056	0.052638354	-0.029051208
P07954	Fumarate hydratase, mitochondrial	FH	2.122799679	0.112272263	0.618370066	0.042362213
Q9Y613	FH1/FH2 domain-containing protein 1	FHOD1	0.352325018	0.101133347	1.11728683	0.231450717
O43427;E9PSD3;H0YCE7	Acidic fibroblast growth factor intracellular-binding protein	FIBP	0.287878562	0.051583608	0.060608097	-0.011646907
Q6UN15;A0A0B4J203	Pre-mRNA 3-end-processing factor FIP1	FIP1L1	0.246214225	-0.024202029	1.021976145	-0.083959897
Q9Y3D6	Mitochondrial fission 1 protein	FIS1	0.129204209	0.025959333	0.108833047	-0.019576708
F8VU90;Q9NYL4	Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase FKBP11	FKBP11	0.514992061	0.106009801	0.165647657	-0.045239449
P62942;Q5W0X3;A0A087WZM5	Peptidyl-prolyl cis-trans isomerase FKBP1A;Peptidyl-prolyl cis-trans isomerase	FKBP1A	0.652333199	-0.085596085	0.174158211	0.016592026
P26885;F5H0N4	Peptidyl-prolyl cis-trans isomerase FKBP2;Peptidyl-prolyl cis-trans isomerase	FKBP2	0.217669965	-0.025429726	0.139236628	-0.023074468
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3	0.380032392	0.039957682	0.583319862	0.081831614
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed	FKBP4	0.86406463	-0.066451391	0.393998488	-0.036107699
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5;Peptidyl-prolyl cis-trans isomerase FKBP5, N-terminally processed	FKBP5	2.359311649	-0.126912753	1.417691722	-0.113051097

Q14318;U3KQ64	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8	1.258881321	0.113468806	0.931603197	0.067507108
Q8NFF5;Q5T196	FAD synthase;Molybdenum cofactor biosynthesis protein-like region;FAD synthase region	FLAD1	0.052769913	0.005203883	0.258571667	0.02521801
Q13045	Protein flightless-1 homolog	FLII	1.314933358	-0.064695676	0.142650506	-0.011216482
Q8TEK8;A0A1B0GTG4;Q8WWW0;A0A075B763	Ras association domain-containing protein 5	FLJ00186;RASSF5	0.088435505	-0.034976006	0.162021942	-0.053104719
Q60FE5;P21333;A0A087WWY3	Filamin-A	FLNA	4.182617434	-0.094986598	1.381629672	0.0339667
O75369;E7EN95	Filamin-B	FLNB	3.546032441	-0.179676692	1.223247537	-0.064094861
O75955;A0A140T9R1;A2AB12;A2AB10;A0A140T9X0;A2AB09	Flotillin-1	FLOT1	1.228087302	0.112025261	1.30729157	0.10353152
J3QLD9;E7EMK3;Q14254	Flotillin-2	FLOT2	1.566913218	0.146450361	0.197905143	0.027574221
I3L1Y9;Q96CP2;I3L410	FLYWCH family member 2	FLYWCH2	0.180335433	-0.051463763	0.397684492	0.112119357
O95466;A0A0A0MR62	Formin-like protein 1	FMNL1	0.541566214	0.051717758	0.366485946	-0.042889595
G3V0J0;R9WNI0;A8MQB8;Q06787;A0A087WXI3;A0A087WR6;Q8IXW7	Fragile X mental retardation protein 1	FMR1	0.076341295	-0.030973879	0.734125136	-0.212038167
P02751;H0Y7Z1	Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3	FN1	7.764164085	-0.661310514	0.340574576	-0.026134173
Q9HA64;I3L2G3;I3L139	Ketosamine-3-kinase	FN3KRP	0.312305551	-0.066681862	0.11721874	-0.028930219
P49354;B3KVN2;E9PQP6;H0YCW1	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	FNTA	0.606569453	-0.106771151	0.488997381	-0.107821465
P85037	Forkhead box protein K1	FOXK1	0.927763192	-0.225401243	0.873288345	-0.208167394
Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1	0.318929508	-0.093820572	0.588066464	-0.150060654
Q05932;Q5JU21;Q5JU20;Q5JU23	Folylpolyglutamate synthase, mitochondrial	FPGS	0.075648555	0.025204341	0.384337948	0.091306051
Q9BZ67	FERM domain-containing protein 8	FRMD8	0.796276659	0.086571693	0.619098074	0.089590708
Q5CZC0	Fibrous sheath-interacting protein 2	FSIP2	0	0.283285141	0	NaN
P02792	Ferritin light chain	FTL	1.56271562	-0.296196302	0.10945296	-0.03757604
A0A1B0GUC3;A0A1B0GV98;A0A1B0GTC5;A0A1B0GU26;A0A1B0GTC3;A0A1B0GVH5;Q9C0B1;A0A1B0GTY1	Alpha-ketoglutarate-dependent dioxygenase FTO	FTO	0.536478278	-0.095861753	1.294254892	-0.141273499
Q9UET6;B7Z4K4	Putative tRNA (cytidine(32)/guanosine(34)-2-O)-methyltransferase	FTSJ1	0.272207666	0.040163994	0.143858663	-0.036556435
Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3	0.153841716	0.011727015	0.796782271	0.05408891
E9PEB5;Q96AE4	Far upstream element-binding protein 1	FUBP1	0.840917975	-0.086000443	0.073821611	-0.010697047
Q96I24	Far upstream element-binding protein 3	FUBP3	0.43727184	-0.04814593	0.340021355	0.03045845
Q9BWH2	FUN14 domain-containing protein 2	FUNDC2	0.901450833	0.06262207	0.822213776	0.074399312
P35637;H3BPE7	RNA-binding protein FUS	FUS	2.584486849	-0.150693893	1.1672576	0.101179123
C9JAX1;Q16595;H7C585	Frataxin, mitochondrial;Frataxin intermediate form;Frataxin(56-210);Frataxin(78-210);Frataxin mature form	FXN	0.029793851	0.012898445	0.076501914	-0.024207878
B4DXZ6;P51114;E9PFF5;E7EU85	Fragile X mental retardation syndrome-related protein 1	FXR1	5.071327083	0.131055196	2.821148618	0.107425054
P51116	Fragile X mental retardation syndrome-related protein 2	FXR2	0.277673255	0.057109642	0.190092906	-0.032007408
Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1	0.260569139	0.022738139	1.403237472	0.077956518
Q9UN86	Ras GTPase-activating protein-binding protein 2	G3BP2	0.024316512	-0.00530529	0.103061088	-0.02187411
P11413;E7EU18;E7EM57;E9PD92	Glucose-6-phosphate 1-dehydrogenase	G6PD	0.751686377	-0.039422989	0.238658646	0.015906016
H6UMI1;O95166;I3L3J4;F5GZY7;Q9H0R8	Gamma-aminobutyric acid receptor-associated protein;Gamma-aminobutyric acid receptor-associated protein-like 1	GABARAP;GABARAPL1	0.629901769	0.2242733	0.575126044	0.170030848
P60520;H3BSM5;H3BQ50	Gamma-aminobutyric acid receptor-associated protein-like 2	GABARAPL2	5.027880463	-0.687417666	2.957003152	-0.291799863
Q06546	GA-binding protein alpha chain	GABPA	0.287051039	-0.08053627	0.761330724	0.12738018
Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1	0.551551407	-0.07971859	0.813130197	-0.120044327
O14976	Cyclin-G-associated kinase	GAK	0	-0.172375679	0	0.05666256
Q14376;Q5QPP3;Q5QPP4	UDP-glucose 4-epimerase	GALE	0.084101159	0.046862221	0.543105266	-0.172270393

P51570	Galactokinase	GALK1	0.779411446	-0.070086161	1.205977336	-0.101867358
B7ZAX5;Q01415	N-acetylglucosamine kinase	GALK2	0.045741173	0.008002599	0.142462002	-0.032313665
Q96C23;B8ZZ75;H7C1B5	Aldose 1-epimerase	GALM	1.440497836	-0.144397863	0.795373918	-0.247159767
Q10471	Polypeptide N-acetylglucosaminyltransferase 2;Polypeptide N-acetylglucosaminyltransferase 2 soluble form	GALNT2	0.012916221	0.002064069	0.304220916	0.037721634
A0A1W2PR36;Q14353	Guanidinoacetate N-methyltransferase	GAMT	0.092233333	-0.024941444	0.227261163	0.060962359
Q14697;F5H6X6	Neutral alpha-glucosidase AB	GANAB	3.492310382	0.11793836	0.141079673	0.010742188
P04406;E7EUT5	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	0.938165978	-0.081244787	0.617518246	0.051083883
Q14C86;F8W9S7;C9IZ08;B0QZ65;B4DGD8	GTPase-activating protein and VPS9 domain-containing protein 1	GAPVD1	1.364075957	-0.10809199	0.453025238	-0.039697647
Q9NY12	H/ACA ribonucleoprotein complex subunit 1	GAR1	0.138106608	-0.021386782	1.349359945	-0.104752223
P41250	Glycine--tRNA ligase	GARS	3.10122074	0.097908974	2.402787124	0.075189273
P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine ligase;Phosphoribosylformylglycinamide cyclo-ligase;Phosphoribosylglycinamide formyltransferase	GART	1.271748283	-0.050472895	2.314002075	-0.058790525
E9PQ74;E9PRR5;O43903;E9PM28	Growth arrest-specific protein 2	GAS2	0.664315887	-0.1536026	0.27102052	0.075504303
Q86YP4	Transcriptional repressor p66-alpha	GATAD2A	1.080004938	-0.151129405	0.555582139	-0.102397919
A0A0U1RRM1;Q8WXI9	Transcriptional repressor p66-beta	GATAD2B	0.205816414	-0.031066895	0.217317107	0.035200755
P04062;A0A0G2JNZ5;A0A0G2JLB3;A0A0G2JNZ0	Glucosylceramidase	GBA	0.104440488	-0.048422178	0.145608831	0.07553196
O75323	Protein NipSnap homolog 2	GBAS	0.095073964	0.043759982	0.130846974	-0.072496096
Q04446;E9PGM4	1,4-alpha-glucan-branching enzyme	GBE1	0.83105199	-0.07576402	0.542163243	-0.04934756
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1	0.076995836	0.019886017	0.092335723	0.026935895
H7C2Z6;H7BXD5;P28676	Grancalcin	GCA	0.278787606	0.106656551	0.825009411	-0.162165324
O75600	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	GCAT	0.13519054	0.038331985	0.249907074	-0.094550451
Q92947	Glutaryl-CoA dehydrogenase, mitochondrial	GCDH	1.045674584	0.104950587	0.069827198	0.007003466
P48506;E1CEI4;A0A0C4DGB2	Glutamate--cysteine ligase catalytic subunit	GCLC	0.260110012	-0.026783307	0.378829658	0.035808563
P48507	Glutamate--cysteine ligase regulatory subunit	GCLM	0.506969748	0.273807621	0.829840791	0.466599941
Q92616	Translational activator GCN1	GCN1L1	0.229472612	0.011914889	1.33195422	-0.043965022
A0A1W2PQV2;P23434;H3BUH9	Glycine cleavage system H protein, mitochondrial	GCSH	0.891322052	0.230006854	0.261274371	0.086653392
P31150	Rab GDP dissociation inhibitor alpha	GDI1	1.653660866	-0.304806201	0.60875	-0.106766383
P50395	Rab GDP dissociation inhibitor beta	GDI2	5.738649977	-0.153347333	1.6472741	-0.040513039
O14893;S4R421;H0YDP6;H0YEL0	Gem-associated protein 2	GEMIN2	0.2424413	-0.191557503	0.356675927	-0.211166382
I3L2C7;P57678	Gem-associated protein 4	GEMIN4	2.368372143	-0.142590523	1.524434489	-0.125213941
Q8TEQ6	Gem-associated protein 5	GEMIN5	2.572422444	-0.114052773	4.951901376	-0.115506172
Q8WXD5	Gem-associated protein 6	GEMIN6	0.067278674	0.03872331	0.858934413	0.352044423
Q7L5D6;C9JPA8;C9JHN8	Golgi to ER traffic protein 4 homolog	GET4	0.636903169	0.277702204	0.022013059	-0.019939931
Q96RP9;C9IZ01;F8WAU4	Elongation factor G, mitochondrial	GFM1	0.334991295	-0.024863879	0.819470106	-0.04961141
Q969S9	Ribosome-releasing factor 2, mitochondrial	GFM2	0.314110229	0.036601384	1.016054121	-0.101075808
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1	1.117182945	-0.06603082	0.289939278	-0.02442646
O75223;B8ZZK2;M0QZK8;H7BZK5	Gamma-glutamylcyclotransferase	GGCT	3.082006575	-0.185415268	0.41450849	-0.037183762
Q92820	Gamma-glutamyl hydrolase	GGH	0.401596731	-0.081151009	1.035944749	-0.136015892

P19440;B5MCK8;A6NGU5;E7E776;P36268	Gamma-glutamyltranspeptidase 1;Gamma-glutamyltranspeptidase 1 heavy chain;Gamma-glutamyltranspeptidase 1 light chain;Putative gamma-glutamyltranspeptidase 3;Putative gamma-glutamyltranspeptidase 3 heavy chain;Putative gamma-glutamyltranspeptidase 3 light chain;Inactive gamma-glutamyltranspeptidase 2	GGT1;GGT2;GGT3 P	1.274236908	-0.12429746	0.027074542	-0.005531311
Q8N2G8;K7ESN3	GH3 domain-containing protein	GHDC	1.910756041	0.187768936	0.372142774	0.071053505
Q9NWU2	Glucose-induced degradation protein 8 homolog	GID8	0.206015196	0.054282188	0.196148848	-0.041682243
Q6Y7W6;11E4Y6;E7ESB6;C9JHW1	PERQ amino acid-rich with GYF domain-containing protein 2	GIGYF2	0.07236006	0.01315244	0.120460498	0.023502986
Q14691	DNA replication complex GINS protein PSF1	GINS1	1.058843794	0.142381032	0.544782482	0.08708477
Q9Y248	DNA replication complex GINS protein PSF2	GINS2	0.738312263	-0.117231051	0.504848274	-0.084929466
Q9BRX5	DNA replication complex GINS protein PSF3	GINS3	0.699047432	0.088168462	0.165229439	-0.032357216
Q9BRT9;E5RFF9	DNA replication complex GINS protein SLD5;DNA replication complex GINS protein SLD5, N-terminally processed;DNA replication complex GINS protein SLD5	GINS4	0.076014064	-0.019089699	0.130571542	0.030157725
A0A0C4DGN6;Q9Y2X7;J3QRU8	ARF GTPase-activating protein GIT1	GIT1	0.751547036	-0.087458611	0.106769514	0.014400482
P06280	Alpha-galactosidase A	GLA	0.415588941	-0.055445353	2.040328308	0.173826218
P16278;E7EQ29	Beta-galactosidase	GLB1	0.857066866	-0.063972473	1.101735715	-0.089108149
Q53GS7	Nucleoporin GLE1	GLE1	0.221856269	0.30828476	0.068170261	-0.078763962
Q92896;H3BM42	Golgi apparatus protein 1	GLG1	1.297432763	-0.107432683	1.057321099	-0.079467456
Q92990	Glomulin	GLMN	0	-0.044413567	0	0.145434062
Q04760	Lactoylglutathione lyase	GLO1	2.339763308	-0.120032628	0.327320551	-0.027207057
F6TLX2;Q9HC38;I3L3Q4	Glyoxalase domain-containing protein 4	GLOD4	0.453381763	-0.062243462	0.082442088	-0.016736031
P35754	Glutaredoxin-1	GLRX	0.625351605	-0.103652318	0.173460163	0.043701172
O76003	Glutaredoxin-3	GLRX3	3.061764231	-0.216307322	0.906476053	-0.082226753
Q86SX6	Glutaredoxin-related protein 5, mitochondrial	GLRX5	0.018544498	0.006601969	0.031223823	0.014724414
O94925	Glutaminase kidney isoform, mitochondrial	GLS	0.963422055	-0.065676053	0.639629636	-0.053138097
F5H0U5;Q9NZD2;H0YFS9	Glycolipid transfer protein	GLTP	0.072970701	-0.048983097	0.398104717	0.159851456
Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein	GLTSCR2	2.689835171	-0.448654493	0.061042437	-0.016302745
P00367;P49448	Glutamate dehydrogenase 1, mitochondrial;Glutamate dehydrogenase 2, mitochondrial	GLUD1;GLUD2	2.721294156	0.148548126	0.305928017	-0.025643667
Q49A26;K7EMM8	Putative oxidoreductase GLYR1	GLYR1	0.128086863	-0.015266101	0.159101925	-0.026168823
O60547	GDP-mannose 4,6 dehydratase	GMDS	1.176114382	-0.060264587	0.624076637	-0.043509801
G3V4P8;P60983;M0QYG8;M0R1D2;M0ROC1;M0QYJ8;O60234	Glia maturation factor beta;Glia maturation factor gamma	GMFB;GMFG	0.742061275	-0.133864085	0.709270921	-0.097296715
Q9P107;K7EJC2	GEM-interacting protein	GMIP	0.319252521	-0.147040558	0.641369692	0.183786392
Q96IJ6;A0A087WUI8	Mannose-1-phosphate guanyltransferase alpha	GMPPA	0.799594805	-0.095088005	0.181611703	-0.03214105
Q9Y5P6	Mannose-1-phosphate guanyltransferase beta	GMPPB	0.875116306	-0.071271896	0.557859215	-0.057409604
P49915	GMP synthase [glutamine-hydrolyzing]	GMPS	1.466292683	-0.072458267	0.690556333	-0.037549655
Q14344	Guanine nucleotide-binding protein subunit alpha-13	GNA13	0.09872371	0.029828072	0.130590338	0.032319705
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2	1.014277191	0.052107175	1.424498162	0.073413531
P08754	Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3	0.770088875	-0.160746574	0.058704875	-0.023216565
P63092;Q5JWF2;S4R3E3	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	GNAS	4.218887508	0.346367518	2.024159629	0.163773537
P62873;F6UT28;B3KVK2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1	2.063019914	0.108363469	2.746925607	0.194284439
P62879;E7EP32;C9JIS1;C9JXA5;C9JZN1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2	0.098154053	-0.017061551	0.919198533	0.09584713

P63244;J3KPE3;D6RAC2;H0YAF8;H0Y8W2;D6REE5;D6RHH4;H0YAM7;D6R9Z1;D6R9L0;D6RFX4	Guanine nucleotide-binding protein subunit beta-2-like 1;Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed	GNB2L1	0.274217519	0.054052671	0.48121474	0.099416097
P36915;A2AB27	Guanine nucleotide-binding protein-like 1	GNL1	0.253606275	0.03246371	0.768452215	0.085688909
Q13823;H0YG10	Nucleolar GTP-binding protein 2	GNL2	0.457466139	0.042494456	0.055781434	-0.007480303
Q9BVP2	Guanine nucleotide-binding protein-like 3	GNL3	3.827718669	0.149628957	0.42497764	-0.031119665
Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	GNL3L	0.202976122	0.034687996	0.134413889	-0.045103709
O15228;Q5TBH8	Dihydroxyacetone phosphate acyltransferase	GNPAT	0.164318674	-0.042643865	0.395861289	-0.077046712
P46926;D6R9P4;D6RAY7;D6RFF8;D6RBI3	Glucosamine-6-phosphate isomerase 1;Glucosamine-6-phosphate isomerase	GNPDA1	2.417963697	-0.141805013	0.045467432	0.005025546
Q96EK6;G3V4W4;G3V5E4	Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1	0.281588508	-0.047347069	0.258838425	0.053490639
P15586;H7C3P4;F6S8M0;F5H4C6;H0YFA9	N-acetylglucosamine-6-sulfatase	GNS	0.270116915	0.07750988	0.319679677	0.07790184
Q08379;A0A1W2PQY5	Golgin subfamily A member 2	GOLGA2	0.497564622	0.085084915	0.117036887	-0.025449435
Q0D2H9;A0A0G2JP71;H3BMP0;H3BV12;A0A0J9YX86;H3BMC3;A0A0G2JPF6;Q08AF8;H3BSY2;F8WBI6;A6NMD2;A6NCC3;A6NC78	Putative golgin subfamily A member 8D;Putative golgin subfamily A member 8F/8G;Golgin subfamily A member 8M;Golgin subfamily A member 8N;Golgin subfamily A member 8J;Golgin subfamily A member 8O;Putative golgin subfamily A member 8I	GOLGA8DP;GOLGA8N;GOLGA8Q;GOLGA8F;GOLGA8M;GOLGA8J;GOLGA8O;GOLGA8IP	0.415716006	-0.061317762	0.531875628	-0.064967791
Q14789	Golgin subfamily B member 1	GOLGB1	1.279524771	0.539203008	0.203212388	0.134126663
F8W785;O00461	Golgi integral membrane protein 4	GOLIM4	1.121892995	-0.209509087	0.686700302	-0.094868215
Q5T5I6;Q9H4A5	Golgi phosphoprotein 3-like	GOLPH3L	0.039529391	0.007967949	0.312550454	-0.047408104
G3V1U5;F5H6U7;Q9Y3E0	Vesicle transport protein GOT1B	GOLT1B	0.295160823	0.078388532	0.234247398	0.090658824
Q9HD26;F5H1Y4	Golgi-associated PDZ and coiled-coil motif-containing protein	GOPC	1.065714175	0.249905904	0.532542562	0.132921219
Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2	0.082149871	0.013087273	0.022427401	0.003927231
P17174	Aspartate aminotransferase, cytoplasmic	GOT1	1.262230121	-0.077035586	0.303598396	0.016431808
P00505	Aspartate aminotransferase, mitochondrial	GOT2	3.224627562	0.157672564	0.334517095	0.024652481
E9PPZ9;O43292;E9PLV6;E9PLG8	Glycosylphosphatidylinositol anchor attachment 1 protein	GPAA1	0.445104593	0.074183464	0.803398222	-0.10570399
A0A0A0MRK1;E9PAV9;Q5T3I0;F8W895	G patch domain-containing protein 4	GPATCH4	0.1662396	0.027609825	0.433006438	0.0486962
P35052;H7C024;H7C410	Glypican-1;Secreted glypican-1	GPC1	0	NaN	0	-0.673166275
P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	GPD1	1.17943939	-0.070901553	0.250416129	-0.020681381
Q8N335;C9JM46	Glycerol-3-phosphate dehydrogenase 1-like protein;Glycerol-3-phosphate dehydrogenase [NAD(+)]	GPD1L	0.210619278	0.030491193	0.391645503	-0.056771278
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2	1.682082182	0.189471881	0.45783904	0.081810633
G3V582;F5H039;Q9NQX3	Gephyrin;Molybdopterin adenylyltransferase;Molybdopterin molybdenumtransferase	GPHN	0.637695771	-0.169179598	0.138924127	-0.050430934
A0A0A0MTS2;P06744;K7EQ48;A0A0J9YXP8;A0A0J9YYH3;A0A0J9YX90	Glucose-6-phosphate isomerase	GPI	1.130260106	-0.085033099	0.290575993	0.02869161
Q92917	G patch domain and KOW motifs-containing protein	GPKOW	0.015266037	-0.003935496	0.877071658	-0.133002281
Q9HCN4	GPN-loop GTPase 1	GPN1	0.890246763	0.166095098	0.21862127	0.056424459
C9JFE4;Q13098;A0A096LP07;A0A096LPJ3;A8K070;J3KSA5	COP9 signalosome complex subunit 1	GPS1	0.683398457	-0.078137716	0.506459278	0.050859451
A0A087WUQ6;P07203	Glutathione peroxidase;Glutathione peroxidase 1	GPX1	0.574534072	0.10971419	0.325083712	-0.064108213
K7EKX7;R4GNE4;K7ENB4;A0A087X2I2;A0A087WT12;K7EJ20;P36969;A0A087X247;K7ERP4;A0A0A0MTT1	Glutathione peroxidase;Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	GPX4	0.875110118	-0.260855961	0.774490728	-0.198357391
Q96SL4	Glutathione peroxidase 7	GPX7	0.074802061	-0.017840068	0.910846565	-0.210878372
P62993	Growth factor receptor-bound protein 2	GRB2	1.385196403	0.119688034	2.358661198	0.204059919
Q9UBQ7;U3KQ56	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	0.765674881	0.122971217	0.027887354	0.005722682
A0A087WT45;Q4V328;A0A075B793;A0A087WXA6	GRIP1-associated protein 1	GRIPAP1	0.06353882	0.012639681	0.121973888	0.022142728
Q9HAV7	GrpE protein homolog 1, mitochondrial	GRPEL1	0.011929659	0.001455625	2.559758638	-0.162161827
H0Y8R1;F5H5I6;H0YAK1;Q12849	G-rich sequence factor 1	GRSF1	0.397119733	-0.072096189	0.311864512	-0.054842631

Q9BQ67	Glutamate-rich WD repeat-containing protein 1	GRWD1	0.356949912	0.037348111	0.379344362	-0.047363917
G3V1A6;P57764;E9PIB2	Gasdermin-D	GSDMD	0.488883531	-0.125771523	0.307713764	-0.07244428
A8MT37;P49840	Glycogen synthase kinase-3 alpha	GSK3A	0.020007796	0.003297551	0.493606722	0.076732
P49841	Glycogen synthase kinase-3 beta	GSK3B	0.405752197	-0.106361707	1.091764432	-0.212863604
P15170;H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1	0.3137975	0.014982224	0.047054575	-0.004180272
P00390	Glutathione reductase, mitochondrial	GSR	0.165681603	0.01526324	1.910818285	0.105738004
P48637	Glutathione synthetase	GSS	1.52288072	-0.108217875	0.208587841	-0.026309649
Q9Y2Q3;E9PFN5;C9JNT3	Glutathione S-transferase kappa 1	GSTK1	2.848509836	0.128275235	1.15923819	-0.084171931
P78417;Q5TA02;Q5TA01	Glutathione S-transferase omega-1	GSTO1	0.107468908	0.019224485	0.715434014	-0.103703181
A0A0C4DFM0;G3V4T6;A0A0A0MR33;G3V267;G3V5T0;O43708;G3V3B9	Maleylacetoacetate isomerase	GSTZ1	0.244009403	0.044845708	1.33473255	-0.372846603
Q00403	Transcription initiation factor IIB	GTF2B	0.690559931	0.08709685	0.02997336	-0.006314596
C9IYL4;P29083	General transcription factor IIE subunit 1	GTF2E1	0	-0.129163742	0	0.238361359
P29084;E5RH41	Transcription initiation factor IIE subunit beta	GTF2E2	2.316088641	-0.214735985	0.311518541	-0.099690437
P35269;M0QXD6	General transcription factor IIF subunit 1	GTF2F1	0.412578798	0.04613781	0.013496917	-0.002242088
P13984	General transcription factor IIF subunit 2	GTF2F2	0.405715162	0.099644979	0.186645753	0.062917391
P32780;E9PI26	General transcription factor IIH subunit 1	GTF2H1	0	0.015740077	0	-0.061620076
Q6P1K8;Q13888	General transcription factor IIH subunit 2-like protein;General transcription factor IIH subunit 2	GTF2H2C;GTF2H2	1.350497766	0.168048859	0.661079415	-0.093838215
P78347	General transcription factor II-I	GTF2I	0.075974774	-0.004346212	0.774000795	-0.028450012
Q12789	General transcription factor 3C polypeptide 1	GTF3C1	0.123292316	0.015277863	1.367119398	-0.110836347
Q8WUA4;H0Y4Q6;A0A087WZD8	General transcription factor 3C polypeptide 2	GTF3C2	0.759455495	0.078144073	0.175726754	-0.0485274
Q9Y5Q9	General transcription factor 3C polypeptide 3	GTF3C3	0.618048206	0.100857099	0.206089666	-0.039459229
Q9UKN8	General transcription factor 3C polypeptide 4	GTF3C4	1.341731979	-0.116379102	2.461201542	-0.170941035
Q9Y5Q8;Q5T7U0;Q5T7U1;Q5T7U4	General transcription factor 3C polypeptide 5	GTF3C5	0.644872762	0.063554128	2.557454817	-0.128311157
O00178	GTP-binding protein 1	GTPBP1	0.051362804	-0.006965955	0.705099596	-0.058198293
A4D1E9;C9J8R7;C9JN11	GTP-binding protein 10	GTPBP10	1.432319442	-0.189660072	1.496345401	-0.162056287
Q969Y2;M0R0S9	tRNA modification GTPase GTPBP3, mitochondrial	GTPBP3	0.513516353	0.119046211	0.176493696	0.055422465
Q9BZE4	Nucleolar GTP-binding protein 1	GTPBP4	0.506018744	0.037151972	0.011840861	-0.001188914
Q9NYZ3	G2 and S phase-expressed protein 1	GTSE1	0.318166018	0.063599269	0.361145017	0.06434377
G3V1V4;Q8WW33	Gametocyte-specific factor 1	GTSF1	0.199270474	0.046837489	2.286719944	0.310973485
B1ANH0;Q16774;B1ANG9;B1ANH2;B1ANH5;B1ANH6	Guanylate kinase	GUK1	0.30134347	-0.065635363	0.418389666	0.082746506
C9JQ42;P46976;G5E9W8	Glycogenin-1	GYG1	0.223582983	-0.053097407	0.175817319	0.04835542
P13807	Glycogen [starch] synthase, muscle	GYS1	2.326931785	-0.198636373	1.030499893	-0.130969683
P07305	Histone H1.0;Histone H1.0, N-terminally processed	H1F0	2.005152506	0.100789388	1.373201634	-0.061559995
Q92522	Histone H1x	H1FX	3.311485637	0.310342789	1.180215373	0.11335214
Q71U19;P0C0S5;C9J0D1;C9J386	Histone H2A.V;Histone H2A.Z;Histone H2A	H2AFV;H2AFZ	0.620136528	0.084573746	0.039787157	0.007188479
P16104	Histone H2AX	H2AFX	0.983612508	0.133190791	0.132503617	-0.025210063
O75367;B4DJC3	Core histone macro-H2A.1;Histone H2A	H2AFY	0.052577944	-0.006322225	0.075566417	-0.009988149
K7EK07;P84243;K7EMV3;B4DEB1;K7ES00	Histone H3;Histone H3.3	H3F3B;H3F3A	0.452238567	-0.103826205	0.277088073	-0.083899498
Q14520	Hyaluronan-binding protein 2;Hyaluronan-binding protein 2 50 kDa heavy chain;Hyaluronan-binding protein 2 50 kDa heavy chain alternate form;Hyaluronan-binding protein 2 27 kDa light chain;Hyaluronan-binding protein 2 27 kDa light chain alternate form	HABP2	1.027810241	0.14453373	0.319750552	0.037120819
Q9P035;H3BPZ1;H3BS72	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	HACD3	0.523654209	0.049613317	0.04881594	0.006857872
E9PF18;Q16836;A0A0A0MSE2;A0A0D9SFP2;A0A1W2PNM1;A0A1W2PQV5;A0A1W2PQ78	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH	2.58994669	0.132204374	0.009455024	0.00123469

P40939	Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase	HADHA	2.915611385	0.119487127	0.062237633	-0.005271594
P55084;F5GZQ3;B5MD38	Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase	HADHB	3.463211438	0.184384664	0.208645751	-0.020405134
H3BPK3;H3BPQ4;Q16775	Hydroxyacylglutathione hydrolase, mitochondrial	HAGH	0.379978707	-0.071479479	0.696905182	-0.097636541
P12081;B4DDD8;B3KWE1;B4E1C5;E7ETE2	Histidine--tRNA ligase, cytoplasmic	HARS	1.962823417	-0.1349322	0.109850451	0.012268702
P49590;B4DQ67	Probable histidine--tRNA ligase, mitochondrial	HARS2	0.4349316	-0.063341141	0.521889042	-0.099900881
O14929	Histone acetyltransferase type B catalytic subunit	HAT1	0.404635056	-0.02832222	0.381148647	-0.036379814
G3V1N2;P69905	Hemoglobin subunit alpha	HBA2;HBA1	2.068288369	0.325119019	0.042100905	0.008722623
Q9Y450;B7Z524;H0YDX7;J3Q T46;H0YESS	HBS1-like protein	HBS1L	2.288377927	-0.191832542	1.87206081	-0.169331551
P53701	Cytochrome c-type heme lyase	HCCS	1.809878765	0.19666481	1.91690767	0.208873113
A6NEM2		HCFC1	0.278296227	-0.032313347	0.150919082	-0.014965693
I3L0E3;Q9Y2R5;E9PE17	28S ribosomal protein S17, mitochondrial	hCG_1984214;MRP S17	0.4121645	-0.059571584	1.891404886	-0.156816165
P14317;E7EVW7	Hematopoietic lineage cell-specific protein	HCLS1	3.593136288	-0.310057958	1.005149674	0.099048932
Q13547;Q5TEE2	Histone deacetylase 1	HDAC1	0.801713373	-0.068566322	2.481090152	-0.093261719
Q92769	Histone deacetylase 2	HDAC2	1.223673107	-0.130537669	1.765749053	-0.147898992
O15379	Histone deacetylase 3	HDAC3	1.299725399	-0.184859753	0.507565766	-0.07556963
H0YNP9;Q8N4P3;H0YKT9	Guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase MESH1	HDDC3	0	0.290283203	0	0.291682053
P51858	Hepatoma-derived growth factor	HDGF	0.418134301	0.026467959	2.04071479	0.079624812
Q7Z4V5;M0R0J3	Hepatoma-derived growth factor-related protein 2	HDGFRP2	0.271648841	-0.041627884	0.154296972	0.021889051
Q08623;E7EVH9	Pseudouridine-5-phosphatase	HDHD1	1.037005647	-0.22795709	0.174201824	-0.050009727
K7ER15;Q9H0R4;K7EMY7	Haloacid dehalogenase-like hydrolase domain-containing protein 2	HDHD2	0.087528506	0.057788976	0.441019192	0.198304812
Q9BSH5	Haloacid dehalogenase-like hydrolase domain-containing protein 3	HDHD3	0	NaN	0	NaN
A0A024R4E5;Q00341;H0Y394	Vigilin	HDLBP	1.07207385	0.073747635	1.305649237	0.07475853
Q9H583;Q5T3Q7	HEAT repeat-containing protein 1;HEAT repeat-containing protein 1, N-terminally processed	HEATR1	0.576229723	0.030240377	0.675537878	-0.043023109
Q7Z4Q2	HEAT repeat-containing protein 3	HEATR3	0.618421913	-0.081597328	0.879229059	-0.081539154
Q9P2D3	HEAT repeat-containing protein 5B	HEATR5B	0.055087965	-0.032326889	0.018156952	-0.007966232
Q6A108;A0A087WXZ7;K7EIX2	HEAT repeat-containing protein 6	HEATR6	0.0376928	-0.012233353	0.129741467	0.036870448
Q9Y5Z4;Q5THN1	Heme-binding protein 2	HEBP2	0.927289176	-0.23406601	0.213372632	-0.060259628
A0A087X2H1;Q9ULT8;G3V4V5	E3 ubiquitin-protein ligase HECTD1	HECTD1	1.287729613	-0.174008687	0.404982621	-0.087950706
A0A087WSW7;F6XU50;A0A0B4J1V9;Q9NRZ9	Lymphoid-specific helicase	HELLS	1.93841675	0.289170265	0.293541865	0.061638196
H3BP08;Q15011;H3BTA8;H3BTT7	Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 1 protein	HERPUD1	6.516488981	2.091318766	4.732193765	1.310110728
H3BS10;H3BP20;P06865;H3BT D4	Beta-hexosaminidase;Beta-hexosaminidase subunit alpha	HEXA	3.363806255	0.138281504	0.010778894	0.001588186
P07686;Q5URX0	Beta-hexosaminidase subunit beta;Beta-hexosaminidase subunit beta chain B;Beta-hexosaminidase subunit beta chain A	HEXB	1.672233342	0.111795743	0.026989801	-0.003271739
O94992	Protein HEXIM1	HEXIM1	0.506963103	0.134436607	0.797450527	0.287563133
Q9BTY7	Protein HGH1 homolog	HGH1	0.465213404	-0.080283483	1.314678956	-0.169929504
O14964;I3L1P5	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS	0.037128489	0.006330808	0.47091484	0.060917219
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH	0.154169062	0.047902743	0.587579653	-0.16719532
Q6NVY1;B9A058	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH	2.49149808	0.137534777	0.31945228	0.023163795
Q9BW72	HIG1 domain family member 2A, mitochondrial	HIGD2A	0.053848039	0.023051548	0.063088559	0.020646381
P49773	Histidine triad nucleotide-binding protein 1	HINT1	0.250818606	-0.036971728	0.228248817	0.025518099
Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	0.903788272	0.072509766	0.861425682	-0.086789131

Q9BW71	HIRA-interacting protein 3	HIRIP3	0.38210621	0.076350784	0.849411608	0.212821515
P16403	Histone H1.2	HIST1H1C	2.958748397	0.218863805	0.140662906	0.01955986
P16402	Histone H1.3	HIST1H1D	0.225998017	-0.718836784	0	NaN
P10412	Histone H1.4	HIST1H1E	0.561410041	0.123327573	0.246618371	-0.053361893
U3KQK0;Q99880;Q99879;Q99877;Q93079;Q5QNW6;P62807;P58876;O60814;P57053	Histone H2B;Histone H2B type 1-L;Histone H2B type 1-M;Histone H2B type 1-N;Histone H2B type 1-H;Histone H2B type 2-F;Histone H2B type 1-C/E/F/G/I;Histone H2B type 1-D;Histone H2B type 1-K;Histone H2B type F-S	HIST1H2BN;HIST1H2BL;HIST1H2BM;HIST1H2BH;HIST2H2BF;HIST1H2BC;HIST1H2BD;HIST1H2BK;H2BFS	0.062895014	0.008203506	1.136227471	-0.089056651
P68431;Q16695;Q6NXT2	Histone H3.1;Histone H3.1t;Histone H3.3C	HIST1H3A;HIST3H3;H3F3C	0.049303272	-0.007359823	0.040297335	0.004103978
P62805	Histone H4	HIST1H4A	0.633172395	0.052693049	0.019014492	0.002086004
Q8IUE6	Histone H2A type 2-B	HIST2H2AB	0.668040234	-0.06244119	3.183572777	-0.233635267
Q71DI3	Histone H3.2	HIST2H3A	0.222389557	-0.115588188	0.264056083	-0.071975708
Q5TEC6	Histone H3	HIST2H3PS2	0.399152088	0.076801618	0.505793602	0.082499822
Q8N257	Histone H2B type 3-B	HIST3H2BB	1.671303493	0.111019135	0.125067252	0.012921333
P52789;E9PB90	Hexokinase-2;Hexokinase	HK2	0.387112259	-0.034312884	0.772413104	-0.055603027
P16188	HLA class I histocompatibility antigen, A-30 alpha chain	HLA-A	1.928105345	-0.08294932	1.625341602	0.105821292
P30490;P18464;P30498	HLA class I histocompatibility antigen, B-52 alpha chain;HLA class I histocompatibility antigen, B-51 alpha chain;HLA class I histocompatibility antigen, B-78 alpha chain	HLA-B	0.434219823	-0.07689031	0.875556396	0.134161313
O19617;A0A140T921;A0A140T9H5;A0A140T9U8;A2AEA2;P10321;A0A140TA05;A0A140T9L3;A0A1W2PRU9	HLA class I histocompatibility antigen, Cw-7 alpha chain	HLA-C	2.066084511	-0.276253064	0.34466428	-0.116230329
Q8TCT9;A0A075B6F6	Minor histocompatibility antigen H13	HM13	0.563683052	0.086647669	0.318200825	0.054619153
F5H345;P08397;F5GY90;A0A1W2PNU5;F5H226	Porphobilinogen deaminase	HMBS	0.692070902	-0.096004168	0.152065715	-0.041972478
Q9NP66;H0YKLO	High mobility group protein 20A	HMG20A	0.890461803	-0.122046789	0.482498038	-0.086688677
P17096	High mobility group protein HMG-I/HMG-Y	HMGA1	1.327724587	0.282278061	0.153491437	0.055660248
P09429;Q5T7C4	High mobility group protein B1	HMGB1	0.559706595	0.050904592	0.399428203	0.046168645
P26583;D6R9A6	High mobility group protein B2	HMGB2	0.905919072	0.101074537	0.182623448	0.027730942
E9PES6;E7ES08;E7EQU1;O15347	High mobility group protein B3	HMGB3	0.785254237	-0.096112887	1.083113667	-0.142589887
P04035	3-hydroxy-3-methylglutaryl-coenzyme A reductase	HMGCR	0	0.95022138	0	0.113431931
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	3.628391132	0.178225835	2.790874345	0.134805361
P05114;A6NEL0;F2Z2W6;F2Z2Y5;H7BXJ5;A6NL93	Non-histone chromosomal protein HMG-14	HMGN1	0.032639159	-0.006709735	0.223812704	0.049777985
P05204	Non-histone chromosomal protein HMG-17	HMGN2	0.586834842	-0.101670583	0.565583267	-0.076075554
Q5JSL0;Q5JSK6;P82970;Q5JSK9	High mobility group nucleosome-binding domain-containing protein 5	HMGN5	1.715059905	-0.123386065	0.10473943	-0.015339216
Q92619;K7ES98;K7EM85;F5H1R4;K7ES92	Minor histocompatibility protein HA-1;Minor histocompatibility antigen HA-1	HMHA1	1.134342564	-0.109146754	1.951077818	-0.171359062
O75330	Hyaluronan mediated motility receptor	HMMR	3.18589809	0.336802165	3.327220565	0.373571396
P09601;B1AHA8	Heme oxygenase 1	HMOX1	9.990766869	1.323902766	4.365049911	0.521772067
A0A087WT44;P30519;I3L159;I3L1F5	Heme oxygenase 2	HMOX2	2.576316093	-0.189781189	1.555449842	-0.203039487
Q9UK76;J3KT51	Hematological and neurological expressed 1 protein;Hematological and neurological expressed 1 protein, N-terminally processed	HN1	0.376911219	-0.073906898	1.360091735	0.268645287
H3BU16;A6NGP5;Q9H910;H3BMT0;H3BTV5;H3BMV3	Hematological and neurological expressed 1-like protein	HN1L	2.752993717	-0.106217702	1.98695298	0.084130287
Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	2.866497051	-0.175160726	0.730938279	-0.070242246
F8W617;P09651;F8VZ49;Q32P51;F8VQT5	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed;Heterogeneous nuclear ribonucleoprotein A1-like 2	HNRNPA1;HNRNPA1L2	4.058600028	-0.201426188	0.74148013	-0.04136912
P22626;A0A087WUI2	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1	0.595069741	-0.030753454	0.166108955	-0.010906219
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	4.540534454	-0.153222402	0.076911688	-0.005512238

D6R9P3;D6RD18;D6RBZ0;Q99729	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB	2.142351689	-0.118109703	0.592437098	-0.040807406
G3V4W0;B4DY08;B2R5W2;G3V4C1;G3V251;G3V5X6;G3V3K6;G3V2D6		HNRNPC	1.583454994	0.086978277	0.072848613	-0.006457011
Q14103;H0Y8G5;H0YA96;D6RAF8	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	0.032140845	0.00408872	0.41942232	0.043841998
A0A087WUK2;O14979	Heterogeneous nuclear ribonucleoprotein D-like	HNRNPD	2.38915869	-0.16068236	2.768817609	-0.127848625
P52597	Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed	HNRNPF	1.4173751	0.191035589	0.880797676	0.098009427
G8JLB6;P31943;E9PCY7;D6RBM0;H0YB39;E5RGV0;D6RIU0	Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed	HNRNPH1	0.630475504	-0.022975922	0.477670005	0.018026988
P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2	4.235982018	0.201306979	1.650116458	0.130874634
P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	1.03069864	0.140039444	1.396943223	0.178112984
P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	2.392611578	-0.124294917	0.657102773	0.043053945
P14866;M0QXS5	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	0.150236108	0.014377594	0.150765033	0.01224486
B7WPG3;C9IYN3;D6W592;Q8WV9	Heterogeneous nuclear ribonucleoprotein L-like	HNRNPLL;HNRPLL	0.253246291	-0.072695414	0.141533666	-0.040526708
P52272;A0A087X0X3;M0R019	Heterogeneous nuclear ribonucleoprotein M	HNRNPM	2.60305411	0.194625219	0.747315645	0.069618861
O43390;B4DT28	Heterogeneous nuclear ribonucleoprotein R	HNRNPR	0.483592977	0.032573064	0.834215983	-0.050778707
Q00839;A0A1W2PPS1;A0A1X7SBS1;Q5RI18;A0A1W2PP35;A0A1W2PPL4;A0A1W2PPH7;A0A1W2PQL0;A0A1W2PP34;A0A0A0MRA5;B7Z4B8;Q9BUJ2;M0R3F1;M0QYZ0	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	3.036929991	0.087433497	0.130919005	0.007616679
Q1KMD3;H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 1	HNRNPUL1	2.863110443	0.151887894	0.382056068	0.02819252
Q5SSJ5;X6RGJ2;B0QZK4;Q5WC8	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2;HNRNPUL2-BSCL2	2.876602012	0.099147479	0.944183702	0.049978574
P37235;E9PC71	Heterochromatin protein 1-binding protein 3	HP1BP3	1.423713436	0.070614179	0.00360598	-0.000379244
Q961R7	Hippocalcin-like protein 1	HPCAL1	1.046323049	0.178764343	0.833461138	0.146394412
P00492	4-hydroxyphenylpyruvate dioxygenase-like protein	HPDL	2.452559381	-0.317053477	1.053011263	-0.181694667
Q99714;Q5H928	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1	2.035859962	-0.100117683	0.063116183	-0.007388115
D6RC0D;Q8NBQ5	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10	3.255113376	0.132040977	0.054771873	0.003736178
Q53GQ0;A0A1B0GV93;A0A1B0GVY6	Estradiol 17-beta-dehydrogenase 11	HSD17B11	0.086879975	-0.008243561	1.350281134	-0.089271545
P51659;E7EWE5;E7ER27;G5E9S2;E7ET17	Very-long-chain 3-oxoacyl-CoA reductase	HSD17B12	0.840708826	0.065752665	0.260822198	0.026800791
P56937	Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2	HSD17B4	1.588132718	0.073683739	0.460829841	-0.024042765
Q92506	3-keto-steroid reductase	HSD17B7	0	NaN	0	-0.324014664
Q6YN16	Estradiol 17-beta-dehydrogenase 8	HSD17B8	0.035536769	-0.014686902	1.227764617	-0.228095373
E9PMQ6;Q00613	Hydroxysteroid dehydrogenase-like protein 2	HSDL2	0.328910596	-0.046210289	1.575095354	-0.146697362
P07900	Heat shock factor protein 1	HSF1	0.242795557	0.123584747	0.248554224	-0.109483719
Q58FG1	Heat shock protein HSP 90-alpha	HSP90AA1	5.944424832	0.187632879	2.827639914	0.07804807
P08238	Putative heat shock protein HSP 90-alpha A4	HSP90AA4P	0.089801863	-0.075788816	0.715813666	0.56000735
Q58FF8	Heat shock protein HSP 90-beta	HSP90AB1	0.466525786	0.029054642	0.842745823	0.043251673
Q58FF6	Putative heat shock protein HSP 90-beta 2	HSP90AB2P	0.027449193	0.003126144	0.314037134	-0.06015714
P14625	Putative heat shock protein HSP 90-beta 4	HSP90AB4P	0.282379349	-0.178497314	0.011966336	0.011648178
P48723	Endoplasmic reticulum chaperone protein	HSP90B1	3.582315163	0.130256653	1.041116696	0.04264005
Q0VDF9	Heat shock 70 kDa protein 13	HSPA13	0.72861631	-0.079245885	0.986694777	-0.101115545
A0A0G2JIW1;P0DMV9;P0DMV8;V9GZ37	Heat shock 70 kDa protein 14	HSPA14	0.418907447	-0.037803968	0.246292474	-0.029348056
P34931;Q53FA3	Heat shock 70 kDa protein 1B;Heat shock 70 kDa protein 1A	HSPA1B;HSPA1A	15.06964577	1.40752538	5.267172692	0.420836131
P34932;A0A087WYCI;A0A087WTS8	Heat shock 70 kDa protein 1-like	HSPA1L	0	0.580889066	0	-0.465677261
E9PDE8;O95757;D6RJ96	Heat shock 70 kDa protein 4	HSPA4	0.845495057	-0.038712184	0.088161606	0.005041758
P11021	Heat shock 70 kDa protein 4L	HSPA4L	0.126675891	0.03731823	0.166552167	0.042115529
P17066	78 kDa glucose-regulated protein	HSPA5	5.567966582	0.207344691	2.084992814	0.090136846
	Heat shock 70 kDa protein 6	HSPA6	3.057428694	0.581092834	0.54452119	0.156179047

E9PN89		HSPA8	0.599586681	0.071949005	1.268556881	0.125880559
A8K7Q2;E9PS65		HSPA8	0.00997852	0.000956217	1.49478399	0.087178548
P38646	Stress-70 protein, mitochondrial	HSPA9	6.531634522	0.149726868	1.529314276	0.045913696
P04792	Heat shock protein beta-1	HSPB1	3.769268885	0.286278725	1.967880777	0.136166573
Q9Y547;A6NIR2;X6R7Y7	Intraflagellar transport protein 25 homolog	HSPB11	1.574474863	-0.210495949	1.475104263	-0.163187663
Q9NZL4	Hsp70-binding protein 1	HSPBP1	1.329760366	-0.089514097	0.458392733	-0.040044785
P10809	60 kDa heat shock protein, mitochondrial	HSPD1	3.42743832	0.121998469	0.033847436	0.002286911
P61604;B8ZZL8	10 kDa heat shock protein, mitochondrial	HSPE1	1.647064571	0.129029592	0.164200281	-0.017915726
Q92598;A0A0A0MSM0	Heat shock protein 105 kDa	HSPH1	7.491684003	0.250242869	3.550057447	0.096390406
Q9BUP3;E9PI87	Oxidoreductase HTATIP2	HTATIP2	0.013728399	-0.005357901	0.182717561	0.058320204
O43719	HIV Tat-specific factor 1	HTATSF1	0.053206427	0.011886915	0.266361271	0.039126714
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1	0.546455498	-0.029844602	0.416141803	-0.018143972
Q9Y4L1;A0A087X054;E9PJ21;A0A087WW14;K7EQK2	Hypoxia up-regulated protein 1	HYOU1	3.723273927	0.130415281	0.952669801	0.041388512
Q9NX55	Huntingtin-interacting protein K	HYPK	0.007385402	0.001995087	0.255461431	0.052956899
P41252;A0A0A0MSX9;J3KR24	Isoleucine--tRNA ligase, cytoplasmic	IARS	0.071399004	-0.005895297	0.119799282	-0.009601275
Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2	2.58119236	0.102660815	1.40739835	-0.040525119
Q5T440	Putative transferase CAF17, mitochondrial	IBA57	1.266222332	0.238869349	0.024140359	0.011500041
P05362;K7EKL8	Intercellular adhesion molecule 1	ICAM1	2.699562125	-0.142697334	1.360875139	-0.087829272
P32942;K7ERN2	Intercellular adhesion molecule 3	ICAM3	2.503813581	-0.293078423	0.991074425	-0.127916336
P14735	Insulin-degrading enzyme	IDE	0.959546554	-0.083856265	0.116777393	0.016990662
O75874;C9J4N6	Isocitrate dehydrogenase [NADP] cytoplasmic	IDH1	1.332226718	-0.085643768	0.079889673	0.007425308
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	IDH2	2.670082642	0.148335775	0.327031188	-0.034729322
P50213;H0YMU3;H0YL72;H0YLI6;H0YKDO	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	1.087091596	0.061095556	1.155796218	-0.086804072
A0A087WZN1;O43837;A0A087X2E5	Isocitrate dehydrogenase [NAD] subunit, mitochondrial;Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B	1.171087569	0.100705783	0.249753402	0.03092289
E7EQB8;P51553;E9PF84;G5E9Q7;H7C1W2	Isocitrate dehydrogenase [NAD] subunit, mitochondrial;Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G	0.212130013	-0.026035945	0.882243184	-0.084345818
Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1	0.068722637	0.007569949	0.096288985	-0.009074529
Q16666	Gamma-interferon-inducible protein 16	IFI16	1.942324113	0.070355733	0.037022219	0.002906799
P13284	Gamma-interferon-inducible lysosomal thiol reductase	IFI30	0.219559066	0.084074656	0.317148037	0.100701014
P80217	Interferon-induced 35 kDa protein	IFI35	0.055020048	0.037957827	0.108988305	0.060751915
Q13325	Interferon-induced protein with tetratricopeptide repeats 5	IFIT5	0.697411169	-0.292174339	2.129243298	-0.287084103
O00458;C9JFH1;H0YEE3	Interferon-related developmental regulator 1	IFRD1	2.272974857	0.976401011	0.356068549	0.167055448
A0A0R4J2F6;Q12894	Interferon-related developmental regulator 2	IFRD2	0.005836407	-0.001264572	0.562570703	-0.081109365
F5GZ09;Q9BW83;B1AH58;H0Y6C7	Intraflagellar transport protein 27 homolog	IFT27	1.024594664	-0.165324211	0.130098551	0.031019211
P78318	Immunoglobulin-binding protein 1	IGBP1	0.117736508	-0.018315315	0.857321455	0.125291824
F8W930;Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	0.500413023	0.052594503	0.001641539	0.000234286
O00425	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	0.697862813	0.036272049	1.536842695	-0.067928632
P11717	Cation-independent mannose-6-phosphate receptor	IGF2R	0.408510856	0.053880692	0.205418436	-0.033156395
A6XND1;A6XND0;P17936;C9JMX4;H0Y485;H0Y5K2;B3KWK7	Insulin-like growth factor-binding protein 3	IGFBP3	0	NaN	3.101832878	-0.606869221
P01591;D6RD17;D6RHJ6	Immunoglobulin J chain	IGJ;JCHAIN	5.50308476	0.5372413	1.757439472	0.221923828
P0DOY3;P0DOY2;P0CF74	Ig lambda-6 chain C region	IGLC6	3.349943521	-0.424598694	0.024648419	0.006134669
A0A0B4J231;P0CG04;B9A064	Ig lambda-1 chain C regions;Immunoglobulin lambda-like polypeptide 5	IGLL5;IGLC1	2.671857163	-0.493950939	0.96766348	-0.236101627
Q13123;E7EQZ7	Protein Red	IK	2.205043755	0.179349581	0.397237059	0.050863266

Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP	0.983705929	-0.133083344	0.578537225	-0.096619765
O95163;F5H2T0	Elongator complex protein 1	IKBKAP	0.035396661	-0.005774498	0.238700247	-0.032566071
O14920;G3V105	Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB	0	NaN	0	1.229614258
A0A087X0G7;A0A087WUW6;A0A087X1B1;Q9Y6K9;A0A087WV30;C9J2V2;C9JN51	NF-kappa-B essential modulator	IKBKG	2.543163519	0.390688419	0.373606156	-0.190884113
Q13422;A0A0A0MRA0;R9R4D9;A0A0A0MST1;A0A087WU46	DNA-binding protein Ikaros	IKZF1	0.792957089	-0.131967862	0.884084195	-0.209047826
Q9UKT9	Zinc finger protein Aiolos	IKZF3	0.138528676	-0.139167658	0.014651417	-0.019486618
Q14005;H0YLH9	Pro-interleukin-16;Interleukin-16	IL16	0.362652445	-0.062044462	0.114816587	-0.019253413
Q12905;B4DY09	Interleukin enhancer-binding factor 2	ILF2	0.355062004	-0.029720942	2.270057012	-0.115189552
Q12906	Interleukin enhancer-binding factor 3	ILF3	0.527905993	-0.049879074	0.017153564	-0.002087593
A0A0A0MTH3;Q13418	Integrin-linked protein kinase	ILK	0.698410467	0.143294779	2.211823537	0.381802368
Q9H0C8;F8SNU7;H7C218	Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP;ILKAP3	0.872263369	-0.092437426	0.212066886	0.026715914
A1L0T0;M0R026	Acetolactate synthase-like protein	ILVBL	0.220200065	0.045758247	0.289761659	-0.069992383
Q16891;B9A067;C9J406;H7C463	MICOS complex subunit MIC60	IMMT	2.529555436	0.124765714	0.57660031	0.025618871
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	IMP3	0.166771726	-0.029629707	0.02894255	-0.004759153
E7ENR5;H0Y714;Q96G21;B9A008;B8ZZ47	U3 small nucleolar ribonucleoprotein protein IMP4	IMP4	0.031484489	0.009187063	0.088381621	-0.019943237
H0YBL1;P29218;E5RIP7;E5RG13	Inositol monophosphatase 1	IMPA1	0.131768172	-0.043501218	0.269339697	0.081819216
P20839;C9J381;C9K0R9	Inosine-5-monophosphate dehydrogenase 1;Inosine-5-monophosphate dehydrogenase	IMPDH1	0.905811817	-0.064149539	1.292693467	-0.089480082
P12268;H0Y4R1	Inosine-5-monophosphate dehydrogenase 2	IMPDH2	2.664024449	-0.083006859	2.591376465	-0.07321167
Q9NQS7	Inner centromere protein	INCENP	2.403447458	0.241388003	2.41888236	0.254445712
Q27J81	Inverted formin-2	INF2	1.039002408	-0.195913951	0.088807465	-0.030403455
Q96PE3	Type I inositol 3,4-bisphosphate 4-phosphatase	INPP4A	0.029810105	-0.006980896	0.039770785	-0.009969393
Q8N201	Integrator complex subunit 1	INTS1	0	0.186205864	0	0.286323547
J3KMZ7;Q9H0H0	Integrator complex subunit 2	INTS2	0.489348846	0.17297856	0.059646955	-0.020990849
Q68E01	Integrator complex subunit 3	INTS3	0.656835844	-0.107827187	0.640053881	-0.124163628
Q96HW7	Integrator complex subunit 4	INTS4	0.061851808	0.016768773	0.198664517	-0.04522226
Q9NVH2	Integrator complex subunit 7	INTS7	0.323629498	0.074491183	1.20718727	0.15240256
Q9UI26;F8WDV0	Importin-11	IPO11	1.391773012	-0.152568181	0.489599727	-0.078347524
Q8TEX9;H0YN14	Importin-4	IPO4	0.268987138	-0.038071632	1.420684598	-0.151599884
O00410;H0Y8C6	Importin-5	IPO5	4.929913623	-0.210055987	2.040583377	-0.088774363
O95373	Importin-7	IPO7	1.725616312	-0.095552762	0.920452126	-0.059575717
O15397	Importin-8	IPO8	0.410595437	0.068430265	0.702863271	-0.107096036
Q96P70	Importin-9	IPO9	0.520401127	-0.077231407	0.333958533	-0.04218324
P46940;A0A0J9YXZ5;H0YLE8	Ras GTPase-activating-like protein IQGAP1	IQGAP1	2.67061756	-0.106442769	0.358759797	-0.021633784
Q13576;F5H7S7;E7EWC2	Ras GTPase-activating-like protein IQGAP2	IQGAP2	1.827019301	0.054688772	0.207500305	-0.008911451
D3YTB5;P51617;H7C224	Interleukin-1 receptor-associated kinase 1	IRAK1	0.160832956	-0.043855349	0.336228156	-0.079156876
Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2	0.576285169	-0.040649732	0.11989886	-0.016145706
Q9H1B7	Interferon regulatory factor 2-binding protein-like	IRF2BPL	0.069598443	0.021251806	0.534413549	-0.134831492
Q15306;F2Z3D5	Interferon regulatory factor 4	IRF4	0.006359643	0.000890414	1.832181994	-0.142857869
C9JAU6;Q13568	Interferon regulatory factor 5	IRF5	0.321428797	0.133493423	0.11229354	0.061232122
Q9H1K1;F5H5N2;B4DNC9;B3KQ30	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	ISCU	0.056194379	-0.014419556	0.044313197	-0.011317253
A0A096LNZ9;A0A096LPJ4;P05161	Ubiquitin-like protein ISG15	ISG15	0	NaN	0	0.094510078
Q96AZ6;H0YMM4	Interferon-stimulated gene 20 kDa protein	ISG20	1.049565413	0.16607062	0.795459421	0.154594103
Q96CN7;D6RGE2	Isochorismatase domain-containing protein 1	ISOC1	0.79762598	-0.234680939	0.239400902	0.120678139
Q96AB3;K7ENV7;K7EKW4	Isochorismatase domain-containing protein 2, mitochondrial	ISOC2	0.811198226	0.078183492	0.042521509	-0.012152672

H3BMU1;H3BUI0;P53990;H3BQF7;J3KR23;F5GXM3	IST1 homolog	IST1	0.139147455	-0.029832204	0.567309514	0.096913338
D6RC18;A8MVI5;Q9ULR0;H0YA89	Pre-mRNA-splicing factor ISY1 homolog	ISY1	0.233064827	-0.135242144	0.635212095	-0.165663719
Q9NPH2	Inositol-3-phosphate synthase 1	ISYNA1	0.21677681	-0.073496977	0.307197536	-0.107490222
Q96J02	E3 ubiquitin-protein ligase Itchy homolog	ITCH	0.18756005	-0.051627159	0.190927867	-0.052922249
P18084;V9GYZ1;V9GZ57	Integrin beta-5;Integrin beta	ITGB5	0.548406696	0.107448578	0.201520673	-0.043798923
P26010;F5H6T4	Integrin beta-7;Integrin beta	ITGB7	7.777642494	0.386236827	2.283430233	0.083329837
Q9BY32	Inosine triphosphate pyrophosphatase	ITPA	1.583506641	-0.113916715	2.17394746	-0.114480337
Q13572;G3V588;G3V5A3;G3V4M9	Inositol-tetrakisphosphate 1-kinase	ITPK1	2.066434297	0.294346142	1.416280856	0.21818018
Q14571	Inositol 1,4,5-trisphosphate receptor type 2	ITPR2	0.213807351	0.078510602	0.201418832	0.078012784
Q14573	Inositol 1,4,5-trisphosphate receptor type 3	ITPR3	0.0553265	0.01008002	0.918632169	-0.127315839
A0A0A0MT83;P26440;H7C4G6;H0YLC3	Isovaleryl-CoA dehydrogenase, mitochondrial	IVD	0.143195087	0.024872144	0.328045318	-0.05312856
Q96ST2;A0A1B0GW95	Protein IWS1 homolog	IWS1	0.253934151	-0.046194077	0.033553528	-0.008136495
B2WTI3;B2WTI4;K7EJU9;Q6NYC1	Bifunctional arginine demethylase and lysyl-hydroxylase JMJD6	JMJD6	0.015846357	-0.003273646	1.491097111	-0.182329814
Q96MG2	Junctional sarcoplasmic reticulum protein 1	JSRP1	1.036672945	0.124253273	1.222075505	0.124123573
P14923	Junction plakoglobin	JUP	1.002517788	0.131453196	0.965268244	-0.116711299
Q15046	Lysine-tRNA ligase	KARS	1.19924819	-0.049549103	0.042363843	0.003046354
E7EUP3;O95251	Histone acetyltransferase;Histone acetyltransferase KAT7	KAT7	0.724594525	0.090219498	0.231671934	-0.042654673
Q9P0J7	E3 ubiquitin-protein ligase KCMF1	KCMF1	0.241364684	-0.054334958	0.111184024	-0.035062154
Q13303;Q5TG80;Q5TG81	Voltage-gated potassium channel subunit beta-2	KCNAB2	0.421155072	0.058595339	0.388576842	0.050333341
Q96CX2	BTB/POZ domain-containing protein KCTD12	KCTD12	2.050921544	-0.130026182	0.003206199	-0.000244459
Q9Y597	BTB/POZ domain-containing protein KCTD3	KCTD3	0.970168048	-0.265444756	0.108012857	0.050238609
Q9NXV2	BTB/POZ domain-containing protein KCTD5	KCTD5	1.189704962	0.232677778	1.229293324	0.337654114
O60341	Lysine-specific histone demethylase 1A	KDM1A	1.20699394	-0.161351522	1.387259029	-0.17453893
I3VM54;Q9Y2K7	Lysine-specific demethylase 2A	KDM2A	0.772463368	0.134474119	0.170697937	0.036584854
Q7LBC6;H0Y9V5	Lysine-specific demethylase 3B	KDM3B	0.221312467	0.07066679	0.053732339	-0.013599968
Q06136;K7ERC8	3-ketodihydrospingosine reductase	KDSR	0.072142688	-0.021796862	0.105551969	0.030292193
Q14145	Kelch-like ECH-associated protein 1	KEAP1	0.706458891	-0.068107923	0.78706307	-0.085373561
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	KHDRBS1	0.554234772	-0.039790471	0.402090354	-0.030053775
A0A087WTP3;Q92945;M0R0I5	Far upstream element-binding protein 2	KHSRP	3.229543115	-0.138740222	0.023325624	0.001962026
Q15397	Pumilio domain-containing protein KIAA0020	KIAA0020	0.011147773	-0.001547813	1.344856668	-0.092457136
Q15004;H0YKX3;H0YMA4;A0A0UIRQM0	PCNA-associated factor	KIAA0101	4.184018961	0.463492076	4.009771191	0.618885994
Q12768;E7EQI7	WASH complex subunit strumpellin	KIAA0196	0.12208357	-0.038525581	0.256809401	-0.063786825
J3KN16;Q5VYK3;R4GMY1	Proteasome-associated protein ECM29 homolog	KIAA0368;ECM29	2.376816325	-0.10351785	1.265894256	-0.063402812
O15091;A0A0A0MTQ0	Mitochondrial ribonuclease P protein 3	KIAA0391	0.410010652	-0.069872856	0.283127975	-0.064276377
A0A087X256;Q2M389;F8VYH7	WASH complex subunit 7	KIAA1033	0.982428809	-0.210993258	0.535788157	-0.135740089
Q69YN4	Protein virilizer homolog	KIAA1429	1.390454272	-0.248009682	0.443935229	-0.118256887
A0A087X211;Q8TCG1	Protein CIP2A	KIAA1524	0.754787392	0.159929975	0.737220334	0.132529004
A0MZ66	Shootin-1	KIAA1598	0.447116907	-0.064033826	0.137835776	0.023378054
Q8IYS2	Uncharacterized protein KIAA2013	KIAA2013	0.117691046	0.021513303	0.164246576	0.022994677
P52732	Kinesin-like protein KIF11	KIF11	0.41088377	0.043430964	0.906803851	0.082075755
Q15058	Kinesin-like protein KIF14	KIF14	0.662693989	0.15180397	0.573311301	0.113884608
Q9NS87;D6RCT7	Kinesin-like protein KIF15;Kinesin-like protein	KIF15	0.772372434	-0.2296381	1.411796518	-0.295031548
O95235	Kinesin-like protein KIF20A	KIF20A	0.604522338	0.117170048	0.981961452	0.186319733
A0A1B0GV47;Q7Z4S6	Kinesin-like protein KIF21A	KIF21A	0.195424384	-0.047490438	0.399373058	0.091738701
Q14807;H3BRB3	Kinesin-like protein KIF22;Kinesin-like protein	KIF22	3.954475592	0.286486626	1.166893767	0.077217738

H7BYN4;Q02241	Kinesin-like protein;Kinesin-like protein KIF23	KIF23	0.053695862	-0.005994479	0.222189805	-0.020190239
O00139	Kinesin-like protein KIF2A	KIF2A	0.915548292	0.127022107	0.04757171	0.010431925
Q99661;Q5JR91	Kinesin-like protein KIF2C;Kinesin-like protein	KIF2C	0.763366476	0.089964231	0.945277835	0.088878632
O95239	Chromosome-associated kinesin KIF4A	KIF4A	0.740099987	-0.050993284	1.994207425	-0.118312836
P33176	Kinesin-1 heavy chain	KIF5B	3.465790506	-0.124752363	2.430858883	-0.087821643
Q9BW19	Kinesin-like protein KIFC1	KIFC1	2.08354353	0.218353271	2.221627404	0.223248482
G3V2E7;F8W6L3;G3V3H3;G3V5R9;E7EVH7;Q07866;G5E9S8;A8MZ87;Q9H0B6Q03164	Kinesin light chain 1;Kinesin light chain 2	KLC1;KLC2	0.215355888	0.040184975	0.105483197	0.018157641
Q1ED39	Histone-lysine N-methyltransferase 2A;MLL cleavage product N320;MLL cleavage product C180	KMT2A	0.949839449	0.118366241	0.68355678	0.152889156
Q1ED39	Lysine-rich nucleolar protein 1	KNOP1	0.084858007	-0.02414163	0.107829425	-0.033860842
V9GY01;Q9Y448;H0YKF8;H0YLA7;H0YM11P50748;E7ES84	Small kinetochore-associated protein	KNSTRN	0.234965381	0.113538106	0.077184257	0.049290021
P52294;C9JY14	Kinetochore-associated protein 1	KNTC1	0.54607248	-0.076009432	0.601813059	-0.071997643
P52292	Importin subunit alpha-5;Importin subunit alpha-5, N-terminally processed	KPNA1	0.884147365	0.167484601	0.148929576	0.045959791
P52292	Importin subunit alpha-1	KPNA2	0.635938799	-0.035592397	1.483986495	0.072775523
O00505	Importin subunit alpha-4	KPNA3	0.764942886	-0.15439415	0.858393469	-0.117566744
O00629	Importin subunit alpha-3	KPNA4	2.06695434	-0.130553563	0.314318105	-0.035678228
O60684;Q5TFJ7;O15131	Importin subunit alpha-7;Importin subunit alpha-6	KPNA6;KPNA5	0.081011368	0.019429525	0.399557752	0.067064921
Q14974;J3KTM9	Importin subunit beta-1	KPNB1	0.899434071	-0.049330076	0.673236024	-0.038205465
P01116	GTPase KRas;GTPase KRas, N-terminally processed	KRAS	1.216315819	0.143948237	0.19496634	0.043014526
Q8N9T8	Protein KRI1 homolog	KRI1	0.548495184	-0.093503952	0.953913008	-0.149026871
Q13601	KRR1 small subunit processome component homolog	KRR1	0.081165527	0.010762533	0.645413784	-0.048879623
P04264;CON_P04264	Keratin, type II cytoskeletal 1	KRT1	0.305584623	-0.76429081	2.728525452	-1.808738073
CON_P13645;P13645	Keratin, type I cytoskeletal 10	KRT10	0.040697515	-0.080034574	2.649346476	-1.157201131
CON_P08779;P08779	Keratin, type I cytoskeletal 16	KRT16	4.708882973	0.889725367	3.203805028	0.3513333
F8VZY9;P05783	Keratin, type I cytoskeletal 18	KRT18	3.629693898	0.43096288	3.176955575	0.381465912
CON_P08727;P08727;C9JM50;CON_P19001	Keratin, type I cytoskeletal 19	KRT19	0	NaN	0	NaN
CON_P35908;P35908	Keratin, type II cytoskeletal 2 epidermal	KRT2	0.356924895	0.296765995	0	-1.072562027
CON_P19013;P19013	Keratin, type II cytoskeletal 4	KRT4	0	NaN	0	NaN
CON_P48668;P48668;CON_P04259;CON_P02538;P02538	Keratin, type II cytoskeletal 6C;Keratin, type II cytoskeletal 6A	KRT6C;KRT6A	0.193212062	-0.102630297	1.190368146	-0.397795677
CON_P35527;P35527	Keratin, type I cytoskeletal 9	KRT9	0.744847341	1.718850327	0.07870234	-0.085828781
Q96EK9	Protein KTI12 homolog	KTI12	1.274887531	-0.530941963	1.072793721	-0.16641744
Q86UP2	Kinectin	KTN1	0.354617364	-0.049434026	0.445167892	-0.057521502
Q9H9P8;C9JVN9;G3V5S1;G3V272	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH	0.137594666	-0.030897141	1.083106684	-0.153754552
Q53H82	Beta-lactamase-like protein 2	LACTB2	0.696183455	-0.100019455	0.728827121	-0.116914431
Q14657	EKC/KEOPS complex subunit LAGE3	LAGE3	0.193642155	-0.079777718	0.424334043	-0.11218586
P11279	Lysosome-associated membrane glycoprotein 1	LAMP1	1.00103859	0.411632538	0.145663646	0.075172424
Q6IAA8;F5GX19;F5H3Y3;H0YF11;F5H479Q9Y2Q5	Ragulator complex protein LAMTOR1	LAMTOR1	0.754528545	-0.124727249	1.119310958	-0.160746384
Q9UHA4	Ragulator complex protein LAMTOR2	LAMTOR2	0.782539996	0.104342461	1.881233055	0.205959956
Q9UHA4	Ragulator complex protein LAMTOR3	LAMTOR3	0.780819069	-0.155146662	0.535700985	-0.117839559
Q0VGL1;A0A087WVU0;A0A087WT92;A0A087WV46;C9JXA7	Ragulator complex protein LAMTOR4;Ragulator complex protein LAMTOR4, N-terminally processed	LAMTOR4	0	0.211874962	0	NaN
R4GMU8;E9PLX3;A0A0C4DG V4;O43504	Ragulator complex protein LAMTOR5	LAMTOR5	1.38278346	0.211941242	0.933753699	0.211603483
O43813;E9PHS0	LanC-like protein 1	LANCL1	0.178826024	-0.033363342	0.054742337	-0.01408577
Q9NS86	LanC-like protein 2	LANCL2	0.379102582	-0.078425725	0.285693272	0.048370361
P28838	Cytosol aminopeptidase	LAP3	1.32907438	-0.048417727	0.386119492	-0.02314345

Q6PKG0;A0A0B4J210;E5RH50	La-related protein 1	LARP1	0.697445207	-0.038923899	0.006264084	0.000567754
Q71RC2;X6RLN4;Q96J85	La-related protein 4	LARP4	1.024248965	0.122706095	4.128213614	0.236181259
Q92615	La-related protein 4B	LARP4B	0.998356431	-0.081738154	1.712450836	-0.127554576
Q4G0J3;H0YA82	La-related protein 7	LARP7	1.588833359	0.099472046	0.26586096	-0.022951444
Q9P2J5	Leucine--tRNA ligase, cytoplasmic	LARS	0.236839147	0.015643438	0.588056281	-0.040658315
E9PHM2;Q15031	Probable leucine--tRNA ligase, mitochondrial	LARS2	0.341196442	0.054515203	0.136351631	-0.028349559
Q9Y4W2	Ribosomal biogenesis protein LAS1L	LAS1L	2.391178514	0.230171204	0.741799765	0.06946373
Q14847;C9J9W2	LIM and SH3 domain protein 1	LASP1	2.963130477	-0.236593882	2.261292046	0.14944458
Q53QV2;B5MBX5;B5MCP4	Protein LBH	LBH	1.514729774	-0.569728661	0.839992694	-0.160158157
Q14739;C9JXK0	Lamin-B receptor	LBR	0.935082412	0.089809736	0.183812102	0.025321643
Q6UWP7;C9KOC3	Lysocardiolipin acyltransferase 1	LCLAT1	0.17084133	0.043339729	0.410407328	-0.070443471
I3L2Q8;Q9UIC8	Leucine carboxyl methyltransferase 1	LCMT1	0.218820347	0.126930078	0.175064312	-0.177899996
P13796	Plastin-2	LCP1	0.633528149	-0.067941666	0.160778212	0.022182465
B5MDU6;Q9H6V9;C9JHU6;B5MCE2;C9JUM0;B4DRG3;B5MCU4;A0A0A0MSH6P00338	UPF0554 protein C2orf43	LDAH;C2orf43;FLJ21820	0.547496071	-0.137337939	0.167140913	-0.047766558
P07195;A8MW50;C9J7H8	L-lactate dehydrogenase A chain	LDHA	2.010490713	-0.154404322	0.126713995	-0.019846598
Q8NC56	L-lactate dehydrogenase B chain;L-lactate dehydrogenase	LDHB	2.699123377	-0.134845734	0.190053151	-0.019590378
Q9Y2U8	LEM domain-containing protein 2	LEMD2	0.292352371	0.03329277	0.156700765	0.047034264
A0A0G2JNN3;A0A087WTE7;C9JMY0;A0A087WUE4;Q96PV6Q8WVC0	Inner nuclear membrane protein Man1	LEMD3	0.302622663	0.04481252	0.154814157	0.027860006
Q32P28	Leukocyte receptor cluster member 8	LENG8	0.428921671	0.068350665	0.735342765	-0.137165769
O95202	RNA polymerase-associated protein LEO1	LEO1	0.084476398	0.029697736	0.329380374	-0.080199877
P09382	Prolyl 3-hydroxylase 1	LEPRE1	0.031046207	0.019974391	0.406475102	0.153062185
P17931	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1	0.359240155	0.034703255	1.529821854	-0.090471903
Q99538	Galectin-1	LGALS1	1.07762568	0.061558406	0.460117831	0.030233701
P18858;F5GZ28;M0R0Q7	Galectin-3	LGALS3	0.218536714	-0.104424	0	NaN
P49916;K7ERZ5;K7EQB6	Legumain	LGMN	3.051390354	-0.314282099	0.876091206	-0.076197306
A0A087WUJ1;Q9H400	DNA ligase 1;DNA ligase	LIG1	0.363348274	0.026160876	0.334978681	-0.020538966
A0A0J9YXC7;P48059;A0A0M3HER1	DNA ligase 3	LIG3	0.443959073	0.063236237	0.598316443	-0.069819768
Q9NUP9;G3V1D4	Lck-interacting transmembrane adapter 1	LIME1	0.211830462	0.068869591	0.711890533	0.218598366
Q9BRT6	LIM and senescent cell antigen-like-containing domain protein 1	LIMS1	0.721493105	0.158658091	0.314338898	0.07054081
P49257	Protein lin-7 homolog C	LIN7C	0.169305429	-0.075970968	0.120103688	-0.075608253
Q12907;D6RBV2;D6RIU4;D6RDX1Q9H0V9	Protein LLP homolog	LLPH	0.534755482	0.097807312	0.096693936	0.048650742
Q9BU23	Protein ERGIC-53	LMAN1	3.213077041	0.200499217	0.655109478	0.054982503
P02545	Vesicular integral-membrane protein VIP36	LMAN2	2.422888995	0.151349703	0.102411537	0.016171773
P20700;E9PBF6;A0A0D9SFE5	VIP36-like protein	LMAN2L	0	-0.054452896	0	-0.183307648
Q03252	Lipase maturation factor 2	LMF2	0.461805197	0.076149305	1.638569152	-0.213247299
Q9UIQ6	Prelamin-A/C;Lamin-A/C	LMNA	0.572759377	0.042606354	2.276549818	0.136886597
K7EKE6;P36776;K7EJE8	Lamin-B1	LMNB1	0.165863497	-0.019363085	0.080668252	0.006063461
Q8NF37;A0A0G2JQ62;A0A0G2JRI7Q92604	Lamin-B2	LMNB2	0.453001525	-0.036924362	0.52289026	-0.035937309
Q14693	Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form	LNPEP	0.363067876	0.099097888	0.113673325	0.037228266
O60711;B7Z5P7	Lon protease homolog, mitochondrial	LONP1	3.80253169	0.136477788	0.124034711	-0.00800705
Q92604	Lysophosphatidylcholine acyltransferase 1	LPCAT1	0.342969326	-0.077315013	0.669638601	-0.126806895
Q14693	Acyl-CoA:lysophosphatidylglycerol acyltransferase 1	LPGAT1	1.053085662	0.113163948	1.148437674	-0.165973981
	Phosphatidate phosphatase LPIN1	LPIN1	0.422267596	0.143792788	1.20769208	0.186779976
	Leupaxin	LPXN	3.109414061	0.155561765	3.598959421	0.236872037

E9PEM5;P50851;H0YAC6	Lipopolysaccharide-responsive and beige-like anchor protein	LRBA	0.029977675	-0.008890788	0.570684364	-0.141626676
P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1	2.559020269	0.204885165	1.237335592	0.137262026
P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC	0.209294755	-0.007557551	1.810837003	-0.056165059
Q5VZK9;A0A0U1RQQ1	Leucine-rich repeat-containing protein 16A	LRRC16A	2.272611145	-0.166540464	1.81248767	-0.16734314
X6RK58;Q8TCA0;A0A0A0MSS8	Leucine-rich repeat-containing protein 20	LRRC20	0	NaN	1.122819676	0.795701345
Q2I0M4	Leucine-rich repeat-containing protein 26	LRRC26	0	0.424841563	0	-0.096224785
Q9H9A6	Leucine-rich repeat-containing protein 40	LRRC40	0.145268508	0.025393486	0.53281875	-0.065887451
A0A0C4DH00;A0A087WTU1;A0A0B4J2G4;Q15345;A0A087WT19	Leucine-rich repeat-containing protein 41	LRRC41	0.501677184	-0.127434921	0.494124927	-0.13442688
Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	1.685672729	-0.101866086	0.928894031	-0.061820984
Q96CX6	Leucine-rich repeat-containing protein 58	LRRC58	0.231713876	-0.080893199	0.803536099	0.083070437
Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59	1.493328564	0.067068418	0.356464231	0.021059036
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	1.143900309	-0.142520269	1.250025022	0.137494405
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1	LRSAM1	0.965072186	0.217919159	0.695074906	0.148642349
Q9UFC0;H7C5S6	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1	0.226874491	0.02845637	0.234675269	-0.032612483
Q9H089	Large subunit GTPase 1 homolog	LSG1	0.199843998	-0.066210111	0.019531321	0.006697337
K7ELG9;Q3MHD2	Protein LSM12 homolog	LSM12	0.582438727	-0.18357722	0.603669146	-0.16396904
Q8ND56;A0A140TA76;K7EMZ9	Protein LSM14 homolog A	LSM14A	2.10565746	-0.206848145	0.192757579	0.034500758
Q9BX40;Q5TBP9	Protein LSM14 homolog B	LSM14B	0.083179474	-0.039839935	0.412485291	-0.132640076
Q9Y333	U6 snRNA-associated Sm-like protein LSm2	LSM2	1.386971167	-0.154912631	0.739141045	-0.06600825
P62310	U6 snRNA-associated Sm-like protein LSm3	LSM3	0.691021623	0.16372776	0.948422759	0.13300902
V9GZ56;Q9Y4Z0;U3KQS7;U3KQK1	U6 snRNA-associated Sm-like protein LSm4	LSM4	0.969032472	0.166303317	0.112748278	-0.021322568
P62312	U6 snRNA-associated Sm-like protein LSm6	LSM6	1.268810064	-0.174538294	0.463985167	-0.044887861
Q9UK45	U6 snRNA-associated Sm-like protein LSm7	LSM7	0.484128439	0.191289457	0.768590936	0.219234975
O95777;F2Z2Y6;C9JIZ0;C9JNV3	U6 snRNA-associated Sm-like protein LSm8	LSM8	1.431066063	-0.111336072	0.143399486	0.02731355
P33241;E9PBD8;E7EMG9	Lymphocyte-specific protein 1	LSP1	1.464949818	0.157670975	1.799499325	0.195678393
P48449;A0A0G2JQD0	Lanosterol synthase	LSS	0.418401422	0.021243095	1.498215334	-0.10708491
P09960	Leukotriene A-4 hydrolase	LTA4H	2.316462454	-0.111354828	1.082508938	-0.052897453
O94822;H7BYG8	E3 ubiquitin-protein ligase listerin	LTN1	0.469451672	-0.044412613	0.526017815	-0.048330625
Q96GA3	Protein LTV1 homolog	LTV1	0.259141853	0.252367655	0.264790883	0.246233622
Q9NQ29;A8MYV2;B8ZZ10	Putative RNA-binding protein Luc7-like 1	LUC7L	0.665711519	0.414441109	0.717052182	0.456508319
Q9Y383;A0A0A6YYJ8	Putative RNA-binding protein Luc7-like 2	LUC7L2	1.235695976	0.071113586	0.666103632	0.033443769
J3KPP4;O95232;D6RDI2	Luc7-like protein 3	LUC7L3	0.124496868	0.015555064	1.047609271	0.059169769
Q9BS40	Latexin	LXN	1.758222918	-0.185529836	0.329491629	-0.066680908
Q9NX58	Cell growth-regulating nucleolar protein	LYAR	1.209686405	-0.141749382	1.049795574	-0.113978704
O75608;E5RGR0;A0A087X1K9;B4DP64	Acyl-protein thioesterase 1	LYPLA1	0.076471502	0.011488914	0.025374877	-0.00458622
O95372;Q5QPQ1;Q5QPQ0;Q5QPQ3;Q5QPQ2;Q5QPQ9	Acyl-protein thioesterase 2	LYPLA2	0.233331354	-0.042093277	0.158062465	-0.041538556
Q5VWZ2	Lysophospholipase-like protein 1	LYPLAL1	0.301333027	-0.051541328	1.567310684	-0.144134204
C9JY28;C9JRX8;F5H189;Q9HD34;C9J799;H7C4Q5	LYR motif-containing protein 4	LYRM4	0.370764285	0.081217448	0.079644733	0.029951731
Q5U5X0	Complex III assembly factor LYRM7	LYRM7	0.085092592	-0.022302055	0.095795407	-0.028732681
Q8WZA0;K7ES95	Protein LZIC	LZIC	2.037998567	-0.212063789	1.361226751	-0.181597074
Q9NQ48;H7C488	Leucine zipper transcription factor-like protein 1	LZTFL1	0.293964091	-0.05354627	0.066658281	-0.01180776
P20645;F5GX30;H0YGE9	Cation-dependent mannose-6-phosphate receptor	M6PR	1.237612145	0.205785433	0.439386725	0.102800051
H3BPE1;H3BQK9;Q9UPN3;H0Y390	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1	0.018679662	-0.006191254	0.928474457	-0.190873146
Q9BQ69	O-acetyl-ADP-ribose deacetylase	MACROD1	0.059314475	0.00769647	0.862812137	-0.091652552
Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1	MAD1L1	0.792511724	-0.182848295	0.734669923	-0.16762956

B4DQT1;B4DVN3;E7ESC7;Q7L5Y9;D6RE80 P43355	Macrophage erythroblast attacher	MAEA	0.593693387	0.398874728	0.067964806	-0.029375394
	Melanoma-associated antigen 1	MAGEA1	0.468998175	0.076111476	0.054500523	0.012876193
Q5H907;Q5H909;Q9UNF1	Melanoma-associated antigen D2	MAGED2	0.905317825	0.122767448	0.601635417	0.093735059
P61326;Q96A72;F5H6N1;F5H6P7 A0A087WU53;Q9H0U3	Protein mago nashi homolog;Protein mago nashi homolog 2	MAGOH;MAGOHB	1.661045197	-0.09691143	0.388756534	-0.038764318
	Magnesium transporter protein 1	MAGT1	2.273870704	0.190774282	0.039981585	0.007244428
Q9BXY0;H0YBV6	Protein MAK16 homolog	MAK16	0.562955549	-0.149172147	2.056963612	-0.216919581
Q96EH3	Mitochondrial assembly of ribosomal large subunit protein 1	MALSU1	1.415611994	-0.125052929	0.176988564	-0.055050659
Q9UDY8	Mucosa-associated lymphoid tissue lymphoma translocation protein 1	MALT1	0.329832428	-0.090854263	1.355078557	-0.394555283
P33908	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	MAN1A1	0.176179263	0.120277405	0.209480977	0.172726631
Q9UKM7;H0YGV7;H0YG20	Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase;alpha-1,2-Mannosidase	MAN1B1	0.207615105	-0.072794406	0.497622926	-0.114447085
Q16706	Alpha-mannosidase 2	MAN2A1	0.347080356	0.071218173	0.125599253	-0.024429639
A8K878;P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF	1.178520959	-0.087476095	0.247234237	0.019607862
Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S	0.991658867	-0.140130679	1.582167782	-0.220554034
Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1	0.661853438	0.048851649	0.74105762	0.053214391
P36507;A0A1B0GUL7;G5E9C7	Dual specificity mitogen-activated protein kinase kinase 2	MAP2K2	0.13607719	0.027307828	0.502799526	0.082209905
P46734	Dual specificity mitogen-activated protein kinase kinase 3	MAP2K3	1.015666019	0.107233365	1.093334942	0.138899167
E7EVA0;P27816	Microtubule-associated protein;Microtubule-associated protein 4	MAP4	1.388181849	-0.072080294	0.853636726	0.037220637
P28482	Mitogen-activated protein kinase 1	MAPK1	0.055983446	-0.016612689	0.360277497	-0.070699374
O15264	Mitogen-activated protein kinase 13	MAPK13	0.954712098	-0.113132159	0.419072682	-0.053070068
B4E0K5;Q16539;E7EX54;B5TY33 P27361;E9PQW4;E9PBK7;E9PJF0;B3KR49	Mitogen-activated protein kinase 14	MAPK14	0.096830392	0.025444031	0.12203654	-0.026876767
	Mitogen-activated protein kinase 3;Mitogen-activated protein kinase	MAPK3	1.013976217	0.071911494	0.339786867	0.044273059
C9J8E1;Q16644	MAP kinase-activated protein kinase 3	MAPKAPK3	1.426960624	0.404633808	0.454588122	0.155762672
Q15691	Microtubule-associated protein RP/EB family member 1	MAPRE1	0.906435242	0.071667671	1.08097024	0.09783268
Q15555;K7EL66;K7ERD8	Microtubule-associated protein RP/EB family member 2	MAPRE2	0.648077709	0.103146235	1.655744082	0.189950307
Q9NX47	E3 ubiquitin-protein ligase MARCH5	MARCH5	2.7108618	0.308208466	0.663836505	0.133284887
P49006	MARCKS-related protein	MARCKSL1	0.024010417	-0.007174174	1.900457495	0.276287397
E9PC69;Q7KZ17	Serine/threonine-protein kinase MARK2	MARK2	1.254119724	0.130300522	0.158046167	0.033378919
P56192	Methionine--tRNA ligase, cytoplasmic	MARS	0.172754488	0.012011846	1.051425141	-0.042866389
Q96GW9	Methionine--tRNA ligase, mitochondrial	MARS2	0.131387608	-0.021919568	2.448296131	-0.163427353
Q96GX5	Serine/threonine-protein kinase greatwall	MASTL	0	0.269958496	0	NaN
P31153	S-adenosylmethionine synthase isoform type-2	MAT2A	0.183638661	-0.014158567	0.100434411	-0.011674245
Q9NZL9	Methionine adenosyltransferase 2 subunit beta	MAT2B	0.560411811	-0.088504155	0.836349004	-0.092683474
A0A0R4J2E8;A8MXP9;P43243;D6REM6;D6R991 Q7Z434	Matrin-3	MATR3	0.34265332	-0.022222837	0.085261906	0.005002975
Q8N884	Mitochondrial antiviral-signaling protein	MAVS	1.460084097	-0.359551366	1.890278053	-0.298902194
Q9UBB5;X6RBL6	Cyclic GMP-AMP synthase	MB21D1	0.40842822	-0.047196706	1.112985736	-0.11411794
	Methyl-CpG-binding domain protein 2	MBD2	0.208721056	-0.053964615	0.562359569	0.119357808
A0A087WT34;A0A087X1H1;A0A0AMTS6;K7EIE8;O95983 H7C4T5	Methyl-CpG-binding domain protein 3	MBD3	0.558201344	-0.075560284	0.581964668	-0.190612411
		MBNL1	1.4602592	-0.383639018	0.225878157	-0.175257365
C9JP00;A0A0A0MQX8;Q9NR56;Q86VM6;O95205;Q5VZF2 Q96N66	Muscleblind-like protein 1;Muscleblind-like protein 2	MBNL1;MBLL;MBNL2	0.562712035	0.091988564	0.191924892	0.030136108
	Lysophospholipid acyltransferase 7	MBOAT7	1.122407027	0.233845711	1.132434308	0.225567818
P43121	Cell surface glycoprotein MUC18	MCAM	2.091236867	-0.272531192	0.651919167	-0.094585737
Q8IVS2	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	MCAT	0.07280378	-0.017518997	1.807531957	-0.194663366

Q96RQ3;E9PHF7;E9PG35;F5G YT8;G5E9X5	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1	0.922929192	0.084195455	0.811836063	-0.060466131
Q9HCC0;D6RD67	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2	1.452112052	0.089952151	0.233310554	-0.018921216
Q96PE7;H7BZS7	Methylmalonyl-CoA epimerase, mitochondrial	MCEE	0.167965246	-0.043080997	0.060463596	-0.023094368
Q8NI22;H7BZ18	Multiple coagulation factor deficiency protein 2	MCFD2	0.280419753	0.052516937	0.823836915	-0.127834956
Q07820;A0A087WT64	Induced myeloid leukemia cell differentiation protein Mcl-1	MCL1	2.992540046	0.389437358	0.155388603	0.037705739
P49736;H0Y8E6	DNA replication licensing factor MCM2	MCM2	0.698218712	0.026309013	0.314511788	-0.017438889
P25205;J3KQ69	DNA replication licensing factor MCM3	MCM3	0.199589429	0.010652224	1.03393446	-0.041100502
P33991	DNA replication licensing factor MCM4	MCM4	1.78678683	0.062169711	0.964988591	-0.035794894
P33992;B1AHB1	DNA replication licensing factor MCM5;DNA helicase	MCM5	1.112299217	0.056306203	0.868247693	-0.048425357
Q14566	DNA replication licensing factor MCM6	MCM6	0.01548277	0.00104777	0.618235085	-0.031710307
P33993	DNA replication licensing factor MCM7	MCM7	1.58344655	0.046185493	1.214574631	-0.051319122
Q9BTE3	Mini-chromosome maintenance complex- binding protein	MCMBP	0.221307182	0.025100072	0.134381201	-0.024539312
Q9ULC4	Malignant T-cell-amplified sequence 1	MCTS1	0.567572843	0.071011861	0.274066762	0.045161247
Q14676	Mediator of DNA damage checkpoint protein 1	MDC1	2.753822566	-0.160585721	2.672882658	-0.107713381
P40925;B9A041;B8ZZ51	Malate dehydrogenase, cytoplasmic	MDH1	1.75893994	-0.163295428	0.560163515	-0.070215861
P40926;G3XAL0	Malate dehydrogenase, mitochondrial;Malate dehydrogenase	MDH2	2.989248875	0.094893138	0.732430898	-0.031033834
Q9NU22	Midasin	MDN1	0.120341612	0.025033951	0.458533207	-0.071105003
P48163	NADP-dependent malic enzyme	ME1	0.699174427	-0.073033015	0.107927958	-0.016818047
A0A1W2PPH1;P23368;A0A1W 2PQH3;A0A1W2PQT3;A0A1W 2PQY8;A0A1W2PR68;A0A1W 2PQF8;A0A1W2PQ37 Q9BV79;H3BM30	NAD-dependent malic enzyme, mitochondrial	ME2	2.51450886	0.115395864	0.090723296	-0.007575353
Q15648	Trans-2-enoyl-CoA reductase, mitochondrial	MECR	0.034479016	0.011849244	0.11674721	-0.023485661
O60244	Mediator of RNA polymerase II transcription subunit 1	MED1	0.659340185	0.21745491	0.90341262	0.239768982
J3KR33;A0JLT2	Mediator of RNA polymerase II transcription subunit 14	MED14	0.349605738	0.087987264	0.00111097	0.000249863
F5H872;Q13503	Mediator of RNA polymerase II transcription subunit 19	MED19	0.219243007	0.243235906	0.288425953	0.173440933
F5GY88;A0A0B4J1W0;O75448; B4DDR8;F5H5K2;E9PFL1 Q9NPJ6;Q5T911	Mediator of RNA polymerase II transcription subunit 21	MED21	0	NaN	0	NaN
Q9Y316	Mediator of RNA polymerase II transcription subunit 24	MED24	0.200212484	0.049410184	0.861647696	-0.092079798
Q7L2J0	Mediator of RNA polymerase II transcription subunit 4	MED4	0.591054	0.089001338	0.128794077	0.031393687
Q14696	Protein MEMO1	MEMO1	0.313609475	-0.026434263	0.260973129	-0.028241793
C9JW74;Q5EB52;C9JRA9;C9JC M6;R4GN52;C9JWU9;C9JSW2 P53582	7SK snRNA methylphosphate capping enzyme	MEPCE	0.375115474	0.048102061	1.71397634	-0.120553017
P50579;F8VRR3;F8VQZ7	LDLR chaperone MESD	MESDC2	0.562171383	0.086028735	0.591542572	0.080348333
Q9UBP6;H0YIH0	Mesoderm-specific transcript homolog protein	MEST	0	0.453105927	0	0.039012909
Q8N6R0	Methionine aminopeptidase 1	METAP1	2.460433985	-0.080636024	0.598182531	-0.042277654
Q86W50;I3L3W3;I3L4V1;I3L36 2;K7EKQ8 H0YI09;Q9H8H3;F8VQX6	Methionine aminopeptidase 2	METAP2	0.656840618	-0.096685092	0.680807965	0.116127332
C9JHF5;Q9GZY8;C9JU19;A0A 0A0MS29 A0A0C4DFN1;Q8IWA4;H7C5H 5	tRNA (guanine-N(7))-methyltransferase	METTL1	1.624360138	-0.12534078	0.40790645	-0.056276321
Q10620;F5H7F6;F5H6X2	Methyltransferase-like protein 13	METTL13	0.336995101	0.02864329	2.374257352	-0.155493736
G3V599;Q96PC5;O15320	Methyltransferase-like protein 16	METTL16	0.371757273	0.173517227	0.709574277	-0.163508797
P16455	Methyltransferase-like protein 7A	METTL7A	0.764458166	0.072295507	0.655989218	-0.074949265
P10620;F5H7F6;F5H6X2	Mitochondrial fission factor	MFF	0	-0.602748871	0	-0.075540066
Q10620;F5H7F6;F5H6X2	Mitofusin-1	MFN1	0	0.026622772	0	0.110740662
G3V599;Q96PC5;O15320	Alpha-1,6-mannosyl-glycoprotein 2-beta- N-acetylglucosaminyltransferase	MGAT2	0.812435603	0.165596008	0.252153679	-0.059873581
P16455	Protein O-GlcNAcase	MGEA5	0.246003188	0.078898748	0.121583123	-0.046114604
P10620;F5H7F6;F5H6X2	Methylated-DNA--protein-cysteine methyltransferase	MGMT	0.102925726	-0.0337684	0.863912595	0.157644908
G3V599;Q96PC5;O15320	Microsomal glutathione S-transferase 1	MGST1	0.25032611	0.028536797	0.25759234	0.024088224
	Melanoma inhibitory activity protein 2;cTAGE family member 5	MIA2;CTAGE5	0.232633481	0.044415474	0.400660213	-0.090214411

Q5JRA6;A0A0AMRH6	Melanoma inhibitory activity protein 3	MIA3	0.469591261	0.044271151	0.163235082	0.023031553
J3KTI2;Q9BRT3	Migration and invasion enhancer 1	MIEN1	1.115145394	-0.253939056	0.366427417	-0.094115448
Q8N108	Mesoderm induction early response protein 1	MIER1	0.040670106	0.010248502	0.048788123	-0.013775571
P14174	Macrophage migration inhibitory factor	MIF	0.108517212	0.029493968	0.181680305	0.051131884
Q8IUf8	Bifunctional lysine-specific demethylase and histidyl-hydroxylase MINA	MINA	0.787463927	-0.097510338	0.241912721	-0.035329183
Q9UNW1	Multiple inositol polyphosphate phosphatase 1	MINPP1	0	-0.346894264	0	NaN
Q99797	Mitochondrial intermediate peptidase	MIPEP	0.261126757	-0.043110975	0.429093544	0.048784765
P46013	Antigen KI-67	MKI67	1.75167177	-0.190318743	0.447660529	-0.051574707
C9J494;Q9H000	Probable E3 ubiquitin-protein ligase makorin-2	MKRN2	1.511486395	0.225150998	0.316704143	0.054485257
Q14165;F5H1S8;H0YG07	Malectin	MLEC	0.270807963	-0.026117007	0.481831853	-0.04963843
H0Y818;P40692	DNA mismatch repair protein Mlh1	MLH1	0.221253309	0.032643318	1.320424592	-0.105482101
Q8NB16;I3L4Z5;I3L2T9	Mixed lineage kinase domain-like protein	MLKL	0.370934671	-0.155272484	0.533009282	0.207781792
Q5TIG5;A8MQ02;J3KN01;P55196	Afadin	MLLT4	0.16093319	-0.062673569	0.319801732	-0.106285095
Q96EY8;S4R3P5;F5H4Z7	Cob(II)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB	0.08249888	-0.011484464	0.92734246	-0.111814817
Q8N4V1	Membrane magnesium transporter 1	MMGT1	0.149901847	0.033439318	0.38570058	-0.075172742
Q96T76;H0Y746	MMS19 nucleotide excision repair protein homolog	MMS19	0.16926493	-0.027679443	0.56370437	-0.078637759
Q9H8S9;Q7L9L4;D6RCK3	MOB kinase activator 1A;MOB kinase activator 1B	MOB1A;MOB1B	0.265341504	-0.043837229	1.111658946	0.136277199
Q96BX8;K7ESA9	MOB kinase activator 3A	MOB3A	0.037296556	0.00933075	1.234071167	-0.198972384
O96007	Molybdopterin synthase catalytic subunit	MOCs2	0.079322825	-0.025694529	0.279293243	0.117931048
O95396	Adenylyltransferase and sulfurtransferase MOCs3;Molybdopterin-synthase adenylyltransferase;Molybdopterin-synthase sulfurtransferase	MOCs3	0	-0.17954731	0	-0.186560631
Q13724;C9J8D4	Mannosyl-oligosaccharide glucosidase	MOGS	1.039763953	0.080184937	0.814545232	-0.074892998
A0A286YFF8;Q7Z3U7	Protein MON2 homolog	MON2	0.378079414	-0.043988228	0.100394681	0.019923528
Q9Y6X9;H7C1V1	MORC family CW-type zinc finger protein 2	MORC2	1.754099725	-0.234262466	0.312750041	-0.072218895
Q14149	MORC family CW-type zinc finger protein 3	MORC3	0	0.038809776	0	-0.151694298
H0YMJ0;H0YLJ3;B3KTM8;Q9UBU8;H0YMT8;H0YM21	Mortality factor 4-like protein 1	MORF4L1	0.038130023	0.036543846	0.04850112	-0.029470921
Q5R3B4;O95563	Mitochondrial pyruvate carrier 2	MPC2	1.673121499	0.324426015	0.549261552	0.111280123
J3QS48;I3L295;J3KTK8;J3QQZ4;J3KT75;J3QW43;J3QRD5;O75352;J3KSI4;I3L405;I3L261;I3L1D2;I3L4E0	Mannose-P-dolichol utilization defect 1 protein	MPDU1	0.058968155	-0.017184893	0.62590539	-0.129606565
A2IDA3;P29372	DNA-3-methyladenine glycosylase	MPG	0.095743773	0.021854401	0.143792599	0.033001582
O00566;U3KQ48	U3 small nucleolar ribonucleoprotein protein MPP10	MPHOSPH10	2.79343725	0.162425041	1.362706865	0.103464444
Q99549	M-phase phosphoprotein 8	MPHOSPH8	0.748827228	-0.1508255	0.155873729	-0.048544566
H3BPB8;P34949;F5GX71;H3BMZ9;H3BPP3;H3BP57;H3BT48;H3BUZ9;H3BPM5;H3BPU7;H3BNY8;H3BT46	Mannose-6-phosphate isomerase	MPI	1.052921191	-0.115572929	1.113735887	-0.138922056
Q00013	55 kDa erythrocyte membrane protein	MPP1	3.535717323	0.31020991	1.4066024	0.145447413
Q9NZW5;B8ZZG1	MAGUK p55 subfamily member 6	MPP6	0.363711767	0.076752345	0.477466724	-0.046886444
P25325;B1AH49	3-mercaptopyruvate sulfurtransferase;Sulfurtransferase	MPST	0.68983326	-0.076017698	0.048281143	0.006022453
O95297;Q9UEL6	Myelin protein zero-like protein 1	MPZL1	0	-0.275009155	0	-0.103503545
P49959;F8W7U8	Double-strand break repair protein MRE11A	MRE11A	0.85120502	0.040312449	1.422625522	-0.066517194
Q9BV20	Methylthioribose-1-phosphate isomerase	MRI1	2.738887866	-0.163868904	0.533083078	-0.046292623
Q6IN84	rRNA methyltransferase 1, mitochondrial	MRM1	1.190285497	-0.438954353	1.86429736	-0.608525912
Q9BYD6;H0Y8N7	39S ribosomal protein L1, mitochondrial	MRPL1	1.250252513	0.169088682	0.086035102	0.021671613
Q7Z7H8	39S ribosomal protein L10, mitochondrial	MRPL10	0.330594034	0.049795151	0.711940637	-0.095283826
Q9Y3B7	39S ribosomal protein L11, mitochondrial	MRPL11	0.555195648	-0.056001981	0.708431044	-0.067346573
P52815	39S ribosomal protein L12, mitochondrial	MRPL12	0.249156619	0.025831223	1.568903318	-0.112998009

Q9BYD1;E5RJ17	39S ribosomal protein L13, mitochondrial	MRPL13	0.694231289	-0.044833501	0.036675629	0.005659421
Q6P1L8	39S ribosomal protein L14, mitochondrial	MRPL14	2.004989604	-0.203519185	2.241432117	-0.226875941
Q9P015;E5RIZ4;E5RHF4	39S ribosomal protein L15, mitochondrial	MRPL15	0.180176442	0.020364126	1.293039441	-0.09483846
Q9NX20	39S ribosomal protein L16, mitochondrial	MRPL16	0.013874845	-0.003499985	1.275807631	-0.113226318
E9PKV2;Q9Nrx2	39S ribosomal protein L17, mitochondrial	MRPL17	0.226495359	-0.053913116	0.88857747	-0.126107852
Q9H0U6	39S ribosomal protein L18, mitochondrial	MRPL18	0.566559411	-0.115699132	0.291738312	-0.071416537
P49406;S4R3W9;A0A0A0MRF4	39S ribosomal protein L19, mitochondrial	MRPL19	1.493766338	-0.143568039	1.480717755	-0.131189664
Q5T653;C9IY40	39S ribosomal protein L2, mitochondrial	MRPL2	0.230187281	-0.461153348	0.975000299	-0.191227277
Q9BYC9	39S ribosomal protein L20, mitochondrial	MRPL20	0.302051012	0.091523616	0.792391547	0.197200267
Q7Z2W9;F5H7V8;H3BUY0	39S ribosomal protein L21, mitochondrial	MRPL21	0.041876153	-0.013461113	0.250372747	-0.077313741
E7ESL0;J3KQY1;Q9NWU5	39S ribosomal protein L22, mitochondrial	MRPL22	0.133131594	0.018216769	0.486976811	-0.054560026
Q96A35;X6RJ73	39S ribosomal protein L24, mitochondrial	MRPL24	0.187853168	-0.063322067	0.239626439	-0.05585893
D6RAN8;H7C5U8;Q9P0M9	39S ribosomal protein L27, mitochondrial	MRPL27	0	-0.568293571	0	-0.437641144
Q13084;A2IDC6;Q4TT37;A2IDC7	39S ribosomal protein L28, mitochondrial	MRPL28	0.541715979	-0.097784678	1.634705941	-0.232866287
H0Y9G6;E7ETU7;P09001;E9PF06;D6RC14	39S ribosomal protein L3, mitochondrial	MRPL3	0.5718518	-0.159236272	0.297737776	-0.089900335
Q9BYC8	39S ribosomal protein L32, mitochondrial	MRPL32	0.057976969	0.023703893	0.287062502	-0.069420815
Q9BZE1;S4R369;A6NHR2	39S ribosomal protein L37, mitochondrial	MRPL37	1.9681352	-0.137137095	1.61406837	-0.096787771
Q96DV4	39S ribosomal protein L38, mitochondrial	MRPL38	0.099901106	-0.016323725	1.47431586	-0.194543521
Q9NYK5;C9JG87	39S ribosomal protein L39, mitochondrial	MRPL39	0.528763051	-0.049133619	1.103142359	-0.096067746
Q9BYD3;K7ES61;X6RAY8;K7ELQ0	39S ribosomal protein L4, mitochondrial	MRPL4	0.209931959	-0.030672391	1.091065912	-0.100448926
Q8IXM3	39S ribosomal protein L41, mitochondrial	MRPL41	0.119659002	0.027265549	0.217330432	0.038392385
H0Y6Y8;B1AL05;Q8N983;H0YBU8	39S ribosomal protein L43, mitochondrial	MRPL43	0.218310194	0.081691106	0.179011702	0.070222219
Q9H9J2	39S ribosomal protein L44, mitochondrial	MRPL44	0.669149897	-0.075386365	0.700118733	-0.0575339
A0A087X2D5;Q9BRJ2;A0A0G2JMS5;A0A087WU62	39S ribosomal protein L45, mitochondrial	MRPL45	0.185653759	0.041465441	0.051261504	-0.012875557
Q9H2W6	39S ribosomal protein L46, mitochondrial	MRPL46	0.021650612	0.006457647	0.775806078	-0.16258653
Q9HD33	39S ribosomal protein L47, mitochondrial	MRPL47	1.482025394	0.111347834	0.012344697	-0.003099124
F5H702;Q96GC5	39S ribosomal protein L48, mitochondrial	MRPL48	0.0326234	0.009720484	0.53197337	-0.106382052
Q13405;H0YDP7	39S ribosomal protein L49, mitochondrial	MRPL49	0.0280904	-0.007052422	0.842974848	-0.12092336
Q8N5N7	39S ribosomal protein L50, mitochondrial	MRPL50	0.533462411	0.111312866	0.050049075	-0.013079961
Q4U2R6;M0R176;A0A087WU28;A0A0B4J2C1	39S ribosomal protein L51, mitochondrial	MRPL51	0.258296414	0.120210648	0	-0.557168961
Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53	0.73848798	-0.064027468	0.385711345	-0.038136482
Q6P161	39S ribosomal protein L54, mitochondrial	MRPL54	0.53260622	0.101325353	0.182276132	-0.037309011
Q7Z7F7;X6R631;X6RIW1	39S ribosomal protein L55, mitochondrial	MRPL55	0.076197144	-0.026076063	0.739600324	-0.188042068
Q9BYD2;Q5SZR1	39S ribosomal protein L9, mitochondrial	MRPL9	0.198623947	0.069515673	0.209731121	0.081283379
P82912	28S ribosomal protein S11, mitochondrial	MRPS11	0.079591804	0.018749873	0.342278111	-0.083861669
O60783	28S ribosomal protein S14, mitochondrial	MRPS14	0.767335756	0.137978236	0.471681248	-0.125090281
A6ND22;Q9Y3D3	28S ribosomal protein S16, mitochondrial	MRPS16	0.002991777	0.000813802	0.256512969	-0.070475578
Q5QPA5;Q9NVS2	28S ribosomal protein S18a, mitochondrial	MRPS18A	0.000175122	-3.43E-05	2.732923564	-0.182374477
Q9Y676;A0A0G2JIC6	28S ribosomal protein S18b, mitochondrial	MRPS18B	1.428306704	-0.173642476	0.6108606	-0.108799299
Q9Y399;Q5T8A0	28S ribosomal protein S2, mitochondrial	MRPS2	0.558797287	-0.088522593	2.145023059	-0.216772715
G5E9W7;G5E9V5;P82650	28S ribosomal protein S22, mitochondrial	MRPS22	0.471022905	-0.063386599	1.29555801	-0.139469783
J3QLR8;Q9Y3D9	28S ribosomal protein S23, mitochondrial	MRPS23	0.843827712	-0.120836894	0.696733665	-0.091210683
P82663;E7EPW2	28S ribosomal protein S25, mitochondrial	MRPS25	0.625738754	-0.068336169	1.475468441	-0.107020696
Q9BYN8	28S ribosomal protein S26, mitochondrial	MRPS26	0.094549546	0.062407176	0.145257422	0.079293569
Q92552;G5EA06;D6RH20;D6RJC7	28S ribosomal protein S27, mitochondrial	MRPS27	1.302930068	-0.148920695	1.179119912	-0.128280322
Q9Y2Q9;H0YAT2;H7C5V3;E5RGC7;E5RFH3	28S ribosomal protein S28, mitochondrial	MRPS28	0.321896081	0.061271985	0.449434117	-0.076870282

Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30	2.182947211	-0.233808835	2.750150846	-0.28407828
Q92665	28S ribosomal protein S31, mitochondrial	MRPS31	0.13274214	-0.026070595	0.559742406	-0.10160319
C9JJ19;P82930	28S ribosomal protein S34, mitochondrial	MRPS34	0.916248245	-0.123209318	0.10259251	-0.01875941
P82673	28S ribosomal protein S35, mitochondrial	MRPS35	0.440798233	-0.112477303	1.546589191	-0.253129323
P82909	28S ribosomal protein S36, mitochondrial	MRPS36	1.695879048	0.190903982	1.45090531	0.156734149
P82675	28S ribosomal protein S5, mitochondrial	MRPS5	0.094276508	-0.04285272	0.305858963	-0.125929197
P82932	28S ribosomal protein S6, mitochondrial	MRPS6	0.492324215	0.089096705	0.440229357	0.087353388
J3QLS3;Q9Y2R9;J3QQS1;J3QK W2;J3KSI8 P82933	28S ribosomal protein S7, mitochondrial	MRPS7	0.181403239	-0.02162075	0.718719162	0.064858754
Q96E11;X6RDS5	28S ribosomal protein S9, mitochondrial	MRPS9	0.21389171	-0.027234395	0.111775975	-0.01921463
Q96E11;X6RDS5	Ribosome-recycling factor, mitochondrial	MRRF	0.249582773	0.059116999	0.150798782	0.028708458
Q9UKD2	mRNA turnover protein 4 homolog	MRTO4	0.02824097	-0.004508336	0.223253169	-0.03287824
P43246;E9PHA6	DNA mismatch repair protein Msh2	MSH2	0.73935077	0.048617045	0.584749472	-0.034194628
P20585	DNA mismatch repair protein Msh3	MSH3	0.221616123	-0.060182254	0.281105173	-0.058007558
P52701;A0A087WWJ1	DNA mismatch repair protein Msh6	MSH6	0.437561687	0.039834976	0.227865667	-0.018309911
B4DHE8;Q96DH6;J3KTC1;B4D M51	RNA-binding protein Musashi homolog 2	MSI2	1.32820605	-0.151900927	1.082322465	-0.136666616
P26038	Moesin	MSN	0.073362404	0.008825302	2.221979508	0.174778303
Q9BUK6	Protein misato homolog 1	MSTO1	0.242548798	-0.237271309	0.058782056	0.042079449
O94776	Metastasis-associated protein MTA2	MTA2	0.041778108	-0.002513568	0.822933723	-0.076374372
B4DUC8;Q13126;J3QSB7	S-methyl-5-thioadenosine phosphorylase;Purine nucleoside phosphorylase	MTAP	0.805179428	-0.079681396	0.155098632	-0.02173233
Q9Y6C9;E9PIE4	Mitochondrial carrier homolog 2	MTCH2	1.623905705	0.1099418	0.835817333	-0.055282593
P00403	Cytochrome c oxidase subunit 2	MT-CO2	1.867469769	0.261546453	0.48664138	0.090689977
Q86UE4;E5RJU9	Protein LYRIC	MTDH	0.384736074	-0.023311615	0.234388872	0.01071771
B5MC22;Q9UDX5;F8WEN7;H7 C417 P11586;F5H2F4	Mitochondrial fission process protein 1	MTFP1	2.358041788	0.516966629	0.871134896	0.158027331
	C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methylenetetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase;C-1-tetrahydrofolate synthase, cytoplasmic, N-terminally processed	MTHFD1	1.258310801	-0.059707324	0.703007876	-0.034322739
A0A087WVM4;B7ZM99;Q6UB 35 P13995;B9A062;B8ZZU9	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L	1.771073585	-0.106621106	2.09605044	-0.138181051
	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial;NAD-dependent methylenetetrahydrofolate dehydrogenase;Methylenetetrahydrofolate cyclohydrolase	MTHFD2	3.819120874	-0.17171669	2.46533538	-0.103896141
P49914;A0A0UIRR23;A0A0A6 YYL1;A0A0UIRQM3 P46199	5-formyltetrahydrofolate cyclo-ligase	MTHFS;ST20- MTHFS MTIF2	0.551190043	-0.089173317	0.006946815	-0.001669566
Q9Y2Z2;E7EW11	Translation initiation factor IF-2, mitochondrial	MTIF2	1.221744603	0.574838638	0.415189869	-1.202976227
Q9Y2Z2;E7EW11	Protein MTO1 homolog, mitochondrial	MTO1	0.668041219	-0.147597631	0.215579736	-0.057900429
P42345	Serine/threonine-protein kinase mTOR	MTOR	1.531412954	0.25952212	0.672993886	0.133875847
Q9NVV4	Poly(A) RNA polymerase, mitochondrial	MTPAP	1.013066089	-0.235939026	0.294980321	0.065338453
P58546	Myotrophin	MTPN	1.726811624	-0.123842557	0.266057054	-0.033397357
Q99707;B1ANE3	Methionine synthase	MTR	1.068506998	0.076869011	0.082733309	-0.009706497
A0A0A0MRK6;Q13505;A0A0C 4DFQ1	Metaxin-1	MTX1	1.526376478	0.137975693	1.386772905	0.109790166
O75431;C9JAZ1;C9JNK6	Metaxin-2	MTX2	0.48930101	0.07151858	0.120572411	-0.020725886
P22033	Methylmalonyl-CoA mutase, mitochondrial	MUT	0.570083525	-0.090515137	0.985225941	-0.110512733
P53602;H3BP35	Diphosphomevalonate decarboxylase	MVD	1.097250309	-0.223794301	0.721853619	-0.155743281
F5H8H2;Q03426;A0A1B0GWC 2 Q14764	Mevalonate kinase	MVK	0.109208115	-0.032870928	1.022654596	-0.178172429
	Major vault protein	MVP	0.368054291	-0.0375398	0.600063328	-0.039240201
Q9BQG0;I3L1L3	Myb-binding protein 1A	MYBBP1A	1.569654026	0.061210314	1.470583927	-0.06398042

P01106;A0A0B4J1R1;H0YBT0;A0A087WVR4;A0A087WUS5 A0A087WV05;Q99417	Myc proto-oncogene protein C-Myc-binding protein	MYC MYCBP	0.266252311 0.312921712	-0.191548506 0.065635045	0.345201992 0.116017413	0.419156551 0.025775592
Q969H8;M0QXF7;M0QYN0	Myeloid-derived growth factor	MYDGF	0.139004336	0.019881248	0.978046556	-0.059360822
Q7Z406;M0QY43	Myosin-14	MYH14	1.688623055	-0.624219418	0	NaN
P35579	Myosin-9	MYH9	0.439514138	-0.02305158	0.276502169	0.014705022
P05976;P08590	Myosin light chain 1/3, skeletal muscle isoform;Myosin light chain 3	MYL1;MYL3	0.081899905	0.016683896	0.799047517	0.119590441
J3QRS3;P19105;O14950;P24844	Myosin regulatory light chain 12A;Myosin regulatory light chain 12B;Myosin regulatory light polypeptide 9	MYL12A;MYL12B;MYL9	0.266941018	-0.032100677	0.668483293	-0.067042033
G8JLA2;F8W1R7;J3KND3;G3V1V0;B7Z6Z4;P60660;F8VFP3;F8VZU9;G3V1Y7;F8W180 A0A0D9SFK2;Q92614	Myosin light polypeptide 6 Unconventional myosin-XVIIIa	MYL6 MYO18A	0.251470973 0.556017741	0.032008489 -0.059523582	1.44551361 0.753205507	0.084526062 -0.076186816
F5H6E2;O00159	Unconventional myosin-Ic	MYO1C	1.097288569	0.220634778	0.020731554	-0.011121432
J3QRN6;O94832;K7EIG7;J3KRL0 F8WE88;Q9Y411;F8W6H6;A0A087WY00 Q8WU39	Unconventional myosin-Id Unconventional myosin-Va Marginal zone B- and B1-cell-specific protein	MYO1D MYO5A MZB1	0.051878207 3.00558417 0.192169701	-0.013724327 -0.061731656 0.029136658	0.026974274 3.43005638 0.306120433	0.006534576 -0.0711085 -0.042408307
B8ZZ87;Q6NZ67;H7C173;H7C202;Q6P582	Mitotic-spindle organizing protein 2B;Mitotic-spindle organizing protein 2A	MZT2B;MZT2A	0	NaN	0	NaN
P41227;F8W808;A8MWP7;C9JN83;C9JW55;Q9BSU3 Q9BXJ9;A0A0B4J1W3	N-alpha-acetyltransferase 10;N-alpha-acetyltransferase 11 N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA10;NAA11 NAA15	1.195732459 2.448017045	-0.093525251 -0.114263852	0.101073203 0.966967915	0.013329188 -0.054182371
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit	NAA25	1.105679595	-0.192809423	0.41391959	-0.092110634
Q86UY6;F5H2C9	N-alpha-acetyltransferase 40	NAA40	0.154263157	0.05807813	0.058027919	-0.010918681
E7EQ69;Q9GZZ1;C9J5D1;A0A087WWJ2 C9JT95;C9JMP5;Q9BQ15	N-alpha-acetyltransferase 50 SOSS complex subunit B1	NAA50 NABP2	2.470258607 0.090994743	0.19953537 0.03629481	0.719834086 0.481773904	0.085542997 -0.171825536
F8VZJ2;H0YHX9;Q13765;E9PAV3;F8W0W4;F8W1N5;F8VNW4	Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACA	0.988825662	-0.103743553	1.438143985	-0.164405505
Q96RE7	Nucleus accumbens-associated protein 1	NACC1	0.080375095	0.011276563	1.155886382	0.084236781
O95544;A0A0A0MR98	NAD kinase	NADK	0.041356852	-0.024489562	0.040883222	-0.036386172
Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1	0.33934467	-0.030672391	0.036375272	0.004021962
Q9UJ70;C9JEV6;H7C3G9;H7C286 P54802	N-acetyl-D-glucosamine kinase Alpha-N-acetylglucosaminidase;Alpha-N-acetylglucosaminidase 82 kDa form;Alpha-N-acetylglucosaminidase 77 kDa form	NAGK NAGLU	0.237432307 0.019973303	-0.04662323 -0.006242816	0.308838144 0.257010879	-0.080761909 -0.126022085
P43490;A0A0C4DFS8	Nicotinamide phosphoribosyltransferase	NAMPT	2.265173908	-0.130317688	2.367604252	-0.089707057
Q9NR45	Sialic acid synthase	NANS	0.080183628	0.009090424	0.019837679	0.00208505
F8VY35;F8VV59;F5H4R6;H0YIV4;P55209;F8W118;F8W543;H0YH88;B7Z9C2;F8W0J6;H0YHC3;F8VRJ2;F8W020;F8VUX1;F8VXI6 Q99733;C9JZ17;A8MXH2;C9JD1;E9PNW0;E9PJJ2;E9PS34;E9PNJ7;E9PKT8 P54920;M0R0Y2;M0R2M1	Nucleosome assembly protein 1-like 1 Nucleosome assembly protein 1-like 4 Alpha-soluble NSF attachment protein	NAP1L1 NAP1L4 NAPA	1.046646445 1.891131315 0.092600657	-0.113379796 -0.113266627 0.00931867	0.006644339 0.113001998 0.441250884	0.001283964 0.009669622 0.040640513
Q99747	Gamma-soluble NSF attachment protein	NAPG	0.520349225	-0.094955444	0.405126943	-0.078692754
Q6XQN6;G5E977;C9J8U2	Nicotinate phosphoribosyltransferase	NAPRT	1.712555236	-0.081413905	0.224682083	-0.019243558
O43776	Asparagine--tRNA ligase, cytoplasmic	NARS	0.021764361	0.001408895	0.712310478	0.027647018
Q96I59;E9PRK2	Probable asparagine--tRNA ligase, mitochondrial	NARS2	0.365442063	0.045974414	0.20832649	-0.024414063
P49321;Q5T624;H0YF33	Nuclear autoantigenic sperm protein	NASP	1.627708838	-0.065959613	0.621484467	-0.041337967
Q9H0A0;A0A087WV29	N-acetyltransferase 10	NAT10	0.767809195	0.05007712	0.144695182	-0.012891452
H0Y5G7;A2RRP1	Neuroblastoma-amplified sequence	NBAS	1.12271555	0.100312233	0.297796156	-0.037210464
H0Y764;Q6ZJN1;H7C3Y7	Neurobeachin-like protein 2	NBEAL2	0.084787594	-0.023014386	0.559586982	-0.117222468

O60934;E5RGU1;A0A0C4DG07	Nibrin	NBN	1.508680501	0.188205719	0.959637816	0.122722626
A0A087WWD4;P13591;A0A087WTF6;A0A087WX77;A0A087WV75;H7BYX6;A0A087WTE4Q15021;E7EN77	Neural cell adhesion molecule 1	NCAM1	3.4083019	-0.277313868	0.410739562	0.046839714
P42695;G3V1A9;E9PKK4	Condensin complex subunit 1	NCAPD2	1.659109736	0.049585025	0.395286408	-0.013808568
Q9BPX3	Condensin-2 complex subunit D3	NCAPD3	0.174973486	0.036177953	0.202152466	-0.036792119
Q86X12;H0Y6U5	Condensin complex subunit 3	NCAPG	0.0580763	-0.008424441	0.667883227	-0.072008133
E9PHA2;Q15003;C9J470	Condensin-2 complex subunit G2	NCAPG2	1.413746053	-0.230831718	0.482601261	-0.133990224
Q09161	Condensin complex subunit 2	NCAPH	1.980357814	-0.120654742	1.774431923	-0.131953875
Q9UBB6;C9J5H8	Nuclear cap-binding protein subunit 1	NCBP1	1.147765875	-0.099064509	1.122081654	-0.124746323
A0A0R4J2G3;A0A0A0MTJ9;Q6PIU2;H7C046	Neurochondrin	NCDN	0.801897191	0.07257239	0.654516292	0.066041629
Q15080;A0A0G2JR51;A0A217FLJ2;B0QY04	Neutral cholesterol ester hydrolase 1	NCEH1	0.580706319	0.1041406	0.248923612	0.047011693
P16333;C9JAB9	Neutrophil cytosol factor 4	NCF4	1.909259629	0.30483977	0.172534649	0.064692815
P55160	Cytoplasmic protein NCK1	NCK1	0.271015628	-0.066496563	0.94988271	0.143787829
P19338;H7BY16	Nck-associated protein 1-like	NCKAP1L	3.484668891	-0.182937622	1.15306892	-0.08279705
Q969V3;K7EMW4;A0A0C4DGP7;K7ENM2;K7ELZ9	Nucleolin	NCL	3.680258997	-0.150133769	2.217591173	-0.075876872
Q9HCD5	Nicalin	NCLN	1.520787914	0.09291331	0.374149838	-0.03245767
A0A088AWL3;O75376	Nuclear receptor coactivator 5	NCOA5	1.40272112	-0.198109309	1.345287609	-0.162991842
Q92542;H0Y6T7;Q5T205;H0Y3Z4	Nuclear receptor corepressor 1	NCOR1	0.812373272	0.240352631	0.364317408	0.076382446
Q9BTX1	Nicestrin	NCSTN	0.595691308	0.134003639	0.710674064	0.139186541
O14777	Nucleoporin NDC1	NDC1	0.683806343	0.07529513	0.711138732	-0.052329381
Q9UHB4	Kinetochore protein NDC80 homolog	NDC80	1.614400065	0.200522423	0.686490303	0.109796842
Q92597;E5RJY1;E7ESM1	NADPH-dependent diflavin oxidoreductase 1	NDOR1	0.220483927	0.070935249	0.800503883	0.150757154
A0A087WXC5;E7ESZ7;O95299;H7C2W5;H7C1Y7;H7C2X4	Protein NDRG1	NDRG1	2.663438389	-0.49673303	0.128953404	0.043838183
K7EQ77;K7EK78;K7EP35;K7EMT4;Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10	0.033875938	-0.006356875	0.823493002	-0.101218541
Q9P0J0;U3KQP3;B4DEZ3;K7EJ1;E7ENQ6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11	1.495952739	-0.223015467	0.525532401	-0.119826698
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13	2.255705734	-0.283358256	2.638617338	-0.194212914
Q16718;A0A087X1G1;H7BYD0;F8WAS3;A0A087WXR5	Cytochrome c oxidase subunit NDUF4	NDUFA4	0.612491905	-0.116888364	0.339897637	0.083613078
A0A0C4DGS0;P56556;R4GN43	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5	0.584025728	-0.063513756	0.691798486	-0.067181905
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6	1.284882995	-0.143389066	1.670405739	-0.156371117
Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8	0.777496381	0.079454422	0.030861326	-0.004344622
O14561;H3BNK3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9	2.615994724	-0.189625104	1.045386854	-0.123310725
Q9Y375;H0YNN4;H0YNB7;H0YL22	Acyl carrier protein, mitochondrial;Acyl carrier protein	NDUFAB1	3.005824927	0.257340749	0.890092425	0.102389018
Q8N183	Complex I intermediate-associated protein 30, mitochondrial	NDUFAB1	0.023274836	0.009979248	0.315541552	-0.149978638
Q9BU61	Mimitin, mitochondrial	NDUFAF2	2.448486802	0.132398605	0.589614753	0.038837751
Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	NDUFAF3	0.413691234	-0.068869909	0.081649855	0.014254888
B3KR61;Q5TEU4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4	0.443344447	0.057724317	0.194823555	-0.029297829
O96000;H3BPJ9;H3BV16	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5	NDUFAF5	0.152816477	0.068603516	0.125419307	-0.044020462
Q9NX14	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10	0.188935228	-0.029346466	0.857138499	0.09144942
	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	NDUFB11	1.059612987	-0.189441681	0.290178649	-0.067128499

O43676;C9JKQ2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3	1.83036743	-0.190826734	1.275516721	-0.141085625
O95168;F2Z3P9;C9JXQ9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	NDUFB4	0.274911817	-0.046589533	0.054155302	0.011951447
H0Y886;O43674;E7EWP0	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	NDUFB5	0.59217818	-0.084397952	0.104458483	0.020799001
O95139;A0A087WZX2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	NDUFB6	0	NaN	0	0.14803791
Q9Y6M9;E9PH64;E7EWZ0;E9P F49	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUFB9	0.744096034	0.159510295	1.215525207	0.243132909
O95298;E9PRJ5;E9PM14;A0A0 87WUM3;E9PQ53	NADH dehydrogenase [ubiquinone] 1 subunit C2;NADH dehydrogenase [ubiquinone] 1 subunit C2, isoform 2	NDUFC2;KCTD14; NDUFC2-KCTD14	1.95005308	0.215714455	2.603991385	0.315511386
B4DJ81;P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1	0.240779202	-0.03738753	0.342449704	-0.049561501
O75306	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUFS2	0.216739962	0.028900782	0.112937634	-0.016100883
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3	0.750152393	-0.082487106	1.459018241	-0.141254425
O43181;D6REP1;D6R916;H0Y9 M8;D6RI09	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4	0.372013843	-0.081432978	0	-0.079153061
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NDUFS5	2.85057244	0.346814728	0.298757935	0.085781988
O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6	0.365257854	-0.114709091	0.14754235	0.04865392
F5H5N1;A0A087WXF6;A0A08 7WTI3;F5GXJ1;O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7	0.854403054	0.140551249	0.448522833	0.070992152
O00217;E9PN51;F8W9K7;E9P KH6;E9PPW7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8	1.460072123	0.305134583	0.30355818	-0.12945226
G3V0I5;P49821;B4DE93;E9PQ P1;E9PLC6;E9PMX3	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1	0.749772415	-0.095069249	0.408476617	0.040845235
E7EPT4;P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2	5.332671913	-0.52535216	3.850910018	-0.317494075
Q15843	NEDD8	NEDD8	0.702030864	-0.215817134	0.119126047	0.045102437
H0Y3X6;A0A0C4DFX9;Q9H3P 2;C9JEM7;H7C2C7;C9JHL4 A0A0X1KG71;Q8WX92	Negative elongation factor A Negative elongation factor B	NELFA NELFB	2.553647875 0.278515031	-0.247662544 0.02856191	0.251677693 0.356292838	-0.027752558 -0.035572052
X6RLT1;H0UI80;Q8IXH7	Negative elongation factor C/D	NELFCD;TH1L	0.401282008	0.054496447	0.803189889	-0.086889267
P18615;A0A0A0MT02;A0A0A0 MSN9;A0A0G2JI50;E9PD43 O60524;G3V5V3	Negative elongation factor E Nuclear export mediator factor NEMF	NELFE NEMF	0.121985159 0.00807282	0.023078601 -0.001642863	0.723682057 0.17154838	0.083425522 -0.029925982
Q9UMX5	Neudesin	NENF	0	NaN	0	NaN
Q99519;E9PIF4	Sialidase-1	NEU1	2.034426652	-0.243442218	0.236034734	0.032335917
Q8NCF5;H3BSZ7	NFATC2-interacting protein	NFATC2IP	1.84455535	-0.185341835	0.494209152	-0.080622355
J3QKY3;B4DYE1;F5H1B7;J9JI E5;Q14494 A0A286YEX4;P08651	Nuclear factor erythroid 2-related factor 1 Nuclear factor 1 C-type	NFE2L1 NFIC	0	NaN	0	NaN
D6RH30;P19838	Nuclear factor NF-kappa-B p105 subunit;Nuclear factor NF-kappa-B p50 subunit	NFKB1	0.405037953	-0.305760384	0.18632412	0.106729984
Q9Y697	Cysteine desulfurase, mitochondrial	NFS1	0.858143475	0.081922213	0.030266724	-0.004313787
Q5T6K7;E9PI99;Q5T6K5;Q139 52;A0A0A0MT00 Q8NEJ9;H0YJ17;G3V4G1	Nuclear transcription factor Y subunit gamma Neuroguinidin	NFYC NGDN	0.077715869 0.69678906	0.01688544 -0.151464144	1.938384219 0.036664255	-0.316597939 -0.005808512
C9JWV4;G5E9Q8;Q9H9Q4;H7 C0G7 Q8NBF2	Non-homologous end-joining factor 1 NHL repeat-containing protein 2	NHEJ1 NHLRC2	1.277095785 0	-0.2633564 -0.051252365	0.094342102 0	-0.038840961 -0.204875946
Q9NX24;D6RC52;D6RCB9	H/ACA ribonucleoprotein complex subunit 2	NHP2	0.82759359	-0.11754926	0.390372688	-0.079239845
B1AHD1;P55769	NHP2-like protein 1;NHP2-like protein 1, N-terminally processed	NHP2L1	0.291501327	0.033587774	2.136626403	-0.086299896
Q9GZT8;E7EXA3;Q6X734	NIF3-like protein 1	NIF3L1	1.51018535	0.13683637	2.580514783	0.18704764
Q9BYG3;C9J808;C9J6C5	MK167 FHA domain-interacting nucleolar phosphoprotein	NIFK	1.153487541	0.071857135	0.119355571	-0.013863246

Q9Y221;J3QLW7	60S ribosome subunit biogenesis protein NIP7 homolog	NIP7	0.444255345	0.094258308	0.190748253	0.044437726
Q9BPW8;H7C2U6	Protein NipSnap homolog 1	NIPSNAP1	1.384124404	0.144891103	0.148646006	0.024359067
C9J715;Q9Y211	Nischarin	NISCH	0.633357613	-0.10445296	0.445531878	-0.063134193
Q86X76	Nitrilase homolog 1	NIT1	0.692899521	-0.134451866	0.355434413	-0.056178729
Q9NQR4	Omega-amidase NIT2	NIT2	1.708453158	-0.150177638	0.493367448	-0.058436712
O15226	NF-kappa-B-repressing factor	NKRF	0.394577406	0.046850204	0.016212333	0.002120654
Q9NVX2;A0A0A0MRH0;K7EN33	Notchless protein homolog 1	NLE1	0.442574473	-0.056246122	0.049625981	0.009500186
Q9BYT8;E9PCB6;H0YAK4	Neurolysin, mitochondrial	NLN	0.335161505	-0.031851133	0.024214762	-0.002952894
P59045;K7EMN8;K7EQV0	NACHT, LRR and PYD domains-containing protein 11	NLRP11	0	0.236070633	0	0.290296555
A0A0G2JMG8;A0A0G2JPQ2;Q9NX02;J3KN39;A0A0G2JNC8;A0A0G2JLX3;A0A0G2JLQ8;A0A0G2JPB6;A0A0G2JP37	NACHT, LRR and PYD domains-containing protein 2	NLRP2	0.503658443	-0.045496623	0.099255388	0.013136864
C9JA08;Q96D46	60S ribosomal export protein NMD3	NMD3	0.16734749	0.02127107	0.110995958	-0.01362292
P15531	Nucleoside diphosphate kinase A	NME1	0.117973225	-0.066288948	0.298074908	0.111461322
Q32Q12;J3KPD9;P22392;E7ERL0	Nucleoside diphosphate kinase;Nucleoside diphosphate kinase B	NME1;NME2;NME3	0.152880963	-0.014399846	0.906173501	0.062373479
Q13232;H3BPR2	Nucleoside diphosphate kinase 3;Nucleoside diphosphate kinase	NME3	0.464772403	0.127806981	0.005820698	-0.00188001
Q9Y5B8;E9PNU1;B4DXC8	Nucleoside diphosphate kinase 7	NME7	0.635938551	0.255715561	0.517892249	0.250190735
Q13287	N-myc-interactor	NMI	0	0.059947332	0	-0.013822556
P30419	Glycylpeptide N-tetradecanoyltransferase 1	NMT1	0.227107934	-0.019096692	0.153925705	0.012458801
Q13423;E9PCX7	NAD(P) transhydrogenase, mitochondrial	NNT	0.955662591	0.060844103	0.518913165	-0.030877431
Q8NC60	Nitric oxide-associated protein 1	NOA1	0.458624797	-0.188610713	0.234232186	-0.094830195
Q9ULX3	RNA-binding protein NOB1	NOB1	1.256189332	-0.078828812	1.055100957	-0.076892535
Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L	1.045198619	0.128804843	0.111695052	-0.02057902
Q8WTT2	Nucleolar complex protein 3 homolog	NOC3L	0.199279365	0.04908371	0.566197235	-0.119351387
Q9BV14	Nucleolar complex protein 4 homolog	NOC4L	1.211700841	0.102735837	0.000852549	0.000118891
Q9BSC4	Nucleolar protein 10	NOL10	0.963271513	-0.06012694	0.889675581	-0.114679972
Q9H8H0	Nucleolar protein 11	NOL11	1.475573567	0.114433924	0.19024852	0.018150965
Q9H6R4;A0A0A0MRW6	Nucleolar protein 6	NOL6	0.735097385	0.084832827	0.302565358	-0.042888641
H7C2B1;Q9UMY1	Nucleolar protein 7	NOL7	1.752838415	0.276461792	0.97469711	0.195129267
Q5SY16	Polynucleotide 5-hydroxyl-kinase NOL9	NOL9	0.187489813	-0.021500905	2.274569741	-0.144522349
A0A0A0MRM9;Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1	0.568231171	-0.036373456	0.285617371	0.018939018
Q5C9Z4	Nucleolar MIF4G domain-containing protein 1	NOM1	0.359648305	-0.106874466	0.627386948	-0.326106071
Q5JPE7;J3KN36;P69849	Nodal modulator 2;Nodal modulator 3	NOMO2;NOMO3	4.374985813	0.224788984	2.951896629	0.146558444
Q15233;H7C367;C9JYS8	Non-POU domain-containing octamer-binding protein	NONO	0.172976297	-0.017762184	1.050345116	0.069314321
Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	NOP10	2.160620638	0.249541918	2.829442132	0.255750338
E9PFK5;P78316	Nucleolar protein 14	NOP14	1.37694106	-0.125320117	1.662937907	-0.155619939
Q9Y3C1	Nucleolar protein 16	NOP16	0.086404389	0.021732966	0.211206558	0.053385417
P46087	Probable 28S rRNA (cytosine(4447)-C(5)-methyltransferase	NOP2	1.318651155	-0.055634181	1.997731997	-0.075028737
O00567;Q5JXT2	Nucleolar protein 56	NOP56	1.65803916	0.070491791	0.579404951	-0.037102699
Q9Y2X3	Nucleolar protein 58	NOP58	1.38243234	0.107292493	0.286558571	0.029530525
Q86U38	Nucleolar protein 9	NOP9	0.174086831	0.030611038	0.628395195	-0.100183805
A0A075B6F9;Q9Y314;M0R3B2;M0R1K2	Nitric oxide synthase-interacting protein	NOSIP	0.172553411	0.03181235	0.18919587	0.038509369
J3KMY5;H0YIZ1;G3V3E8;E7E7MS2;G3V3D1;P61916;G3V2V8	Epididymal secretory protein E1	NPC2	0.904092554	-0.145071602	0.440010528	0.140018463
E9PLK3;P55786	Puromycin-sensitive aminopeptidase	NPEPPS	2.909140074	-0.150732358	0.994277773	-0.056042989
Q8TAT6	Nuclear protein localization protein 4 homolog	NPLOC4	0.129877002	-0.020796458	1.31425625	0.143724759
P06748	Nucleophosmin	NPM1	1.622428031	0.151268641	2.077466328	0.161050161

O75607	Nucleoplasmin-3	NPM3	0.092396783	-0.012474696	0.654115281	-0.050438245
B4DLR8;P15559;H3BNV2;H3B RK3	NAD(P)H dehydrogenase [quinone] 1	NQO1	3.023796032	0.213722547	1.13386754	0.139004389
Q5TD07;P16083;Q5TD05	Ribosyl-dihydroxynicotinamide dehydrogenase [quinone]	NQO2	0.221339707	-0.038490295	0.913910799	0.154013316
Q86WQ0;U3KQ53	Nuclear receptor 2C2-associated protein	NR2C2AP	0.484514163	-0.112338066	0.09350276	-0.028172557
F8W6G1		NRBP1	0.816093415	-0.136494954	0.292557669	-0.082491557
B1AKJ5;O43847;G3V1R5;F5H7 V1	Nardilysin	NRD1	1.449744073	-0.078032176	0.176853096	0.013751348
O95478;A0A0A0MQZ6	Ribosome biogenesis protein NSA2 homolog	NSA2	0.141114071	-0.01580588	0.226488475	0.0352904
Q15738;C9JDR0	Sterol-4-alpha-carboxylate 3- dehydrogenase, decarboxylating	NSDHL	0.508554192	-0.035948118	1.340418147	-0.097739538
I3L0N3;P46459	Vesicle-fusing ATPase	NSF	0.610608523	0.056221008	0.316696053	0.026626587
Q9UNZ2;F2Z2K0	NSFL1 cofactor p47	NSFL1C	1.08132933	-0.090415955	0.939711906	0.079249064
Q8WV22;I3L113	Non-structural maintenance of chromosomes element 1 homolog	NSMCE1	0.391374032	0.077996254	0.164391071	0.031988144
Q9NXX6	Non-structural maintenance of chromosomes element 4 homolog A	NSMCE4A	0.090727509	-0.054651896	0.23952474	0.137472153
Q08J23	tRNA (cytosine(34)-C(5))- methyltransferase	NSUN2	0.076401889	0.00822703	1.073831195	-0.081833204
Q96CB9	5-methylcytosine rRNA methyltransferase NSUN4	NSUN4	1.446023219	0.191698456	0.018725559	0.003806973
Q96P11	Probable 28S rRNA (cytosine-C(5))- methyltransferase	NSUN5	0.48525505	-0.043999354	1.502474075	-0.090444565
Q8TEA1	Putative methyltransferase NSUN6	NSUN6	0.368126224	0.095305125	0.17642758	0.064293543
J3KRC4;Q8TCD5;J3KXSX6	5(3)-deoxyribonucleotidase, cytosolic type	NT5C	0.961212414	-0.126785596	0.266840852	-0.066319784
P49902;Q5JUV6	Cytosolic purine 5-nucleotidase	NT5C2	0.423849785	-0.068382581	0.450712194	-0.08288002
X6RM59;Q9H0P0;B9A035	5-nucleotidase;Cytosolic 5-nucleotidase 3A	NT5C3A	0.626252208	0.135790634	0.005258007	0.00381279
Q5TFE4;Q5QPD0	5-nucleotidase domain-containing protein 1	NT5DC1	0.439635267	-0.142645836	0.81197679	-0.238740921
Q9H857	5-nucleotidase domain-containing protein 2	NT5DC2	0.738546446	-0.140617371	0.806782032	-0.15807279
P78549;H3BRL9	Endonuclease III-like protein 1	NTHL1	0.074774129	0.051022371	0.096737317	0.056794008
Q9BV86	N-terminal Xaa-Pro-Lys N- methyltransferase 1;N-terminal Xaa-Pro- Lys N-methyltransferase 1, N-terminally processed	NTMT1	0.079072375	-0.012861888	0.421555451	-0.056600253
Q9BSD7;Q5TDF0	Cancer-related nucleoside-triphosphatase	NTPCR	0.095406764	-0.020545642	0.751675458	-0.103057226
P53384	Cytosolic Fe-S cluster assembly factor NUBP1	NUBP1	0.412100192	-0.062581698	0.306195766	-0.070358276
Q9Y5Y2;H3BNF0;H3BNS4;H3 BQR2	Cytosolic Fe-S cluster assembly factor NUBP2	NUBP2	0.981900768	0.122374852	0.117294601	-0.023574193
Q02818;H7BZ11	Nucleobindin-1	NUCB1	0.960772505	0.071364721	0.204404438	0.017987251
E9PKG6;V9HW75;A0A087WS V8;P80303;Q2L696	Nucleobindin-2;Nesfatin-1	NUCB2;HEL-S- 109;Nucb2	0.198312621	0.044644992	0.176709773	-0.055234464
Q9H1E3	Nuclear ubiquitous casein and cyclin- dependent kinase substrate 1	NUCKS1	0.713613573	-0.092216174	0.818525318	-0.138238907
Q9Y266	Nuclear migration protein nudC	NUDC	0.110986118	-0.018773397	0.734112233	0.090405146
Q96RS6	NudC domain-containing protein 1	NUDCD1	0.26107609	0.02280585	0.962578843	0.06198438
Q8WVJ2;E5RFP0	NudC domain-containing protein 2	NUDCD2	1.409432381	0.158638318	1.535051055	0.183694522
Q8IVD9	NudC domain-containing protein 3	NUDCD3	0.898716425	0.101323764	1.635290822	0.213363965
P36639	7,8-dihydro-8-oxoguanine triphosphatase	NUDT1	0.172759288	-0.046276728	0.700469548	-0.116561254
Q96DE0	U8 snoRNA-decapping enzyme	NUDT16	2.008976927	-0.194570541	0.186485169	-0.026673635
P50583	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	NUDT2	0.248513426	0.033514341	0.850737655	0.092557589
O43809;H3BND3	Cleavage and polyadenylation specificity factor subunit 5	NUDT21	0.716161113	-0.062386195	1.761607491	-0.115705172
O95989	Diphosphoinositol polyphosphate phosphohydrolase 1	NUDT3	0.457991757	-0.062620799	0.798134	-0.087152163
A6NFX8;Q9UKK9;A6NJU6	ADP-sugar pyrophosphatase	NUDT5	2.409962267	-0.198226929	1.003348863	-0.096017838
Q8WV74	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	NUDT8	0.080618381	0.016259193	1.881380455	-0.217100779
D6RAW2;H7C386;Q9BW91	ADP-ribose pyrophosphatase, mitochondrial	NUDT9	0.213716078	0.067226028	0.369866652	-0.136580149
Q9BZD4;E9PQC4;B1AQT4;E9P P32	Kinetochore protein Nuf2	NUF2	0.723053345	0.188359896	0.401789102	0.114471436

Q7Z417	Nuclear fragile X mental retardation-interacting protein 2	NUFIP2	0.688733481	-0.073161443	0.209511693	0.026422501
P57740	Nuclear pore complex protein Nup107	NUP107	0.07089734	0.013001442	0.343009477	0.037702878
Q8WUM0	Nuclear pore complex protein Nup133	NUP133	0.36406818	0.031099637	0.988538187	-0.068051338
P49790	Nuclear pore complex protein Nup153	NUP153	2.825423133	-0.085013707	1.711065304	0.055534363
O75694;E9PF10	Nuclear pore complex protein Nup155	NUP155	0.015633411	-0.000978788	2.463961404	-0.097239812
Q12769;G3V198;E9PR16	Nuclear pore complex protein Nup160	NUP160	1.626566418	0.117382367	0.150355845	-0.020450592
Q5SRE5	Nucleoporin NUP188 homolog	NUP188	2.472596078	0.177354177	0.080602321	0.009810448
Q92621	Nuclear pore complex protein Nup205	NUP205	0.946902954	0.049040476	0.292499088	-0.024519285
Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210	2.720668499	0.125260989	1.378840091	-0.073381424
P35658;A0A0A0MSW3	Nuclear pore complex protein Nup214	NUP214	0.48110644	0.035746574	0.071234085	0.006146431
Q8NFH5;C9IYQ7;F8WCF5;F8WEL4	Nucleoporin NUP53	NUP35	0.518709377	0.08628273	0.054709681	0.012159665
Q8NFH4;F8VTY2	Nucleoporin Nup37	NUP37	1.127599054	0.116684914	0.122680011	0.02099673
Q8NFH3	Nucleoporin Nup43	NUP43	0.181895898	0.034286817	0.308620945	-0.058890025
Q9UKX7	Nuclear pore complex protein Nup50	NUP50	2.515825671	-0.181379	0.533211874	-0.03485775
Q7Z3B4	Nucleoporin p54	NUP54	0.301677503	0.051777522	0.318353927	-0.071744283
P37198;M0QXN5	Nuclear pore glycoprotein p62	NUP62	0.523475492	0.048156738	0.391494534	-0.033287684
Q9BW27;J3KT10;J3QL54;J3QLD4	Nuclear pore complex protein Nup85	NUP85	2.33142637	0.130893071	1.274860776	0.073056221
Q99567;J3KMX1	Nuclear pore complex protein Nup88	NUP88	0.686669437	0.048370679	0.089518533	0.008001963
Q8N1F7;H3BVG0	Nuclear pore complex protein Nup93	NUP93	0.92462074	0.039632797	0.165651692	0.012950897
P52948;H7C3P6	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nuclear pore complex protein Nup96	NUP98	0.194454341	0.022482236	0.602303704	-0.066492716
Q5JRG1;H7BYF2;Q9BVL2	Nucleoporin p58/p45	NUPL1	0.307271852	-0.178557078	0.425093784	-0.128540675
O15504;C9JYA1	Nucleoporin-like protein 2	NUPL2	0.395736159	0.083389282	0.384594046	0.08655262
Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1	2.381197829	0.314756076	4.107640991	0.431161245
P61970;H3BRV9	Nuclear transport factor 2	NUTF2	0.314723957	0.06238842	0.515066468	0.101256053
O15381	Nuclear valosin-containing protein-like	NVL	0.347489412	-0.063334465	0.082526961	0.018226941
Q9UBU9;E9PIN3	Nuclear RNA export factor 1	NXF1	0.621365524	-0.045483907	0.619441638	-0.061258316
P04181	Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form;Ornithine aminotransferase, renal form	OAT	4.27483758	-0.238516172	2.844322496	-0.153018316
Q9NX40;D6RG39;D6RIT9;D6RDK6;D6RBN5;D6RDI5;D6RA54;D6RC55	OClA domain-containing protein 1	OClAD1	0.43213862	0.072635015	0.473431707	0.083305677
Q56VL3	OClA domain-containing protein 2	OClAD2	0.439281913	-1.040294965	0.268163854	0.130952517
Q5SWX8	Protein odr-4 homolog	ODR4	0.918776659	0.138951937	0.404627561	-0.08271726
Q02218;E9PCR7;A0A0D9SFS3;E9PDF2;E9PFG7	2-oxoglutarate dehydrogenase, mitochondrial	OGDH	2.556181505	-0.112052917	2.52871515	-0.099847158
Q8N543;A0A0A0MTR2;H3BUA6	Prolyl 3-hydroxylase OGFOD1	OGFOD1	0.093065073	0.013588905	0.807288449	-0.080843608
Q6N063;F5H145	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2	OGFOD2	0.063481114	0.048787753	0.218669338	-0.09098657
A0A0A0MRN5;Q9NNT2	Opioid growth factor receptor	OGFR	1.840388038	-0.13511912	2.836704039	-0.263147354
O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT	1.283497211	-0.088263512	1.542830934	-0.109018962
J3KQ32;Q9NTK5	Obg-like ATPase 1	OLA1	1.08427205	-0.080579758	0.360384617	0.034689585
O60313;E5KJL9	Dynamin-like 120 kDa protein, mitochondrial;Dynamin-like 120 kDa protein, form S1	OPA1	0.06385605	0.00503095	0.634193725	-0.045372963
Q13415	Origin recognition complex subunit 1	ORC1	4.974573956	0.508387884	3.294204591	0.411241849
Q13416	Origin recognition complex subunit 2	ORC2	0.197598539	0.14439888	1.024600999	0.422615719
Q9UBD5	Origin recognition complex subunit 3	ORC3	0.211386071	0.041423798	0.455007993	-0.074288368
O43929;CON_Q2YDI2	Origin recognition complex subunit 4	ORC4	0.478770901	-0.090820313	0.964931479	-0.148713748

O43913	Origin recognition complex subunit 5	ORC5	1.066866287	0.158949534	0.038218095	0.008245468
Q9Y5N6;H3BTQ7;H3BT22	Origin recognition complex subunit 6	ORC6	0.647008036	0.120202065	0.560983568	0.09684817
F8VXD5;Q53FV1	ORM1-like protein 2	ORMDL2	0	-0.146348953	1.729407289	0.291925812
P22059	Oxysterol-binding protein 1	OSBP	0.074320774	0.011814753	0.017751178	-0.002740224
Q9BXB4	Oxysterol-binding protein-related protein 11	OSBPL11	1.356349987	-0.132395426	0.866180242	-0.101295471
Q9H4L5	Oxysterol-binding protein-related protein 3	OSBPL3	0.345786424	0.076664925	0.036643571	0.008758545
Q9BZF1	Oxysterol-binding protein-related protein 8	OSBPL8	0.314492949	0.061761538	0.217215705	-0.046299299
Q96SU4	Oxysterol-binding protein-related protein 9	OSBPL9	1.270403583	0.1658535	0.507429641	0.089889208
Q9NPF4	Probable tRNA N6-adenosine threonylcarbamoyltransferase	OSGEP	0.154774054	-0.035571734	0.608510256	-0.115887642
Q92882	Osteoclast-stimulating factor 1	OSTF1	0.171909831	0.019075394	1.023191542	0.105924288
F5GYN4;J3KR44;Q96FW1;F5H6Q1;F5GGYJ8	Ubiquitin thioesterase OTUB1	OTUB1	2.699456045	-0.163420041	1.896203051	-0.093830109
A0A087X0W9;Q8N6M0	OTU domain-containing protein 6B	OTUD6B	0.085631401	-0.027640661	0.521893613	-0.119378408
S4R3Q9;J3KNA0;Q15070;C9JC63;E7EYV0	Mitochondrial inner membrane protein OXA1L	OXA1L	0.895429644	-0.146316719	0.741095964	-0.129313469
P55809;E9PDW2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1	1.015063879	0.100514412	0.16896548	0.019606908
H0YC07;Q8N573	Oxidation resistance protein 1	OXR1	0.326856144	-0.039483706	1.231628479	-0.141331037
Q9NWU1;C9JQ2	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	OXSM	1.283242546	0.095238686	0.251670714	-0.033619563
O95747;C9JIG9	Serine/threonine-protein kinase OSR1	OXSR1	3.145193486	-0.135663986	3.909452009	-0.14811643
P13674	Prolyl 4-hydroxylase subunit alpha-1	P4HA1	1.844487241	0.408277194	1.379089355	0.303492228
P07237;H7BZ94;H0Y3Z3	Protein disulfide-isomerase	P4HB	0.003026036	-0.000167211	0.742387785	-0.033264796
Q9UQ80;F8VR77	Proliferation-associated protein 2G4	PA2G4	0.145359831	-0.017766317	0.075155502	-0.009912491
Q9BRP4;F5H0C4;F5H103;F5H3I1;F5H5D4	Proteasomal ATPase-associated factor 1	PAAF1	0.352973563	-0.048230807	0.184789149	0.025348981
P11940;E7EQV3;A0A087WTT1;E7ERJ7;H0YAR2	Polyadenylate-binding protein 1;Polyadenylate-binding protein	PABPC1	2.860844884	-0.091924667	1.432497124	-0.064899445
B1ANR0;Q13310;H0Y5F5	Polyadenylate-binding protein;Polyadenylate-binding protein 4	PABPC4	0.208542331	-0.023856799	1.465757115	-0.098662694
Q86U42;B4DEH8;G3V4T2	Polyadenylate-binding protein 2	PABPN1	0.866138956	-0.087361654	1.015873127	-0.099140485
Q6VY07;B4DF77	Phosphofurin acidic cluster sorting protein 1	PACS1	0.054612992	0.012494723	0.32684573	-0.083575249
F6U236;Q9BY11	Protein kinase C and casein kinase substrate in neurons protein 1	PACSIN1	0.280298678	-0.091594696	0	NaN
A0A0U1RR22;Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2	0.444155991	-0.158835888	0.343325528	-0.131748676
Q8N7H5	RNA polymerase II-associated factor 1 homolog	PAF1	0.362653211	-0.044836362	0.474291244	-0.049898783
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1	0.308006041	0.024495125	2.008808124	0.118705114
P68402	Platelet-activating factor acetylhydrolase IB subunit beta	PAFAH1B2	1.506412422	-0.177761396	0.743727288	-0.111955961
Q15102;M0R389;M0R1K3	Platelet-activating factor acetylhydrolase IB subunit gamma	PAFAH1B3	0.312999702	-0.062228839	0.31504224	-0.051528613
P22234;E9PBS1	Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase	PAICS	0.341033534	-0.040892283	0.060921521	0.00936381
Q9H074;D6REB4	Polyadenylate-binding protein-interacting protein 1	PAIP1	1.339570225	-0.179874102	0.279267347	0.049713135
Q9NWT1	p21-activated protein kinase-interacting protein 1	PAK1IP1	0.949833068	-0.076858521	1.477759895	-0.092573484
Q13177	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34	PAK2	3.386615846	-0.147573789	1.034945736	-0.051211993
Q9ULE6	Paladin	PALD1	0.034296282	0.010401408	0.091249824	-0.029486974
H3BQM0;Q8NDF8	Non-canonical poly(A) RNA polymerase PAPD5	PAPD5	0.108191421	0.017366727	1.359344963	-0.100727399
G3XAH6;P51003;A0A0C4DGK1	Poly(A) polymerase alpha	PAPOLA	1.268211707	-0.209762573	0.829441335	-0.127519608
O43252	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1;Sulfate adenylyltransferase;Adenylyl-sulfate kinase	PAPSS1	0.099468212	0.051561038	0.677667713	0.211407661
Q99497;K7ELW0;K7EN27	Protein deglycase DJ-1	PARK7	4.008128744	-0.179742495	1.521742376	-0.066660881
O95453;H3BRK1	Poly(A)-specific ribonuclease PARN	PARN	0.296079961	0.035774867	0.042157197	-0.005725861

P09874	Poly [ADP-ribose] polymerase 1	PARP1	0.800575225	0.03213501	0.105622837	-0.005281448
Q9UKK3	Poly [ADP-ribose] polymerase 4	PARP4	2.144811334	0.372844378	1.646332582	0.289428075
A0A087WZB5;Q9HB11;B0QYP8	Beta-parvin	PARVB	1.050558677	0.106482188	0.121181364	-0.023965518
Q9Y5B6	PAX3- and PAX7-binding protein 1	PAXBP1	1.258444602	-0.305330594	0.46170855	-0.127014796
Q9BVG4;A6NDF3	Protein PBDC1	PBDC1	1.473659448	-0.209731102	1.632057977	-0.21404171
Q96KB5;E5RFX4	Lymphokine-activated killer T-cell-originated protein kinase	PBK	0.122357319	-0.018770218	0.060128766	0.014193853
Q86U86;E7EVG2;H0Y5B5	Protein polybromo-1	PBRM1	0.153437243	-0.014978091	0.499192465	-0.037163734
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	PBXIP1	0	0.535791397	0	0.296718597
Q15365	Poly(rC)-binding protein 1	PCBP1	0.041645017	-0.006717364	0.509913403	0.058959325
F8VRH0		PCBP2	0.808229104	-0.16151619	0.188647875	0.040117264
Q15366	Poly(rC)-binding protein 2	PCBP2	0.065637871	-0.008402824	0.304955998	0.034890811
F8WB19;E7EUY3;E7ETT1;E9DR0;C9JQS9;E7EX59;P05166;E7ENC1;E9PEC3;E7ETT4	Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB	1.56598392	-0.150196393	0.913209534	-0.149130821
O94913;E9PKN0;E9PQ01	Pre-mRNA cleavage complex 2 protein Pcf1	PCF11	0.178632026	-0.090277195	1.35244127	-0.347130108
Q5JVF3	PCI domain-containing protein 2	PCID2	0.535240782	-0.079387029	0.421617322	-0.057504336
Q16822;A0A0A0MS74;H0YM31;H0YML5;B4DW73	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	PCK2	1.294726737	0.15937074	0.135728339	-0.026789983
A0A0A0MRJ6;H7BY58;P22061;F6S8N6	Protein-L-isoaspartate O-methyltransferase;Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	0.6252683	0.075825055	1.36664312	0.131283124
P12004	Proliferating cell nuclear antigen	PCNA	0.095492809	-0.005913417	0.131257969	0.006191254
Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP	0.052981571	0.007084846	1.456358227	0.127737363
P48539	Purkinje cell protein 4	PCP4	4.525093363	-0.541300774	0.377800634	0.064056396
Q9UHG3;F8W8W4	Prenylcysteine oxidase 1	PCYOX1	0.156259685	0.022205353	0.897206794	-0.063114166
Q8NBM8;E7EVZ5	Prenylcysteine oxidase-like	PCYOX1L	0.802010338	0.160154661	0.07662448	-0.021074613
C9JEJ2;P49585;C9J050;H7C1T3;H7BZNI	Choline-phosphate cytidylyltransferase A	PCYT1A	2.80357776	0.158070882	5.393804516	0.318707784
Q99447;I3L1L9;I3L1R7;I3L2Q1	Ethanolamine-phosphate cytidylyltransferase	PCYT2	0.450420928	-0.078817685	0.35254507	-0.055214246
Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1	4.829793169	-0.524626414	0.960715535	-0.040242513
C9J363;Q9BUL8;C9J5C3;H7C5M9;C9JSA3;C9JND6;C9J6F3	Programmed cell death protein 10	PDCD10	1.018609096	0.108722687	0.140831736	0.02253596
Q14690	Protein RRP5 homolog	PDCD11	1.825381802	0.057713826	1.170648532	-0.059303284
Q53EL6	Programmed cell death protein 4	PDCD4	5.38302531	0.263226509	1.597101222	0.052059809
O14737;K7EQA1	Programmed cell death protein 5	PDCD5	1.727281037	-0.181227366	0.559017047	-0.064293861
O75340;A0A024QZ42	Programmed cell death protein 6	PDCD6	0.27319357	0.074630737	0.046325978	-0.016268412
Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP	1.369894211	-0.086337407	0.109624364	-0.011129061
Q13371	Phosducin-like protein	PDCL	0.240950428	0.05834198	1.756385389	0.140308062
Q9H2J4;H7BZP2	Phosducin-like protein 3	PDCL3	0.244958625	-0.030846596	0.035254697	0.005812327
Q8NB37;H0YER3;H0YE25;H0YF25	Parkinson disease 7 domain-containing protein 1	PDDC1	0.414708664	-0.044068019	0.108568799	-0.022550265
Q6L8Q7;F6T1Q0	2,5-phosphodiesterase 12	PDE12	0.674600293	-0.028240204	1.436493582	-0.085692724
Q9HBH1	Peptide deformylase, mitochondrial	PDF	1.148188819	0.134689331	0.2589996	-0.057807922
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1	3.600356308	0.121734937	0.720788682	0.036178589
P11177;C9J634;F8WF02	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB	2.428042878	0.196595192	0.1470309	0.019829114
Q13087;H0Y4J5	Protein disulfide-isomerase A2	PDIA2	0.226888458	-0.03693517	0.303587565	0.049895922
P30101	Protein disulfide-isomerase A3	PDIA3	3.598642672	0.055992762	0.317718437	0.010365804
P13667	Protein disulfide-isomerase A4	PDIA4	3.116492184	0.086775462	0.286256036	0.014713923
Q14554	Protein disulfide-isomerase A5	PDIA5	0.114953273	0.023252805	0.253473103	0.040481885
Q15084	Protein disulfide-isomerase A6	PDIA6	0.014131328	-0.001106898	1.493508884	-0.067808787

Q15118;C9IYB4	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	PDK1	0.556092271	-0.090805372	0.518557766	-0.104897817
Q15120	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial	PDK3	0.414357218	-0.077021917	0.322399998	-0.068289121
O00151	PDZ and LIM domain protein 1	PDLIM1	3.326111902	-0.126635551	0.433679038	0.021083196
Q96HC4;H0Y8Y3	PDZ and LIM domain protein 5	PDLIM5	1.07415763	-0.185921669	0.42251953	-0.112978617
Q8NCN5;A8MT40;H3BQG3	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR	0.027002447	-0.009261131	0.705073641	-0.15380319
Q29RF7	Sister chromatid cohesion protein PDS5 homolog A	PDS5A	0.099833111	-0.01587677	1.165876163	-0.108870506
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	PDS5B	0.098847144	0.01219972	0.610203499	-0.085371335
H3BND4;Q6P996;Q86XE2	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1	0.619587087	-0.091390928	0.192628097	-0.034884453
O00764;F2Z2Y4	Pyridoxal kinase	PDXK	0.04563234	-0.006613413	0.296895626	-0.037347158
Q96GD0	Pyridoxal phosphate phosphatase	PDXP	1.474402968	-0.213280678	1.99150292	-0.222876867
Q15121;B1AKZ5	Astrocytic phosphoprotein PEA-15	PEA15	0.074152173	-0.039727656	0.748514015	0.250711441
P30086	Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimulating peptide	PEBP1	0.110524884	-0.015772502	0.510814494	0.063928286
Q9UBV8	Peflin	PEF1	1.382013135	0.211685816	1.036307596	0.192475955
A0A087WXX2;A0A087WUL4;A0A087WX23;Q86TG7;A0A087WZG9;B4DSP0	Retrotransposon-derived protein PEG10	PEG10	1.331584919	0.100160917	0.148881878	0.021493912
Q9BRX2	Protein pelota homolog	PELO	2.957395074	0.35816129	1.974373021	0.260176659
C9JFV4;Q8IZL8;E7EV54;I3L445	Proline-, glutamic acid- and leucine-rich protein 1	PELP1	0.351428584	0.051968257	0.272897259	-0.037233353
P12955	Xaa-Pro dipeptidase	PEPD	2.297770146	-0.09850057	0.200121068	-0.015433311
O00541;B5MCF9;B3KXD6	Pescadillo homolog	PES1	0.387062052	0.026721001	0.973888355	-0.055404663
O96011;H7C3V6	Peroxisomal membrane protein 11B	PEX11B	0.017050036	-0.005461057	0.717026582	-0.134711266
O75381;K7EK59	Peroxisomal membrane protein PEX14	PEX14	0.227827335	0.041093953	0.805264661	-0.187785339
E9PMM3;Q9Y5Y5;E9PQW0;E9PP98	Peroxisomal membrane protein PEX16	PEX16	0.04281144	0.014767965	0.314105483	0.0599521
P40855;Q5QNY5;B7Z8B3;E9PS71	Peroxisomal biogenesis factor 19	PEX19	0	NaN	0	NaN
O15067	Phosphoribosylformylglycinamide synthase	PFAS	2.37377851	-0.099129677	2.138378648	-0.097408613
E5RGS4;O60925	Prefoldin subunit 1	PFDN1	0.473711196	-0.177706623	0.154553045	0.065421677
Q9UHV9	Prefoldin subunit 2	PFDN2	2.081318386	-0.203071594	0.847167907	-0.099445343
E9PQY2;Q9NQP4	Prefoldin subunit 4	PFDN4	1.510938101	-0.187242826	0.915088289	-0.128837903
Q99471;H3BPF6	Prefoldin subunit 5	PFDN5	1.857251796	-0.092697144	1.094194263	0.08221817
O15212;A2AB88	Prefoldin subunit 6	PFDN6	0.006350927	0.001782417	0.496693631	0.098773003
P17858	ATP-dependent 6-phosphofructokinase, liver type	PFKL	0.795370558	-0.044313749	1.103636397	-0.054701487
P08237	ATP-dependent 6-phosphofructokinase, muscle type	PFKM	2.217510061	-0.073171933	0.605274539	0.020715714
Q01813	ATP-dependent 6-phosphofructokinase, platelet type	PFKP	3.683519957	-0.133544604	1.152113675	-0.044365247
P07737;K7EJ44	Profilin-1	PFN1	1.397352471	-0.060692469	0.45054114	0.022140503
P18669	Phosphoglycerate mutase 1	PGAM1	1.510944433	-0.119202932	0.164656234	0.024007161
Q96HS1;F5GXG4	Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5	0.104004619	0.011576335	0.047413571	-0.007274946
P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD	1.743884913	-0.078497887	1.093992403	0.056059519
P00558	Phosphoglycerate kinase 1	PGK1	0.798275684	-0.054000854	0.318993859	0.025213242
O95336;M0R261;M0R1L2	6-phosphogluconolactonase	PGLS	1.757943542	-0.147081693	1.76571517	-0.105569204
P36871	Phosphoglucomutase-1	PGM1	0.371995805	-0.111515045	0.117389935	-0.038168907
Q96G03	Phosphoglucomutase-2	PGM2	1.863660341	-0.177717527	0.858662253	-0.092157364
H0Y8I3;J3KN95;O95394;H0Y987;A0A087WT27	Phosphoacetylglucosamine mutase	PGM3	0	NaN	0	NaN
A6NDG6	Phosphoglycolate phosphatase	PGP	1.057903889	-0.08063221	0.090037949	-0.015133222
O00264	Membrane-associated progesterone receptor component 1	PGRMC1	1.62106891	0.174811999	0.771966883	0.081519127
O15173;U3KQM0	Membrane-associated progesterone receptor component 2	PGRMC2	0.044711445	-0.006154696	1.92082333	-0.118940036

Q9H814	Phosphorylated adapter RNA export protein	PHAX	2.570207506	-0.305021922	0.788878837	-0.096919696
P35232;C9JW96;C9JZ20;E7ESE2;E9PCW0	Prohibitin	PHB	0.471998822	0.046835581	0.075950821	-0.010278384
J3KPX7;Q99623;F5GY37;F5GWA7;F5H3X6	Prohibitin-2	PHB2	1.794419378	0.138358752	0.0576986	-0.007013003
E7EX82;Q8NDX5;C9JAU4;H7C4H9	Polyhomeotic-like protein 3	PHC3	0.230723005	0.053951263	1.22242685	0.240402317
Q8WUB8;S5FZ81	PHD finger protein 10	PHF10	0.049853883	0.014764786	0.126193873	0.024915314
Q7RTV0	PHD finger-like domain-containing protein 5A	PHF5A	0.201230239	0.036396345	0.006760824	-0.001378377
Q5JRC6;A0A0D9SGE8;Q8IWS0	PHD finger protein 6	PHF6	1.311238413	0.124781291	0.469154895	0.046762149
A0A286YF22;O43175;A0A2C9F2M7;A0A286YFA2;A0A286YFL2	D-3-phosphoglycerate dehydrogenase	PHGDH	1.125668284	0.098421733	0.570416591	0.063449542
Q8WWQ0	PH-interacting protein	PHIP	0.020099666	0.007357915	0.627202933	-0.158177694
Q93100	Phosphorylase b kinase regulatory subunit beta	PHKB	0.313491969	0.078028997	0.0197211	-0.005381902
J3KNN3;P15735;H3BTI9;H3BP07;H3BTW6	Phosphorylase b kinase gamma catalytic chain, liver/testis isoform	PHKG2	0.690059076	0.19200236	0.010371453	-0.003436661
Q9NRX4	14 kDa phosphohistidine phosphatase	PHPT1	0.281280375	-0.086168289	0.309003486	0.091123581
Q13492	Phosphatidylinositol-binding clathrin assembly protein	PICALM	0.203899156	-0.05059274	0.570133368	0.104223887
Q92643;A6NEM5;B1AK81	GPI-anchor transamidase	PIGK	0.151489583	0.032189369	0.731141064	-0.11101977
Q96S52	GPI transamidase component PIG-S	PIGS	1.622962121	0.078674952	0.187256077	0.014370282
A0A1W2PP57;A0A1W2PPC3;A0A1W2PPS0;A0A1W2PNP0;Q969N2;A0A1W2PPQ7;A0A1W2PRZ8;A0A1W2PQN1;A0A1W2PP53;A0A1W2PPR6;A0A1W2PP13;F6W983;A0A1W2PR92;A0A1W2PQY1;A0A1W2PRH2;A0A1W2PQ52	GPI transamidase component PIG-T	PIGT	1.185623294	0.15375646	0.239406787	-0.040708224
Q9H490	Phosphatidylinositol glycan anchor biosynthesis class U protein	PIGU	0.468753404	0.040960948	2.1112469	-0.144024531
Q9NWS0;M0R3A4;M0QYA2;M0R028;M0QZM3;M0QYF4	PIH1 domain-containing protein 1	PIH1D1	0.470687323	-0.258310509	0.018569552	-0.00259463
A8MYT4;A0A1W2PS05;Q8NEB9	Phosphatidylinositol 3-kinase;Phosphatidylinositol 3-kinase catalytic subunit type 3	PIK3C3	0.04689739	0.021197637	0.17639108	-0.067592621
P27986;E5RJY0;H0YBC2	Phosphatidylinositol 3-kinase regulatory subunit alpha	PIK3R1	0.916106279	-0.349467913	0.411648789	-0.12285773
Q99570	Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4	0.356597584	-0.036493937	1.538228956	-0.093192736
Q13526;K7EN45	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	PIN1	0.62281656	-0.073361397	0.842721338	-0.078566551
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4	1.310269956	-0.250041962	0.076859551	-0.026242892
P12273	Prolactin-inducible protein	PIP	0	NaN	0	NaN
P48426;H7BXS3	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	PIP4K2A	0.223249156	-0.034536044	0.187629854	0.029256821
Q8TBX8	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C	0.272326353	0.042318217	0.129682437	-0.025778898
A6PW57;Q99755	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	PIP5K1A	0	0.206792068	0	0.099967194
O00625	Pirin	PIR	0.527538683	-0.11650308	1.24849258	0.112188339
Q9GZP4;X6R8S9	PITH domain-containing protein 1	PITHD1	0.321005047	-0.041000366	0.316848428	0.04539903
F5GWE5;Q00169;I3L4H1;I3L4C0;I3L459	Phosphatidylinositol transfer protein alpha isoform	PITPNA	0.254349767	-0.060592333	0.444230085	-0.098838806
P48739;A0A0A0MSW4;B3KYB6;B3KYB7	Phosphatidylinositol transfer protein beta isoform	PITPNB	1.417093588	-0.126954079	1.601360902	-0.136434873
Q5JRX3;A0A0A0MRX9	Presequence protease, mitochondrial	PITRM1	1.943948353	0.070282618	2.2243689	0.091245651
P14618;B4DNK4	Pyruvate kinase PKM;Pyruvate kinase	PKM	3.006126183	-0.069326401	0.11207676	0.005718231
Q99640;A6NHV6;B4DZM6	Membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase	PKMYT1	0.037111265	-0.009183566	0.145737666	-0.025141716
Q16512	Serine/threonine-protein kinase N1	PKN1	0.462713434	-0.073835055	0.163354121	-0.025883993
Q99959	Plakophilin-2	PKP2	0.046906415	-0.012329006	0.119513676	0.023818906
Q8NCC3;H3BM47;B4DJW4;H3BPT3;H3BMU8	Group XV phospholipase A2	PLA2G15	0.006377494	-0.001983325	0.203222283	-0.055055936
P47712	Cytosolic phospholipase A2;Phospholipase A2;Lysophospholipase	PLA2G4A	0.46454672	0.053866069	0.496802956	0.053782145
Q9Y263;E5RIM3	Phospholipase A-2-activating protein	PLAA	2.169378828	0.130087217	1.984086844	0.113608996

Q4KWH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-1	PLCH1	0.471446735	0.096633752	0.318226378	0.042879581
Q8IV08	Phospholipase D3	PLD3	2.446160585	-0.326752663	0.815832479	-0.122207959
F5H2B5;Q96BZ4	Phospholipase D4	PLD4	0.497164808	-0.112009557	0.601184148	-0.166556867
Q15149	Plectin	PLEC	4.174839986	-0.126346588	1.133659425	-0.035616239
Q8TD55	Pleckstrin homology domain-containing family O member 2	PLEKHO2	1.095915202	0.247783343	0.925206419	0.224370003
O60664;K7ERZ3;K7EL96	Perilipin-3	PLIN3	6.032655034	-0.34068807	0.482882028	-0.0368433
P53350	Serine/threonine-protein kinase PLK1	PLK1	0.68373997	0.051042239	2.511921894	0.131526629
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1	1.035354819	-0.121848742	0.27883154	-0.033506711
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3	0.103260059	0.009604772	1.469821518	-0.081398646
O43660	Pleiotropic regulator 1	PLRG1	0.002966399	-0.000628471	0.105528479	0.019322395
Q14651;C9JAM8	Plastin-1	PLS1	0.010747149	0.004062335	0.041561732	-0.01849397
A0A0A0MSQ0;P13797	Plastin-3	PLS3	2.064926452	-0.173310598	0.455433155	-0.061392466
Q9Y4D7	Plexin-D1	PLXND1	0.185412731	0.336877823	0.148350904	0.276053429
Q8IYS1	Peptidase M20 domain-containing protein 2	PM20D2	0.843338221	0.119186401	0.133903399	0.024781545
P29590;H3BT57;H3BT29	Protein PML	PML	0.166647872	0.017712593	0.523048805	-0.046141624
O15305;H3BV55;H3BPH4;H3BRM0	Phosphomannomutase 2;Phosphomannomutase	PMM2	0.345550797	-0.04861927	1.212058129	-0.118870417
Q10713	Mitochondrial-processing peptidase subunit alpha	PMPCA	1.624035533	0.108942668	0.046009044	0.004328728
O75439;G3V0E4	Mitochondrial-processing peptidase subunit beta	PMPCB	0.241143299	0.013839404	1.603362438	-0.091085752
Q15126	Phosphomevalonate kinase	PMVK	0.232678638	0.027482986	1.104571477	-0.102499008
M0QYH2;Q96T60;M0R3C8;A0A0D9SFL2;M0QYI1	Bifunctional polynucleotide phosphatase/kinase;Polynucleotide 3-phosphatase;Polynucleotide 5-hydroxyl-kinase	PNKP	1.069648421	0.107789358	0.021639669	-0.004056295
Q9H307	Pinin	PNN	0.513512933	0.058686574	0.011843415	0.002374013
Q9NRX1	RNA-binding protein PNO1	PNO1	0.215978936	0.030804952	0.187573232	-0.029893875
P00491;G3V5M2	Purine nucleoside phosphorylase	PNP	1.499183431	-0.110254606	0.078370349	-0.00876077
Q8IY17	Neuropathy target esterase	PNPLA6	0.150341491	-0.076429367	0.26421508	-0.093459924
Q9NVS9;J3QQV6;J3QQZ9;A0A286YFL3	Pyridoxine-5-phosphate oxidase	PNPO	0.270664184	-0.073590914	0.117734214	-0.034665426
Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1	0.153464801	0.011943181	0.841646397	-0.050695101
Q9H488	GDP-fucose protein O-fucosyltransferase 1	POFUT1	0.088720531	0.047891299	0.137115407	-0.067136447
Q8NBL1	Protein O-glycosyltransferase 1	POGLUT1	0.574057375	-0.111237208	0.779959019	-0.136705399
Q7Z3K3	Pogo transposable element with ZNF domain	POGZ	0.000941987	0.000212987	0.686599731	-0.127549171
A0A087WU64;A6NMQ1;P09884	DNA polymerase;DNA polymerase alpha catalytic subunit	POLA1	0.015644283	-0.001097679	0.616708667	-0.035527865
Q14181	DNA polymerase alpha subunit B	POLA2	0.087213558	0.016501745	0.500763625	0.050052007
M0R2B7;P28340;M0QZR8	DNA polymerase;DNA polymerase delta catalytic subunit	POLD1	0.272313354	-0.025331497	1.432311746	-0.096178373
A0A087WWF6;P49005;F8W8R3;C9JLE1	DNA polymerase delta subunit 2	POLD2	1.586847565	0.094977061	0.198359237	0.020108223
Q15054;E9PM91;E9PNC0;E9PRK3	DNA polymerase delta subunit 3	POLD3	0.861084906	-0.208655357	0.677578267	-0.194512049
Q9Y2S7;B4DEM9	Polymerase delta-interacting protein 2	POLDIP2	0.027863705	0.004116694	0.006753065	0.0012544
F6VRR5;Q9BY77;F8WCX5;Q8WUT1	Polymerase delta-interacting protein 3	POLDIP3	1.099091069	-0.107786814	1.320297408	-0.084180514
Q9NRF9	DNA polymerase epsilon subunit 3	POLE3	0.223321761	-0.063909721	0.093532945	0.039853223
O95602;B9ZVN9	DNA-directed RNA polymerase I subunit RPA1;DNA-directed RNA polymerase	POLR1A	0.146148492	-0.023812294	0.208818558	-0.028098424
Q9H9Y6	DNA-directed RNA polymerase I subunit RPA2	POLR1B	0.049393171	0.010036786	0.356628707	-0.055294673
O15160;E7EQB9;D6RDJ3;HOY723	DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C	0.614220801	-0.090207736	1.219854737	-0.157317162
Q9GZS1	DNA-directed RNA polymerase I subunit RPA49	POLR1E	0.279273898	-0.066889445	0.922733147	-0.148442904
P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A	1.058826672	-0.059203784	0.127094345	-0.011580785
C9J2Y9;P30876;A0A1W2PPT5;C9J4M6	DNA-directed RNA polymerase;DNA-directed RNA polymerase II subunit RPB2	POLR2B	0.964460217	0.081334432	0.356675562	-0.032245318

P19387	DNA-directed RNA polymerase II subunit RPB3	POLR2C	0.788271376	0.126004537	0.002841352	0.0006965
O15514;E9PB93;E9PHV4	DNA-directed RNA polymerase II subunit RPB4	POLR2D	0.134846583	-0.092745463	0.294809693	0.219004949
A0A0A0MQR7;P19388;A0A087WVZ9;A0A087WWX0	DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E	1.17295846	0.139812787	0.030416875	-0.006193161
P62487	DNA-directed RNA polymerase II subunit RPB7	POLR2G	1.27941292	0.097787539	0.612570271	0.053025881
C9JLU1;P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H	1.092139892	-0.091436386	0.75754181	-0.062903404
P36954;K7EKS1	DNA-directed RNA polymerase II subunit RPB9	POLR2I	3.013840936	-0.290148608	0.767428639	0.091270765
A0A0B4J2F8;F6S314;E2QRJ6;P52435;D6RAG0;E7EP90;A0A0B4J1Z8;A6NFM0;E7EWC6;H0Y980;Q9H1A7;Q9GZM3	DNA-directed RNA polymerase II subunit RPB11-a;DNA-directed RNA polymerase II subunit RPB11-b2;DNA-directed RNA polymerase II subunit RPB11-b1	POLR2J3;POLR2J;POLR2J2	0.914411962	0.148980776	0.906381054	-0.150191625
P62875	DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L	0.779964012	-0.185351372	1.066362698	-0.221086502
Q9BU14;E9PHH9	DNA-directed RNA polymerase III subunit RPC3	POLR3C	1.186975363	0.148333549	0.361244439	0.077454249
P05423	DNA-directed RNA polymerase III subunit RPC4	POLR3D	0.68601999	-0.199384054	0.345224365	-0.125507037
O00411	DNA-directed RNA polymerase, mitochondrial	POLRMT	0.389877663	-0.051072439	0.462261104	-0.075640678
A0A087WY75;A0A075B7F8;A8CG34;Q96HA1	Nuclear envelope pore membrane protein POM 121C;Nuclear envelope pore membrane protein POM 121	POM121C;POM121	0.039953125	0.010525703	0.544384172	-0.101903598
Q9Y244	Proteasome maturation protein	POMP	0.574047616	0.228368759	3.909529941	1.134586016
Q99575	Ribonucleases P/MRP protein subunit POP1	POP1	0.362995746	-0.058440526	0.337504138	-0.066545486
Q969H6	Ribonuclease P/MRP protein subunit POP5	POP5	0.18847186	-0.024824905	1.689990817	-0.136351395
P16435;H0Y4R2;E7EMD0	NADPH--cytochrome P450 reductase	POR	0.367172302	-0.036466916	0.786803981	-0.058952332
Q6S8J3;A5A3E0;P0CG38	POTE ankyrin domain family member E;POTE ankyrin domain family member F;POTE ankyrin domain family member I	POTEE;POTEF;POTEI	2.173027458	-0.828073819	0.804857178	-0.440893491
A0A0C4DG88;P14859	POU domain protein;POU domain, class 2, transcription factor 1	POU2F1	0.281816656	-0.047784424	0.400402777	-0.072329839
Q15181;Q5SQT6	Inorganic pyrophosphatase	PPA1	0.318704488	-0.029892286	0.156373187	0.016807556
Q9H2U2;D6R967;H0Y9D8	Inorganic pyrophosphatase 2, mitochondrial	PPA2	1.245878861	0.110574404	0.545551649	-0.076587359
A0A0A6YYI3;A0A0B4J1V8;Q9NQ55;A8MV53;C9J3W3	Suppressor of SWI4 1 homolog	PPAN-P2RY11;PPAN	1.366149364	-0.109004021	0.037836095	-0.005655924
Q06203	Amidophosphoribosyltransferase	PPAT	2.465024922	-0.212011655	2.329270284	-0.181211472
F8W0Q9;F8WF16;B7Z8L1;F8W6A0;Q8NEY8	Periplin-1	PPHLN1	0.817558565	0.196730932	0.325585305	-0.065852737
P62937;F8WE65;C9J5S7	Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase A, N-terminally processed;Peptidyl-prolyl cis-trans isomerase	PPIA	1.096854045	-0.078495661	0.61701929	-0.044693629
P23284	Peptidyl-prolyl cis-trans isomerase B	PPIB	0.69483264	0.044286728	0.224973998	-0.0195357
Q08752	Peptidyl-prolyl cis-trans isomerase D	PPID	0.105465667	-0.015308062	0.501292636	-0.05468305
Q9UNP9;E9PEQ6;E9PKY5	Peptidyl-prolyl cis-trans isomerase E;Peptidyl-prolyl cis-trans isomerase	PPIE	0.949905322	-0.1397597	1.867091299	-0.232853572
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF	2.723675016	0.147045135	0.872201152	-0.068141619
C9JN15;Q13427;E9PG73;C9JM79	Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase G	PPIG	0.189191847	0.039538066	0.542761187	-0.105628332
C9JQD4;O43447;H0YEL5	Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase H	PPIH	0.099843831	0.011814117	0.299065871	-0.022950808
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1	PPIL1	0.110773474	0.029701869	0.160666398	-0.05695947
H7BZ14;Q9H2H8;B8ZZ77	Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3	0.360041541	-0.041748365	0.228175457	-0.054126422
Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4	1.207595281	-0.212144184	0.583845437	-0.068002701
A0A087WZV0;O43314;H0Y9S9	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2	PPIP5K2	0.196716898	0.056961695	0.041047713	-0.011086146
K7EKI8;O60437;K7EQ71	Periplakin	PPL	0.070854061	-0.017057737	0.179218972	-0.039798419
C9JIR6;O75688;B8ZZF0	Protein phosphatase 1B	PPM1B	0.015110176	-0.009746075	0.291529693	-0.124768734
O15355	Protein phosphatase 1G	PPM1G	0.632360841	0.081098874	0.696206828	0.08271726

Q9ULR3	Protein phosphatase 1H	PPM1H	0.585964012	-0.141246796	0.239172605	-0.063075066
Q9Y570	Protein phosphatase methylesterase 1	PPME1	0.073249182	0.010999997	0.066970279	-0.010139147
P50336	Protoporphyrinogen oxidase	PPOX	1.740949043	-0.165453911	0.323931705	-0.06976827
P62136;E9PMD7	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;Serine/threonine-protein phosphatase	PPP1CA	0.28666027	-0.018138885	0.655193322	-0.034844716
P62140;E7ETD8;C9JP48	Serine/threonine-protein phosphatase PP1-beta catalytic subunit;Serine/threonine-protein phosphatase	PPP1CB	0.176179597	-0.035563469	0.81172972	-0.106852531
Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	PPP1R10	1.428618321	-0.201918284	0.035834502	-0.010481199
O14974;F8VZN8	Protein phosphatase 1 regulatory subunit 12A	PPP1R12A	0.533121315	-0.092179298	0.149306466	-0.022197723
Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B	2.439676268	-0.272516886	0.09004507	-0.022843043
P41236;E7EMN6;G1AUC5;Q6N XS1;E7EUI7	Protein phosphatase inhibitor 2;Protein phosphatase inhibitor 2-like protein 3	PPP1R2;PPP1R2P3	0.948149974	-0.428252538	0.543518814	-0.275979678
H7C003;C9J177;Q15435;B5MB Z8;C9JD73	Protein phosphatase 1 regulatory subunit 7	PPP1R7	1.95699729	-0.196311315	2.11090616	-0.175642331
Q12972	Nuclear inhibitor of protein phosphatase 1;Activator of RNA decay	PPP1R8	1.517880189	-0.140429179	0.925630274	-0.073287646
P6775;P62714	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform;Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CA;PPP2CB	0.199194031	0.031615257	0.451866224	0.079008102
P30153;B3KQV6;C9J9C1	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	PPP2R1A	0.44042055	-0.037297885	0.947118261	0.065187136
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B	1.503502964	-0.183276812	0.438577328	-0.072910945
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A	0.077949507	0.004944166	0.584113622	-0.049093564
Q15257;F6WIT2;A6PVN5;A6P VN9;Q5T949;Q5T948	Serine/threonine-protein phosphatase 2A activator	PPP2R4	2.075601358	-0.08025233	0.608159625	-0.030070623
H0YJ75;Q13362;Q96B13	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	PPP2R5C	1.207293499	0.803285122	0.863875006	0.511252562
E9PFR3;Q14738;H0Y8C4	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D	0.253702123	-0.037712415	0.856710768	-0.076018016
Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	PPP2R5E	0.119697483	0.030179342	0.10468133	0.02194341
Q08209;E7ETC2;E9PPC8;E9PK 68;Q5F2F8;P16298	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	PPP3CA;PPP3CB	0.35616209	-0.121773084	0.553665984	-0.213784854
H7BYZ3;F6U1T9;D3YTA9;P63 098	Calcineurin subunit B type 1	PPP3R1	0.668820272	-0.280744267	0.326724075	-0.108046246
P60510;H3BTA2;I3L4X0;H3BV 22	Serine/threonine-protein phosphatase 4 catalytic subunit;Serine/threonine-protein phosphatase	PPP4C	0.237287002	-0.033969561	1.736093689	-0.175131162
Q9NY27;F8WCA1;C9IZ04	Serine/threonine-protein phosphatase 4 regulatory subunit 2	PPP4R2	0.020831673	-0.008428574	0.086328939	0.037300873
H0YDU8;P53041;A8MU39	Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase 5	PPP5C	1.4241206	-0.111166318	0.046707022	0.005704562
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit;Serine/threonine-protein phosphatase 6 catalytic subunit, N-terminally processed	PPP6C	0.241750973	0.024933179	0.028817991	0.003869057
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1	2.041910888	0.152053515	0.908772611	0.063519478
H7BXH2;E9PKF6;Q5H9R7;E9P QP7	Serine/threonine-protein phosphatase 6 regulatory subunit 3	PPP6R3	2.654187786	-0.312421799	0.548358347	-0.091989199
A0A2C9F2P4;A0A286YFF7;P5 0897;Q5T0S4;A0A286YFE3;A0 A286YFL8;E9PK48	Palmitoyl-protein thioesterase 1	PPT1	2.780411493	-0.486434937	0.428866743	-0.120772362
F5H7P7;Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	PPWD1	0.795142793	-0.10772419	0.495818385	-0.054463387
O60828	Polyglutamine-binding protein 1	PQBP1	1.086573141	-0.153746923	1.29583588	0.129055023
O43663	Protein regulator of cytokinesis 1	PRC1	0.697496441	0.095907211	1.005819777	0.086771647
Q92733	Proline-rich protein PRCC	PRCC	0.022575175	-0.005019506	1.418651701	0.217882156
P42785;E9PLY4;E9PNF7;E9PQ B5;E9PL85;E9PNJ1;E9PQN3;E 9PKN6;E9PIG4	Lysosomal Pro-X carboxypeptidase	PRCP	0.345832655	-0.300620556	0.004077687	-0.00350666

Q06830;A0A0A0MSI0	Peroxiredoxin-1	PRDX1	0.104296964	-0.013856888	0.510268048	0.044819514
P32119;A6NIW5	Peroxiredoxin-2	PRDX2	1.496923871	-0.118802389	0.231018698	-0.021442731
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	3.36254216	0.161569277	0.322874867	0.021597226
Q13162;H7C3T4	Peroxiredoxin-4	PRDX4	3.371432922	0.182213783	0.284623121	0.015510559
P30044	Peroxiredoxin-5, mitochondrial	PRDX5	0.450777329	-0.03602918	0.959552682	-0.075181325
P30041	Peroxiredoxin-6	PRDX6	2.226388965	-0.095461528	0.434821993	0.022391001
Q9HCU5;B5MC98	Prolactin regulatory element-binding protein	PREB	1.567096191	0.110442162	0.174938775	0.021826744
P48147	Prolyl endopeptidase	PREP	1.912679405	-0.190402349	2.11337984	-0.155072848
Q4J6C6	Prolyl endopeptidase-like	PREPL	0.119920497	0.03598175	0.514535021	0.158868599
P49642	DNA primase small subunit	PRIM1	0.115128688	-0.012592316	0.223336064	-0.024785678
P49643	DNA primase large subunit	PRIM2	0.930444833	0.08647124	0.040912176	-0.004298528
Q13131	5-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1	0.348555863	0.085125605	0.030006622	0.010279655
P17612	cAMP-dependent protein kinase catalytic subunit alpha	PRKACA	1.341895409	-0.155168851	0.902997809	-0.11663119
F8VYY9;P54619;H0YHF8;F8V PF5	5-AMP-activated protein kinase subunit gamma-1	PRKAG1	0.053236172	-0.017694028	0.059401225	0.020880858
P10644;K7EM13;K7EPB2	cAMP-dependent protein kinase type I-alpha regulatory subunit;cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed	PRKAR1A	1.655076252	0.174882889	2.598868745	0.201057116
H7BYW5;P31321;C9JSK5	cAMP-dependent protein kinase type I-beta regulatory subunit	PRKAR1B	0.050699447	-0.015006828	0.097473791	-0.023131943
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A	0.201716812	-0.020557086	0.104670541	-0.010898908
Q05655	Protein kinase C delta type;Protein kinase C delta type regulatory subunit;Protein kinase C delta type catalytic subunit	PRKCD	0.82501394	-0.201839193	1.090473632	-0.174954096
P41743	Protein kinase C iota type	PRKCI	0.075951577	0.012035052	0.078943614	-0.015894254
K7ELL7;P14314	Glucosidase 2 subunit beta	PRKCSH	1.529792044	0.191285451	0.924567998	0.128138542
B4DTS2;Q9BZL6	Serine/threonine-protein kinase;Serine/threonine-protein kinase D2	PRKD2	0.322448477	0.167662621	0.142252028	0.08186245
P78527	DNA-dependent protein kinase catalytic subunit	PRKDC	2.042285267	0.055054983	2.704752609	-0.060283025
O75569;F8WEG8;G5E9Q4;C9J MM3	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	PRKRA	0.235742268	0.042729696	0.517646401	-0.095160484
E9PKG1;H7C2I1;Q99873;A0A0 87X1W2;E9PQ98;E9PIX6;H0Y DE4;E9PNR9	Protein arginine N-methyltransferase 1	PRMT1	0.324705527	-0.0270799	0.086412907	-0.007481257
O60678;A0A0A0MSN7	Protein arginine N-methyltransferase 3	PRMT3	0.41853502	-0.054765701	0.846074667	-0.081933657
O14744	Protein arginine N-methyltransferase 5;Protein arginine N-methyltransferase 5, N-terminally processed	PRMT5	1.072771906	-0.088514646	1.023387157	-0.073957125
O94903;E5RG77	Proline synthase co-transcribed bacterial homolog protein	PROSC	0.467153047	-0.093936284	0.0319932	0.005830447
Q9UMS4	Pre-mRNA-processing factor 19	PRPF19	0.97834787	0.04226462	0.521941224	0.029814402
O43395	U4/U6 small nuclear ribonucleoprotein Prp3	PRPF3	0.644775048	-0.079574903	0.193367818	-0.034267743
Q8WWY3;E7EVX8;E7EU94;E7 ESX0;E7EN72	U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31	1.616039491	0.089507103	0.669877359	0.044139544
Q8NAV1	Pre-mRNA-splicing factor 38A	PRPF38A	0.273545722	0.059011141	0.056100765	0.008777301
O43172	U4/U6 small nuclear ribonucleoprotein Prp4	PRPF4	1.152445912	0.087109566	0.165140265	-0.022431056
O75400	Pre-mRNA-processing factor 40 homolog A	PRPF40A	0.0394785	0.004412015	0.579416853	-0.047609647
Q13523;H0YDJ3	Serine/threonine-protein kinase PRP4 homolog	PRPF4B	0.278232009	-0.049854279	0.092652738	-0.01628081
O94906	Pre-mRNA-processing factor 6	PRPF6	2.401144459	0.184887886	1.157213483	0.106911977
Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8	1.753548585	0.078711192	0.177715688	-0.011158625
P60891;B1ALA9;B7ZB02	Ribose-phosphate pyrophosphokinase 1	PRPS1	0.142156765	-0.018857638	0.733062863	0.078586896
P11908;H7C540	Ribose-phosphate pyrophosphokinase 2	PRPS2	3.450765558	-0.114109039	2.952481073	-0.103384972
Q14558;B4DP31;C9J168	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1	0.960976527	-0.151876767	1.11497779	-0.153955142
O60256;E7EPA1;C9JJS3;C9K0 K7;I3L0S1	Phosphoribosyl pyrophosphate synthase-associated protein 2	PRPSAP2	1.986427078	-0.144806226	0.575129925	-0.041866302

P48634	Protein PRRC2A	PRRC2A	2.955891987	-0.272356987	2.019271589	-0.143724442
Q5JSZ5	Protein PRRC2B	PRRC2B	0	-0.071004868	0	0.172489166
E7EPN9;Q9Y520	Protein PRRC2C	PRRC2C	2.320966772	0.186714172	4.060026371	0.283594449
A6XMV8;A0A0J9YYC8;A6XMV9;P07478	Trypsin-2	PRSS2	3.313991558	-0.388644536	0.656958212	-0.095931053
Q86TP1	Protein prune homolog	PRUNE	0.420280813	-0.149153392	0.770632938	-0.212548256
C9JIZ6;P07602	Prosaposin;Saposin-A;Saposin-B-Val;Saposin-B;Saposin-C;Saposin-D	PSAP	0.82825398	-0.157707214	0.866743305	0.151302338
Q9Y617	Phosphoserine aminotransferase	PSAT1	1.776380062	0.187183062	2.200152054	0.222305934
O75475	PC4 and SFRS1-interacting protein	PSIP1	2.281467584	-0.300978343	0.611913146	-0.103579203
X5D2R7;P28062;Q5JNW7;A0A140T998	Proteasome subunit beta type;Proteasome subunit beta type-8	PSM8;PSMB8	1.7803942	-0.165245374	0.828567738	-0.075490952
P25786;F5GX11	Proteasome subunit alpha type-1	PSMA1	1.938807944	-0.045791626	2.187594085	0.059295336
A0A024RA52;P25787;C9JCK5	Proteasome subunit alpha type;Proteasome subunit alpha type-2	PSMA2	0.859895372	-0.089545568	0.580498921	0.064941724
P25788	Proteasome subunit alpha type-3	PSMA3	0.105291542	0.014659246	1.280032941	0.099911372
P25789;HOYMZ1;H0YN18;HOYL69;HOYMA1;HOYKT8;HOYMI6;H0YKSO;HOYLC2	Proteasome subunit alpha type-4;Proteasome subunit alpha type;Proteasome subunit beta type	PSMA4	0.024193648	0.002711296	1.161841231	0.074241956
P28066	Proteasome subunit alpha type-5	PSMA5	0.368848168	-0.023331006	2.056617475	0.117782911
P60900;G3V295;G3V5Z7;G3V3I1	Proteasome subunit alpha type-6;Proteasome subunit alpha type	PSMA6	0.850295796	-0.061204274	0.859248535	0.0605793
O14818	Proteasome subunit alpha type-7	PSMA7	0.581406648	-0.056012472	1.854243952	0.112276077
P20618	Proteasome subunit beta type-1	PSMB1	0.48400448	0.028890292	0.102063402	0.007784843
P40306;J3QQN1	Proteasome subunit beta type-10	PSMB10	1.187199296	-0.199723244	1.741305275	-0.266177654
P49721	Proteasome subunit beta type-2	PSMB2	0.028719563	0.002620061	1.827861849	0.127921422
P49720;A0A087WUL2;A0A087WXQ8;A0A087WY10	Proteasome subunit beta type-3	PSMB3	1.38462872	-0.130905787	0.587809356	0.061436653
P28070	Proteasome subunit beta type-4	PSMB4	1.796365111	0.127743721	2.503772741	0.213807424
P28074	Proteasome subunit beta type-5	PSMB5	2.752127547	-0.151314735	3.568288547	0.158546766
P28072;A0A087X214	Proteasome subunit beta type-6;Proteasome subunit beta type	PSMB6	0.661783127	-0.105044683	1.007435385	0.129282951
Q99436	Proteasome subunit beta type-7	PSMB7	0.339423148	0.031557401	3.991407769	0.269337336
A2ACR1;P28065;A0A0G2JJA7;A2ACR0	Proteasome subunit beta type;Proteasome subunit beta type-9	PSMB9	1.413392951	-0.187484423	0.014025632	-0.002117157
P62191	26S protease regulatory subunit 4	PSMC1	0.286048476	-0.020562172	3.56591457	0.132266363
P35998;A0A1W2PQS1	26S protease regulatory subunit 7	PSMC2	2.630631224	0.130160014	4.105448394	0.209781011
R4GNH3;P17980;E9PM69;E9PKD5;E9PMD8;E9PN50	26S protease regulatory subunit 6A	PSMC3	4.821780459	0.204127947	5.39992296	0.235345523
P43686	26S protease regulatory subunit 6B	PSMC4	0.558771776	0.040063222	3.19342771	0.185365359
P62195;J3QSA9;J3KRP2;J3QH6;J3QQM1	26S protease regulatory subunit 8	PSMC5	2.326111047	0.110186577	4.573733453	0.167555491
A0A087X211;P62333	26S protease regulatory subunit 10B	PSMC6	1.252208122	0.080740293	4.975423633	0.189926147
Q99460;A0A087WW66	26S proteasome non-ATPase regulatory subunit 1	PSMD1	0.455430876	-0.025746346	2.259988747	0.074193001
B1AJY7;O75832;B1AJY5	26S proteasome non-ATPase regulatory subunit 10	PSMD10	0.110506361	-0.022783279	0.162013648	0.034415245
O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11	1.182318858	0.086805979	2.156372255	0.150926908
O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12	0.959742682	0.049379031	3.202729911	0.15471077
Q9UNM6;J3KNQ3;A0A087WUL9;E9PL38;H0YD73	26S proteasome non-ATPase regulatory subunit 13	PSMD13	0.182758912	0.015756289	2.233077587	0.138067563
O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14	3.928033913	0.167895635	4.307733485	0.163315773
Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2	4.83944426	0.164259911	6.063075563	0.222184499
O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3	0.919055762	0.062782605	2.458166011	0.123143196
P55036;Q5VWC4;A6PVX3	26S proteasome non-ATPase regulatory subunit 4	PSMD4	4.559097295	-0.232134819	0.353338942	0.0295976
Q16401	26S proteasome non-ATPase regulatory subunit 5	PSMD5	1.936254965	-0.142300924	1.586263737	-0.103032748
Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6	1.014158706	0.099673907	1.651544013	0.136968613

P51665;H3BNT7;H3BTM8	26S proteasome non-ATPase regulatory subunit 7	PSMD7	1.059400397	0.079372724	1.736669145	0.097167651
R4GMR5;P48556;K7EJR3;K7EJC1	26S proteasome non-ATPase regulatory subunit 8	PSMD8	0.02263213	0.002503713	3.066343274	0.139595668
J3KN29;O00233;F5H5V4;F5GX23;F5H7X1	26S proteasome non-ATPase regulatory subunit 9	PSMD9	0.140866596	0.027952512	0.503377488	0.079371777
Q06323	Proteasome activator complex subunit 1	PSME1	2.251458219	-0.124772072	1.182023444	-0.062759082
A0A087X1Z3;Q9UL46;H0YM70	Proteasome activator complex subunit 2	PSME2	2.39739039	-0.159263611	0.421892577	0.040301323
P61289;K7ESG5;K9J957;B3KQ25;A0A087WTV2;K7ENH2	Proteasome activator complex subunit 3	PSME3	0.541516067	-0.047351201	0.222570427	-0.029240608
Q14997	Proteasome activator complex subunit 4	PSME4	0.312960344	0.051075935	0.839576733	0.11108621
Q5QPM7;Q92530;Q5QPM9	Proteasome inhibitor PI31 subunit	PSMF1	0.887448159	-0.220499039	0.061199488	0.024129868
O95456	Proteasome assembly chaperone 1	PSMG1	0.732610664	-0.079589208	0.081463266	-0.012071292
Q969U7;K7ENR6;V9GZ55	Proteasome assembly chaperone 2	PSMG2	0.644097856	-0.10232385	0.522552382	0.075037638
Q9BT73	Proteasome assembly chaperone 3	PSMG3	1.241609553	-0.218611399	0.987410514	-0.160994212
Q5JS54;D6RB92;D6REN3;E2QRC7;H7C465	Proteasome assembly chaperone 4	PSMG4	0.46051904	0.109004656	0.076965414	-0.026770592
Q8WXF1;X6RDA4	Paraspeckle component 1	PSPC1	0.070795317	-0.007198334	1.205003076	-0.086360296
C9JB13;P78330	Phosphoserine phosphatase	PSPH	2.664441599	0.2783343	1.070294702	0.137423833
A6NLN1;P26599;A0A0U1RRM4	Polypyrimidine tract-binding protein 1	PTBP1	3.614456689	-0.214359283	1.312411055	-0.089368502
O95758	Polypyrimidine tract-binding protein 3	PTBP3	0.018230694	0.004343669	0.23472372	-0.065330823
Q96EY7	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	PTCD3	0.593413431	-0.091448784	0.89375796	-0.115614573
P48651	Phosphatidylserine synthase 1	PTDSS1	1.297394094	0.253120422	0.684376922	0.167513529
Q9H7Z7;A6NH0;X6RJ95	Prostaglandin E synthase 2;Prostaglandin E synthase 2 truncated form	PTGES2	0.88404247	-0.111532847	1.373477999	-0.157125791
A0A087WYT3;Q15185;B4DDC6	Prostaglandin E synthase 3	PTGES3	0.036790169	-0.004692396	0.051019751	-0.006726901
Q14289	Protein-tyrosine kinase 2-beta	PTK2B	0.355026602	-0.039696376	1.463145992	-0.140920639
B8ZZQ6;P06454;B8ZZA1;B8ZZW7;H7C2N1	Prothymosin alpha;Prothymosin alpha, N-terminally processed;Thymosin alpha-1	PTMA	2.66560303	-0.547561328	0.862422643	0.2167298
Q12974;E9PMY3;E9PML8;E9PJCO;E9PRR9	Protein tyrosine phosphatase type IVA 2	PTP4A2	0.221920795	0.061934471	0.091590879	-0.028295835
P18031;B4DSN5	Tyrosine-protein phosphatase non-receptor type 1;Tyrosine-protein phosphatase non-receptor type	PTPN1	2.380207482	0.216922442	0.860840732	0.133907636
Q06124;A0A1W2PPU4	Tyrosine-protein phosphatase non-receptor type 11	PTPN11	0.243948175	-0.041416486	0.50948117	0.074325879
K7EQG9;P17706	Tyrosine-protein phosphatase non-receptor type;Tyrosine-protein phosphatase non-receptor type 2	PTPN2	0.200401784	0.07942613	0.017772289	-0.007978821
Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23	PTPN23	0.27738042	0.053801219	0.861794116	0.131372134
P29350;F5H0N8	Tyrosine-protein phosphatase non-receptor type 6	PTPN6	1.33142336	-0.131561915	0.993404482	-0.10690403
J3KR55;P35236	Tyrosine-protein phosphatase non-receptor type 7	PTPN7	0.248704875	0.044459343	0.04665466	-0.011804263
Q86Y79;A0A096LP34;A0A096LP22	Probable peptidyl-tRNA hydrolase	PTRH1	0.310326447	-0.08118089	0.157058676	0.059992472
J3KQ48;Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2	0.556487257	0.076713562	0.50298642	0.062735558
Q6GMV3	Putative peptidyl-tRNA hydrolase	PTRHD1	0.787065383	-0.129310608	0.145089854	0.026778221
A0A0J9YYL3;A0A0J9YXJ8;A0A0J9YVP6;A0A0J9YXX5;Q9UHX1;A0A0J9YVR6;E9PQ56;A0A0J9YWM1;H0YEM1	Poly(U)-binding-splicing factor PUF60	PUF60	0.697919464	-0.031118075	0.169566014	-0.010743141
H0YDK8;Q5T1Z4;Q5T1Z8;E9PR38;H0YEH2;Q14671	Pumilio homolog 1	PUM1	0.273744177	0.051740964	0.248292185	-0.047036489
A0A0C4DG68;A0A0A0MR59;Q8TB72	Pumilio homolog 2	PUM2	0.177886607	0.053303719	0.766217118	-0.133196513
Q00577	Transcriptional activator protein Pur-alpha	PURA	0.948429238	0.242251968	0.627009319	0.143694592
Q96QR8	Transcriptional activator protein Pur-beta	PURB	1.314127054	0.121756872	2.223917321	0.157593409
F5H1S9;G8JLB3;Q9Y606	tRNA pseudouridine synthase;tRNA pseudouridine synthase A, mitochondrial	PUS1	0.859882353	0.065167745	0.874961843	-0.081001282
Q96PZ0;E7EUH7	Pseudouridylate synthase 7 homolog	PUS7	0.968596849	-0.064251582	0.873897121	-0.066492081
P20472;B8ZZ19;H0Y3U0;B1AH72	Parvalbumin alpha	PVALB	2.181962017	-0.11545531	0.719424754	-0.041679064
B4DJV5;Q13610	Periodic tryptophan protein 1 homolog	PWP1	0.604364478	0.113823891	0.022409775	-0.006840706
Q15269;A0A0B4J2E5	Periodic tryptophan protein 2 homolog	PWP2	1.12436615	0.053802172	1.003840437	-0.06588014

H7C4V0;E9PD56;H7BYG4;W5RWE6;A0A0C4DG95;Q7Z7A4;U3KQS4 Q9ULZ3;H3BP42	PX domain-containing protein kinase-like protein	PXX	0	-0.309924126	0	-0.330586243
P32322;E2QRB3;J3KQ22;J3QL24;J3QKT4;J3QLK9;J3QL23;J3QL32	Apoptosis-associated speck-like protein containing a CARD	PYCARD	1.840805581	-0.21009318	0.446584886	-0.226717631
Q96C36;A0A087WTV6;A0A087WZR9;J3KR12	Pyroline-5-carboxylate reductase 1, mitochondrial;Pyroline-5-carboxylate reductase	PYCR1	0.090152775	-0.01093483	0.63995618	0.056617101
A0A0A0MQS1;Q53H96	Pyroline-5-carboxylate reductase 2;Pyroline-5-carboxylate reductase	PYCR2	3.616322285	-0.148739497	1.96342146	-0.101815224
P11216	Pyroline-5-carboxylate reductase 3	PYCRL	0.273365288	0.034965197	0.622186441	-0.066038767
Q96123	Glycogen phosphorylase, brain form	PYGB	2.81694873	-0.133673032	2.246876721	-0.13561662
P47897	Protein preY, mitochondrial	PYURF	0.716061574	-0.402042961	0.103329819	-0.032288869
P09417	Glutamine--tRNA ligase	QARS	1.679512925	-0.112744013	2.207800404	-0.099582354
A0A140TA86;Q5XKP0;K7EIR2;A0A140TA84 Q96PUS;F5GXS8;F5GYM3;H0YG47 Q2TAL8	Dihydropteridine reductase	QDPR	0.349090832	-0.03749307	0.214803841	0.017901738
Q6ZRP7;H0Y430	Protein QIL1	QIL1;C19orf70	0.669912448	0.078145027	0.567144582	0.084706942
Q9BXR0;K7ESP6;K7EJ21	Protein quaking	QKI	0.592575033	-0.05802695	2.543422347	-0.141438802
Q9H974	Glutamine-rich protein 1	QRICH1	0.011644514	0.004012616	0.220572619	0.078754934
P61026	Sulfhydryl oxidase 2;Sulfhydryl oxidase	QSOX2	0.409161195	-0.08760198	0.539704498	-0.106038094
Q15907	Queuine tRNA-ribosyltransferase	QTRT1	1.660179243	-0.180052439	0.250211438	-0.048571905
Q6WKZ4;E7EX40	Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1	0.139651996	0.025957108	0.036618094	0.007396698
P61106;X6RFL8	Ras-related protein Rab-10	RAB10	0.300474589	0.028431575	0.028307314	0.00303332
Q9NP72;A0A087X163;H0Y6T8;Q5W0J0 P62820;E7END7	Ras-related protein Rab-11B	RAB11B	0.680449531	-0.041793823	0.738392809	-0.040352186
Q9H0U4;E9PLD0	Rab11 family-interacting protein 1	RAB11FIP1	0.072306098	0.034562492	0.075654288	0.034004784
Q9UL25	Ras-related protein Rab-14	RAB14	0.179590872	0.020855586	0.140558471	-0.016912142
H3BN55;P51159;H3BS49;H3BVH7;H3BUD9 P61019;E9PKL7;Q8WUD1	Ras-related protein Rab-18	RAB18	0.847127186	-0.064017932	0.686556274	-0.062500318
Q15771;E9PS06;E9PMJ1;E9PJQ5;E9PRF7;E9PNB9;H0YDK7 F5H157;Q15286	Ras-related protein Rab-1A	RAB1A	1.17781103	0.095276197	2.794394404	0.141940435
O95716;P20336	Ras-related protein Rab-1B	RAB1B	0.569902152	0.134813627	0.828400755	0.18874232
Q15042	Ras-related protein Rab-21	RAB21	0.101711201	0.020896276	0.201867121	-0.032135646
Q9H2M9	Ras-related protein Rab-27A	RAB27A	0.319379344	0.058139483	0.499395523	0.089918137
Q8TBN0;E9PK89	Ras-related protein Rab-2A;Ras-related protein Rab-2B	RAB2A;RAB2B	0.540343494	-0.07033062	0.590125685	-0.055742582
P20339	Ras-related protein Rab-30	RAB30	0.957923931	-0.193144162	0.979460487	-0.23767217
P61020;F8VUA5	Ras-related protein Rab-35	RAB35	0.1224329	0.046696345	1.492194035	0.18555514
P51148;F8VVK3;K7ER18;K7ERQ8 P20340;Q9NRW1;J3KR73;C9JU14 Q9H0N0;Q53S08	Ras-related protein Rab-3D;Ras-related protein Rab-3A	RAB3D;RAB3A	0.99265026	-0.219089826	0.694333525	-0.140679677
P51149;C9J592;C9J8S3;C9J4V0;C9IZZ0 P61006	Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1	0.216597273	0.041120847	0.057656447	0.011808077
P51151	Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2	0.643842254	-0.072443962	0.742614362	-0.102474848
Q7Z6M1;Q5T1S5	Guanine nucleotide exchange factor for Rab-3A	RAB3IL1	1.084213061	-0.242109299	0.348106252	-0.101533572
Q9Y3P9	Ras-related protein Rab-5A	RAB5A	0.031961296	-0.007417043	0.20477371	-0.032297516
Q5R372;A0A0C4DG54;A0A0U1RQY6 Q92696;H0YLG7	Ras-related protein Rab-5B	RAB5B	0.127247753	0.059354146	0.189500293	0.074374517
Q5HY18;C9JXM3	Ras-related protein Rab-5C	RAB5C	0.764150953	0.048522949	1.858290497	0.129691442
	Ras-related protein Rab-6A;Ras-related protein Rab-6B	RAB6A;RAB6B	0.407147049	0.0478309	0.027532451	0.005287806
	Ras-related protein Rab-6C	RAB6C	1.954727839	-0.370563348	0.16460405	-0.062847805
	Ras-related protein Rab-7a	RAB7A	0.106704714	-0.014077187	0.115753331	-0.01444753
	Ras-related protein Rab-8A	RAB8A	0.495670046	-0.088088036	0.167208204	0.03050073
	Ras-related protein Rab-9A	RAB9A	0.213874542	-0.14452076	1.106934963	-0.163047791
	Rab9 effector protein with kelch motifs	RABEPK	1.31451099	-0.166226514	0.786724304	-0.165075429
	Rab GTPase-activating protein 1	RABGAP1	0.048693867	-0.017758052	0.059951	0.020598412
	Rab GTPase-activating protein 1-like	RABGAP1L	0.003805634	0.000531642	0.69432857	-0.079606692
	Geranylgeranyl transferase type-2 subunit alpha	RABGGTA	0.826686138	-0.422140312	1.336754397	-0.692487272
	Rab-like protein 3	RABL3	0.028813821	0.007665634	0.13063822	0.034169515

Q3YEC7;G3V154;F2Z2T0;HOY4Z8 P63000;P60763	Rab-like protein 6	RABL6	3.251702898	-0.252705574	1.363171018	-0.156370799
	Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrate 3	RAC1;RAC3	1.88134767	0.135035515	1.60346527	0.11639595
P15153;B1AH77;B1AH80;B1AH78 Q9H0H5	Ras-related C3 botulinum toxin substrate 2	RAC2	0.516713783	-0.035118421	0.202199494	0.018714905
	Rac GTPase-activating protein 1	RACGAP1	1.440961062	-0.113376935	0.325574032	0.050072034
Q9NS91;F8WE49	E3 ubiquitin-protein ligase RAD18	RAD18	0.440262078	0.308019956	0.052184448	0.035593987
O60216	Double-strand-break repair protein rad21 homolog	RAD21	0.092278053	-0.014253298	0.700015987	-0.090328534
P54725;K7ENJ0;K7ELW1	UV excision repair protein RAD23 homolog A	RAD23A	1.689482612	-0.134194056	0.19022226	-0.024481455
P54727;Q5W0S5	UV excision repair protein RAD23 homolog B	RAD23B	0.357028026	-0.033308983	1.154295745	0.088389715
Q92878	DNA repair protein RAD50	RAD50	0.826018115	0.058733304	0.306636085	-0.032450676
P78406;E9PQ57	mRNA export factor	RAE1	0.539458051	0.065583547	0.295332462	0.027345022
P11233;H7C3P7;C9JPE8;P11234 Q9UKM9;Q5QPL9;Q5QPM1;Q5QPM2	Ras-related protein Ral-A;Ras-related protein Ral-B	RALA;RALB	0.499191896	0.069812457	0.144278544	-0.037496885
	RNA-binding protein Raly	RALY	1.91545715	0.11686039	0.299027535	0.025495211
B5MDF5;J3KQE5;P62826;F5H018;HOYFC6	GTP-binding nuclear protein Ran	RAN	0.981180366	-0.074825287	1.363373234	-0.088167508
P43487;F6WQW2;C9JXG8;C9JJ34;C9JGV6 P49792	Ran-specific GTPase-activating protein	RANBP1	0.138837122	-0.02595075	0.007475033	-0.002038002
	E3 SUMO-protein ligase RanBP2	RANBP2	3.615427975	0.119338989	1.929850684	0.063239415
B7Z7F3;Q9H6Z4;K7EI14	Ran-binding protein 3	RANBP3	0.110682463	-0.022643407	0.605912776	0.072310766
Q96S59	Ran-binding protein 9	RANBP9	0.164301482	-0.047963778	0.000181217	-6.71E-05
P46060	Ran GTPase-activating protein 1	RANGAP1	0.875736745	0.036001841	1.754385803	0.06854407
Q9HD47	Ran guanine nucleotide release factor	RANGRF	0.556153593	-0.070526123	0.009190135	0.003054619
P61224;F5GX62;E7ESV4;F5H7Y6;F5H004;A6NIZ1;F5H6R7;F5H0B7;F5H500;F5H823;B7ZB78;F5GZG1;F5GYB5 P52306	Ras-related protein Rap-1b;Ras-related protein Rap-1b-like protein	RAPIB	0.034692901	-0.004781723	0.054724876	0.006563505
	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1	2.343898475	-0.117031733	0.456693714	-0.040221532
P61225;F6U784;P10114	Ras-related protein Rap-2b;Ras-related protein Rap-2a	RAP2B;RAP2A	0.538281784	0.066942851	0.488499948	0.063266436
Q9Y3L5	Ras-related protein Rap-2c	RAP2C	0.730780428	0.144757398	0.022289915	-0.004324595
P54136	Arginine--tRNA ligase, cytoplasmic	RARS	2.948829401	-0.126512527	2.744673611	-0.108121554
Q5T160	Probable arginine--tRNA ligase, mitochondrial	RARS2	0.219171691	-0.069476446	0.111110332	-0.034255981
E9PGC0;P20936	Ras GTPase-activating protein 1	RASA1	0.064499796	-0.013069789	0.783465558	-0.138174057
O95294	RasGAP-activating-like protein 1	RASAL1	1.260924983	0.173296928	0.011867044	0.002486547
Q86YV0	RAS protein activator like-3	RASAL3	0.958767443	0.125673294	0.285932208	-0.06846269
A0A087WZ13;E9PAU2;Q8IY67	Ribonucleoprotein PTB-binding 1	RAVER1	0.638559162	0.036080996	0.419408191	0.020183563
P06400	Retinoblastoma-associated protein	RB1	0.097793073	-0.012536685	3.088778518	-0.147981644
Q09028;HOYF10	Histone-binding protein RBBP4	RBBP4	1.199401849	0.086070061	1.728201505	0.117058118
Q15291	Retinoblastoma-binding protein 5	RBBP5	0.318703616	0.036872546	1.574444776	0.153102875
Q7Z6E9;I3L3Y2;H3BUN0	E3 ubiquitin-protein ligase RBBP6	RBBP6	0.159688575	0.037616158	0.40214237	0.101226807
Q16576;E9PC52;Q5JP01	Histone-binding protein RBBP7	RBBP7	0.242689202	0.027212779	0.772404045	0.073143323
A0A0G2JSB3;I3L1D4;B0QYY7;S4R469;F8VR27;F8VZY7;B0QYV1;B0QYY4;A0A087X2B1;A0A0G2JRA5;J3KNW3;B7Z1U7;F8VZG9;A0A286YEU2;O43251;Q9NWB1;B0QYY6;A0A0G2JRD1;S4R3K7;J3QZ22;J3QRF4;F8VRS4;A6NFN3 A0A0A0MR66;P98175	RNA binding protein fox-1 homolog;RNA binding protein fox-1 homolog 2;RNA binding protein fox-1 homolog 1;RNA binding protein fox-1 homolog 3	RBFOX1;RBFOX2;RBFOX3	0	0.096831322	0	0.226486206
Q9NTZ6	RNA-binding protein 10	RBM10	0.90545601	0.058038076	0.78809192	0.054676056
B9ZVT1;Q8IXT5	RNA-binding protein 12	RBM12	1.02154547	-0.08523496	0.962640656	-0.083547274
Q96PK6	RNA-binding protein 12B	RBM12B	0.166521106	0.029809952	1.547966227	-0.162092845
A0A087WWP4;Q96T37	RNA-binding protein 14	RBM14	1.494352232	0.080952962	0.147065471	0.01389122
	Putative RNA-binding protein 15	RBM15	0.330936402	0.042863846	0.278320314	0.035847982
Q96I25;Q5W011;Q5W010;HOY6J6;Q5W012	Splicing factor 45	RBM17	0.153348947	-0.037496885	0.027309765	-0.005857786

Q9Y4C8	Probable RNA-binding protein 19	RBM19	0.093368246	-0.015910467	0.107125471	-0.018758138
Q9NW64	Pre-mRNA-splicing factor RBM22	RBM22	1.028862793	-0.125565847	0.178746819	-0.044753393
P49756	RNA-binding protein 25	RBM25	0.056082344	-0.004994392	0.190847838	0.0175155
A0A087X0H9;Q5T8P6	RNA-binding protein 26	RBM26	0.509137147	0.360364914	0.143964768	0.110435486
U3KPZ7;Q9P2N5	RNA-binding protein 27	RBM27	1.110541554	-0.244476	0.746300502	-0.14258798
Q9NW13	RNA-binding protein 28	RBM28	0.399493813	-0.021952947	0.086150512	0.007261912
P98179	RNA-binding protein 3	RBM3	0.825555501	-0.124469121	0.010419051	0.002268155
A2A2V2;P42696	RNA-binding protein 34	RBM34	0.269309084	0.038625399	0.038441289	-0.008445422
F6VZ39;Q9H0Z9;E9PSF1;Q9B X46	RNA-binding protein 38;RNA-binding protein 24	RBM38;RBM24	0.284148859	-0.057799339	0.124277822	-0.039162318
Q14498;A0A0U1RQH7;H0Y4X 3	RNA-binding protein 39	RBM39	0.632986983	0.037013054	0.050065104	0.004281362
Q9BWF3;E9PB51;D6R9K7;J3Q RR5	RNA-binding protein 4	RBM4	1.784945132	0.06839625	0.771193574	0.036423683
K7EP90;Q9BTD8;K7ER08;K7E Q03	RNA-binding protein 42	RBM42	0.309204251	-0.063206673	0.376584532	-0.081742605
B7Z8Z7;A0AV96;D6R9D6;D6R BS9;D6REZ6	RNA-binding protein 47	RBM47	0.155771578	0.026303291	0.794491823	0.100231806
P52756	RNA-binding protein 5	RBM5	1.553121822	0.239816793	0.122457838	0.044836553
E9PGM9;P78332;F8WCA5	RNA-binding protein 6	RBM6	0.164146446	-0.090894318	0.278100862	-0.133241781
J3KPD3;Q9Y580;G3V1T9;I3L5 21;F5GXV8;F5GY08	RNA-binding protein 7	RBM7	0.00667198	0.003140767	0.240517058	0.076254018
Q9Y5S9;A0A0J9YW13	RNA-binding protein 8A	RBM8A	0.783798506	-0.09158198	0.1225263	-0.02109623
P38159;H0Y6E7;H3BT71;Q96E 39;H3BUY5	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-like-1	RBMX;RBMXL1	3.507108961	-0.331433614	0.248037825	-0.03235213
A0A1W2PP04;Q9Y388	RNA-binding motif protein, X-linked 2	RBMX2	0.823982702	-0.088021278	0.385820163	-0.18713665
P18754;C9JW69;C9JRH2;C9JM J4;C9J3R0;C9JQZ4	Regulator of chromosome condensation	RCC1	0.248028385	-0.01653862	0.183966503	-0.017095566
Q9P258	Protein RCC2	RCC2	0.325323365	-0.023251851	0.436924429	-0.034182549
Q9Y2P8;Q5VZU3	RNA 3-terminal phosphate cyclase-like protein	RCL1	0.437696991	-0.039355596	1.159342206	-0.139271736
Q15293	Reticulocalbin-1	RCN1	0.061942013	-0.016961416	0.009829542	-0.002524058
Q14257;H0YL43	Reticulocalbin-2	RCN2	0.346456072	0.056576729	0.008311425	-0.001843452
Q9UKL0;Q9P2K3;E9PQE5;B4D V59	REST corepressor 1;REST corepressor 3	RCOR1;RCOR3	1.168065183	-0.135320028	0.700676113	-0.145991325
B7ZKW8;Q6JBY9;F6T4W9	CapZ-interacting protein	RCS1	4.305943875	-0.398787816	0.830297427	-0.076228142
Q8TC12;G3V2G6	Retinol dehydrogenase 11	RDH11	0.785089213	0.101127307	0.553550496	0.098475138
Q8NBN7;G8JLA1	Retinol dehydrogenase 13	RDH13	0.506875576	-0.074942589	1.385123315	-0.13738505
P35241	Radixin	RDX	2.425660335	-0.222528776	0.012350256	0.003219287
P46063	ATP-dependent DNA helicase Q1	RECQL	0.117156574	0.009500186	0.58600239	-0.044145266
E5RGS2;Q9H6H4	Receptor expression-enhancing protein;Receptor expression-enhancing protein 4	REEP4	0.017053711	0.004906178	0.839553695	-0.137772083
Q00765;E2QRG8	Receptor expression-enhancing protein 5;Receptor expression-enhancing protein	REEP5	5.699958571	-0.691800435	0.035457219	-0.006256739
Q2TAM5;A0A087X0W8;Q0420 6;E9PKV4;A0A087WVP0;E9PK H5;E9PI38;E9PQS6	Transcription factor p65	RELA	0.598499193	-0.070780118	0.621905499	-0.074663162
Q9BWE0	Replication initiator 1	REPIN1	0.430809431	-0.093663534	0.331665349	0.046443939
Q15258;Q5T092;A0A0A0MR06 ;Q5T091;Q5T093	Protein RER1	RER1	0.00230652	0.000736237	0.861887836	0.124524434
H7BZ81;Q6NUM9;H7BZ16;H7 C3J0	All-trans-retinol 13,14-reductase	RETSAT	0.174508648	-0.045291646	0.127358895	0.054670588
H0YGR4;Q9Y3B8;H0YG54;F5 GYG5	Oligoribonuclease, mitochondrial	REXO2	0.940207853	0.09875679	1.308435304	0.099876404
Q9GZR2	RNA exonuclease 4	REXO4	0.197872534	-0.041492144	0.130305159	-0.022950808
P35251	Replication factor C subunit 1	RFC1	1.014585483	0.132546425	0.475867038	-0.07800293
P35250;A0A087WVY3;H7C5P4	Replication factor C subunit 2	RFC2	0.385074672	0.036859194	0.79370643	-0.066971143
P40938	Replication factor C subunit 3	RFC3	0.592971253	0.047492663	0.421015961	-0.034564018
P35249;C9JZI1;C9J8M3	Replication factor C subunit 4	RFC4	0.015760196	-0.00169309	0.538586316	-0.039252599
P40937	Replication factor C subunit 5	RFC5	0.43387342	0.021186829	0.619448986	-0.027249972

Q14699;G3XAJ6;C9JWQ9;F8W AR1;C9JRN3;C9JHG2 O43566	Raftlin	RFTN1	0.993566274	-0.189706167	0.588822929	-0.137991269
	Regulator of G-protein signaling 14	RGS14	0.808555021	-0.141196823	0.239752146	0.071063805
Q15382;C9J931	GTP-binding protein Rheb	RHEB	1.381328296	0.153290431	1.74149948	0.181978544
P61586;C9JNR4;C9JX21;Q5JR0 8;P08134;Q5JR07;E9PQH6;Q5J R05 P62745	Transforming protein RhoA;Rho-related GTP-binding protein RhoC	RHOA;RHOC	0.193457553	0.024649302	0.225290216	0.023698171
	Rho-related GTP-binding protein RhoB	RHOB	0	NaN	0	NaN
P84095	Rho-related GTP-binding protein RhoG	RHOG	0.063853065	0.013733546	0.043895732	0.007987658
Q8IXI2;H7BXZ6	Mitochondrial Rho GTPase 1;Mitochondrial Rho GTPase	RHOT1	0.292302334	-0.09026947	1.393122639	-0.232058907
Q8IXI1	Mitochondrial Rho GTPase 2	RHOT2	2.379121591	0.113234838	0.975647565	-0.06029892
Q9NPQ8;H0YEN0	Synembryn-A	RIC8A	0.011695961	0.004695257	0.171106433	-0.05759271
Q6R327;D6R9S6	Rapamycin-insensitive companion of mTOR	RICTOR	0	0.157142639	0.191409736	-0.166664124
Q5UIP0	Telomere-associated protein RIF1	RIF1	1.371953972	-0.118090312	1.499419022	-0.120665868
Q06587	E3 ubiquitin-protein ligase RING1	RING1	0.279488512	-0.05081749	0.240670243	-0.03942585
Q9BRS2	Serine/threonine-protein kinase RIO1	RIOK1	0.3300505	-0.061842346	0.526859404	0.079412142
Q9BVS4	Serine/threonine-protein kinase RIO2	RIOK2	0.306561699	0.051207225	0.233381733	0.040015539
Q13546	Receptor-interacting serine/threonine- protein kinase 1	RIPK1	0.472626598	0.068079821	0.066057161	0.01350708
Q6F5E8	Leucine-rich repeat-containing protein 16C	RLTPR	0.71874366	0.112374942	0.425532065	0.078179359
Q96DB5;H0YB83;E5RH53;E5R GC8	Regulator of microtubule dynamics protein 1	RMDN1	0.369484067	0.140156555	0.15283784	0.054257584
Q96TC7;H0YMB1	Regulator of microtubule dynamics protein 3	RMDN3	0.615365225	-0.067273458	1.981860865	-0.164587021
Q9H871	Protein RMD5 homolog A	RMND5A	0	NaN	0	NaN
O75792	Ribonuclease H2 subunit A	RNASEH2A	0.738115037	0.117453257	0.066474155	0.014277776
A0A087WXR7;Q5TBB1	Ribonuclease H2 subunit B	RNASEH2B	0.174208656	0.078830719	0.096333181	0.028734525
H0YEF3;Q8TDP1;E9PN81;E9P KP0;H0YE52;H0YCP5	Ribonuclease H2 subunit C	RNASEH2C	0.696817832	0.139013926	0.287590106	-0.077317238
D6REQ6;D6RHI9;O00584;H0Y AE9	Ribonuclease T2	RNASET2	0.763746479	0.174577713	0.034756985	-0.010832787
O15541	RING finger protein 113A	RNF113A	0.012335984	-0.004873276	0.151359739	0.057979584
A0A096LNV3;A0A096LP02;Q9 Y508	E3 ubiquitin-protein ligase RNF114	RNF114	0.644922419	-0.167565664	1.489440183	-0.189792315
K7E1Y6;Q9BV68;U3KQF4	E3 ubiquitin-protein ligase RNF126	RNF126	0.85731005	-0.127673467	1.127173415	-0.215686162
Q5VTR2	E3 ubiquitin-protein ligase BRE1A	RNF20	0.201820261	0.062325478	0.890132345	0.204641024
Q8ND24;E9PN76	RING finger protein 214	RNF214	0.139044227	-0.023087819	0.783763939	-0.153971354
Q5VTB9;Q5TDE7;Q5TDE8	E3 ubiquitin-protein ligase RNF220	RNF220	0.437625917	-0.140510241	0	-0.059757868
O75150;H3BP71	E3 ubiquitin-protein ligase BRE1B	RNF40	1.285855239	0.181713104	0.465705662	0.077694893
P13489	Ribonuclease inhibitor	RNH1	1.246271334	-0.052535693	0.218557039	-0.023180008
O43148;K7EP06	mRNA cap guanine-N7 methyltransferase	RNMT	0.229028311	-0.026597977	1.242515252	-0.093212763
Q9HC36;I3L0T6;I3L443	rRNA methyltransferase 3, mitochondrial	RNMTL1	0.033254784	-0.017314911	0.184014754	0.087035179
Q9H4A4;A6NKB8	Aminopeptidase B	RNPEP	2.331878553	-0.098051071	0.852303195	-0.040635745
H3BV80;H3BMM9;H3BTC0;Q1 5287;H3BPG5;H3BMS0 O75695	RNA-binding protein with serine-rich domain 1	RNPS1	1.163511331	0.104937236	0.164440428	-0.020492554
	Protein XRP2	RP2	0.214906404	-0.032103856	0.305408987	-0.062509219
P27694	Replication protein A 70 kDa DNA- binding subunit;Replication protein A 70 kDa DNA-binding subunit, N-terminally processed	RPA1	1.719097686	0.054484367	1.583089065	0.032256126
P15927;Q5TEJ7	Replication protein A 32 kDa subunit	RPA2	0.287945468	0.045172373	0.774560717	0.086959521
P35244;B5MC59	Replication protein A 14 kDa subunit	RPA3	0.741714669	-0.054885546	0.437241118	-0.031545639
Q9HG6T3	RNA polymerase II-associated protein 3	RPAP3	0.479499059	-0.049770991	0.173671664	0.025565147
Q96AT9;C9J6A7;C9J9T0;C9IZ U8	Ribulose-phosphate 3-epimerase	RPE	1.048202872	-0.115236918	0.005050996	0.000935555
Q9H7B2;Q5VXN0	Ribosome production factor 2 homolog	RPF2	0.277717071	0.026768684	0.221353599	-0.025330861
P49247	Ribose-5-phosphate isomerase	RPIA	0.411686407	-0.103176117	1.206377449	-0.214210192
X1WI28;P27635	60S ribosomal protein L10	RPL10	0.374691983	-0.071304957	0.175817619	-0.038432757

F8W7C6;A0A087WV22;H7C123;H7C2C5		RPL10	0.364642578	0.052242597	0.358870488	0.052522341
P62906	60S ribosomal protein L10a	RPL10A	1.311900323	-0.081883113	0.609536525	-0.057049751
P62913;Q5VVC8;Q5VVC9	60S ribosomal protein L11	RPL11	0.903025158	-0.093997955	1.042433684	-0.101056099
P30050	60S ribosomal protein L12	RPL12	2.729652793	-0.153857549	2.097239015	-0.109074275
P26373;J3QSB4	60S ribosomal protein L13	RPL13	0.240524327	0.035204252	0.41483424	0.063663801
P40429;M0QYS1;Q8J015	60S ribosomal protein L13a	RPL13A;RPL13a	0.2682109	0.038829168	0.330200844	0.047195117
P50914;E7EPB3	60S ribosomal protein L14	RPL14	0.462792634	-0.068199476	1.004901549	-0.124697049
P61313;E7EQV9;E7ENU7	60S ribosomal protein L15;Ribosomal protein L15	RPL15	0.2628053	-0.03213342	0.446469949	0.058060328
A0A087WXM6;J3QQT2;J3KRX5;A0A0A6YYL6;P18621;J3QLC8;A0A0A0MRF8;J3KRB3;A0A087WWH0;J3QS96	60S ribosomal protein L17	RPL17;RPL17-C18orf32	1.656578399	-0.145250956	0.404022078	-0.042811076
J3QQ67;Q07020;G3V203;H0YH A7;F8VYV2;A0A075B7A0;F8VUA6	60S ribosomal protein L18	RPL18	0.136161344	-0.020732562	0.28047086	-0.045692444
Q02543;M0R3D6;M0R1A7;M0R117;M0R0P7	60S ribosomal protein L18a	RPL18A	0.151281804	0.034285545	0.406917714	0.077132861
J3QR09;J3KTE4;P84098	Ribosomal protein L19;60S ribosomal protein L19	RPL19	0.475723458	0.099546115	0.487129093	0.10545667
P46778;G3V1B3;M0R181	60S ribosomal protein L21	RPL21	0.078509401	-0.010640462	0.638181365	0.063246727
P35268	60S ribosomal protein L22	RPL22	0.564768453	-0.063567479	0.404538335	-0.048012733
P62829;J3KT29;C9JD32;B9ZVP7	60S ribosomal protein L23	RPL23	0.521135952	-0.05183061	0.086059677	0.007858594
P62750;H7BY10;K7EJV9;K7ERT8;A8MUS3;K7EMA7	60S ribosomal protein L23a	RPL23A	1.324977311	-0.153807958	0.098284957	-0.013619423
C9XB8;C9JNW5;P83731	60S ribosomal protein L24	RPL24	1.645344926	-0.114659627	1.872032011	-0.116852125
P61254;J3QR17;J3QQQ9;J3QV1;J3QRC4;J3KTJ8	60S ribosomal protein L26	RPL26	0.767594419	-0.094009717	0.008569985	-0.001622518
P61353;K7ELC7;K7EQQ9	60S ribosomal protein L27	RPL27	1.136793275	-0.07244873	1.231060461	-0.090632757
P46776;E9PLL6;E9PJD9	60S ribosomal protein L27a	RPL27A	1.222952472	-0.080051422	0.080998974	0.00816981
H0YKD8;P46779;H0YMF4;H0YLP6	60S ribosomal protein L28	RPL28	0.130456897	0.017464638	0.566936426	0.057258606
P47914	60S ribosomal protein L29	RPL29	0.210523274	-0.052501678	0.072352843	-0.015659332
P39023;G5E9G0;H7C422;H7C3M2;B5MCW2	60S ribosomal protein L3	RPL3	0.181422367	0.017734528	1.008296462	0.072119395
P62888;E5R199	60S ribosomal protein L30	RPL30	0.111116188	-0.0181036	0.220811673	0.032836914
P62899;H7C2W9;C9JU56;B7Z4E3;B7Z4C8	60S ribosomal protein L31	RPL31	0.23463636	-0.028153737	0.217878808	0.020851771
D3YTB1;F8W727;P62910	60S ribosomal protein L32	RPL32	0.244501791	-0.036283493	0.076064815	0.011932691
P49207	60S ribosomal protein L34	RPL34	1.635071153	-0.129931768	0.13574387	-0.012556712
P42766;F2Z388	60S ribosomal protein L35	RPL35	2.072417862	-0.193579992	1.447941344	-0.122099241
P18077;C9K025;F8WBS5;F8WB72	60S ribosomal protein L35a	RPL35A	0.942402906	-0.050706863	0.034611275	-0.003027916
Q9Y3U8;J3QSB5	60S ribosomal protein L36	RPL36	0.028543563	0.007482847	0.265915369	0.050678571
H0Y5B4;H7BZ11;J3KQN4;P83881;R4GN19	60S ribosomal protein L36a	RPL36A;RPL36A-HNRNP2	0.55348149	-0.066911379	2.737439073	0.172005971
Q969Q0	60S ribosomal protein L36a-like	RPL36AL	0.382313259	-0.198246129	1.270570868	0.188998731
C9J4Z3;P61513;M0R0A1;Q6P4E4;E9PEL3;M0R2L6	60S ribosomal protein L37a	RPL37A	1.188442162	0.201697032	1.315291897	0.244540532
P63173;J3KT73;J3QL01;J3KSP2	60S ribosomal protein L38	RPL38	1.168464602	-0.183614413	0.679312435	-0.099404335
P36578;H3BM89	60S ribosomal protein L4	RPL4	3.006585318	-0.144447962	0.626520895	-0.038448334
P46777	60S ribosomal protein L5	RPL5	0.012884315	0.001344363	0.076447687	0.006758372
Q02878	60S ribosomal protein L6	RPL6	0.075526935	0.010351817	0.436597647	0.04595089
P18124;A8MUD9	60S ribosomal protein L7	RPL7	1.131753532	-0.083625158	0.536442077	-0.038626989
P62424;Q5T8U2	60S ribosomal protein L7a	RPL7A	1.687444991	-0.062753042	0.269219271	-0.014602025
Q6DK11;R4GMU7	60S ribosomal protein L7-like 1	RPL7L1	0.050076937	-0.015028318	0.388014054	-0.058055242
P62917;E9PKZ0;E9PKU4;G3V1A1	60S ribosomal protein L8	RPL8	0.441288805	-0.047563553	0.018192291	0.002182325
P32969;H0Y9V9;D6RAN4;E7ESEO	60S ribosomal protein L9	RPL9	2.395152201	-0.142108281	1.197060298	-0.093753815
P05388;F8VU65;F8VW21;F8VPE8;F8VQY6;F8VRK7;Q8NHW5	60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-like	RPLP0;RPLP0P6	1.915777342	-0.094635328	1.411724418	-0.049036026
P05386	60S acidic ribosomal protein P1	RPLP1	0.502330102	-0.178972244	0.276894505	-0.126621882

P05387	60S acidic ribosomal protein P2	RPLP2	0.62748175	-0.08671538	0.298695073	-0.046841939
P04843;B7Z4L4	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1	0.95637501	0.058942159	0.318539007	0.024431229
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2	1.081752891	0.105229378	0.136239767	0.018870036
O95059	Ribonuclease P protein subunit p14	RPP14	0.575198005	-0.15213426	0.125155218	-0.041341464
P78346;Q5VU11;Q5VU10	Ribonuclease P protein subunit p30	RPP30	2.557833421	-0.099370639	3.847962701	-0.174103737
P78345	Ribonuclease P protein subunit p38	RPP38	0	0.007339478	0	-0.01093483
A0A087X1N3;O75818;F8WC38;X6RLL4	Ribonuclease P protein subunit p40	RPP40	0.910455515	-0.083417257	0.606805381	-0.065389951
A0A0C4DGQ6;Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A	0.685480893	-0.079834302	1.946220596	-0.151389758
Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B	0.698676323	-0.068262418	1.004647418	-0.093551318
Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2	1.200464338	-0.108489037	0.04028253	0.006590525
P46783	40S ribosomal protein S10	RPS10	0.544054071	-0.062169711	0.151002735	0.018820445
P62280;M0QZC5	40S ribosomal protein S11	RPS11	0.636133724	-0.056709607	0.806791076	0.071404775
P25398	40S ribosomal protein S12	RPS12	1.773654682	-0.126718203	0.71925265	-0.068470319
P62277;J3KMX5	40S ribosomal protein S13	RPS13	2.105344788	-0.182505608	1.315421406	-0.107767105
P62263;E5RH77;H0YB22	40S ribosomal protein S14	RPS14	0.823756731	-0.080601374	0.133678896	0.009535789
K7ELC2;P62841;K7EM56;A0A0B4J2B4;S4R417;K7EQJ5;K7EJ78;S4R456	40S ribosomal protein S15	RPS15	0.560610536	-0.080846786	0.374872617	0.05093956
H3BN98;I3L246		RPS15A	0.158747184	0.024044037	0.110365121	-0.017811775
P62249;M0R210;M0R3H0;M0R1M5	40S ribosomal protein S16	RPS16	1.009455117	-0.068912506	0.364693979	-0.032703718
P08708;H0YN88;A0A075B716	40S ribosomal protein S17	RPS17	2.155163628	-0.117542267	0.132986136	-0.01045386
P62269	40S ribosomal protein S18	RPS18	0.040449929	-0.008299828	0.818984796	0.11044693
P39019;A0A075B6E2	40S ribosomal protein S19	RPS19	0.795151757	-0.126503627	0.237794687	0.048095067
Q86WX3;F8WFE7	Active regulator of SIRT1	RPS19BP1	0.402397263	-0.054191907	0.223241727	-0.053650538
P15880;H0YEN5;E9PQD7;I3L404;E9PMM9;E9PPT0	40S ribosomal protein S2	RPS2	1.946359227	-0.097736359	0.783590707	-0.052027067
P60866;E5RFX2	40S ribosomal protein S20	RPS20	1.182950331	-0.139442126	0.589707138	-0.088366508
Q8WVC2;P63220;Q9BYK1	40S ribosomal protein S21	RPS21	0.645055245	-0.08449014	0.189162912	-0.033886274
P62266;D6RD47	40S ribosomal protein S23	RPS23	0.963550351	-0.088903745	0.275808831	-0.027782758
E7ETK0;A0A087WUS0;P62847	40S ribosomal protein S24	RPS24	1.300054252	0.079125086	1.482679306	0.091928164
P62851	40S ribosomal protein S25	RPS25	1.048488717	-0.183151881	0.670194739	-0.129443169
P62854;Q5JNZ5	40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1	RPS26;RPS26P11	3.804730682	-0.246564865	1.1824547	-0.124844869
P42677;Q5T4L4	40S ribosomal protein S27	RPS27	0.023258029	0.008032481	0.193595476	0.046335538
P62979;J3QS39;J3QTR3;F5H6Q2;F5GYU3;F5H2Z3;F5H265;B4DV12;F5H388;F5H747;F5GXK7;J3QKN0;Q5PY61;Q96C32;P0CG47;P0CG48	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin	RPS27A;UBB;UBC	6.640221987	0.608316422	4.180854815	0.23912398
H0YMV8;Q71UM5;C9JL16	40S ribosomal protein S27;40S ribosomal protein S27-like	RPS27L	0.015143784	0.007522583	0.566256694	0.243532308
P62857	40S ribosomal protein S28	RPS28	0.045728213	0.015139898	1.180291916	0.235683123
P62273;A0A087WTT6	40S ribosomal protein S29	RPS29	0.137182712	-0.090774218	1.472018946	0.479562759
P23396;E9PL09;E9PPU1;F2Z2S8;H0YCJ7;H0YEU2	40S ribosomal protein S3	RPS3	2.459625089	-0.121385574	1.307824083	-0.065296809
P61247;D6RG13;D6RAT0;D6RB09;E9PFI5;H0Y9Y4;H0Y8L7;D6R9B6	40S ribosomal protein S3a	RPS3A	0.868197968	-0.077486038	0.246408585	-0.023708979
P62701	40S ribosomal protein S4, X isoform	RPS4X	1.085007273	-0.055647214	0.441571354	-0.029177348
M0R0F0;P46782;M0R0R2;M0QZN2	40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed	RPS5	0.005693874	-0.000671069	0.235730781	-0.025750478
P62753;A2A3R5	40S ribosomal protein S6	RPS6	1.222285173	-0.105782509	0.652145527	-0.066225688

E9PGT3;Q15418	Ribosomal protein S6 kinase;Ribosomal protein S6 kinase alpha-1	RPS6KA1	0.676695603	0.075149854	1.088267903	0.087629
P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3	0.129096152	0.019423485	0.624779724	-0.069049199
Q9UBS0	Ribosomal protein S6 kinase beta-2	RPS6KB2	0.045794785	0.020112038	0.724170659	0.116486073
P62081;B5MCP9	40S ribosomal protein S7	RPS7	2.954579353	-0.196187973	1.731811923	-0.099898974
P62241;Q5JR95	40S ribosomal protein S8	RPS8	3.253928371	-0.169380824	2.241924628	-0.080430667
A0A024R4M0;P46781;B5MCT8;C9JM19	40S ribosomal protein S9	RPS9	1.084703419	-0.109620412	0.482196503	-0.054045995
C9J9K3;A0A0C4DG17;P08865;F8WD59	40S ribosomal protein SA	RPSA	1.435871602	-0.102930705	1.045537019	-0.082247416
Q92600	Cell differentiation protein RCD1 homolog	RQCD1	0.971243223	0.158056577	0.121765872	0.02771155
Q7L523;Q5VZM0	Ras-related GTP-binding protein A	RRAGA;RRAGB	0.344968323	0.118186951	0.306174737	0.048591614
A0A0A0MRV0;Q9P2E9;A0A087WVV2;F8W7S5	Ribosome-binding protein 1	RRBP1	1.63734052	0.110363007	1.98220986	0.11366272
P23921;E9PL69	Ribonucleoside-diphosphate reductase large subunit	RRM1	0.004506754	-0.000480334	1.544305381	0.123867671
P31350;A0A286YFD6;C9JXC1	Ribonucleoside-diphosphate reductase subunit M2	RRM2	5.009708369	0.39899381	5.374816187	0.436147054
P56182	Ribosomal RNA processing protein 1 homolog A	RRP1	0.171527083	-0.020329793	2.273613839	-0.157253901
Q5JTH9	RRP12-like protein	RRP12	2.100378652	0.104026794	0.349654885	0.025050481
Q9Y3B9	RRP15-like protein	RRP15	0.116885933	0.020757039	0.096322129	-0.018946966
Q14684	Ribosomal RNA processing protein 1 homolog B	RRP1B	0.440034055	-0.036289533	1.751989205	-0.108050028
Q9Y3A4	Ribosomal RNA-processing protein 7 homolog A	RRP7A	0.137841249	-0.038343747	0.127653745	-0.0572354
O43818	U3 small nucleolar RNA-interacting protein 2	RRP9	0.382131232	0.047387441	0.099186892	-0.01576678
Q15050	Ribosome biogenesis regulatory protein homolog	RRS1	0.027928883	0.005222321	0.012684438	0.002701124
Q96T23;H7C306;H0YDG9;H0YER1	Remodeling and spacing factor 1	RSF1	0.238976144	0.105965296	0.300754536	-0.107592265
O76021;J3QSV6;I3L3U9	Ribosomal L1 domain-containing protein 1	RSL1D1	0.050549267	0.002840042	1.107701906	0.030779521
Q96I27;C9J367;H7C5Q0;C9J713	Serine/Arginine-related protein 53	RSRC1	1.348312456	-0.240224393	0.075757469	-0.019855372
Q15404	Ras suppressor protein 1	RSU1	0.513868337	-0.074905713	0.277873223	0.038631439
O00442	RNA 3-terminal phosphate cyclase	RTCA	0.161424773	0.03139782	0.113991903	0.022066116
Q9Y310	tRNA-splicing ligase RtcB homolog	RTCB	0.062361554	0.004133542	0.001485059	0.000105222
Q92541	RNA polymerase-associated protein RTF1 homolog	RTF1	0	-0.075848103	0	-0.281056404
Q9BY42;A0A0A0MQR2;A2A2L6	Protein RTF2 homolog	RTFDC1	1.649252517	0.378201803	1.924647118	0.429732641
A8MT72;Q2NKQ5;Q16799	Reticulon;Reticulon-1	RTN1	0.000297228	-6.85E-05	0.047561077	-0.008634663
O95197	Reticulon-3	RTN3	1.975870946	0.308828354	0.857270859	0.119622231
F8W914;Q9NQC3;H7C106	Reticulon;Reticulon-4	RTN4	0.35515683	0.033373197	0.090557219	0.009065628
Q86UN3	Reticulon-4 receptor-like 2	RTN4RL2	0.538108287	-0.062358538	1.656696609	0.205261548
Q96T51;J3KPP6	RUN and FYVE domain-containing protein 1	RUFY1	1.520582468	-0.203029315	2.144604141	-0.216091474
Q9Y265;E7ETRO	RuvB-like 1	RUVBL1	0.422535415	-0.026232402	1.695875831	-0.079199473
Q9Y230;M0R0Y3	RuvB-like 2	RUVBL2	0.385163247	-0.026846568	0.120148153	-0.009013176
Q9H446;E5RJE3;E5RGS5;E5RGO3	RWD domain-containing protein 1	RWDD1	0.481516837	-0.127875519	0.202670935	-0.052352142
A0A0G2JKR7;P28702;A0A087WZ88;P48443	Retinoic acid receptor RXR-beta;Retinoic acid receptor RXR-gamma	RXRB;RXRG	1.257899259	0.16118749	0.483310711	0.138570086
P31949	Protein S100-A11;Protein S100-A11, N-terminally processed	S100A11	2.022750851	-0.146093369	0.81324449	-0.062584877
P26447	Protein S100-A4	S100A4	0.129339038	-0.01919651	0.676184622	0.080387115
R4GN98;P06703	Protein S100;Protein S100-A6	S100A6	0.399777549	0.067255656	0.147403745	0.033832932
P05109	Protein S100-A8;Protein S100-A8, N-terminally processed	S100A8	0	NaN	0	NaN
P06702	Protein S100-A9	S100A9	0	NaN	0	NaN
Q9NTJ5;E9PGZ4	Phosphatidylinositol phosphatase SAC1	SACMIL	0.552313427	0.047503153	0.033829305	-0.005171458
Q9NZJ4	Sacsin	SACS	0.030767988	-0.009988785	0.212908621	-0.070143064
Q9UBE0;M0QZS6;B3KNJ4;M0QX65	SUMO-activating enzyme subunit 1;SUMO-activating enzyme subunit 1, N-terminally processed	SAE1	0.879421399	-0.084827423	0.542348523	-0.0541598

Q15424	Scaffold attachment factor B1	SAFB	1.51431856	-0.172726631	0.079159678	0.014234543
Q14151	Scaffold attachment factor B2	SAFB2	6.001783976	-0.490560532	1.939831323	-0.093605995
Q6SPF0;E9PIW9	Atherin	SAMD1	0.003345312	-0.001244227	0.47654921	-0.133014043
Q5K651;C9JKF1	Sterile alpha motif domain-containing protein 9	SAMD9	1.211273425	-0.246975263	0.538860378	-0.188379288
Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	0.171415459	-0.009768486	1.460071904	-0.051133156
Q9Y512	Sorting and assembly machinery component 50 homolog	SAMM50	1.439837192	0.102550824	0.234482625	-0.025034904
X6RAL5;O00422;H7BZW6;U3 KPY7	Histone deacetylase complex subunit SAP18	SAP18	0.31824857	0.026737531	0.3772817	-0.03232797
O75446	Histone deacetylase complex subunit SAP30	SAP30	0.552897544	0.102172375	0.415897281	-0.27078867
J3QQJ0;Q9UHR5;X6R3T8;J3Q LH3	SAP30-binding protein	SAP30BP	0.12707211	0.024218241	0.597602498	-0.092773438
Q9NR31;Q5SQT8	GTP-binding protein SAR1a	SAR1A	0.862414404	-0.115091324	0.296638596	-0.025708516
Q9Y6B6;D6RD69;D6RDB2;D6 RAA2;D6R9R5;Q9H029	GTP-binding protein SAR1b	SAR1B;DKFZp434B2017	1.509342347	-0.218946139	0.311988143	0.049993515
Q9UL12;A0A0A0MT55;Q5SYV 1	Sarcosine dehydrogenase, mitochondrial	SARDH	3.151950134	0.168099403	1.529220527	-0.108517329
H0YHG0;P82979;F8VZQ9	SAP domain-containing ribonucleoprotein	SARNP	1.662556222	-0.158169746	0.668605961	-0.065036456
Q5T5C7;P49591	Serine--tRNA ligase, cytoplasmic	SARS	0.138713367	-0.023522695	0.16638009	0.024084409
M0QWZ7;Q9NP81;B4DJM9;M 0R2C6	Serine--tRNA ligase, mitochondrial	SARS2	0.055648528	-0.061046346	0.299367972	0.295498466
O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1	0.07566889	-0.005630175	0.994228513	0.044616699
Q15020;F8VV04	Squamous cell carcinoma antigen recognized by T-cells 3	SART3	1.761568587	0.083396276	0.29568535	-0.020235697
Q9Y3A5;A0A087X020	Ribosome maturation protein SBDS	SBDS	0.108122679	-0.013627052	0.074325637	-0.00972271
A3KN83	Protein strawberry notch homolog 1	SBNO1	0.861792022	-0.116890272	0.135852124	0.037609418
F8VXG7;Q99590;A0A0A0MTP 7	Protein SCAF11	SCAF11	2.776432782	-0.343887011	0.754488463	-0.185862859
O95104	Splicing factor, arginine/serine-rich 15	SCAF4	0.18639941	0.038649368	0.236524181	0.040598679
A0A0A0MT33;Q9UPN6	Protein SCAF8	SCAF8	0.148603248	-0.047228177	0.064406913	-0.021952629
O15126;A0A087WXB0;A0A087 WZA6	Secretory carrier-associated membrane protein 1	SCAMP1	0.518872081	-0.228773435	0.579494934	-0.099438032
O15127	Secretory carrier-associated membrane protein 2	SCAMP2	0.82626386	0.09236304	0.169004189	0.027485847
O14828	Secretory carrier-associated membrane protein 3	SCAMP3	1.220838049	-0.104298592	0.63302941	-0.056788762
B7ZKQ9;Q8WTV0;F5H4X0	Scavenger receptor class B member 1	SCARB1	0.282227074	-0.040275892	1.133021619	-0.114397367
A0A1W2PPX5;A0A1W2PQR6; A0A1W2PQB7;A0A1W2PS43; Q14108;A0A1W2PRS1;A0A1W 2PRF6;A0A1W2PPU6	Lysosome membrane protein 2	SCARB2	1.939342497	0.119529724	0.16214361	-0.013542175
O00767	Acyl-CoA desaturase	SCD	0.166722744	-0.038924853	0.375315964	-0.083014806
Q8WVM8	Sec1 family domain-containing protein 1	SCFD1	1.919645604	-0.118431727	2.417242133	-0.160854975
Q8WU76	Sec1 family domain-containing protein 2	SCFD2	0.27143077	-0.085854022	0.29722426	-0.108549245
O43819	Protein SCO2 homolog, mitochondrial	SCO2	0.524263436	0.231781006	0.614685561	-0.179158783
P22307;H0YF61	Non-specific lipid-transfer protein	SCP2	1.503679247	0.128703117	0.196173059	0.027002652
Q9HB40	Retinoid-inducible serine carboxypeptidase	SCPEP1	1.403805406	0.171540451	3.240282437	0.33366394
A0A0G2JNZ2;A0A0G2JPP5;Q1 4160;A0A0G2JMS7	Protein scribble homolog	SCRIB	0.377484465	-0.057262103	0.295388251	-0.047202746
J3QRJ1;J3QL71;Q96FV2;J3QR8 4	Secernin-2	SCRN2	1.956082428	-0.239376386	2.352896889	-0.364969889
E9PS17;E9PK59;Q96KG9;E9PP N3	N-terminal kinase-like protein	SCYL1	1.648749883	-0.107671738	1.384332603	-0.062811852
F8VSC5;A0A0U1RQQ9;Q6P3 W7	SCY1-like protein 2	SCYL2	1.019706228	-0.158324877	0.817522399	-0.103713226
Q9NVU7;E7EW05	Protein SDA1 homolog	SDAD1	0.485714527	-0.06034406	0.610468022	-0.110833486
P18827;E9PHH3;H7C1K4	Syndecan-1	SDC1	6.420296066	-0.729045041	1.74425473	-0.213407199
Q6IQ49	Protein SDE2 homolog	SDE2	0.189706716	0.063593864	0.5308509	0.153886795
Q99470	Stromal cell-derived factor 2	SDF2	0.241794071	0.107992808	0.055757295	-0.025729497
Q9HCN8	Stromal cell-derived factor 2-like protein 1	SDF2L1	0.338417971	0.040476163	0.02905533	-0.004627546
Q9BRK5;H0Y3T6;G3V1E2	45 kDa calcium-binding protein	SDF4	1.003472	-0.141070684	0.750773706	0.09254392
P31040;D6RFM5;A0A087X113	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA	5.008369361	-0.378686587	2.015881511	-0.125927925

A0A087WXX8;A0A087WWT1;P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB	0	-0.00472641	0	-0.974323273
Q96GA7;F8VYZ3;H0YID3	Serine dehydratase-like	SDSL	1.140138309	-0.158631325	0.220243449	-0.04933548
H0YNG3;P67812;H0YNX5;H0YNA5	Signal peptidase complex catalytic subunit SEC11;Signal peptidase complex catalytic subunit SEC11A;Signal peptidase I	SEC11A	0.501354338	0.075223605	0.494472647	-0.06834348
B4DI03;K7EJQ7;Q9BY50;A0A0AMR04	Signal peptidase complex catalytic subunit SEC11;Signal peptidase complex catalytic subunit SEC11C	SEC11L3;SEC11C	1.836328375	0.202370008	0.29563952	-0.04399999
P55735;A8MXL6	Protein SEC13 homolog	SEC13	1.347188435	0.23702685	1.248542258	0.229231517
Q92503;K7EJ08	SEC14-like protein 1	SEC14L1	0.773837124	0.317922274	1.406883105	-0.121884346
F1T011;J3KNL6;O15027;X6RG P5 O75396	Protein transport protein Sec16A Vesicle-trafficking protein SEC22b	SEC16A SEC22B	0.00413717 0.574183943	-0.000557899 0.073796272	1.004428264 0.229499327	0.081469218 0.02817599
F5H365;Q15436	Protein transport protein Sec23A	SEC23A	0.148405523	0.024724642	1.096758272	0.143929799
Q15437	Protein transport protein Sec23B	SEC23B	4.209197927	0.141514142	2.713341068	0.13724041
Q9Y6Y8	SEC23-interacting protein	SEC23IP	0.221060084	0.033438683	1.549299303	-0.123483976
O95486	Protein transport protein Sec24A	SEC24A	0.880526761	-0.15623188	0.016126098	-0.004622142
O95487	Protein transport protein Sec24B	SEC24B	0.237121141	-0.092989604	0.426791855	-0.166848501
P53992;G5EA31	Protein transport protein Sec24C	SEC24C	0.090782713	-0.009023666	0.157539884	-0.017415365
O94855;E9PDM8	Protein transport protein Sec24D	SEC24D	0.915680603	0.095265071	1.061777465	0.129706701
D6REX3;Q94979;D6RHZ5;H7B XG7;H0YAB3 B4DR61;P61619	Protein transport protein Sec31A Protein transport protein Sec61 subunit alpha isoform 1	SEC31A SEC61A1	1.184300196 4.121373362	0.032524109 0.305765788	0.536291013 2.813770897	0.015540441 0.229532242
P60468	Protein transport protein Sec61 subunit beta	SEC61B	6.19746051	0.588187218	3.557660922	0.288564046
F8WF48;Q99442;F8WCJ7	Translocation protein SEC62	SEC62	1.798112606	0.187324206	0.253083675	0.039922396
Q9UGP8	Translocation protein SEC63 homolog	SEC63	0.022250245	0.004665375	0.321881179	-0.049721718
Q96EE3;K7ELV2;K7EP88;K7ENI5 Q9UBV2	Nucleoporin SEH1 Protein sel-1 homolog 1	SEH1L SEL1L	1.800880893 0.557810458	0.16587925 0.14588356	0.274364997 0.090498071	0.041569074 0.028880437
A0A087X1G7;A0A0B4J1S4;O60613;A0A0J9YX89 A0A087X0Q9;Q9BVL4	15 kDa selenoprotein Selenoprotein O	SELENOF SELO	1.234276727 0.943357856	0.184818268 0.237584114	0.789544607 0.185894116	0.170952797 0.050595284
A0A087WVA1;P62341;Q6IAK0	Selenoprotein T	SELT	0.23801103	0.043357213	0.029815698	0.008382797
P04279	Semenogelin-1;Alpha-inhibin-92;Alpha-inhibin-31;Seminal basic protein	SEMG1	0	NaN	0	NaN
Q02383	Semenogelin-2	SEMG2	0	-5.499720891	0	NaN
J3QT09;Q9BQF6	Sentrin-specific protease 7	SEN7	0.220812136	-0.056336721	0.135842122	-0.032441457
P49903;Q5T5U6	Selenide, water dikinase 1	SEPHS1	2.096119475	-0.175414403	1.754343097	-0.154150009
B5MCX3;Q15019;C9J2Q4	Septin-2	SEPT2	0.083060703	0.008749326	0.196888845	0.022303581
B1AMS2;Q14141	Septin-6	SEPT6	1.389874578	-0.082112948	0.018410275	0.001519839
E7ES33;E7EPK1;Q16181;G3V1 Q4 Q9UHD8	Septin-7 Septin-9	SEPT7 SEPT9	0.922442634 2.569573042	-0.060085932 -0.13297685	0.282995071 0.08755105	-0.013209343 0.006810824
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1	2.605498814	-0.161353429	0.8862955	0.060086886
P84101;F8WBN3;B9A031;C9JQ Z0;B8ZZY7;F8WBV6 P30740	Small EDRK-rich factor 2 Leukocyte elastase inhibitor	SERF2 SERPINB1	1.849255891 1.875031033	-0.115484238 -0.141875585	2.280099331 2.858907699	0.221685727 -0.149522463
A0A024QZX5;A0A087X1N8;P35237 P50454;E9PR70;E9PPV6;E9PK H2;E9PK86;E9PM15 Q01105;A0A0C4DFV9;A0A087 X027;P0DME0 Q8WTS6;D6RJA0	Serpin B6 Serpin H1 Protein SET;Protein SETSIP Histone-lysine N-methyltransferase SETD7	SERPINB6 SERPINH1 SET;SETSIP SETD7	2.135157652 7.460457916 2.025644627 0.16440219	-0.122929891 0.447855949 -0.107595762 0.0790809	1.080377582 0.790446605 1.273628281 0.384742048	-0.059487025 0.044467608 -0.055830002 -0.197658348
Q15637	Splicing factor 1	SF1	0.139292667	-0.019675891	0.018367368	-0.003596624
Q15459	Splicing factor 3A subunit 1	SF3A1	1.411802316	-0.070111593	0.178511977	0.012007395
Q15428;K7EMT0	Splicing factor 3A subunit 2	SF3A2	1.532941101	0.11067009	2.09567905	0.148753166

Q12874	Splicing factor 3A subunit 3	SF3A3	0.182899583	-0.017498016	0.272320246	-0.015012105
O75533	Splicing factor 3B subunit 1	SF3B1	0.9238304	0.042496999	0.102183299	0.006635984
Q13435;E9PPJ0	Splicing factor 3B subunit 2	SF3B2	0.255103619	0.022216797	0.866710995	0.062898954
Q15393	Splicing factor 3B subunit 3	SF3B3	0.078531805	0.005553563	0.861336675	-0.033283552
Q15427;Q5SZ64	Splicing factor 3B subunit 4	SF3B4	0.477724018	-0.07360522	0.079042985	0.018177986
Q9BWI5	Splicing factor 3B subunit 5	SF3B5	0.080063146	0.017754873	0.132643375	0.020735741
Q9Y3B4	Splicing factor 3B subunit 6	SF3B6	1.348689289	0.122030576	0.296263497	-0.025184631
P31947	14-3-3 protein sigma	SFN	1.705797197	-0.135399818	0.384753233	-0.034501394
P23246	Splicing factor, proline- and glutamine-rich	SFPQ	1.457539897	0.089676539	0.218464605	0.018235207
Q9H9B4	Sideroflexin-1	SFXN1	1.634513286	0.126711845	0.585680467	-0.049078306
O43765;K7EMD6	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA	0.767602546	-0.072238286	0.157704804	-0.018847466
Q9H788	SH2 domain-containing protein 4A	SH2D4A	0.015216103	0.008943748	0.908372747	-0.325233269
O75368	SH3 domain-binding glutamic acid-rich-like protein	SH3BGRL	0.479966967	-0.133793513	0.0521907	0.018359502
Q5T123;Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3BGRL3	0.093047884	0.021419525	2.408755485	0.245254199
Q9Y3L3	SH3 domain-binding protein 1	SH3BP1	0.699375238	0.187828732	0.303909313	-0.161074066
M0QYE0;M0R0I3;Q99961	Endophilin-A2	SH3GL1	0.034899447	0.007922745	0.181041626	-0.051934052
A0A087WW40;Q9Y371	Endophilin-B1	SH3GLB1	0	NaN	0	0.458545685
B7ZC38;Q9NR46;B7ZC39	Endophilin-B2	SH3GLB2	0.504084913	0.039880435	0.645739698	0.049640338
P29353;X6R6D0	SHC-transforming protein 1	SHC1	0.049453934	0.01988856	0.366425465	0.066798846
Q8NEM2	SHC SH2 domain-binding protein 1	SHCBP1	2.858588952	0.241991679	1.954918542	0.192946752
P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1	1.956539589	-0.117380142	1.624444731	-0.102364858
P34897;H0YIZ0	Serine hydroxymethyltransferase, mitochondrial;Serine hydroxymethyltransferase	SHMT2	1.086608789	0.078280131	0.302056513	-0.028177579
Q99720;Q5T1J1	Sigma non-opioid intracellular receptor 1	SIGMAR1	0.383908002	0.164490382	0.33262512	0.148062865
D6REA1;Q9H173	Nucleotide exchange factor SIL1	SIL1	0.654651651	0.069158872	0.556226824	-0.049034437
Q96ST3	Paired amphipathic helix protein Sin3a	SIN3A	0.210094119	-0.028149287	0.179466572	-0.020513535
Q8IX90	Spindle and kinetochore-associated protein 3	SKA3	0.114806704	-0.03469696	0.679593341	0.214426295
Q15477	Helicase SKI2W	SKIV2L	1.587886072	0.071976344	0.056679359	0.005942345
P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2	0.094358232	0.008688291	0.303277276	0.025402069
P63208;E5RJR5;E7ERH2;F8W8N3	S-phase kinase-associated protein 1	SKP1	1.324350288	0.145955722	0.775920774	0.079877853
P53985;Q5T8R5	Monocarboxylate transporter 1	SLC16A1	0.446433853	-0.129080455	0.298767998	0.085382144
O15427;J3QRP8;J3QLE3;J3KT M6;J3QRU2;J3KT83;J3QRA0;J3QQS9;J3QQV2;J3QSC3	Monocarboxylate transporter 4	SLC16A3	0.093004763	-0.044237709	0.379436832	-0.189936638
P43007	Neutral amino acid transporter A	SLC1A4	0.656344803	-0.089730263	0.19611403	0.034248352
Q15758;M0QXM4	Neutral amino acid transporter B(0);Amino acid transporter	SLC1A5	1.294467611	-0.138719559	1.123009838	0.123792013
P53007;B4DP62	Tricarboxylate transport protein, mitochondrial	SLC25A1	0.155324198	-0.106816292	0.326086769	-0.212465858
Q9UBX3;F6RGN5	Mitochondrial dicarboxylate carrier	SLC25A10	0.246596492	0.021269162	2.789274358	-0.140810649
Q02978;I3L1P8	Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11	0.354658515	0.051635742	0.377712494	-0.052806536
O75746	Calcium-binding mitochondrial carrier protein Aralar1	SLC25A12	0.520016611	0.072413445	0.568063259	-0.064915339
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13	0.758297486	0.059315681	0.841384078	-0.070615451
B0QYW5;F6RTR7;F8WE74;O43808	Peroxisomal membrane protein PMP34	SLC25A17	0.119737049	0.037830671	0.120965602	-0.033309937
Q9HC21	Mitochondrial thiamine pyrophosphate carrier	SLC25A19	0.763281361	0.044542948	0.951559901	-0.101932208
O43772;C9JPE1	Mitochondrial carnitine/acylcarnitine carrier protein	SLC25A20	0.879335719	0.163732847	0.287408283	-0.062496821
Q9H936;E9PJH7;A0A0D9SFE1;A0A0D9SE19;K4DIB8;K4DIA8;E9PS95;K4DIB6;K4DIB3	Mitochondrial glutamate carrier 1	SLC25A22	0.746194537	0.040871302	0.663345192	-0.043276787
Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24	1.304478034	0.128143946	0.482932791	-0.060660998
Q6KCM7	Calcium-binding mitochondrial carrier protein SCaMC-2	SLC25A25	0.363101155	-0.109804153	0.922474635	-0.297531128

Q00325	Phosphate carrier protein, mitochondrial	SLC25A3	1.781529142	0.1614453	0.342487583	0.041227659
Q9H2D1	Mitochondrial folate transporter/carrier	SLC25A32	0.634546433	-0.087374369	0.646475009	-0.078505516
P12235;V9GYGO	ADP/ATP translocase 1	SLC25A4	0	0.14600563	0	0.272975922
P05141	ADP/ATP translocase 2;ADP/ATP translocase 2, N-terminally processed	SLC25A5	1.730454743	0.260122935	0.422485742	0.108493487
P12236	ADP/ATP translocase 3;ADP/ATP translocase 3, N-terminally processed	SLC25A6	1.40446061	0.083573977	0.286983543	-0.039675077
Q6P1M0	Long-chain fatty acid transport protein 4	SLC27A4	1.240109596	-0.049173355	1.534311825	-0.117961884
Q99808	Equilibrative nucleoside transporter 1	SLC29A1	0.467015337	-0.096356074	0.23365821	0.052117984
P11166	Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1	0.352376739	0.045053482	0.450532627	-0.057918549
Q9UGQ3;F2Z2F6	Solute carrier family 2, facilitated glucose transporter member 6	SLC2A6	0.637261659	-0.102739716	1.186638427	-0.219138209
O00400;H7C562	Acetyl-coenzyme A transporter 1	SLC33A1	0	NaN	0	NaN
P78383;D6RE58;D6RB73;D6R HG0 Q8TB61	Solute carrier family 35 member B1	SLC35B1	0.964166644	0.438035965	1.13057499	0.269554138
U3KPU7;U3KQS2;O43826;U3K QL4 F8VX04;Q9H2H9	Adenosine 3-phospho 5-phosphosulfate transporter 1 Glucose-6-phosphate translocase	SLC35B2 SLC37A4	0.047258101 0.822204423	0.012037913 0.15882225	0.387255539 0.159306003	-0.075694402 0.043078931
Q8WUX1;C9JJU1;C9JMY2;C9J HH7;C9JWG4;C9JNK4 E5RIP4;Q15043;E5RFZ8;E5RG A7;E5RJ40;E5RJG5 Q92504	Sodium-coupled neutral amino acid transporter 1 Sodium-coupled neutral amino acid transporter 5 Zinc transporter ZIP14 Zinc transporter SLC39A7	SLC38A1 SLC38A5 SLC39A14 SLC39A7	0.650133129 1.099915941 0.054082429 0.125906493	0.357449055 -0.159251849 -0.05514876 0.049179554	0 0.252376687 0.049824929 0.964963648	0.096729755 -0.049447378 -0.042536418 0.153269768
F5GZS6;J3KPF3;P08195	4F2 cell-surface antigen heavy chain	SLC3A2	0.010002425	0.001427333	0.08565641	0.012805303
Q8NB15;H0YD64;E9PS74	Solute carrier family 43 member 3	SLC43A3	0.330619707	-0.135578156	0.594846639	-0.132750829
A0A087X0M4;Q9BWU0	Kanadaplin	SLC4A1AP	0.1477102	-0.026976903	1.193590502	-0.086548487
Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	0.332735699	0.082661947	0.707750987	0.132646879
Q96CW6;A0A087X0P9	Probable RNA polymerase II nuclear localization protein SLC7A6OS	SLC7A6OS	0.517144747	-0.216287613	0.104011014	0.038755417
O14745;J3QRP6	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1	1.139247868	-0.090728442	1.777786057	0.130920092
Q9GZT3;A0A087WUN7;H0YJ4 0;G3V4X6;G3V2S9;H0YJW7	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP	1.503083045	0.215227127	0.53499344	0.096955299
Q9NWH9;H7C3F4	SAFB-like transcription modulator	SLTM	0.088987241	0.027509371	0.280880667	0.071659088
B7Z5N5;Q15796;K7EJX0;P840 22;H3BVD1;O15198	Mothers against decapentaplegic homolog;Mothers against decapentaplegic homolog 2;Mothers against decapentaplegic homolog 3;Mothers against decapentaplegic homolog 9	SMAD2;SMAD3;SMAD9	0.271262305	-0.03743426	0.390659478	-0.043574015
K7EIU8;Q13485;A0A087WUF3	Mothers against decapentaplegic homolog;Mothers against decapentaplegic homolog 4	SMAD4	0.295575642	0.063542048	0.770335993	0.087470373
Q8IYB5;A0A087X1X9	Stromal membrane-associated protein 1	SMAP1	0.51182518	-0.08867391	0.086919591	-0.022296588
Q8WU79;A0A087WV97;X6RC C3 P51531;A0A0U1RQZ9;F6VDE0 A0A0A0MT49	Stromal membrane-associated protein 2 Probable global transcription activator SNF2L2	SMAP2 SMARCA2 SMARCA4	1.441027605 0.072093241 1.750190945	0.223700841 -0.009670893 0.133485476	1.459494601 1.318765175 0.346162178	0.213850657 -0.109417915 0.022075335
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	2.014120625	0.089755694	0.047898344	0.004854838
Q12824;C9JTA6;A0A0G2JSE9; G5E975;B5MCL5;A0A0U1RRB 8 Q92922	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 SWI/SNF complex subunit SMARCC1	SMARCB1 SMARCC1	0.62964954 0.138827703	-0.069832802 -0.015714327	1.049501608 0.787134931	-0.108838717 -0.06318442
F8VXC8;Q8TAQ2	SWI/SNF complex subunit SMARCC2	SMARCC2	0.408503269	-0.04547596	0.573314528	-0.056271871
Q96GM5;F8VUB0;F8VRQ4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	SMARCD1	0.155843681	-0.045026843	0.129035326	0.048020999
J3KMX2;B9EGA3;Q92925;J3Q WB6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	SMARCD2	0.582855469	0.10167853	0.017477023	0.004063924
Q969G3;B4DGM3;J3QKS7;K7E MQ8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	SMARCE1	0.726537582	0.075230916	0.017221273	-0.00271829

Q14683;G8JLG1	Structural maintenance of chromosomes protein 1A;Structural maintenance of chromosomes protein	SMC1A	0.364639953	0.029109319	1.412968436	-0.043150902
O95347	Structural maintenance of chromosomes protein 2	SMC2	0.532554978	0.035429637	0.010933018	-0.001054764
Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3	0.178563622	0.012640635	1.183957113	-0.046823502
Q9NTJ3;E9PD53	Structural maintenance of chromosomes protein 4;Structural maintenance of chromosomes protein	SMC4	3.537623247	0.181428591	0.305619869	0.024131139
C9JMN1;Q96SB8;A0A0A0MR Y1	Structural maintenance of chromosomes protein 6	SMC6	0	NaN	0	NaN
A6NHR9;J3KTL8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1	0.29319879	0.01861318	1.821126789	-0.089142164
L0R8F8		SMCR7L	0.926251118	-0.153072484	0.40258303	-0.089128812
G3V5Z3;Q6IN85;H0YIY8;G3V 5A2	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1	0.092792332	-0.030183792	0.073621566	-0.017673492
Q5MIZ7	Serine/threonine-protein phosphatase 4 regulatory subunit 3B	SMEK2	0.151746044	-0.061909676	0.152574293	0.054607073
J3KRA9;Q96Q15;H3BQN7	Serine/threonine-protein kinase SMG1	SMG1	0.451870461	0.126450539	0.303511344	-0.076758703
Q9H0W8	Protein SMG9	SMG9	2.160966315	0.283649445	1.167911931	0.174788793
A0A0G2JRX5;A0A0G2JRY6;A 0A1W2PRV5;E7EQZ4;Q16637; H0YBZ9;A0A0G2JQN8;B4DP6 1	Survival motor neuron protein	SMN1;SMN2	0	0.081027985	0	0.595031738
O75940	Survival of motor neuron-related-splicing factor 30	SMNDC1	0.112343325	-0.022099813	0.515423475	0.099544207
H7BXF4;B1PBA3;Q9NXC4;H7 C1Q6;H7C0W5	Sphingomyelin phosphodiesterase 4	SMPD4	2.606455559	0.219613711	0.36830338	0.064398448
F8VWW8;Q92485	Acid sphingomyelinase-like phosphodiesterase 3b	SMPDL3B	0.536035342	-0.128614426	0.069481706	-0.020485242
P52788;H7C2R7	Spermine synthase	SMS	0.916930437	-0.095148404	0.045404647	-0.006147067
Q2TAY7	WD40 repeat-containing protein SMU1;WD40 repeat-containing protein SMU1, N-terminally processed	SMU1	0.988880128	0.079106967	0.26695941	0.030424754
O00161;H3BNE1;H3BR18;H3B M38;H3BPJ0;H3BV99;H3BP15; H3BQY9	Synaptosomal-associated protein 23;Synaptosomal-associated protein	SNAP23	0.061206272	0.017062187	0.466297706	0.116164716
O95295	SNARE-associated protein Snapin	SNAPIN	1.904531754	-0.277740479	0.171425252	-0.04735597
Q7KZF4	Staphylococcal nuclease domain-containing protein 1	SND1	1.043587048	-0.036671321	0.358596006	-0.011398951
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200	0.533840025	0.019758224	0.647401189	-0.031007131
Q96D17	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40	0.820483574	0.084038417	0.190691283	0.021987279
P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70	0.611839727	-0.052611033	0.240694521	-0.020197233
P09012;M0QZG7;M0R268;M0R 221;M0R2B8	U1 small nuclear ribonucleoprotein A	SNRPA	0.233605371	0.035620689	0.789481588	0.086739858
P09661;H0YKK0	U2 small nuclear ribonucleoprotein A	SNRPA1	2.306281574	-0.101264	0.799968907	-0.036664327
P08579	U2 small nuclear ribonucleoprotein B	SNRPB2	1.624237825	-0.139953613	0.166718622	0.014285723
A0A0A0MRR7;P09234	U1 small nuclear ribonucleoprotein C	SNRPC	0.848167362	-0.096526464	0.891972759	0.093212763
P62314;J3QLI9	Small nuclear ribonucleoprotein Sm D1	SNRPD1	0.014956593	0.00288868	0.016836865	0.003218969
P62316;K7ERG4	Small nuclear ribonucleoprotein Sm D2	SNRPD2	1.01012851	-0.081940333	1.424262887	-0.097693443
P62318;H3BT13	Small nuclear ribonucleoprotein Sm D3	SNRPD3	1.756930325	0.124277433	2.159547211	0.107202848
P62304;A6NHK2	Small nuclear ribonucleoprotein E	SNRPE	0.088267067	-0.021520615	0.000540196	-0.000149409
P62306	Small nuclear ribonucleoprotein F	SNRPF	0.433830905	0.374796391	0	0.220805645
P62308;A8MWD9;Q49AN9;F5 H013;C9JVQ0	Small nuclear ribonucleoprotein G;Putative small nuclear ribonucleoprotein G-like protein 15	SNRPG;SNRPGP15	0.191233165	0.023935954	0.68794973	0.052510897
J3QLE5;P63162;P14678;J3KRY 3;S4R3P3	Small nuclear ribonucleoprotein-associated protein N;Small nuclear ribonucleoprotein-associated proteins B and B	SNRPN;SNRPB	0.034348136	-0.006196976	0.454775983	-0.061071396
A0A140TA73;Q13425;A0A0G2 JM75;J3KT21;H0YCS0	Beta-2-syntrophin	SNTB2	0.261824445	0.108507347	0.376360852	0.123152097
Q13573;G3V4X8;G3V3A4	SNW domain-containing protein 1	SNW1	0.650663254	0.053044319	1.044462273	0.077882767
Q13596;H0YK42	Sorting nexin-1	SNX1	0.131058706	-0.024016062	0.053359986	0.010540326
A0A087X0R6;Q9UMY4	Sorting nexin-12	SNX12	1.519810609	-0.21979173	0.187785479	-0.056918144
Q15036	Sorting nexin-17	SNX17	2.772692669	0.1683321	1.872077364	0.187966029
O60749	Sorting nexin-2	SNX2	1.419117834	-0.146535873	1.147641023	-0.119272868
Q96L92	Sorting nexin-27	SNX27	0.222462278	0.073866208	0.633842644	-0.162418365

O60493	Sorting nexin-3	SNX3	1.813472662	0.136870066	0.24176849	0.038363457
Q9Y5X3;Q5QPE5;A0A087WU Y5;Q5QPE4	Sorting nexin-5	SNX5	1.889747336	-0.084623973	1.988126979	-0.066178004
A0A0A0MRI2;Q9UNH7	Sorting nexin-6;Sorting nexin-6, N-terminally processed	SNX6	0.723936759	-0.076278369	0.000215386	-2.29E-05
Q9Y5X1	Sorting nexin-9	SNX9	0.896232776	-0.106928507	1.010652477	-0.092510859
B1APM4;P35610	Sterol O-acyltransferase 1	SOAT1	0.430957497	0.080075582	0.221527702	0.048570633
P00441;H7BYH4	Superoxide dismutase [Cu-Zn]	SOD1	3.634728248	-0.250917435	0.751108008	0.0704813
A0A0C4DFU2;P04179;A0A0C4 DFU1;F5H3C5;F5H4R2;F5GYZ 5;G8JLJ2;A0A0C4DG56 P18583	Superoxide dismutase;Superoxide dismutase [Mn], mitochondrial	SOD2	3.296310266	0.266955694	0.896385577	0.085920334
Q00796;H0YLA4	Protein SON	SON	0.262850714	0.018637657	0.312378337	-0.019862811
Q96R06	Sorbitol dehydrogenase	SORD	1.414588973	-0.104348818	0.800920415	-0.065661112
A0A087X2D8;O60271	Sperm-associated antigen 5	SPAG5	4.156978239	0.48183918	3.615059699	0.295109749
Q8NB90	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9	0.028291587	0.006597201	0.760083066	0.086377462
Q8NBT2;K7EJH0;K7EMX1;K7 EJV2;K7ESQ2	Spermatogenesis-associated protein 5	SPATA5	0.550176213	-0.265561676	0.520765108	-0.170030149
Q9Y6A9;C9JBL1;X6R2S6	Kinetochores protein Spc24	SPC24	0.429745815	0.086929003	0.290259711	-0.040692329
A0A087WUC6;E9PI68;Q15005; E9PL01;H0YE04 P61009	Signal peptidase complex subunit 1	SPCS1	1.234415484	0.298432668	0.053198196	-0.030939102
Q5M775	Signal peptidase complex subunit 2	SPCS2	1.939245765	0.199546814	0.002337652	0.00057443
Q9NZD8;H0YMB7;H0YKB0;H 3BRR0	Signal peptidase complex subunit 3	SPCS3	0.6028598	0.059307098	0.05539301	-0.009373665
O43291;K7EKQ0;K7EM91;K7E S15;K7EQZ3 P10451;D6R9C5	Cytospin-B	SPECC1	1.186716069	0.200790087	0.719646014	0.142856598
P35270	Masparidin	SPG21	0.512544857	0.120276769	0.400212242	0.05395476
Q8WW59	Kunitz-type protease inhibitor 2	SPINT2	0.700718014	-0.209621429	1.113697275	0.339331945
Q13813;A0A0D9SF54;A0A0D9 SGF6	Osteopontin	SPP1	1.93698946	-0.51310126	2.877863652	0.609271685
Q01082;A0A087WUZ3	Sepiapterin reductase	SPR	0.191384068	-0.075169563	0.284523684	-0.074309985
O15020;A4QPE4	SPRY domain-containing protein 4	SPRYD4	0.986117182	0.115848859	0.290346808	0.044830958
O15269	Spectrin alpha chain, non-erythrocytic 1	SPTAN1	2.775796277	0.096401532	1.880977824	0.078537623
O15270	Spectrin beta chain, non-erythrocytic 1	SPTBN1	0.023371832	-0.002580007	0.002443117	-0.000231107
Q9NUV7	Spectrin beta chain, non-erythrocytic 2	SPTBN2	0.056412398	-0.021050199	0.072852848	0.03057766
Q14534;E7EVQ6	Serine palmitoyltransferase 1	SPTLC1	0.706040331	0.195348104	0.762967889	-0.192918142
Q9Y6N5;H3BNX3	Serine palmitoyltransferase 2	SPTLC2	0.61700044	0.309914112	0.68702617	0.253502051
Q13501;E7EMC7	Serine palmitoyltransferase 3	SPTLC3	0.168127631	-0.050766627	0.393374082	-0.110261917
Q8N5C6	Squalene monooxygenase	SQLE	3.309418688	0.412654559	1.52587832	0.205033938
Q8WXA9	Sulfide:quinone oxidoreductase, mitochondrial	SQRDL	2.577814613	0.156390508	1.091513145	0.07903258
A0A075B7B5;B7ZM87;O75044; A0A286Y3;G5EA48;P0DMP 2;P0DJJ0;Q7Z6B7	Sequestosome-1	SQSTM1	6.159616556	0.550900459	4.178158201	0.295125008
C9J0K6;P30626;B4DHQ6	S1 RNA-binding domain-containing protein 1	SRBD1	0.699638068	0.4337732	0.465896626	0.297977606
P19623	Splicing regulatory glutamine/lysine-rich protein 1	SREK1	0.539529277	-0.104746183	0.824466916	-0.158578555
P37108;H0YLA2	SLIT-ROBO Rho GTPase-activating protein 2;SLIT-ROBO Rho GTPase-activating protein 2B;SLIT-ROBO Rho GTPase-activating protein 2C;SLIT-ROBO Rho GTPase-activating protein 1	SRGAP2;SRGAP1;SRGAP2B;SRGAP2C	0	-0.050039291	0	-0.002252579
P09132;A0A087WYR0;A0A087 WWU9	Sorcin	SRI	1.053765684	-0.154568354	0.537253474	0.090299924
P61011;G3V4F7	Spermidine synthase	SRM	3.612376624	-0.146093686	2.459355781	-0.106874148
Q9UHB9	Signal recognition particle 14 kDa protein	SRP14	0.278137236	0.043422063	0.32794817	0.04254818
O76094	Signal recognition particle 19 kDa protein	SRP19	0.715182706	-0.118769964	0.650667029	-0.054870605
P49458;E9PE20	Signal recognition particle 54 kDa protein	SRP54	1.213913806	0.067938169	0.286805128	0.014129957
H3BLV9;Q96SB4	Signal recognition particle subunit SRP68	SRP68	0.781840006	0.034129461	0.667866713	-0.024195035
	Signal recognition particle subunit SRP72	SRP72	0.138826567	0.009874026	0.668560362	0.034431775
	Signal recognition particle 9 kDa protein	SRP9	0.67444452	0.083407402	2.329337303	0.220388095
	SRSF protein kinase 1	SRPK1	0.135666382	-0.029822667	0.070459997	0.016219775

P78362;H7C521;H7C5L6	SRSF protein kinase 2;SRSF protein kinase 2 N-terminal;SRSF protein kinase 2 C-terminal	SRPK2	1.172971585	0.251435916	0.115261764	-0.056377729
P08240	Signal recognition particle receptor subunit alpha	SRPR	0.488381984	0.051067034	0.611693272	-0.074481964
Q9Y5M8;H7C4H2	Signal recognition particle receptor subunit beta	SRPRB	0.854938981	0.064965566	0.382760744	0.031825066
A9Z1X7;Q8IYB3;E9PCT1;M0R088	Serine/arginine repetitive matrix protein 1	SRRM1	0.102595803	0.017852465	0.174244239	0.031206449
Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2	2.010530461	-0.097613335	1.608379082	-0.084506353
Q9BXP5;H7C3A1	Serrate RNA effector molecule homolog	SRRT	0.306530051	0.038712184	1.223264094	0.090578715
J3KTL2;Q07955	Serine/arginine-rich splicing factor 1	SRSF1	0.131759465	-0.009655952	0.722752559	-0.039655685
Q5JRI1;O75494	Serine/arginine-rich splicing factor 10	SRSF10	0.817831924	0.16481781	0.163840234	0.043584188
Q5T760;Q05519;B4DWT1	Serine/arginine-rich splicing factor 11	SRSF11	0.352413369	-0.051137924	1.191532235	-0.131915728
J3KP15;Q01130;J3QL05	Serine/arginine-rich splicing factor 2	SRSF2	0.46962003	-0.057375272	0.164577242	-0.020402273
P84103;A0A087X2D0	Serine/arginine-rich splicing factor 3	SRSF3	0.612091116	0.060162544	1.181927076	0.061462402
A0A0D9SEM4;Q08170	Serine/arginine-rich splicing factor 4	SRSF4	0.324690522	0.084882927	0.026481361	0.008033943
Q13243;B4DJK0;B4DUA4;G3V5K8	Serine/arginine-rich splicing factor 5	SRSF5	0.024916875	0.004983902	0.039519446	0.00635306
Q13247	Serine/arginine-rich splicing factor 6	SRSF6	0.256153095	-0.022313754	0.137521123	-0.011441231
A0A0B4J1Z1;C9JAB2;Q16629	Serine/arginine-rich splicing factor 7	SRSF7	0.353264416	0.03143088	0.334142563	-0.032150586
Q13242;H0YIB4;S4R3G0	Serine/arginine-rich splicing factor 9	SRSF9	0.54962272	0.024882634	1.795495664	-0.051210086
Q9BYN0	Sulfiredoxin-1	SRXN1	1.874616127	0.470085462	3.168850597	0.864695676
P05455	Lupus La protein	SSB	0.136822184	0.011219978	0.150854821	0.012150764
Q04837;A0A0G2JLD8;E7EUY5;C9K0U8	Single-stranded DNA-binding protein, mitochondrial	SSBP1	1.534921171	0.220595996	0.03841048	-0.009757042
D6RAC5;A0A087WVT6;A0A087X159;P81877;Q9BWW4;U3KQ46	Single-stranded DNA-binding protein 2;Single-stranded DNA-binding protein 3	SSBP2;SSBP3;SSBP4	0.180779581	-0.059007327	0.53193525	-0.261169815
O43805	Sjogren syndrome nuclear autoantigen 1	SSNA1	1.114575986	-0.120784124	0.220992596	-0.039180756
P43307;C9J3L8;C9J5W0;E9PAL7;C9JZQ1	Translocon-associated protein subunit alpha	SSR1	1.254205377	0.121622086	0.03110593	0.005369822
C9JA28;Q9UNL2;C9J365	Translocon-associated protein subunit gamma	SSR3	0.854801803	0.460588773	0.837068573	0.480026881
P51571;A6NLM8	Translocon-associated protein subunit delta	SSR4	3.760174431	0.149363518	1.167267927	0.062589645
Q08945	FACT complex subunit SSRP1	SSRP1	0.665604076	-0.042324702	1.950631938	-0.097958883
H0YEB6;O60232;G3V1B8	Sjogren syndrome/scleroderma autoantigen 1	SSSCA1	2.346819256	-0.236094157	0.725738286	-0.077136676
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	SSU72	0.453836345	0.041017532	0.173756801	-0.030673345
P50502;H7C311;Q3KNR6;Q8IZP2;F6VDH7;Q8NFI4	Hsc70-interacting protein;Putative protein FAM10A4;Putative protein FAM10A5	ST13;ST13P4;ST13P5	0.156679919	0.027673721	1.489796601	0.172512372
Q9Y5Y6	Suppressor of tumorigenicity 14 protein	ST14	4.24584615	-0.290949821	1.360877446	-0.117371877
Q8WVM7;Q68DW7	Cohesin subunit SA-1	STAG1;DKFZp781D1416	0.523557622	0.252405326	0.317935933	0.212786833
Q8N3U4	Cohesin subunit SA-2	STAG2	0.147175831	0.017912865	0.941428439	-0.076499621
Q92783	Signal transducing adapter molecule 1	STAM	0.031527315	-0.009942436	0.056655921	0.017159144
O95630;C9JK83	STAM-binding protein	STAMPB	0.390108827	0.084266663	0.419170992	0.072287877
Q9NSY2	StAR-related lipid transfer protein 5	STARD5	0.66600956	-0.168110847	0.614045907	-0.161225319
Q9NQZ5	StAR-related lipid transfer protein 7, mitochondrial	STARD7	0.494559812	0.151355362	0.032924195	0.013168589
P42224;J3KPM9	Signal transducer and activator of transcription 1-alpha/beta;Signal transducer and activator of transcription	STAT1	0.313311891	-0.089392344	0.190390845	0.036233266
P52630;B4DLC8	Signal transducer and activator of transcription 2	STAT2	0.526570521	0.120901426	0.003826373	-0.000833511
P40763;G8JLH9	Signal transducer and activator of transcription 3;Signal transducer and activator of transcription	STAT3	0.513085797	0.042819659	0.545293499	-0.07195123
P51692	Signal transducer and activator of transcription 5B	STAT5B	0	0.43879954	0	0.390060425
A0A1W2PNW1;P42226	Signal transducer and activator of transcription 6	STAT6	0.675120666	0.148911794	0.232494685	-0.074524244
O95793;Q5JW30;A0A087X1A5	Double-stranded RNA-binding protein Staufen homolog 1	STAU1	0.521456684	0.05579567	1.855615352	0.123228391
P31948	Stress-induced-phosphoprotein 1	STIP1	0.503692704	-0.04086113	0.562372235	0.043375015
O94768;C9JZJ1;U3KQF8	Serine/threonine-protein kinase 17B	STK17B	0.104109795	-0.046551895	0.879611039	-0.234846306

B4DR80;Q9Y6E0;H0Y630;Q5J V98	Serine/threonine-protein kinase 24;Serine/threonine-protein kinase 24 36 kDa subunit;Serine/threonine-protein kinase 24 12 kDa subunit	STK24	0.817100945	-0.148566882	1.095249371	-0.184315364
Q8NBY1;B4E0Y9;Q9P289	Serine/threonine-protein kinase 26	STK26	1.111154386	-0.11117363	1.124500745	-0.111604373
Q13043;F5H5B4	Serine/threonine-protein kinase 4;Serine/threonine-protein kinase 4 37kDa subunit;Serine/threonine-protein kinase 4 18kDa subunit	STK4	0.151772928	0.023195903	0.022800955	0.003491402
P16949;A2A2D0	Stathmin	STMN1	1.975759287	-0.153339386	0.252213405	-0.026576996
P27105	Erythrocyte band 7 integral membrane protein	STOM	0.383072987	0.038814227	0.779930198	0.087859154
Q9UJZ1;A0A087WYB4	Stomatin-like protein 2, mitochondrial	STOML2	1.747545765	0.111100515	0.060296137	-0.006276449
Q9Y3F4	Serine-threonine kinase receptor- associated protein	STRAP	1.908367953	-0.0907348	0.493661774	0.016740481
Q96S19	Spermatid perinuclear RNA-binding protein	STRBP	0.018415468	0.00346152	0.055301587	-0.008380254
O43815	Striatin	STRN	1.686494392	-0.65018177	0.982276397	-0.316496849
P08842	Steryl-sulfatase	STS	0.120615398	0.100083033	1.072264124	-0.169013023
P46977	Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit STT3A	STT3A	2.164994455	0.151729902	0.841706335	0.075861295
Q8TCJ2	Dolichyl-diphosphooligosaccharide-- protein glycosyltransferase subunit STT3B	STT3B	2.518162644	0.154845238	0.527822171	0.065087636
Q9UNE7;H3BTA3;H3BUD0;H3 BS86	E3 ubiquitin-protein ligase CHIP	STUB1	0.439677428	0.051897685	0.205750463	0.030335108
Q13190;H7C3X5;E9PNU4	Syntaxin-5	STX5	0.05417065	0.01970768	0.541855425	0.117973646
O15400	Syntaxin-7	STX7	0.801598287	-0.315523148	0.661008436	-0.270650864
A0A1B0GWF2;A0A1B0GVQ5; A0A0D9SG72;A0A1B0GTP9;P 61764;A0A1B0GW76 Q15833;M0R0M7	Syntaxin-binding protein 1 Syntaxin-binding protein 2	STXBP1 STXBP2	2.889945339 0.308114428	-0.239490509 -0.052158038	0.945348321 0.524400548	-0.130779902 -0.084252357
O00186	Syntaxin-binding protein 3	STXBP3	1.196116333	-0.314180311	1.819169823	-0.339662234
P53999	Activated RNA polymerase II transcriptional coactivator p15	SUB1	0.865833169	0.185839017	0.750491415	0.183964411
Q9P2R7;Q5T9Q5	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2	0.942720826	0.082072258	0.069266682	0.008583705
P53597	Succinyl-CoA ligase [ADP/GDP- forming] subunit alpha, mitochondrial	SUCLG1	2.872778237	0.12495931	0.268552279	0.021749179
Q96I99;E9PDQ8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	SUCLG2	1.865985388	0.080520312	0.120393932	-0.008951505
Q8IWX8;V9GZ08	SURP and G-patch domain-containing protein 1	SUGP1	2.468111168	-0.438437653	0.885129866	-0.285572942
M0R3F6;M0R2Z9;Q8IX01	SURP and G-patch domain-containing protein 2	SUGP2	0.030840098	0.036968613	0.220785299	0.149845028
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog	SUGT1	1.37001491	-0.13326931	0.41955479	0.044821421
J3KQJ1;Q8NBJ7;C9JL30;A8M XB9;C9J660;H7C3B2;F8WA42 B8ZZN6;P63165;B8ZZ67	Sulfatase-modifying factor 2 Small ubiquitin-related modifier 1	SUMF2 SUMO1	0.995550389 1.31328689	0.210855484 -0.200873693	0.711024075 0.162987041	0.184647242 0.032259115
P61956	Small ubiquitin-related modifier 2	SUMO2	1.580946756	-0.200112025	0.103967327	0.020659765
H0Y742;H0Y6N5;E9PHI4;O949 01;H7C2K3	SUN domain-containing protein 1	SUN1	1.54099469	0.194675128	0.253481488	-0.062291145
Q9UH99;B0QY60	SUN domain-containing protein 2	SUN2	1.38986737	0.172452291	0.506459709	-0.064644814
Q9Y5B9	FACT complex subunit SPT16	SUPT16H	1.156335034	0.053606987	0.225059094	-0.011503855
O00267	Transcription elongation factor SPT5	SUPT5H	2.25236902	0.123678207	0.598636426	0.043580373
Q7KZ85	Transcription elongation factor SPT6	SUPT6H	0.240093987	0.022200902	0.014659324	0.001998901
Q8IYB8	ATP-dependent RNA helicase SUPV3L1, mitochondrial	SUPV3L1	0.164683307	0.037522952	0.804163596	-0.127754847
Q15526;A0A087WYS9	Surfeit locus protein 1	SURF1	0.243408564	-0.061912855	0.822929566	-0.143591881
Q5T8U5;O15260;B7Z1G8	Surfeit locus protein 4	SURF4	0.655046965	0.178617795	0.149258883	0.055791219
O75683	Surfeit locus protein 6	SURF6	0.249354946	0.044370969	0.570937863	0.056493759
J3QQW9;Q15022	Polycomb protein SUZ12	SUZ12	0.098550957	0.018916766	0.323350579	-0.050857862
Q96A49	Synapse-associated protein 1	SYAP1	0.579496895	-0.085419655	0.727738222	0.090497017
O95926	Pre-mRNA-splicing factor SYF2	SYF2	0.283328067	-0.236233997	0.116553345	0.130731106

P43405	Tyrosine-protein kinase SYK	SYK	1.879114142	0.111397743	0.084644317	-0.007816633
Q92797;A0A087WUE9	Symplekin	SYMPK	1.508805779	0.074710846	0.42790701	-0.053989728
O60506	Heterogeneous nuclear ribonucleoprotein Q	SYNCRIP	0.262605004	-0.027986209	0.258073717	-0.026817958
G3V533;Q6ZMZ3	Nesprin-3	SYNE3	1.463985652	-0.322477341	1.000187679	-0.262811661
O43760;K7ELD9;K7ENG9;K7E LS8	Synaptogyrin-2	SYNGR2	1.036277039	0.178297679	0.23345537	0.054862022
C9JIE4;A0A075B7B1;O15061	Synemin	SYNM	1.032225084	0.307099342	0.712098248	0.129958344
Q86TM6	E3 ubiquitin-protein ligase synoviolin	SYVN1	1.947546145	0.368311246	0.650760048	0.107071241
Q15750	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1	0	-0.076202393	0	0.120727539
Q9Y6A5	Transforming acidic coiled-coil-containing protein 3	TACC3	0.168754325	0.035570463	1.155313317	0.155676842
Q9BSH4	Translational activator of cytochrome c oxidase 1	TACO1	1.136051043	-0.11883831	2.328260509	-0.158046087
Q92804;A0A075B7D9	TATA-binding protein-associated factor 2N	TAF15	1.265075657	-0.193857511	0.263392163	-0.067735354
J3KR72;P49848;C9JIS2;E5RHA 1;C9J088;C9JFL8;C9JTY6	Transcription initiation factor TFIID subunit 6	TAF6	0	0.073259354	0.18910163	-0.080329132
Q9Y6J9	TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L	TAF6L	0.389862996	0.088764509	0.224949813	-0.072944641
Q15545	Transcription initiation factor TFIID subunit 7	TAF7	0.697024751	0.151564916	0.47902245	0.116831303
Q16594;D6RIE8;D6RHW1;D6RIY1;D6RGK3;D6RIV9;Q9HBM 6	Transcription initiation factor TFIID subunit 9;Transcription initiation factor TFIID subunit 9B	TAF9;TAF9B	0.159268504	0.03472964	0.304095263	-0.066987356
P37802;X6RJP6	Transgelin-2	TAGLN2	0.036452815	0.008345286	0.913631356	0.148214976
P37837;F2Z393	Transaldolase	TALDO1	0.927606548	-0.052185376	1.37128788	0.088048299
Q96BW9;A0A0G2JQ92	Phosphatidate cytidylyltransferase, mitochondrial	TAMM41	0.418848104	-0.138285319	0.815682654	-0.607528051
A0A140T9T7;Q03518	Antigen peptide transporter 1	TAP1	0.368300722	-0.085573196	0.915571669	-0.224500338
A0A0G2JLV0;A0A087WYD6;Q03519;A0A140T9S0;E7ENX8	Antigen peptide transporter 2	TAP2	0.568181147	0.083082199	0.210656647	-0.032524109
A0A0G2JKZ1;A2AB90;A0A0G2JH37;A0A0A0MSV9;O15533;A0A0A0MT98;Q6PIN7	Tapasin	TAPBP	3.616781121	0.460328738	1.765600919	0.235209147
Q9BX59	Tapasin-related protein	TAPBPL	0.79517811	0.121052424	0.068838542	0.022430102
Q13148;B1AKP7;G3V162;A0A087X260;A0A087WYY0;A0A087WX29;A0A087WXQ5;A0A087WV68;A0A1W2PNU8	TAR DNA-binding protein 43	TARDBP	0.039835919	0.009269714	0.598210201	0.107130686
P26639	Threonine--tRNA ligase, cytoplasmic	TARS	0.53891953	0.040496508	0.471461024	0.035868963
Q9BW92;U3KQG0;F6S7Q7	Threonine--tRNA ligase, mitochondrial	TARS2	0.410644839	-0.042247772	0.658027378	-0.062551816
Q9NVG8	TBC1 domain family member 13	TBC1D13	2.621240808	-0.203250249	1.646880701	-0.185392062
Q8TC07	TBC1 domain family member 15	TBC1D15	0.705507697	0.049794197	0.215570832	0.020536423
O60343	TBC1 domain family member 4	TBC1D4	0.300548435	-0.146561941	0.09332456	-0.075078964
Q92609;C9J3F6	TBC1 domain family member 5	TBC1D5	1.741595584	-0.204796791	0.403635063	-0.07501634
E5RIW3;E5RJD8;O75347;E5RH G6	Tubulin-specific chaperone A	TBCA	0.808089593	-0.068210284	2.847008037	0.177862167
Q99426;K7EP07;K7EK42	Tubulin-folding cofactor B	TBCB	0.080863329	-0.010503133	0.235161891	0.026715914
Q15814	Tubulin-specific chaperone C	TBCC	1.148905215	-0.230774562	0.694968568	-0.105527401
J3KR97;Q9BTW9	Tubulin-specific chaperone D	TBCD	0.381346939	-0.065225919	0.24672223	-0.028993289
Q15813	Tubulin-specific chaperone E	TBCE	0.375206052	-0.027717272	0.14730616	-0.01305294
Q9UHD2	Serine/threonine-protein kinase TBK1	TBK1	0.072608667	-0.023495515	0.758989642	0.194585323
Q9BZK7;A0A0D9SF63	F-box-like/WD repeat-containing protein TBL1XR1	TBL1XR1	0.904371476	-0.092865626	0.182919475	0.026354154
E9PF19;Q9Y4P3;Q96E41	Transducin beta-like protein 2	TBL2	0.304004421	0.022229195	0.566093598	-0.035523733
Q12788;J3KNP2	Transducin beta-like protein 3	TBL3	1.480473596	0.089495341	0.170012306	-0.017620405
P62380;Q7Z6U1;Q7Z6U2	TATA box-binding protein-like protein 1	TBPL1	0	NaN	0	NaN
Q969Z0	Protein TBRG4	TBRG4	0.674022325	-0.056710879	1.523308498	-0.111619314
A0A1W2PPZ5;P23193;A0A1W2PRL9	Transcription elongation factor A protein 1	TCEA1	0.534069991	0.043209712	1.242412349	0.091303825
E5RHG8;Q15369;R4GMY8	Transcription elongation factor B polypeptide 1	TCEB1	0.950370911	0.090085983	0.814406425	0.081278165
B8ZZU8;Q15370;I3L0M9	Transcription elongation factor B polypeptide 2	TCEB2	1.054843921	0.059446017	3.038321509	0.095653852

A0A024RAC6;Q14241	Transcription elongation factor B polypeptide 3	TCEB3	0.314716827	-0.067723592	0.34373119	0.047197024
O14776;G3V220	Transcription elongation regulator 1	TCERG1	0.174963818	0.025471687	0.264054316	-0.024099668
Q13488;E9PNA6;E9PM12	V-type proton ATPase 116 kDa subunit a isoform 3;V-type proton ATPase subunit a	TCIRG1	0.432667051	0.068518003	1.041121283	-0.14118735
Q13428;J3KQ96;E7ETY2	Treacle protein	TCOF1	0.446315789	-0.06020546	0.89249328	-0.098468145
P17987;E7ERF2;E7EQR6;F5H282	T-complex protein 1 subunit alpha	TCP1	1.984866589	-0.078228315	0.442702176	-0.025509834
H0YJ44;Q9NUW8;G3V2F4;E7E PD8	Tyrosyl-DNA phosphodiesterase 1	TDP1	0	0.037794113	0	NaN
O95551	Tyrosyl-DNA phosphodiesterase 2	TDP2	3.048595344	-0.288545926	1.693945378	-0.226780891
Q55ZR4;F6TB26;Q9Y2W6;E9PKN8	Tudor and KH domain-containing protein	TDRKH	0.878222337	0.15047404	0.079958153	-0.020049604
Q9NZ01	Very-long-chain enoyl-CoA reductase	TECR	1.266770133	0.099218051	0.091414442	0.010759672
Q9Y4R8;H3BRS3	Telomere length regulation protein TEL2 homolog	TELO2	0.539570938	0.048367818	0.045245371	0.003598531
Q15554;U3KQ35;H3BR06;H3BTA7	Telomeric repeat-binding factor 2	TERF2	0.055562575	0.018425624	0.73848833	-0.144719124
Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1	TERF2IP	0.728714587	-0.062453906	0.681778358	0.070771853
Q9UGI8	Testin	TES	3.356751875	0.283231735	3.249536083	0.305040042
Q9NXF1	Testis-expressed sequence 10 protein	TEX10	0.002093403	-0.000964801	0.63761336	-0.178405762
A0A087WTU3;Q9Y619;C9JXQ7;C9JHH5	Testis-expressed sequence 264 protein	TEX264	0.279274179	-0.093031883	0.101067262	-0.030105273
Q00059;H7BYN3	Transcription factor A, mitochondrial	TFAM	1.234854708	0.141405741	0.161685134	-0.026074409
Q01664	Transcription factor AP-4	TFAP4	0.219589047	0.082406998	0.004131547	0.002017339
Q9H5Q4	Dimethyladenosine transferase 2, mitochondrial	TFB2M	0.492043268	-0.103737831	0.260429429	-0.094940503
Q14186;Q5JSB5	Transcription factor Dp-1	TFDP1	0	NaN	0	NaN
Q92734;C9JUE0;C9JJP5;C9JTY3	Protein TFG	TFG	1.03930622	-0.127223333	0.471175762	0.058490117
Q9UBB9	Tuftelin-interacting protein 11	TFIP11	0.772696021	-0.095761935	2.418909155	-0.194181124
P02786;G3V0E5	Transferrin receptor protein 1;Transferrin receptor protein 1, serum form	TFRC	1.445469345	0.128608386	0.414751295	-0.069650332
Q96EK4	THAP domain-containing protein 11	THAP11	0.895357617	-0.124983788	0.642131329	-0.119079272
Q8WUY1;H0YAR9	Protein THEM6	THEM6	0.690879879	0.084584872	0.17671913	0.024242719
A0A0D9SFD2;Q8N1K5	Protein THEMIS	THEMIS	0.454223787	0.056735039	0.658843364	-0.096562703
Q8IYQ7	Threonine synthase-like 1	THNSL1	0.191003197	0.056001027	0.447475211	-0.109721502
A0A087WWS1;Q96FV9	THO complex subunit 1	THOC1	1.25305354	-0.113759041	0.83414864	-0.072750092
Q8NI27;A0A0C4DG98	THO complex subunit 2	THOC2	2.090644869	-0.136645635	2.477458828	-0.160569509
Q96J01;D6RGZ2	THO complex subunit 3	THOC3	0.091226989	0.017113686	0.111858969	-0.02083238
Q13769;F8WCP5;C9JXG5	THO complex subunit 5 homolog	THOC5	0.033862542	0.01005427	0.117863077	-0.023876508
Q86W42	THO complex subunit 6 homolog	THOC6	0.905953121	0.073816935	0.512114261	-0.047456423
Q619Y2;A0A024R341	THO complex subunit 7 homolog	THOC7;NIF3L1BP1	0.332734003	0.085436185	0.699939677	0.08470726
P52888;K7EP46	Thimet oligopeptidase	THOP1	2.835828372	-0.174145063	0.683495953	-0.069855372
Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3	1.263746831	0.128980319	0.798983587	0.08241876
Q9NXG2	THUMP domain-containing protein 1	THUMPD1	2.994211112	-0.191311836	0.25224283	-0.02481842
Q9BV44;H7C3J3	THUMP domain-containing protein 3	THUMPD3	0.02616744	-0.003206253	1.339900797	0.098904928
F8W8I6;P31483;E5RGV5;E5RG67	Nucleolysin TIA-1 isoform p40	TIA1	1.313972318	-0.141352971	0.634899304	-0.086076419
Q01085;E7ETJ9;E7ETC0	Nucleolysin TIAR	TIAL1	0.130680022	0.02068615	0.116860628	0.019263585
Q9NQ88;A0A0U1RQD1	Fructose-2,6-bisphosphatase TIGAR	TIGAR	2.894879525	-0.212466558	0.56598265	-0.099166743
Q9UNS1	Protein timeless homolog	TIMELESS	0.359113807	0.061569214	0.013489499	-0.00250721
Q9Y5L4;K7EIT2	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13	0.832409744	-0.147628148	0.341528414	-0.056194305
Q99595	Mitochondrial import inner membrane translocase subunit Tim17-A	TIMM17A	1.501897659	-0.315495809	0.58128774	0.144899368
Q9BVV7	Mitochondrial import inner membrane translocase subunit Tim21	TIMM21	1.718156295	0.193618774	1.113214095	-0.146216393

O14925;Q5SRD1	Mitochondrial import inner membrane translocase subunit Tim23;Putative mitochondrial import inner membrane translocase subunit Tim23B	TIMM23;TIMM23B	0.062085591	0.01498216	0.107053438	-0.0332009
O43615;M0QXU7	Mitochondrial import inner membrane translocase subunit TIM44	TIMM44	1.912039036	0.10624218	0.361743071	-0.032042503
Q3ZCQ8;M0R2F8;M0R003;M0R0C3;M0R1Y4	Mitochondrial import inner membrane translocase subunit TIM50	TIMM50	0.222283593	0.043223699	0.089632519	0.0228405
O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A	0.588832033	0.133757591	0.429791326	0.103559812
G3XAN8;Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B	TIMM8B	1.356530514	-0.154112498	0.632224943	-0.103420893
Q9Y5J7;A0A1W2PRH9;A0A1W2PQ55;G3V502;G3V2F3	Mitochondrial import inner membrane translocase subunit Tim9	TIMM9	1.193304271	-0.151831945	1.083511962	-0.121205966
Q9NPL8;G3XA94	Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1	2.704971106	-0.388331731	0.267147388	-0.052901904
Q9BVBW5;H3BTH1;H3BU04	TIMELESS-interacting protein	TIPIN	1.243663445	-0.315822601	0.461888965	0.146377087
O75663	TIP41-like protein	TIPRL	0.991276472	0.214887619	1.388389555	0.267664591
P04183;K7ERV3;K7ESS2;K7ERJ1	Thymidine kinase, cytosolic;Thymidine kinase	TK1	2.008573407	0.110144933	3.714025645	0.208716075
P29401;A0A0B4J1R6	Transketolase	TKT	2.534975737	-0.097055435	0.098435192	0.005404154
A0A0D9SES8;H0YKT5;H0YKN8;H0YL70;Q04726;F5H7D6;H0YNT2;H0YNI7;H0YKH0;H0YLW9;H0YLI3	Transducin-like enhancer protein 3	TLE3	0.464326212	-0.104943911	0.658302166	-0.11672624
Q9Y490	Talin-1	TLN1	3.343861457	-0.065722466	0.962591487	0.030247053
H0Y858;Q9NR96	Toll-like receptor 9	TLR9	0.1250671	-0.054121971	0.219761558	-0.093810717
Q99805	Transmembrane 9 superfamily member 2	TM9SF2	0.475627387	0.079417229	0.504315055	0.05685393
Q9HD45;Q5TB53	Transmembrane 9 superfamily member 3	TM9SF3	1.528196865	0.098415693	1.152529766	0.072125753
A0A0C4DFM1;Q92544	Transmembrane 9 superfamily member 4	TM9SF4	0.140753701	-0.038328489	0.119953243	0.022264163
D6RA57;H0Y9X1;Q96EY4;D6RE67;D6RC31	Translation machinery-associated protein 16	TMA16	0.441623686	0.107326508	0.343069703	-0.439649105
Q9Y2S6;A0A024R1R8	Translation machinery-associated protein 7	TMA7;hCG_2014768	0.048760168	0.018206596	1.450583417	0.317098935
J9JIE6;Q9UM00;J3KS45;J3QY2;J3KTQ7	Transmembrane and coiled-coil domain-containing protein 1	TMCO1	0.442346242	0.070082982	0.209416492	0.041347186
P49755;G3V2K7	Transmembrane emp24 domain-containing protein 10	TMED10	2.178942963	0.191693942	1.043293003	0.101286888
Q15363;F5GX39;E7EQ72	Transmembrane emp24 domain-containing protein 2	TMED2	1.798993294	0.254151026	0.488903544	0.088441213
Q9Y3Q3;G3V1J9;F5H4M7	Transmembrane emp24 domain-containing protein 3	TMED3	0.313672263	0.103389104	0.819060641	0.181956927
Q7Z7H5;F8W7F7	Transmembrane emp24 domain-containing protein 4	TMED4	1.741237826	0.235579173	0.595092712	0.079181671
Q9Y3A6;B1AKT3	Transmembrane emp24 domain-containing protein 5	TMED5	1.528237962	0.159444173	0.075500432	-0.01071008
A0A0A6YYA0;Q9Y3B3	Transmembrane emp24 domain-containing protein 7	TMED7-TICAM2;TMED7	0.665304469	0.094027837	0.011372677	0.002488454
Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9	1.29192508	0.169665337	0.013747933	0.004281044
Q9BVC6	Transmembrane protein 109	TMEM109	0.307409547	0.102691523	0.964986177	-0.339219411
P17152	Transmembrane protein 11, mitochondrial	TMEM11	0	NaN	0	NaN
Q9H061	Transmembrane protein 126A	TMEM126A	0.768798919	0.183680534	0.253280862	0.065250397
Q8TBQ9	Protein kish-A	TMEM167A	0.861327087	0.143553734	0.033562195	-0.009249051
I3L0A0;Q13404;A0A0A0MSL3;G3V2F7	Ubiquitin-conjugating enzyme E2 variant 1	TMEM189-UBE2V1;UBE2V1	0.697389952	-0.087031682	0.033667268	-0.00610892
Q6UW68;K7EPR0;K7ELQ9;K7EM09	Transmembrane protein 205	TMEM205	0.000661328	-0.000722567	0.345782084	0.198330561
Q6NUQ4	Transmembrane protein 214	TMEM214	2.136464916	0.139062564	1.180108336	0.06666247
Q5JWB9;A0A087WTT2;Q96A57	Transmembrane protein 230	TMEM230	0	-0.670089722	0	0.119533539
Q9NV96;Q3MIR4	Cell cycle control protein 50A;Cell cycle control protein 50B	TMEM30A;TMEM30B	0.29014521	0.091819763	0.392379236	0.156828403
P57088;D6RAA6	Transmembrane protein 33	TMEM33	0.210204417	-0.040690104	1.076155077	-0.151547432
Q9BTV4	Transmembrane protein 43	TMEM43	0.655084578	0.080178897	1.032600169	-0.093190193
O94886;X6RI56	CSC1-like protein 1	TMEM63A	0.451117142	-0.167261759	1.490097542	-0.488041878
Q9BUB7	Transmembrane protein 70, mitochondrial	TMEM70	0.356640727	0.15891552	0.018173078	-0.00747172

Q5BJF2;J3KT68	Transmembrane protein 97	TMEM97	1.312618248	0.108543777	0.052452973	0.011052322
Q9NYL9;H0YNJ8;H0YKU1	Tropomodulin-3	TMOD3	0.063025479	-0.008184433	0.260830484	0.028784434
P42167;G5E972	Lamina-associated polypeptide 2, isoforms	TMPO	2.664647228	0.127790769	0.751000489	0.062952042
P42166	beta/gamma;Thymopoietin;Thymopentin Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO	0.021463426	-0.001912117	0.595874316	-0.026062012
P63313;CON__P21752	Thymosin beta-10	TMSB10	1.38269446	-0.793590546	1.352714373	0.415273666
P62328	Thymosin beta-4;Hematopoietic system regulatory peptide	TMSB4X	6.745679732	-0.680270195	0.023768618	0.002985636
Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1	0.113797243	-0.012864113	0.252057303	-0.042141596
Q9Y320	Thioredoxin-related transmembrane protein 2	TMX2	0.376144434	0.025416056	0.245811238	0.016542753
Q96JJ7	Protein disulfide-isomerase TMX3	TMX3	0.757601129	0.143718719	0.327922092	0.076059977
Q9H1E5	Thioredoxin-related transmembrane protein 4	TMX4	0.368933755	0.06447347	0.333074011	-0.054677327
D6RCM8;O95379;E5RIJ3	Tumor necrosis factor alpha-induced protein 8	TNFAIP8	1.187756467	-0.258836428	0.550182491	-0.184165001
Q92973	Transportin-1	TNPO1	0.596242738	-0.044312477	0.952265557	-0.052519162
O14787;A0A075B780	Transportin-2	TNPO2	0.09525857	0.020622571	0.403089657	-0.079735438
Q9Y5L0;C9J7E5;E9PFH4	Transportin-3	TNPO3	0.483732866	-0.060886065	0.682983711	-0.068622589
Q68CZ2;E9PCX8	Tensin-3	TNS3	1.287764793	-0.099491437	0.821537411	-0.076809565
Q96GM8	Target of EGR1 protein 1	TOE1	0.327411564	-0.080771764	0.540605556	-0.130206426
O60784;V9GZ68;V9GYF4;BOQY02;Q6UW50;B0QY01 Q15388	Target of Myb protein 1	TOM1	0.110356301	-0.042890072	0.858052581	0.283105373
Q9NS69	Mitochondrial import receptor subunit TOM20 homolog	TOMM20	0.192344145	0.034046173	0.214628721	-0.034416835
Q15785	Mitochondrial import receptor subunit TOM22 homolog	TOMM22	1.382078847	0.238491376	1.278263589	0.21357886
O96008	Mitochondrial import receptor subunit TOM34	TOMM34	1.089132041	-0.078214963	0.676909064	-0.049663544
Q8N4H5;F8W8Z9;H3BUX3;H0YFG9 O94826	Mitochondrial import receptor subunit TOM40 homolog	TOMM40	3.608944924	0.229285876	1.810246024	0.148878098
P11387	Mitochondrial import receptor subunit TOM5 homolog	TOMM5	0.190767273	-0.07489268	1.339959218	-0.356259346
P11388	Mitochondrial import receptor subunit TOM70	TOMM70A	5.251880778	0.273425738	1.192285635	0.050755501
Q02880;E9PCY5	DNA topoisomerase 1	TOP1	3.197478324	0.125160853	1.230885341	0.056831042
Q92547;H0Y817	DNA topoisomerase 2-alpha	TOP2A	0.040604716	-0.002675056	0.184461209	0.01096948
O14656	DNA topoisomerase 2-beta;DNA topoisomerase 2	TOP2B	1.506451932	0.048656146	1.333283616	-0.051652273
A0A0A0MSK5;Q5JTV8;J3KN66;H0Y4R4 Q8NFQ8	DNA topoisomerase 2-binding protein 1	TOPBP1	0.156865675	0.058669726	0.150291515	0.045573711
Q5JU69	Torsin-1A	TOR1A	0.065250614	-0.029517651	0.605173555	-0.524959469
O94842	Torsin-1A-interacting protein 1	TOR1AIP1	1.348958184	-0.130303065	2.046137625	-0.114853541
A6NNK5;Q12888	Torsin-1A-interacting protein 2	TOR1AIP2	0.47554034	0.066399892	0.041415188	-0.008866946
Q96S44;Q5JZ02	Torsin-2A	TOR2A	1.486157004	-0.244661013	1.06096457	-0.263259252
P55327	TOX high mobility group box family member 4	TOX4	1.539387585	0.192991257	0.383233282	0.047174835
O43399;A0A087WYR3;A0A087WZ51 P60174	Tumor suppressor p53-binding protein 1	TP53BP1	1.711012043	-0.195075989	0.230520647	-0.022468567
F5H7S3;H7BYY1;B7Z596;HOYKX5	TP53-regulating kinase	TP53RK	0.802304582	-0.128656069	1.191617184	-0.135679881
P06753	Tumor protein D52	TPD52	1.506920966	-0.129760742	0.326910009	-0.040723483
P67936;K7ENT6;K7ERG3	Tumor protein D54	TPD52L2	1.116387747	-0.058751424	0.129567679	0.009278297
P51580	Triosephosphate isomerase	TP11	0.408660353	-0.050024668	0.31504679	0.04291598
O14773	Tropomyosin alpha-3 chain	TPM1	0.173550432	-0.079984665	0.423078897	0.164210637
P29144;Q5VZU9	Tropomyosin alpha-4 chain	TPM3	0.636482371	-0.089123726	0.108135315	0.019038518
P12270	Thiopurine S-methyltransferase	TPM4	0.126376184	0.023214658	1.513028917	0.183068911
Q9Y3C4	Tripeptidyl-peptidase 1	TPMT	0.108579531	-0.028618813	0.433189758	0.09758091
P42167;G5E972	Tripeptidyl-peptidase 2	TPP1	0.672741083	-0.117170334	0.32076761	0.053062439
P29144;Q5VZU9	Nucleoprotein TPR	TPP2	3.134472588	-0.195088387	0.852615316	-0.065256437
P12270	EKC/KEOPS complex subunit TPRKB	TPR	0.822142108	0.027742386	0.099573807	0.006629944
Q9Y3C4	EKC/KEOPS complex subunit TPRKB	TPRKB	0.688176678	-0.085764885	2.256355029	-0.185390155

P13693;J3KPG2;Q5W0H4;A0A0B4J2C3;E9PJF7Q9ULW0	Translationally-controlled tumor protein Targeting protein for Xklp2	TPT1 TPX2	2.022085664 4.093704728	-0.116498311 0.249866803	0.967973 5.189937768	-0.074604988 0.296129227
Q13595	Transformer-2 protein homolog alpha	TRA2A	0.377389484	0.051253319	2.124977979	-0.169591586
P62995;H7BXF3;H7C2L4	Transformer-2 protein homolog beta	TRA2B	0.021866576	-0.002776782	0.885760951	0.068234762
J3KPT4;Q9H4I3	TraB domain-containing protein	TRABD	0.19944302	-0.025034904	0.524275324	-0.07460467
Q15628	Tumor necrosis factor receptor type 1-associated DEATH domain protein	TRADD	0.015813801	-0.005239169	0.443043328	-0.106935819
G3XAN4;Q15629	Translocating chain-associated membrane protein 1	TRAM1	0.041997958	-0.009054502	0.581357376	-0.065172195
Q12931	Heat shock protein 75 kDa, mitochondrial	TRAP1	1.400521048	0.066918373	1.492525306	-0.056159973
Q9Y5R8	Trafficking protein particle complex subunit 1	TRAPPC1	0.443268098	-0.123250961	0.374739811	0.137256877
P0D182;P0DI81;F5H785	Trafficking protein particle complex subunit 2B; Trafficking protein particle complex subunit 2	TRAPPC2B;TRAPPC2	0.375761105	-0.121061325	0.500876725	-0.277897517
O43617;A0A087WWM0;A0A087WYS5;A6NKE1	Trafficking protein particle complex subunit 3	TRAPPC3	0.079846534	-0.016482035	0.081438994	-0.021808306
Q9Y296;E9PKS9;E9PQE8;J3KP27;E9PN70;G3V1A0;G5EA23Q8IUR0	Trafficking protein particle complex subunit 4	TRAPPC4	1.390932736	0.224246343	1.25656999	0.125596682
J3QQJ5;Q9Y2L5;J3KSL8	Trafficking protein particle complex subunit 5	TRAPPC5	0.06915637	-0.009220123	0.330643812	0.055438677
Q9NSU2;C9J052	Trafficking protein particle complex subunit 8	TRAPPC8	0.034187237	-0.017883142	0.150316862	0.069183985
P36406	Three-prime repair exonuclease 1	TREX1	1.851088804	0.345591927	1.736373088	0.254157639
Q14258	E3 ubiquitin-protein ligase TRIM23	TRIM23	0.025496742	0.003460248	0.20254153	-0.037698428
Q12899;A2AE48	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25	0.231263872	-0.019676208	1.176483881	-0.072710991
P14373;A0A0G2JIZ4	Tripertite motif-containing protein 26	TRIM26	1.682385577	0.200632413	0.671923801	0.091746012
Q13263	Zinc finger protein RFP	TRIM27	2.229517364	0.196858724	0.041282751	-0.005696932
Q96LD4	Transcription intermediary factor 1-beta	TRIM28	0.294977189	0.01791509	0.537263413	-0.029671669
Q9BRZ2;C9JI91	Tripertite motif-containing protein 47	TRIM47	0.977206128	0.074643771	0.109323389	0.009137154
F5GZP3;H3BRJ5;Q8IWR1	E3 ubiquitin-protein ligase TRIM56	TRIM56	0.755810533	-0.144269307	0.467115652	-0.077487628
O75962;E7EPJ7;E7EWP2	Tripertite motif-containing protein 59	TRIM59	0	NaN	0.733359739	-0.40632652
Q14669	Triple functional domain protein	TRIO	0.388987044	0.094421387	0.29825366	-0.091580073
Q15645;H0YAL2	E3 ubiquitin-protein ligase TRIP12	TRIP12	0.03540252	-0.008192698	0.203572165	-0.039058367
Q15650;H0YL91	Pachytene checkpoint protein 2 homolog	TRIP13	0.139038021	-0.01682663	1.051991127	-0.06749026
Q9NXH9;K7EQQ8	Activating signal cointegrator 1	TRIP4	0.44688364	-0.107255936	0.36771515	-0.091421127
Q7L0Y3;C9JVB6	tRNA (guanine(26)-N(2))-dimethyltransferase	TRMT1	0.570708863	-0.062035878	0.387469412	-0.055355708
Q9UI30;F5GG77;F5GYQ2	Mitochondrial ribonuclease P protein 1	TRMT10C	0.255134743	-0.03108565	0.768322604	-0.065105756
Q7Z2T5	Multifunctional methyltransferase subunit TRM112-like protein	TRMT112	1.301068975	0.122108142	0.111607838	0.014057159
Q9UJA5	TRMT1-like protein	TRMT1L	1.46723225	0.118771871	0.231972979	0.022702217
H0Y2Q1;Q96FX7	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6	0.439672083	0.035699526	0.115805529	-0.0127786
Q96Q11	tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A	TRMT61A	0.143948705	-0.043337822	0.017243678	0.005320231
P10155	CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1	0.014453396	-0.001887004	2.556996157	-0.172081947
Q9BX84;Q96LV9	60 kDa SS-A/Ro ribonucleoprotein	TROVE2	4.177695053	-0.237030665	2.55519986	-0.122014364
Q86TN4;H0YGY9;F5H6B6;F5H8A0	Transient receptor potential cation channel subfamily M member 6	TRPM6	0.738840513	0.215248108	1.601023525	0.228914261
A0A0B4J2A0;Q9UHI6	tRNA 2-phosphotransferase 1	TRPT1	0.50294786	-0.125354767	1.096260436	-0.22612985
H0Y4W2;F2Z2U4;Q9Y4A5	Sedoheptulokinase	TRPV1;SHPK	0.393975493	-0.091751734	0.31282122	-0.07261467
Q8WWH5	Transformation/transcription domain-associated protein	TRRAP	0.225533272	-0.112359683	0.183594501	-0.071247419
E7EQB3;Q9BSV6;B0V3J0;A9C4B9;A0A0G2JNK5	Probable tRNA pseudouridine synthase 1	TRUB1	0	0.018476963	0.091355802	-0.019775391
P43897;C9JT21	tRNA-splicing endonuclease subunit Sen34	TSEN34	0.484997911	0.214335124	0.305473169	-0.047591527
F5H442;Q99816	Elongation factor Ts, mitochondrial;Elongation factor Ts	TSEFM	3.746479632	0.169489861	1.360588197	0.075772921
	Tumor susceptibility gene 101 protein	TSG101	0.136958964	-0.026849429	0.422981729	-0.068871498

E9PGT1;Q15631;H7C1D4	Translin	TSN	3.628532947	-0.179448764	2.161208238	-0.104300181
Q99598;C4P0D6;C4P0D8;C4P0D4;Q5VVQ1	Translin-associated protein X	TSNAX;DISC1	0.640072822	0.051167488	1.805267172	0.104269663
B1AH87;P30536	Translocator protein	TSPO	0.045848138	-0.072356669	0.34852468	0.348359934
Q9H0U9	Testis-specific Y-encoded-like protein 1	TSPYL1	0.842894	0.541936556	0.572855138	-0.297515043
Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1	0.4901734	0.053934733	0.266194597	-0.0271101
Q969E8	Pre-rRNA-processing protein TSR2 homolog	TSR2	0	NaN	0	NaN
Q9UJK0	Ribosome biogenesis protein TSR3 homolog	TSR3	0.557713096	-0.130066554	0.4228738	-0.102654775
A8MUM1;Q53HC9;F8WDS8;C9J0U9;D3YTH5	Protein TSSC1	TSSC1	0.019582497	0.007513046	0.169074373	0.039531072
Q16762	Thiosulfate sulfurtransferase	TST	0.89597742	0.127967008	1.087332522	0.211549441
Q13630;E9PP14;A0A0J9YX13;E9PKL9;E9PLH9	GDP-L-fucose synthase	TSTA3	0.118005552	0.018337886	0.644245	0.068828265
Q8NFU3;R4GNF9	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1	0.570411774	-0.085840543	0.085647374	-0.014527639
Q99614;H0YB37	Tetratricopeptide repeat protein 1	TTC1	0.658578594	0.070091565	2.13292701	0.228437106
Q6P3X3	Tetratricopeptide repeat protein 27	TTC27	0.345528006	-0.065858205	0.743149592	-0.093145053
Q6PGP7	Tetratricopeptide repeat protein 37	TTC37	0.409553209	-0.031383832	0.345886712	-0.029243151
O95801	Tetratricopeptide repeat protein 4	TTC4	0.740606855	-0.139098485	0.201843732	0.045564016
H0YDR3;Q8N5M4;E9PKV8	Tetratricopeptide repeat protein 9C	TTC9C	0.517279363	0.073033015	0.636781899	0.082936923
Q9UNY4	Transcription termination factor 2	TTF2	1.685103328	0.272113101	0.015123232	0.004045486
O43156	TELO2-interacting protein 1 homolog	TTI1	0.433321449	-0.110684713	0.238594478	-0.06201299
Q6NXR4;E5RIH5	TELO2-interacting protein 2	TTI2	0.372354738	-0.099785233	0.240338718	-0.084860229
Q14166	Tubulin--tyrosine ligase-like protein 12	TTL12	0.748324331	-0.042433103	1.402243184	-0.088788986
Q71U36;Q13748	Tubulin alpha-1A chain;Tubulin alpha-3C/D chain	TUBA1A;TUBA3C	0.173116838	-0.016605377	0.08189624	0.007231394
Q9BQE3;F5H5D3;A0A1W2PQ	Tubulin alpha-1C chain	TUBA1C	0.161286612	0.047472954	0.667143366	0.121171316
M2P68366	Tubulin alpha-4A chain	TUBA4A	0.3046965	0.024684906	0.849129743	0.068648656
Q5JP53;P07437;Q5ST81	Tubulin beta chain	TUBB	1.015740471	-0.092277527	0.393885469	0.050250371
Q9BVA1;Q13885	Tubulin beta-2B chain;Tubulin beta-2A chain	TUBB2B;TUBB2A	0.227384366	0.035944303	0.023967213	0.004587809
P04350	Tubulin beta-4A chain	TUBB4A	0	NaN	0	NaN
P68371	Tubulin beta-4B chain	TUBB4B	0.742634803	0.063744863	0.894546216	0.074852626
Q3ZCM7;A0A075B736;Q5SQY0	Tubulin beta-8 chain	TUBB8	0.026956416	-0.007054647	0.157366891	0.039355278
P23258;Q9NRH3;K7EIS0	Tubulin gamma-1 chain;Tubulin gamma-2 chain;Tubulin gamma chain	TUBG1;TUBG2	1.469864043	-0.090047518	0.714339212	-0.061711629
F2Z2B9;Q9BSJ2	Gamma-tubulin complex component 2	TUBGCP2	0.53413576	0.141666094	0.030472113	-0.010304769
Q96CW5;A0A087WU06	Gamma-tubulin complex component 3	TUBGCP3	1.301812977	-0.458267339	1.302263564	-0.347024536
Q9UGJ1;H3BPU4	Gamma-tubulin complex component 4	TUBGCP4	0.033075047	0.006233533	0.170489801	0.042072932
P49411	Elongation factor Tu, mitochondrial	TUFM	3.133504847	0.117619197	0.529143598	0.03368187
F5H0R1;Q9H6E5;H3BRB1	Speckle targeted PIP5K1A-regulated poly(A) polymerase	TUT1	1.199684231	0.219759305	0.33809482	0.080302874
Q12792;F8VS81	Twinfilin-1	TWF1	0.375776574	-0.052318573	0.41173443	0.05347983
Q6IBS0;D6RG15	Twinfilin-2	TWF2	1.753495935	-0.09024334	0.283424726	0.024885178
Q3B726	DNA-directed RNA polymerase I subunit RPA43	TWISTNB	0.446468034	0.073561668	0.101189723	0.025729497
P40222	Alpha-taxilin	TXLNA	0.396993522	0.029677709	2.186618237	0.106666247
Q9NUQ3	Gamma-taxilin	TXLNG	0.396907937	-0.044994036	0.13947008	0.012418429
P10599	Thioredoxin	TXN	1.619056401	-0.135118167	0.788371157	-0.066934903
Q99757;M0QXH0	Thioredoxin, mitochondrial	TXN2	1.347634919	0.133927981	0.764630464	0.04469045
O95881	Thioredoxin domain-containing protein 12	TXNDC12	1.362228139	0.151061694	0.022098813	-0.004348437
H0Y997;Q96J42	Thioredoxin domain-containing protein 15	TXNDC15	0.046292032	-0.029938062	0.659892767	0.218009472
Q9BRA2;I3L2R6;I3L0K2;I3L3M7	Thioredoxin domain-containing protein 17	TXNDC17	0.53505059	-0.066643397	0.142044251	-0.024902662
Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5	1.251172637	0.108217239	0.534608398	0.066313426

O14530;F8WCJ3;B8ZZX4	Thioredoxin domain-containing protein 9	TXNDC9	0.297521794	-0.046027819	1.566036485	0.180758794
O43396;K7ER96	Thioredoxin-like protein 1	TXNL1	1.992716121	0.053206126	5.082265315	0.169977824
Q9NX01	Thioredoxin-like protein 4B	TXNL4B	0.44540207	0.224871699	0.326934483	0.203844833
A0A087WSW9;A0A087WSY9; Q16881;F8WR09;A0A182DW13; E9PIR7;E2QRB9 P19971;C9JG13	Thioredoxin reductase 1, cytoplasmic	TXNRD1	1.049693033	-0.066661517	1.223466185	0.054842313
P04818	Thymidylate synthase	TYMP	2.038118081	-0.198743502	0.37323117	-0.057373683
P0DN76;Q01081	Splicing factor U2AF 35 kDa subunit	U2AF1	0.212458541	0.025600433	0.111626383	-0.014860153
P26368;K7ENG2	Splicing factor U2AF 65 kDa subunit	U2AF2	2.536709764	-0.087984721	1.65193929	-0.083391507
O15042;E7ET15	U2 snRNP-associated SURP motif- containing protein	U2SURP	0.644555022	-0.044425011	0.32714493	-0.028350512
Q16222	UDP-N-acetylhexosamine pyrophosphorylase;UDP-N- acetylgalactosamine pyrophosphorylase;UDP-N- acetylglucosamine pyrophosphorylase	UAP1	1.269020155	-0.078968048	0.902288825	-0.037398338
Q3KQV9	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	UAP1L1	0.024499821	0.006000837	0.195789224	-0.040576935
P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1	2.769366559	-0.088278453	0.707046802	-0.038148244
Q9UBT2	SUMO-activating enzyme subunit 2	UBA2	2.593418944	-0.163917542	1.103281785	-0.107250214
Q8TBC4;F8W8D4	NEDD8-activating enzyme E1 catalytic subunit	UBA3	1.754264323	-0.107500076	1.649011174	-0.085014979
Q9GZZ9;E7EQ61;E7EWE1;C9J 5W5;C9JRV9 A0AVT1	Ubiquitin-like modifier-activating enzyme 5	UBA5	3.025782993	-0.202129046	0.282667121	0.030337969
Q5T6F2	Ubiquitin-like modifier-activating enzyme 6	UBA6	1.264431591	-0.109551112	0.908464934	-0.087841034
F8W726;Q14157	Ubiquitin-associated protein 2	UBAP2	3.557991958	-0.280922254	1.344524584	-0.123672167
A0A0D9SG71;P49459;A0A0R4 J2E5;A0A0D9SEZ6;P63146	Ubiquitin-associated protein 2-like	UBAP2L	3.225527993	-0.252974192	0.437570602	-0.03986009
A0A087WY85;P61077;D6RFM 0;D6RAH7;H9KV45;A0A0A0M QU3;P62837;D6RAW0;D6RA11 P51965;C9J2P0;H7C061;B7Z30 6	Ubiquitin-conjugating enzyme E2 A;Ubiquitin-conjugating enzyme E2 B	UBE2A;UBE2B	0.470719061	-0.112269592	0.906307356	0.11202844
Q969T4;R4GND1;A0A1B0GX6 5;A0A087X283 P62253	Ubiquitin-conjugating enzyme E2 D1 D3;Ubiquitin-conjugating enzyme E2 D2	UBE2D3;UBE2D2	0.167440782	-0.041187604	0.08046516	-0.01940155
P60604	Ubiquitin-conjugating enzyme E2 E1	UBE2E1	1.516907151	-0.134495417	1.246954359	-0.154964447
C9JZG9;C9JZY6;P62256;H7C4 M9;C9J8Q9 P63279;H3BQ99;B0QYN7;H3B PC4 Q9Y385	Ubiquitin-conjugating enzyme E2 E3	UBE2E3;UBE2E2	0.534782885	-0.132331562	0.58791918	-0.117439461
P61086;D6RDM7	Ubiquitin-conjugating enzyme E2 G1, N-terminally processed	UBE2G1	0.826421164	0.092424774	1.240578344	0.157409859
P68036;A0A1B0GUS4	Ubiquitin-conjugating enzyme E2 G2	UBE2G2	0.84365429	0.143131256	0.533580382	0.092989922
Q9C0C9;K7ES11	Ubiquitin-conjugating enzyme E2 H	UBE2H	0.378279064	0.068053563	0.074511419	-0.015137672
Q7Z7E8	SUMO-conjugating enzyme UBC9	UBE2I	0.36696965	0.055898348	0.055397934	-0.009823163
Q16763;K7EPJ1	Ubiquitin-conjugating enzyme E2 J1	UBE2J1	2.520486081	0.26083374	1.517129225	0.164405505
Q9NPDS	Ubiquitin-conjugating enzyme E2 K	UBE2K	0.020210149	-0.003022512	2.813269687	0.169697444
Q15819;G3V113;H0YBP9	Ubiquitin-conjugating enzyme E2 L3	UBE2L3	0.497066518	-0.06941541	0.516932377	0.064494133
Q9H832;I3L4C5	Ubiquitin/ISG15-conjugating enzyme E2 L6	UBE2L6	1.647786167	0.13927269	0.569049185	0.112979253
Q05086;A0A1B0GVL3;A0A0D 9SG77 Q15386	NEDD8-conjugating enzyme Ubc12	UBE2M	0.134278666	0.018178304	2.426576931	0.128131866
Q14139;B7Z7P0	Ubiquitin-conjugating enzyme E2 N;Putative ubiquitin-conjugating enzyme E2 N-like	UBE2N;UBE2NL	0.43025252	-0.03460598	0.484567735	0.037745158
O95155	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O	0.552204882	-0.040004094	0.126640461	0.012074788
	Ubiquitin-conjugating enzyme E2 Q1	UBE2Q1	0.02759404	-0.010426203	0.460441391	0.110597928
	Ubiquitin-conjugating enzyme E2 S	UBE2S	0.092934634	0.015894254	1.546538747	0.153392792
	Ubiquitin-conjugating enzyme E2 T	UBE2T	0.044506524	0.011255582	1.056041394	0.154205958
	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2	0	-0.16053009	0	0.337093353
	Ubiquitin-conjugating enzyme E2 Z	UBE2Z	0.513235423	-0.105703354	0.397234815	-0.107660802
	Ubiquitin-protein ligase E3A	UBE3A	1.019362937	-0.161073049	0.954612927	-0.209082603
	Ubiquitin-protein ligase E3C	UBE3C	0.417892872	-0.080715815	0.32764954	-0.063253721
	Ubiquitin conjugation factor E4 A	UBE4A	0.16138192	-0.034499486	0.352645439	0.059423765
	Ubiquitin conjugation factor E4 B	UBE4B	0.522041476	-0.075491587	1.05320884	0.174479485

H3BRL3;O14562;H3BUM8	Ubiquitin domain-containing protein UBF1	UBFD1	0.308341221	0.110805035	0.225049486	-0.103563309
Q9Y5Z9	UbiA prenyltransferase domain-containing protein 1	UBIAD1	0.829952983	-0.150899092	1.046100192	-0.220544815
Q5HY81;P11441	Ubiquitin-like protein 4A	UBL4A	1.082788679	-0.240842056	0.252013813	-0.083646266
H3BV23;H3BUV9;Q96S82	Ubiquitin-like protein 7	UBL7	0	NaN	0	NaN
Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1	UBLCP1	0.241352784	-0.079282443	0.305804719	-0.104595184
Q9NZI7	Upstream-binding protein 1	UBP1	0.141863033	0.038521767	0.23144973	0.066902161
Q9UMX0	Ubiquilin-1	UBQLN1	0.248416027	0.046140989	0.421090082	0.100125949
Q9UHD9	Ubiquilin-2	UBQLN2	0.204670446	0.060683886	1.656893262	0.161813418
Q9NRR5	Ubiquilin-4	UBQLN4	1.596236225	-0.100367228	0.305729251	-0.024946849
Q8IWW8	E3 ubiquitin-protein ligase UBR2	UBR2	1.300563484	0.219808006	0.456645651	0.107224941
Q6ZT12	E3 ubiquitin-protein ligase UBR3	UBR3	0	0.242714882	0	0.175902176
Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4	0.313538765	0.029660543	0.765634004	0.060865084
O95071;E7EMW7	E3 ubiquitin-protein ligase UBR5	UBR5	0.245458292	-0.024536133	0.741236211	-0.062729836
Q8N806;H0YJM2;H0YJA0;G3V3Q6;E9PCJ7	Putative E3 ubiquitin-protein ligase UBR7	UBR7	0.045467503	0.011429787	0.252015477	0.059638977
E9PKP7;P17480	Nucleolar transcription factor 1	UBTF	0.042502711	-0.006457011	2.107306676	-0.140467644
E9PRQ7;Q04323;A0A087WTZ5;E9PJ81	UBX domain-containing protein 1	UBXN1	0.583681815	0.079451561	0.420230081	0.07189846
Q92575	UBX domain-containing protein 4	UBXN4	1.001548255	0.171807925	1.027495548	0.178714116
O94888;C9JAT7	UBX domain-containing protein 7	UBXN7	1.965844206	-0.088791529	2.460641123	-0.15205129
P15374;A0A087WTB8;Q5TBK7	Ubiquitin carboxyl-terminal hydrolase isozyme L3;Ubiquitin carboxyl-terminal hydrolase	UCHL3	0.253945051	-0.048987707	0.040056809	-0.008199056
Q9Y5K5;Q5LJA5;Q5LJA9;H0Y6Y4;Q5LJB0;H0Y4E0	Ubiquitin carboxyl-terminal hydrolase isozyme L5;Ubiquitin carboxyl-terminal hydrolase	UCHL5	0.748038645	0.021481832	0.482060105	0.023397764
Q9BZX2	Uridine-cytidine kinase 2	UCK2	0.960266126	-0.046897252	1.030038863	-0.072781245
Q9NWZ5;Q5JWV1	Uridine-cytidine kinase-like 1	UCKL1	1.407743186	0.33599329	1.536374447	0.240175883
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	1.035207608	-0.113099098	0.131175199	0.023628871
Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L	0.983177931	0.212027868	1.941893767	0.338259888
O94874	E3 UFM1-protein ligase 1	UFL1	0.079499274	-0.010212262	0.196206744	-0.024906476
P61960;H0Y614	Ubiquitin-fold modifier 1	UFM1	1.60014398	-0.176484426	0.590905038	-0.087087631
Q9NUQ7;D6RGX2;H0YA18	Ufm1-specific protease 2	UFSP2	0.558328594	-0.06016318	0.304238743	-0.032581965
O60701	UDP-glucose 6-dehydrogenase	UGDH	1.988081534	0.17787838	2.857108115	0.163866679
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1	2.323519809	0.109662056	0.555596476	-0.030515989
A0A087WYS1;E7EUC7;Q16851	UTP--glucose-1-phosphate uridylyltransferase	UGP2	1.36235762	-0.090461731	0.01012329	0.001053174
A0A087WTW0;A0A087WVR3;Q96T88;A0A087WWG9	E3 ubiquitin-protein ligase UHRF1	UHRF1	1.108254607	-0.081717173	2.068093893	-0.100255648
P11172;E9PFD2	Uridine 5-monophosphate synthase;Orotate phosphoribosyltransferase;Orotidine 5-phosphate decarboxylase	UMPS	0.277856974	-0.030833562	1.019514429	-0.10451285
A0A1W2PNX8;Q9H3U1	Protein unc-45 homolog A	UNC45A	0.159748147	0.018439929	0.940018782	0.06788667
Q9H1C4;E9PNE5	Protein unc-93 homolog B1	UNC93B1	0.141415799	0.050551414	0.722577778	0.19124953
Q92900	Regulator of nonsense transcripts 1	UPF1	0.044332175	0.004712741	0.142916497	-0.014146169
Q9HAU5	Regulator of nonsense transcripts 2	UPF2	1.082504403	-0.151479721	0.15704175	0.031124751
A0A087WYC8;Q9BZI7	Regulator of nonsense transcripts 3B	UPF3B	0.125816462	-0.032593727	0.529003322	-0.126449903
Q9NVA1;B1AKV4;F6UTR7;B1AKV3	Ubiquinol-cytochrome-c reductase complex assembly factor 1	UQCC1	0.074942681	-0.026425616	0.374814479	-0.096620496
Q9UDW1	Cytochrome b-c1 complex subunit 9	UQCR10	0.281785118	-0.054046949	0.600654159	-0.103093783
P14927;B7Z2R2	Cytochrome b-c1 complex subunit 7	UQCRB	0.180433021	0.032671611	0.531810714	-0.080675443
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1	1.94457639	0.089415232	0.626398469	0.039274851
P22695;H3BRG4;H3BSJ9	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2	1.493401825	0.103016218	0.266934357	-0.027660052

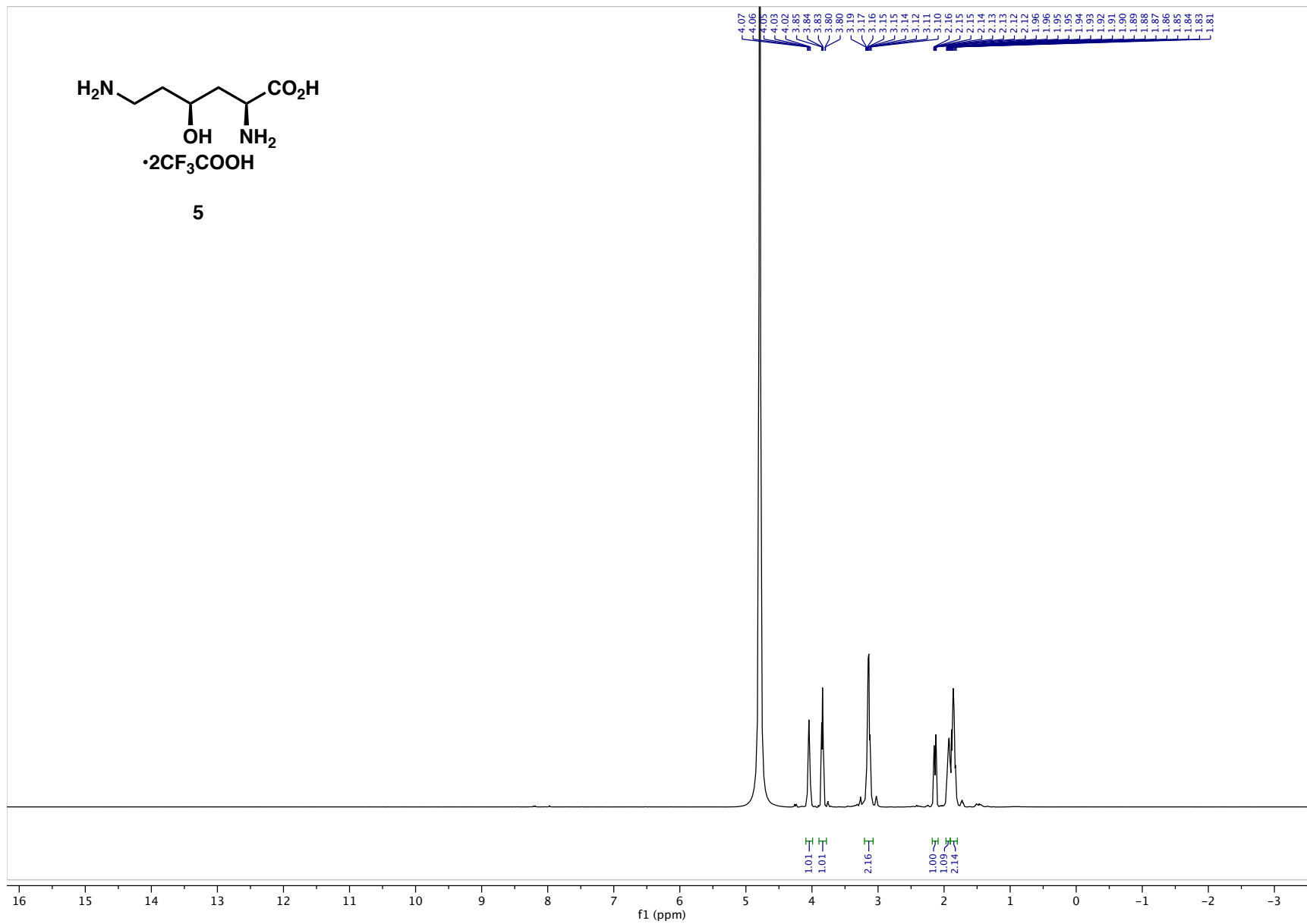
P47985;POC7P4	Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex subunit 11;Putative cytochrome b-c1 complex subunit Rieske-like protein 1	UQCRFS1;UQCRFS1P1	2.418422291	0.155507723	0.002233082	0.000211398
P07919;A0A096LP55	Cytochrome b-c1 complex subunit 6, mitochondrial;Cytochrome b-c1 complex subunit 6	UQCRH;UQCRHL	0.418244571	0.11432457	0.269612884	0.083383242
O14949	Cytochrome b-c1 complex subunit 8	UQCRQ	0.609120312	0.115199725	0.210223128	-0.048981667
O60287	Nucleolar pre-ribosomal-associated protein 1	URB1	0.606899419	-0.104433378	0.682869081	-0.091050148
Q14146	Unhealthy ribosome biogenesis protein 2 homolog	URB2	1.196336148	-0.135289828	0.856540463	-0.116219838
Q9BTM9	Ubiquitin-related modifier 1	URM1	1.023211586	0.256721751	0.718751635	0.237495104
P06132;A0A1B0GVN9;A0A1B0GVZ4;H0Y5R6	Uroporphyrinogen decarboxylase	UROD	2.617477831	-0.180967649	1.251889133	-0.062170029
Q961X5	Up-regulated during skeletal muscle growth protein 5	USMG5	1.507637874	0.083408674	0.219017675	-0.026799838
O60763	General vesicular transport factor p115	USO1	0.989247602	0.062385877	0.802460228	0.046354612
Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10	1.176946381	-0.209393501	0.983597134	-0.141073863
G5E9A6;P51784	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 11	USP11	1.461297747	-0.157098134	0.363500604	-0.043812116
Q92995	Ubiquitin carboxyl-terminal hydrolase 13	USP13	0.196061754	-0.041632334	0.017058658	-0.003973643
P54578;A6NJA2	Ubiquitin carboxyl-terminal hydrolase 14;Ubiquitin carboxyl-terminal hydrolase	USP14	0.016223609	0.002300898	0.702548585	0.067694028
Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15	USP15	0.258000652	-0.030544281	3.0579781	-0.148329735
Q9Y5T5	Ubiquitin carboxyl-terminal hydrolase 16	USP16	0.53494455	0.122847557	0.624436665	0.124191602
E7ESU0;E7EST9;B5MEG5;O94966	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 19	USP19	0.769046125	0.105334918	1.02417181	0.096910477
Q9UPT9	Ubiquitin carboxyl-terminal hydrolase 22	USP22	0	-0.357551098	0.093849888	0.050298532
H0YLB7;H0YKU8;Q6JHV3;H0YM14;Q9Y614	Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 3	USP3	1.587391419	-0.167311668	1.143422197	-0.072776477
Q53GS9;A0A087X1B2;B9A018	U4/U6.U5 tri-snRNP-associated protein 2	USP39	1.034694096	-0.053129514	0.627521347	-0.057661692
Q13107;H7C189	Ubiquitin carboxyl-terminal hydrolase 4;Ubiquitin carboxyl-terminal hydrolase	USP4	0.505333242	0.130937099	0.211930238	0.049648762
Q96K76	Ubiquitin carboxyl-terminal hydrolase 47	USP47	0.308791421	-0.041589737	0.435182032	0.103438282
P45974	Ubiquitin carboxyl-terminal hydrolase 5	USP5	0.515217234	0.050917625	0.98414691	0.068498611
Q93009;H3BND8	Ubiquitin carboxyl-terminal hydrolase 7;Ubiquitin carboxyl-terminal hydrolase	USP7	3.716907166	0.067543666	0.003071805	-0.000102043
P40818	Ubiquitin carboxyl-terminal hydrolase 8	USP8	2.162141129	-0.226892344	0.53155411	-0.102328014
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X	0.84319843	0.079788844	0.140399347	0.022040367
Q9Y3A2	Probable U3 small nucleolar RNA-associated protein 11	UTP11L	2.52877119	0.25135231	0.351583109	0.058984121
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A	UTP14A	0.594413772	0.066654523	0.321156804	-0.031255404
Q8TED0;H0Y8P4	U3 small nucleolar RNA-associated protein 15 homolog	UTP15	0.015623559	0.002441088	1.158583012	-0.122828801
Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18	0.276780044	0.030208906	0.14651069	-0.018989881
O75691	Small subunit processome component 20 homolog	UTP20	0.44710424	-0.062023163	0.656230822	-0.084267934
Q9NQZ2	Something about silencing protein 10	UTP3	1.060371989	-0.122452736	0.023668461	-0.003599167
Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	UTP6	1.008089513	0.068134308	0.023433791	-0.003521283
Q08AM6;H3BUU8	Protein VAC14 homolog	VAC14	1.479950741	-0.102229436	0.315697348	-0.051225344
Q15836;K7ENK9;K7EKX0;J3QRU4;F8WCA0;L7N2F9;P63027	Vesicle-associated membrane protein 3;Vesicle-associated membrane protein 2	VAMP3;VAMP2	0.695238315	-0.117185593	0.017216718	-0.005926132
P51809	Vesicle-associated membrane protein 7	VAMP7	0.171159348	-0.027465185	0.071283019	-0.014088949
Q9BV40;C9JXZ5;B8ZZT4	Vesicle-associated membrane protein 8	VAMP8	1.434478449	-0.465584437	0.33033896	-0.051991145
Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA	0.687167373	-0.054456075	0.069832387	-0.009879112
O95292;E5RK64	Vesicle-associated membrane protein-associated protein B/C	VAPB	0.035209763	-0.009080251	0.158806878	0.034584999
P26640;A0A140T936	Valine-tRNA ligase	VARS	0.465629459	0.043413798	0.167117614	0.018803596
P50552;K7ENR7;K7ENL7	Vasodilator-stimulated phosphoprotein	VASP	0.153920892	-0.045499229	1.097458172	-0.238127772

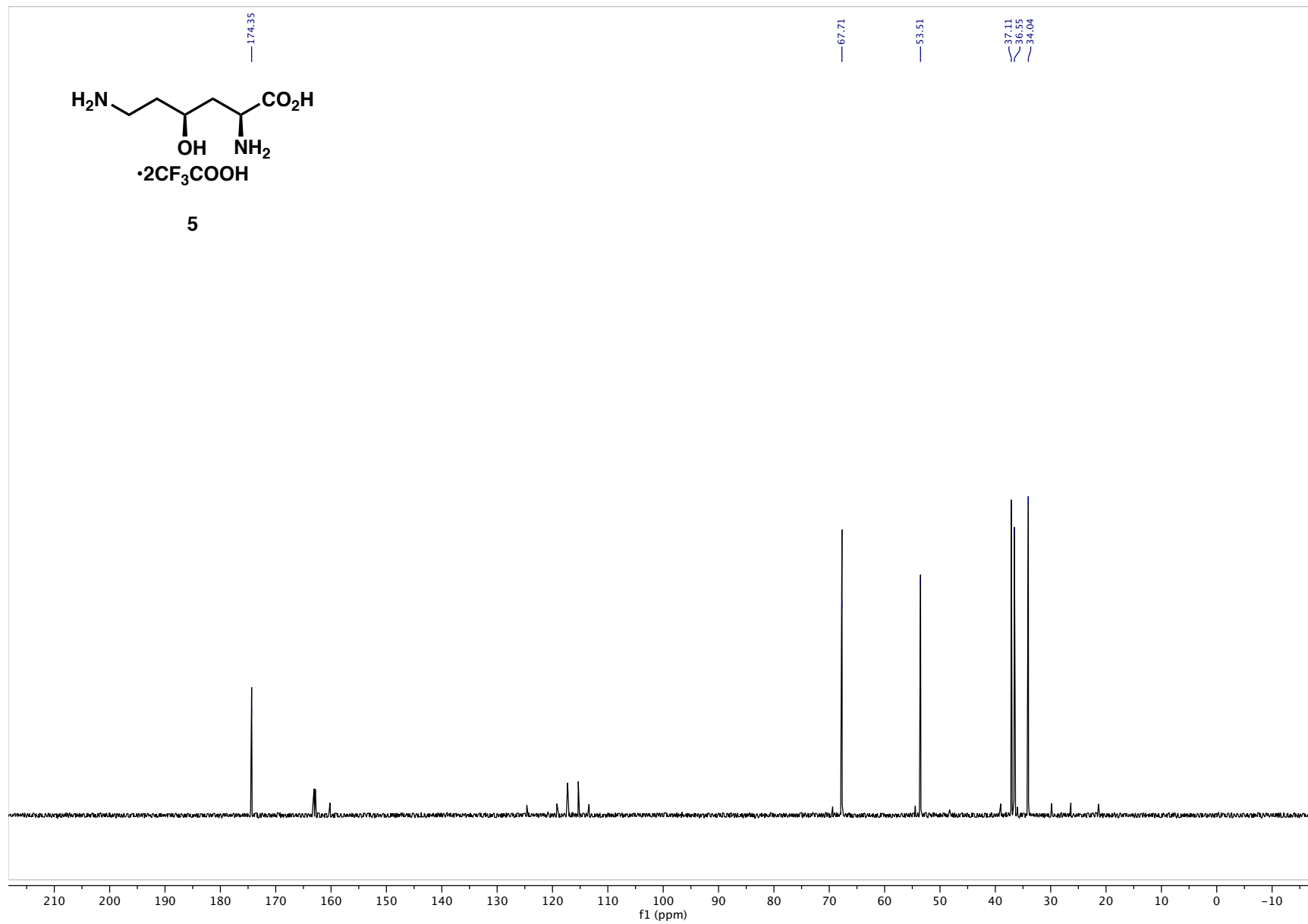
A0A0A0MR07;P15498;F5H5P4;Q96D37 P52735	Proto-oncogene vav	VAV1	0.129188359	0.034433047	0.578018359	-0.130973816
P61758;B4DWR3	Guanine nucleotide exchange factor VAV2	VAV2	0.561478346	-0.100141207	0.240808051	-0.059857368
P18206	Prefoldin subunit 3	VBP1	0.984019064	-0.0831906	0.038926341	-0.007149696
P55072	Vinculin	VCL	1.637057592	-0.115416527	0.022289265	-0.002831459
P21796;C9J187	Transitional endoplasmic reticulum ATPase	VCP	0.949242308	0.035432498	4.586025447	0.16534996
A0A0A0MR02;P45880;Q5JSD2;Q5JSD1 Q9Y277;E5RJN6;E5RHZ6	Voltage-dependent anion-selective channel protein 1	VDAC1	1.81115211	0.127237002	0.06046538	0.006749153
P08670;BOYJC4	Voltage-dependent anion-selective channel protein 2	VDAC2	1.493237862	0.089863777	1.171832705	-0.054917018
Q9BQE4;A0A182DW14;E9PN30 I3L3B4;F8W9H0;E9PLN8;Q9BQB6 Q8N0U8	Voltage-dependent anion-selective channel protein 3	VDAC3	2.395094933	0.14559714	0.999736641	0.096260389
Q9BQE4;A0A182DW14;E9PN30 I3L3B4;F8W9H0;E9PLN8;Q9BQB6 Q8N0U8	Vimentin	VIM	6.117880601	-0.30205218	0.895944738	-0.047510783
Q9BQE4;A0A182DW14;E9PN30 I3L3B4;F8W9H0;E9PLN8;Q9BQB6 Q8N0U8	Selenoprotein S	VIMP	0.410492047	0.128541279	0.899253692	-0.251580048
Q9BQE4;A0A182DW14;E9PN30 I3L3B4;F8W9H0;E9PLN8;Q9BQB6 Q8N0U8	Vitamin K epoxide reductase complex subunit 1	VKORC1	0.362067263	0.447238286	0.275798499	0.354526997
Q9BQE4;A0A182DW14;E9PN30 I3L3B4;F8W9H0;E9PLN8;Q9BQB6 Q8N0U8	Vitamin K epoxide reductase complex subunit 1-like protein 1	VKORC1L1	0.641503012	-0.600632858	0.873901177	-0.386681875
Q709C8	Vacuolar protein sorting-associated protein 13C	VPS13C	0.355171977	0.05277888	0.312624613	0.04899025
Q9H269;Q5JUB0;Q5JUA9	Vacuolar protein sorting-associated protein 16 homolog	VPS16	0.724817409	-0.132725398	0.383346973	-0.082211812
Q9P253	Vacuolar protein sorting-associated protein 18 homolog	VPS18	0.049776021	-0.036901792	0	-0.199006399
Q9BRG1;K7ENE3;K7EKV4	Vacuolar protein-sorting-associated protein 25	VPS25	0.95597468	0.219208082	1.227299735	0.253361066
O75436;S4R3Q6	Vacuolar protein sorting-associated protein 26A	VPS26A	0.810105441	-0.109375318	0.258773275	0.030778249
F8VXU5;Q9UBQ0	Vacuolar protein sorting-associated protein 29	VPS29	0.138207176	0.018821398	0.30309477	0.035822233
H3BMM5;Q96AX1	Vacuolar protein sorting-associated protein 33A	VPS33A	0.080978951	0.064421527	0.102180244	-0.054144224
Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35	0.078658844	0.008232752	0.884544432	0.057956378
F5H4M0;Q9H9H4;F5H1F6	Vacuolar protein sorting-associated protein 37B	VPS37B	0	0.147505442	0	-0.274847031
A0A087WU65;Q9NRW7;B7Z7 G7;A0A1B0GX16 Q9UN37;I3L4J1	Vacuolar protein sorting-associated protein 45	VPS45	1.17333708	-0.170160294	0.010488317	-0.002754847
O75351	Vacuolar protein sorting-associated protein 4A	VPS4A	0.68286693	-0.095762889	0.27858594	-0.062839508
Q9UID3	Vacuolar protein sorting-associated protein 4B	VPS4B	0.1414387	-0.019129117	0.353074042	0.042267799
Q8N1B4;A0A0G2JIG2	Vacuolar protein sorting-associated protein 51 homolog	VPS51	0.108755368	0.022935549	0.329665977	0.066773733
F6VX93;Q5VIR6	Vacuolar protein sorting-associated protein 52 homolog	VPS52	0.180820338	-0.040277735	0.496196964	-0.084918594
Q99986;H0YJ50	Vacuolar protein sorting-associated protein 53 homolog	VPS53	0.14099447	-0.025189082	0.091029232	0.02317524
Q86Y07	Serine/threonine-protein kinase VRK1	VRK1	1.278575798	-0.105167389	1.107182079	-0.13728714
Q8IV63;M0R073;M0QYA8	Serine/threonine-protein kinase VRK2	VRK2	0.031941994	0.009019852	0.483972866	-0.083450953
Q5TGM0;A0A087WY55;Q9NP79 A3KMH1	Inactive serine/threonine-protein kinase VRK3	VRK3	2.45932526	-0.278136317	1.686239995	-0.215398026
H3BRY6;B4DVT3;B4DJL6;Q96SY0 Q9BTA9;A0A0A0MRT2	Vacuolar protein sorting-associated protein VTA1 homolog	VT A1	0.365271303	0.041591009	0.155246225	-0.034766833
Q7Z5K2	von Willebrand factor A domain-containing protein 8	VWA8	0.615359843	0.099002838	0.612013141	-0.08218352
P23381	von Willebrand factor A domain-containing protein 9	VWA9	0.217871574	-0.021395048	0.811068156	-0.058741252
P42768;C9J3B7	WW domain-containing adapter protein with coiled-coil	WAC	1.513037959	-0.235030365	2.05796538	-0.337350527
Q9Y6W5	Wings apart-like protein homolog	WAPAL	0.173542062	0.046121915	0.22829353	0.060640017
Q9Y2W2	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	WARS	0.48149706	-0.033903758	0.347171595	0.027155558
Q96151	Wiskott-Aldrich syndrome protein	WAS	0.388070502	-0.071651459	0.038863052	-0.012530963
O43709	Wiskott-Aldrich syndrome protein family member 2	WASF2	1.603656484	-0.18192927	0.583408339	-0.059232076
O75717	WW domain-binding protein 11	WBP11	0.003041344	0.000700633	0.098141929	-0.023838043
O75083	Williams-Beuren syndrome chromosomal region 16 protein	WBSCR16	1.809061672	-0.209403483	0.526828167	-0.096534411
Q9BZH6;S4R3Z0	Probable 18S rRNA (guanine-N(7))-methyltransferase	WBSCR22	1.75484562	0.078812281	1.783499523	0.094645182
Q9GZL7	WD repeat and HMG-box DNA-binding protein 1	WDHD1	0.38548379	-0.059013685	0.291140148	-0.049921036
	WD repeat-containing protein 1	WDR1	0.934976739	-0.060333252	0.054650481	0.005778631
	WD repeat-containing protein 11	WDR11	1.134485906	0.463948441	0.890841639	0.455653667
	Ribosome biogenesis protein WDR12	WDR12	0.720088886	0.07890892	0.43259256	0.054534912

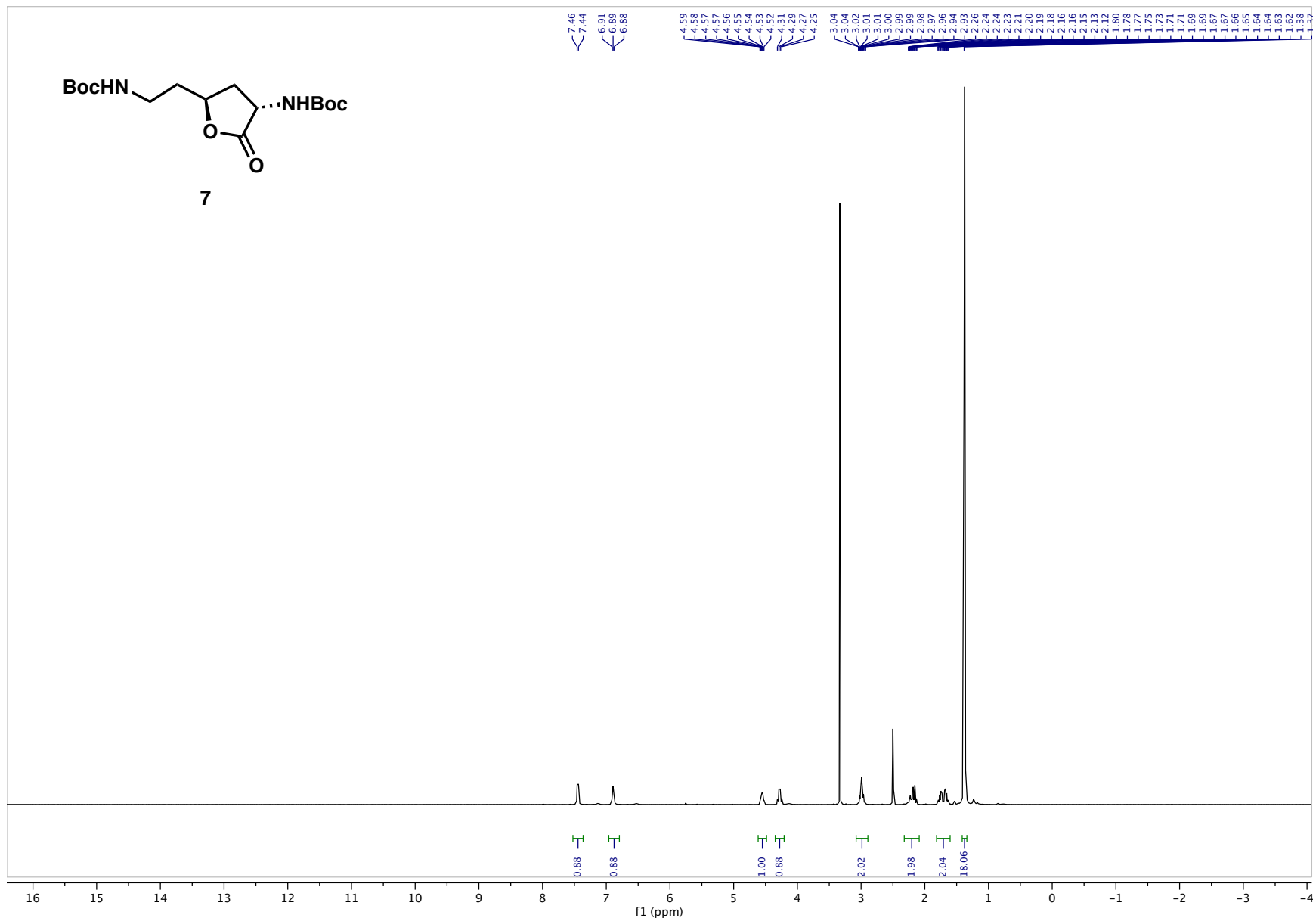
U3KQC1;Q9BV38;A0A0A0MQ U0;K7EIRO Q9H7D7	WD repeat-containing protein 18	WDR18	0.584560109	0.036783536	1.580386874	0.089340846
	WD repeat-containing protein 26	WDR26	0.008828467	-0.001713435	0.61414314	0.099733988
Q9UNX4	WD repeat-containing protein 3	WDR3	0.153336029	-0.015428225	1.146390214	-0.074751218
A0A0A0MTB8;Q8NI36	WD repeat-containing protein 36	WDR36	2.5107211	0.127380053	0.650904322	0.040909767
P57081	tRNA (guanine-N(7))-methyltransferase non-catalytic subunit WDR4	WDR4	0.057833697	-0.008433978	0.104546584	0.019955953
Q15061	WD repeat-containing protein 43	WDR43	1.349422481	-0.109278997	1.451609936	-0.114038785
O15213;H0Y6G3	WD repeat-containing protein 46	WDR46	0.038578724	0.006040255	0.37109491	0.044829686
P61964	WD repeat-containing protein 5	WDR5	3.879077183	0.111341476	0.901396819	0.037430445
Q9H977;B9A049	WD repeat-containing protein 54	WDR54	0	NaN	0	NaN
A0A087X295;Q9NNW5;E9PDU 5	WD repeat-containing protein 6	WDR6	0.351764657	-0.167001724	0.836652627	-0.293020248
Q9GZS3;H0YN81;H0YL19;H0 YMF9;H3BQA8	WD repeat-containing protein 61;WD repeat-containing protein 61, N-terminally processed	WDR61	0.304407304	-0.02736028	0.262952344	0.026672045
Q9NW82;D6RIW8	WD repeat-containing protein 70	WDR70	0.569905339	-0.11796999	0.170788115	-0.041190306
E9PS41;Q6RFH5	WD repeat-containing protein 74	WDR74	2.64482574	0.151931127	2.989974567	0.203101476
Q8IWA0	WD repeat-containing protein 75	WDR75	1.254590297	0.114480972	0.45692298	-0.046580315
Q9BQA1;H0Y711	Methylosome protein 50	WDR77	1.25535235	-0.139696757	0.069797077	-0.015318553
Q6UXN9	WD repeat-containing protein 82	WDR82	0.348185155	0.051229477	0.633801529	0.079302152
Q9BRP8	Partner of Y14 and mago	WIBG	2.371034561	-0.273271243	0.456272674	-0.066997846
O43516;E9PB87	WAS/WASL-interacting protein family member 1	WIPF1	0	NaN	0	NaN
Q9Y4P8	WD repeat domain phosphoinositide- interacting protein 2	WIPI2	0.113344954	-0.030454954	0.467607121	-0.100957235
Q96S55	ATPase WRNIP1	WRNIP1	0.170991948	0.031968117	0.450901113	-0.078076681
Q15007;A0A087X1R4	Pre-mRNA-splicing regulator WTAP	WTAP	0.306374337	0.040555636	0.061672317	-0.013594309
Q9HCS7	Pre-mRNA-splicing factor SYF1	XAB2	2.20091719	0.149231593	1.056093223	0.081168175
Q01831;E7EUB5	DNA repair protein complementing XP-C cells	XPC	0.668383357	-0.162647533	1.107682435	-0.29995362
Q9NQW7;Q5T6H7	Xaa-Pro aminopeptidase 1	XPNPPE1	0.029913056	0.007048925	0.22772058	-0.049754779
Q9NQH7	Probable Xaa-Pro aminopeptidase 3	XPNPPE3	0.401555085	-0.168518829	0.748478098	-0.271238136
O14980	Exportin-1	XPO1	0.811432242	-0.039243698	0.216920682	-0.01150767
Q9HAV4	Exportin-5	XPO5	0.045986722	-0.003653208	0.702106683	-0.059354782
Q96QU8	Exportin-6	XPO6	1.244016774	-0.281899897	0.592388866	-0.116261482
E7ESC6;Q9UIA9	Exportin-7	XPO7	0.897420277	-0.099358241	0.322616011	-0.04374218
O43592	Exportin-T	XPOT	2.318921492	-0.066204389	1.235339295	-0.042223295
P18887;F5H8D7	DNA repair protein XRCC1	XRCC1	0.199359379	0.04468441	1.482556189	-0.156837781
Q13426	DNA repair protein XRCC4	XRCC4	0.380109316	-0.071053187	0.389255913	-0.07114315
P13010	X-ray repair cross-complementing protein 5	XRCC5	3.61107756	-0.126345952	1.13591547	-0.031294187
P12956;B1AHC9	X-ray repair cross-complementing protein 6	XRCC6	0.513011094	0.014913241	1.494244178	-0.055252393
Q8IZH2;H7C5E4	5-3 exoribonuclease 1	XRN1	0.372791289	0.060264905	0.191304546	0.041096687
Q9H0D6	5-3 exoribonuclease 2	XRN2	0.133267892	0.01522541	0.346247164	-0.032818476
Q86Y38	Xylosyltransferase 1	XYLT1	0	NaN	0	NaN
A0A0C4DFW8;B4DT06;Q9H1B 5	Xylosyltransferase 2	XYLT2	0.920585943	-0.181937599	0.908343613	-0.192470868
P54577;A0A0C4DGZ5	Tyrosine--tRNA ligase, cytoplasmic;Tyrosine--tRNA ligase, cytoplasmic, N-terminally processed;Tyrosine--tRNA ligase	YARS	0.15739437	0.015468915	0.14413078	0.014489174
Q9Y2Z4;H0YHS6	Tyrosine--tRNA ligase, mitochondrial;Tyrosine--tRNA ligase	YARS2	0.054452809	0.014446576	0.410229046	-0.098483404
P67809;H0Y449	Nuclease-sensitive element-binding protein 1	YBX1	3.210470396	-0.218052228	0.306122952	-0.031228701
P16989	Y-box-binding protein 3	YBX3	2.414664512	-0.508266131	0.629836477	-0.120493571
E9PIZ0;C9JST7;A6NGW1;O950 70	Protein YIF1A	YIF1A	0	0.219381332	0	0.165014267
D6RGY8;D6RFI3;E7EQR8;Q9G ZM5;H0Y9A1	Protein YIPF3;Protein YIPF3, 36 kDa form III	YIPF3	0.515393576	-0.107700348	1.122990391	-0.253197988

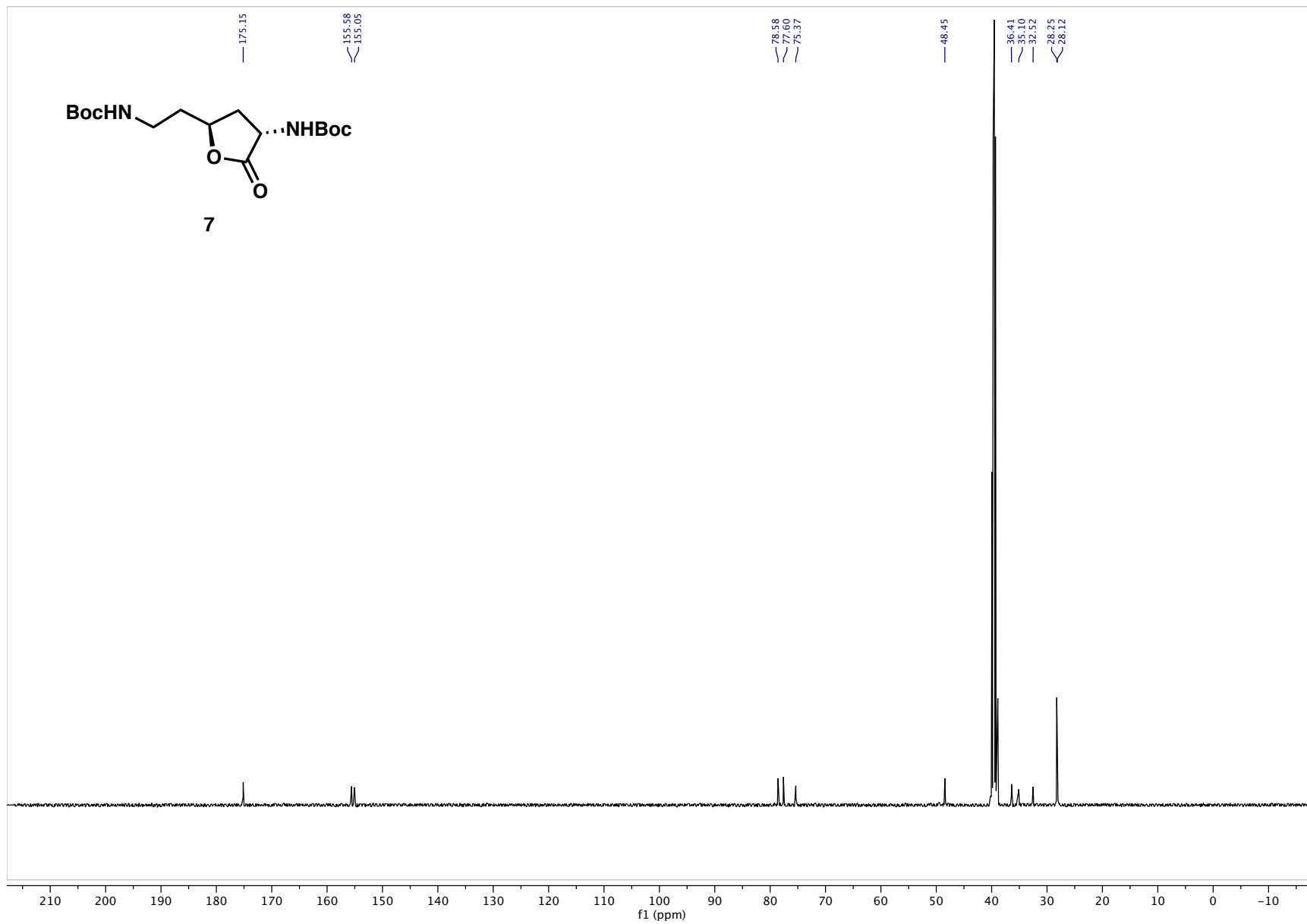
O15498	Synaptobrevin homolog YKT6	YKT6	1.389008687	-0.15840594	0.519409915	-0.066159248
Q96TA2;Q96I63	ATP-dependent zinc metalloprotease YME1L1	YME1L1	2.604440037	0.160116514	0.666369936	0.058679581
Q86U90	YrdC domain-containing protein, mitochondrial	YRDC	1.477934216	-0.168866793	0.286395362	-0.061740557
J3QR07;Q96MU7	YTH domain-containing protein 1	YTHDC1	1.030741156	0.098983765	0.544303407	-0.055678368
Q9H6S0;D6RA70	Probable ATP-dependent RNA helicase YTHDC2	YTHDC2	0.095155794	0.02325662	0.067829616	-0.010652542
Q9Y5A9	YTH domain-containing family protein 2	YTHDF2	2.718750158	-0.205377897	0.108208492	-0.011077245
A0A087WY31;A0A024R7W5;A0A087X0Q1;Q7Z739 P31946	YTH domain-containing family protein 3 14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	YTHDF3 YWHAB	0.036818932 1.818061685	0.012401899 -0.168890635	0.211792103 0.387731262	-0.041895231 -0.045014381
P62258;B4DJF2;I3L3T1	14-3-3 protein epsilon	YWHAE	0.919512461	-0.066069603	0.110155723	0.011404673
P61981	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	YWHAG	2.236188725	-0.089183807	1.154578903	0.069978396
Q04917;A2IDB2	14-3-3 protein eta	YWHAH	2.050770495	-0.134719849	0.553364938	0.043635368
P27348;E9PG15	14-3-3 protein theta	YWHAQ	1.739951417	-0.101535479	0.412984372	-0.041903814
P63104;B0AZS6;E7EX29;B7Z2 E6;HOYB80 P25490;HOYJV7	14-3-3 protein zeta/delta Transcriptional repressor protein YY1	YWHAZ YY1	1.258321052 1.262451334	-0.073916435 0.361551603	0.424961172 0.40913774	0.028386116 0.113652547
Q8N4Q0	Zinc-binding alcohol dehydrogenase domain-containing protein 2	ZADH2	0	-0.262535095	0	-0.156850815
Q9ULJ3	Zinc finger and BTB domain-containing protein 21	ZBTB21	0	NaN	0	0.208731651
Q8NAP3;A0A1B0GV48;D6RB C4	Zinc finger and BTB domain-containing protein 38	ZBTB38	0.679725698	0.141017151	0.199844375	-0.070768801
D3DPQ2;A0A087X0V4;A8K0B 5;Q8IWT0 O75152;E9PQ61;E9PBY7	Protein archease Zinc finger CCCH domain-containing protein 11A	ZBTB80S ZC3H11A	0.623935964 0.257807619	-0.054817518 0.029657364	0.040090067 1.506210288	0.004359563 -0.143828392
G3V256;Q6PJT7;G3V3Y4;G3V 516;HOYJA2 Q8WU90	Zinc finger CCCH domain-containing protein 14 Zinc finger CCCH domain-containing protein 15	ZC3H14 ZC3H15	0.076079238 0.711438334	0.02320226 -0.077267965	0.340845758 0.706267922	0.080807686 0.06308047
E7ERS3;Q86VM9	Zinc finger CCCH domain-containing protein 18	ZC3H18	0.072072237	-0.01854229	0.051463295	0.013451576
M0QY97;Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4	0.091454578	-0.027338982	0.089585943	0.024657885
I3L2K5;Q8IWR0;I3L3S2;I3L3F 9;I3L1Y3;I3L382;I3L323 Q7Z2W4;C9J6P4	Zinc finger CCCH domain-containing protein 7A Zinc finger CCCH-type antiviral protein 1	ZC3H7A ZC3HAV1	0 0.202171792	NaN 0.01740551	0 1.148800972	NaN 0.060927709
C9J0I9;Q86WB0	Nuclear-interacting partner of ALK	ZC3HC1	0.075458638	0.024273618	1.731773519	-0.238962173
Q6NZY4;F5H6J5;F5GX80	Zinc finger CCHC domain-containing protein 8	ZCCHC8	0.095973994	-0.029266357	0.183482184	0.057791074
Q6FIF0;H0YMR5;H0YLR2;H0 YME2;H0YK21;H0YK54 Q15911	AN1-type zinc finger protein 6 Zinc finger homeobox protein 3	ZFAND6 ZFHX3	0.427535482 0.551819194	0.075486183 -0.13974762	2.824211063 0.157646286	0.383662542 0.066572825
A0A0A6YYC7;Q96JP5	E3 ubiquitin-protein ligase ZFP91	ZFP91-CNTF;ZFP91	0	-0.993904114	0	-1.031150818
E9PQ47;E9PNY1;O95159;E9P MQ3;E9PQA5;E9PJX1;E9PJ47 Q96KR1	Zinc finger protein-like 1 Zinc finger RNA-binding protein	ZFPL1 ZFR	1.34050294 0.213357699	-0.171590805 -0.035839081	1.108161887 0.101047014	-0.103710175 0.015899658
Q8N5A5;V9GY48	Zinc finger CCCH-type with G patch domain-containing protein	ZGPAT	0.271462241	0.099558703	1.804623836	0.190987015
O75844	CAAX prenyl protease 1 homolog	ZMPSTE24	1.693458862	-0.055642128	0.685935766	-0.0684913
A0A087WV57;A0A087WYS3; H7C4X9;A0A087WVZ6;Q9UL U4;Q5TH12 J3QRS9;X6R4W8;O43670	Protein kinase C-binding protein 1 BUB3-interacting and GLEBS motif-containing protein ZNF207	ZMYND8 ZNF207	1.094238542 0.150775934	0.081545448 -0.026432037	1.743962317 0.025605252	-0.100957616 -0.00440375
P17028	Zinc finger protein 24	ZNF24	0.427913368	-0.184499741	0.15338614	-0.060140292
Q9Y2X9	Zinc finger protein 281	ZNF281	0.096969263	0.048515956	0	0.072769801
Q5BKZ1;A0A0A0MRN4	DBIRD complex subunit ZNF326	ZNF326	0.169984547	-0.021983782	0.36224147	0.043673197
D6RBR7;Q9Y3S2;D6R9C8;D6R 8Y9 M0QXZ5;Q96B54	Zinc finger protein 330 Zinc finger protein 428	ZNF330 ZNF428	0.83555253 0.639130532	0.111038208 -0.229894638	0 0.285845502	-0.036422094 -0.103122075
A9J4F5;O00488	Zinc finger protein 593	ZNF593	0	NaN	0.647951439	0.320775032
Q86UK7;H3BQQ2	Zinc finger protein 598	ZNF598	0.189808084	0.041769981	0.309871116	0.071967125

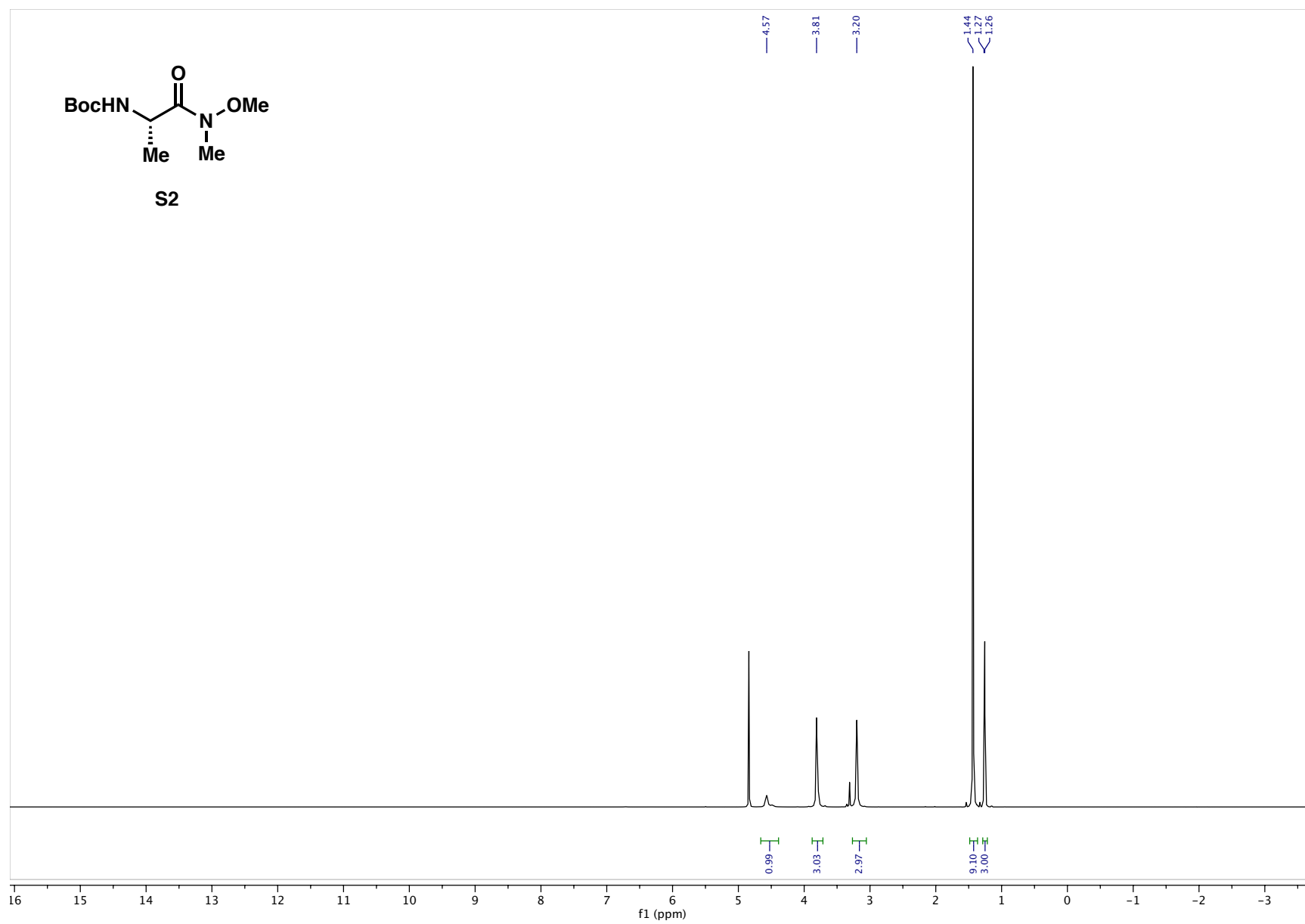
Q969S3	Zinc finger protein 622	ZNF622	1.29559772	-0.383155632	0.724423555	-0.261346245
Q14966	Zinc finger protein 638	ZNF638	2.908383811	-0.279278437	0.873794799	-0.104940414
Q9Y5V0;H0YC70;E5RHH4;H0 YAP1;E5RHR6	Zinc finger protein 706	ZNF706	0.592249247	-0.154759089	0.029284703	-0.00769488
H7C0E5;O75312;H7BZM7	Zinc finger protein ZPR1	ZPR1	0.294915334	0.045640945	0.474117714	0.060534795
O95218	Zinc finger Ran-binding domain- containing protein 2	ZRANB2	0.113303476	0.033890724	0.834913056	0.178241094
O43264	Centromere/kinetochore protein zw10 homolog	ZW10	1.023428573	-0.095712662	0.266696352	-0.025685946
Q9H900	Protein zwilch homolog	ZWILCH	1.17693494	-0.107638359	2.255103853	-0.169868151

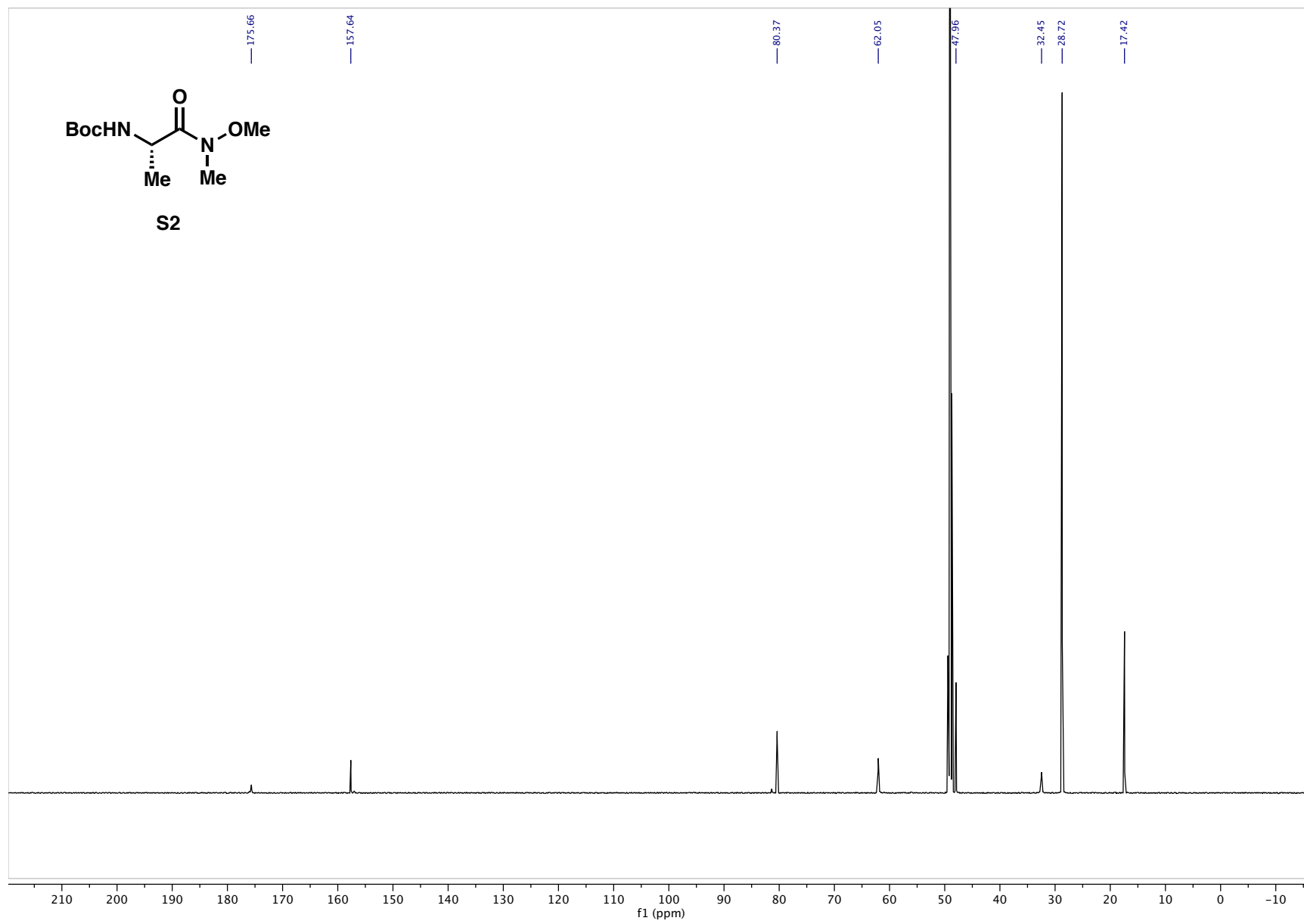


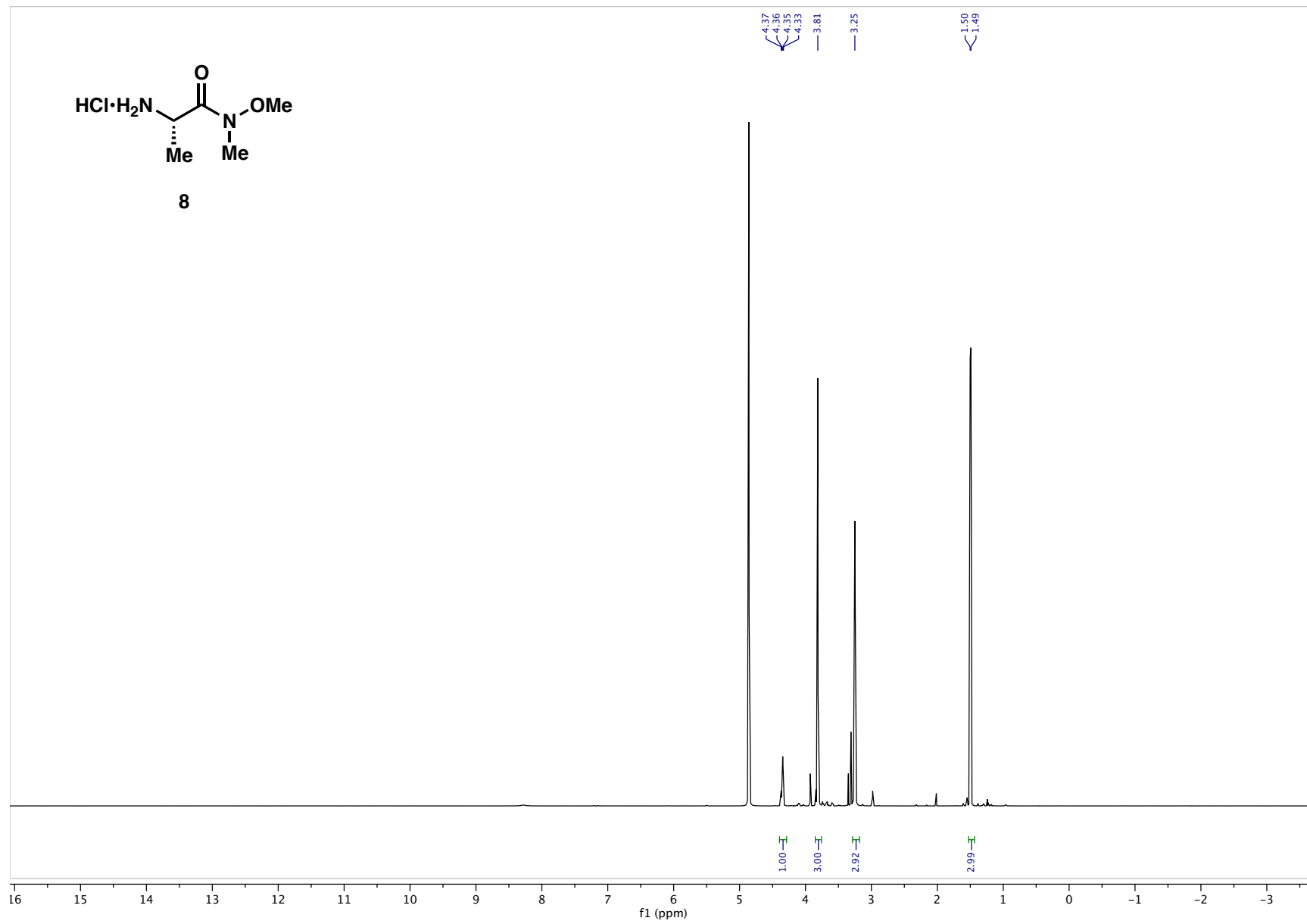
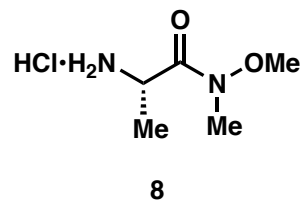


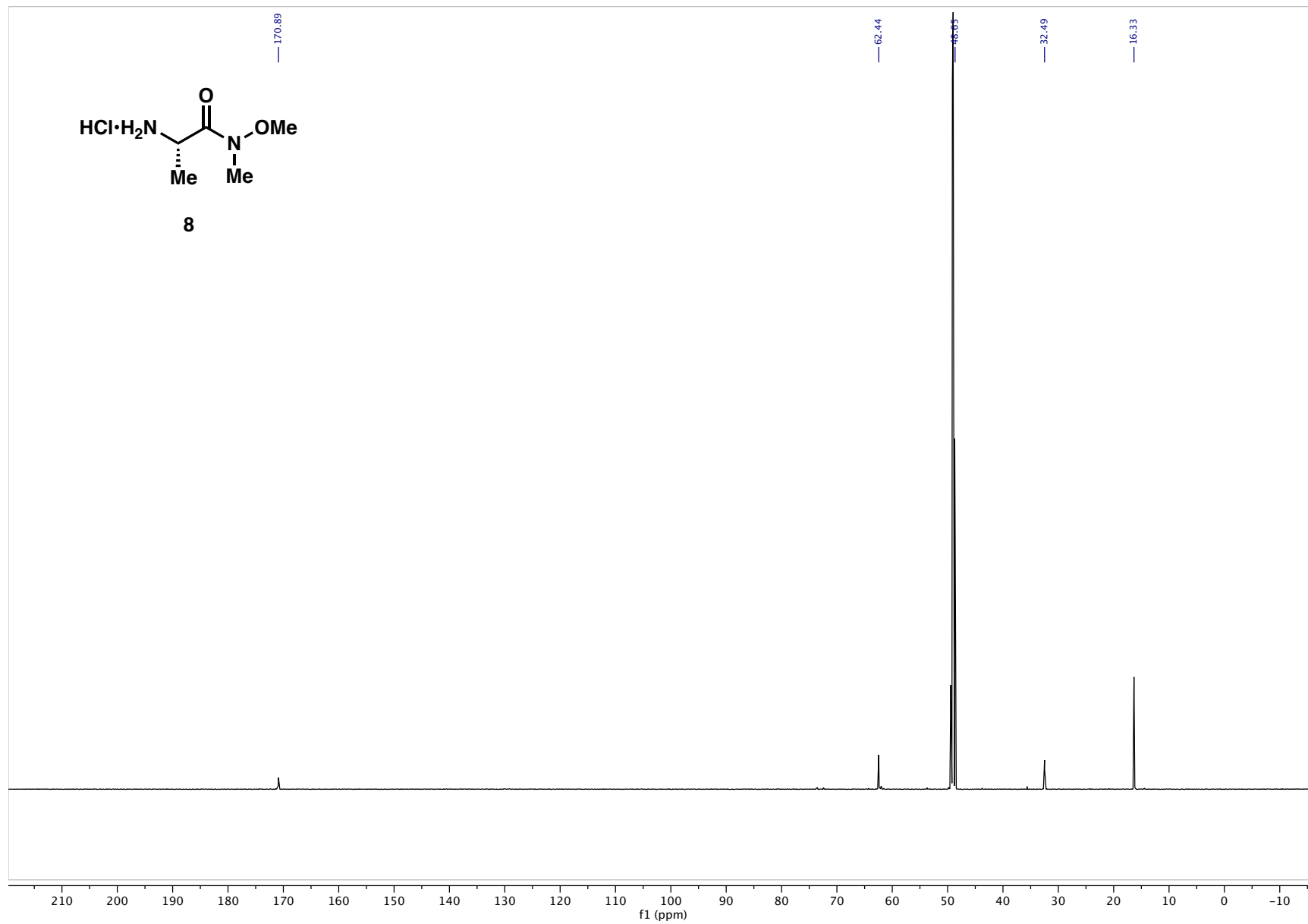


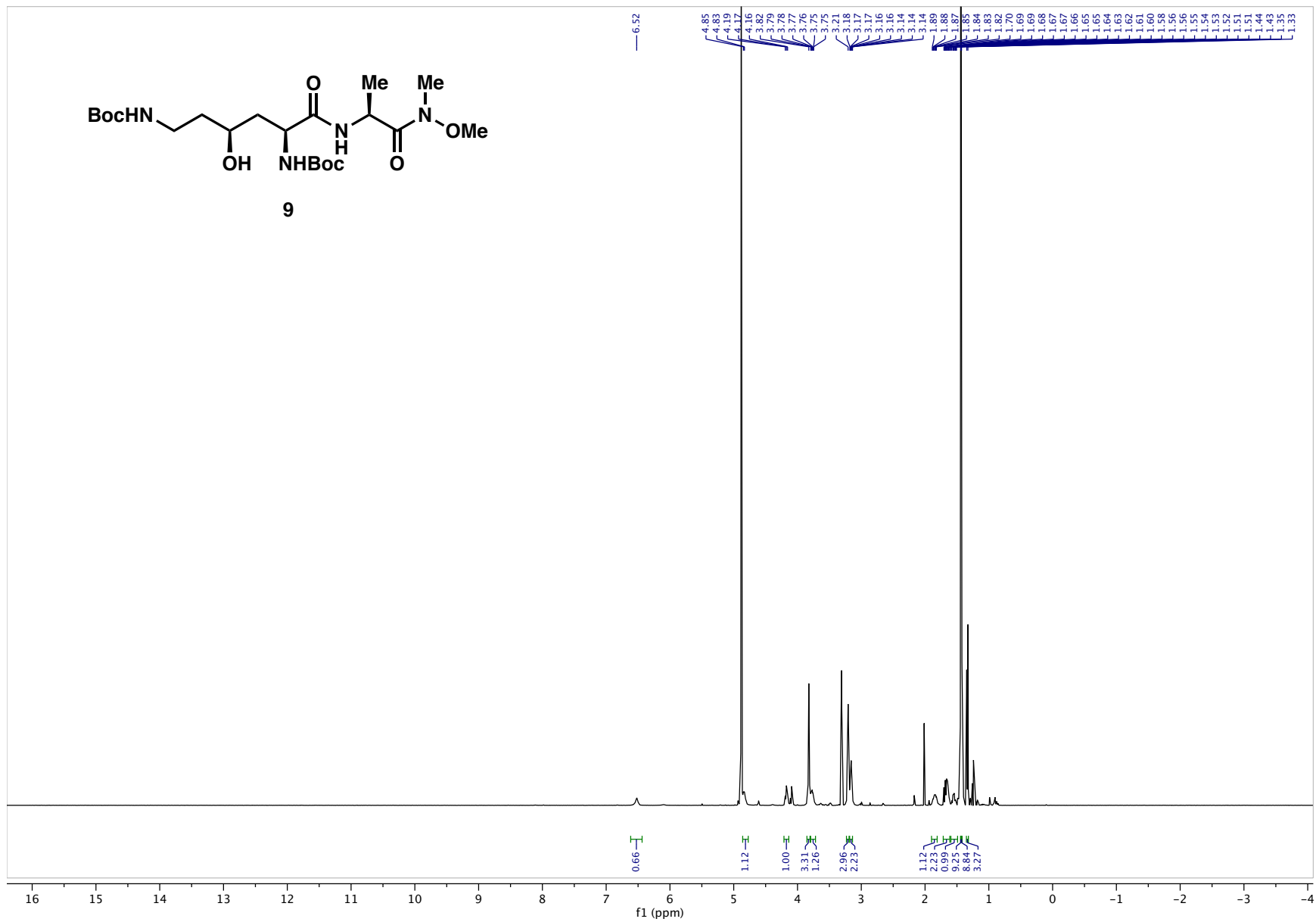


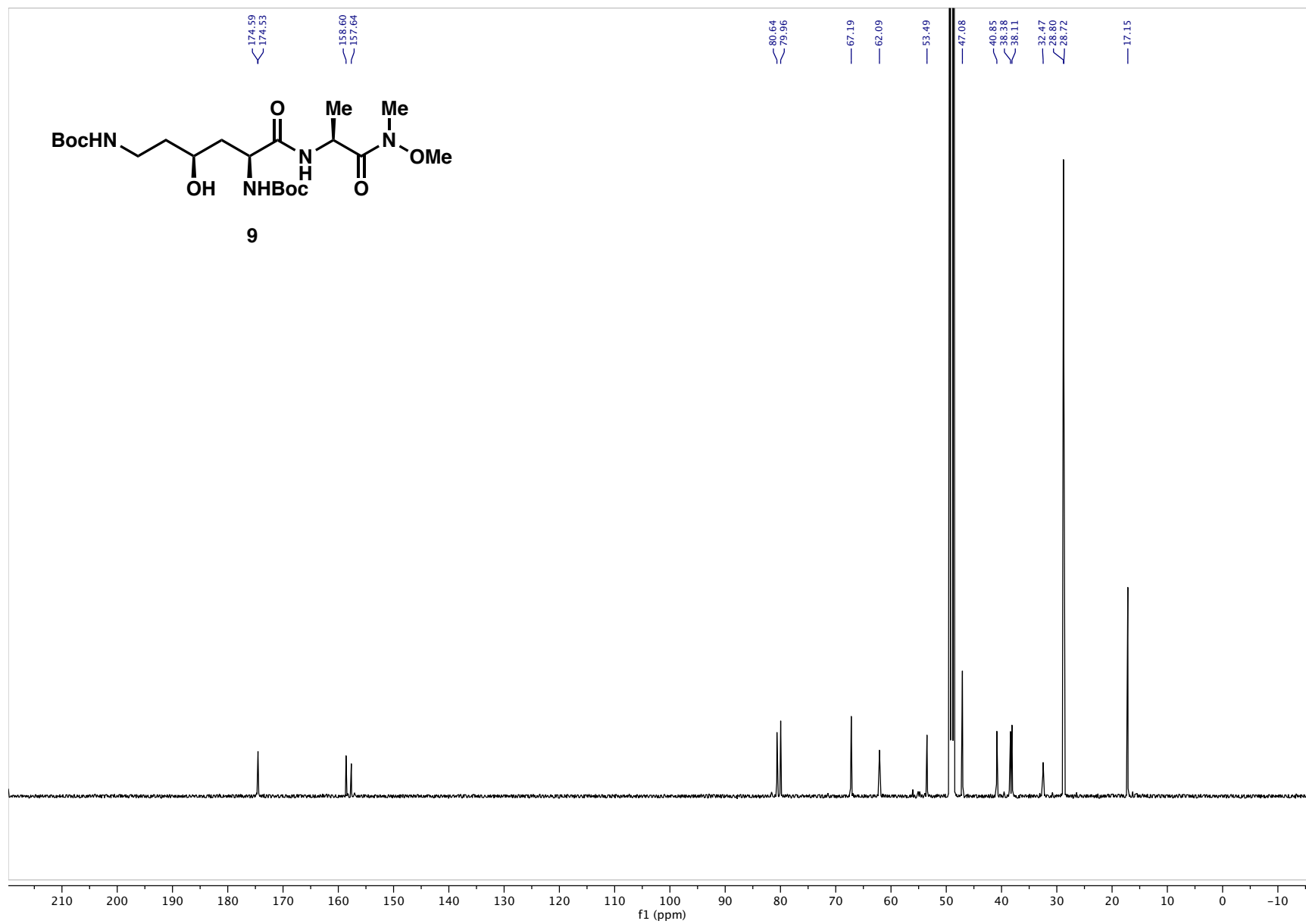


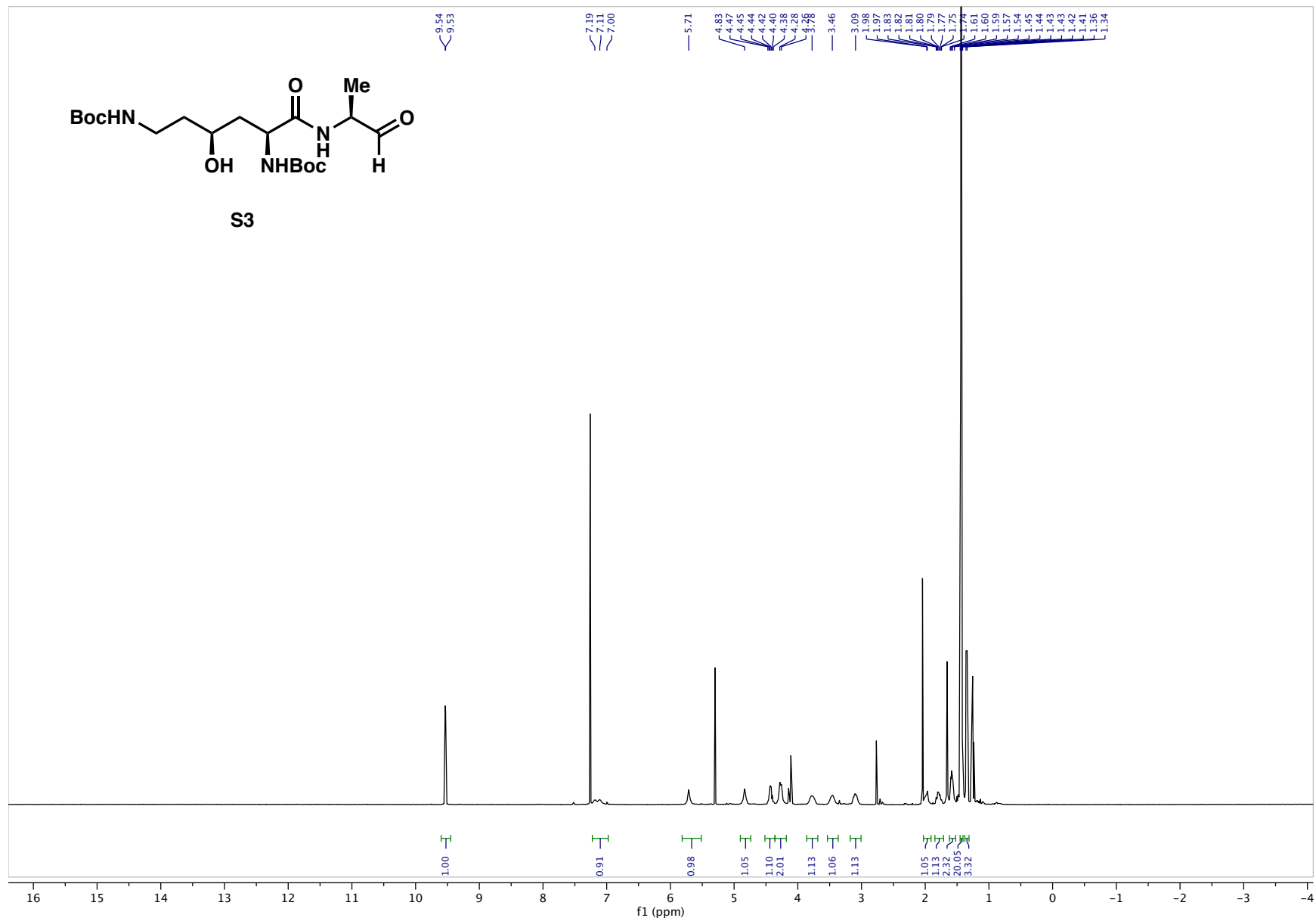




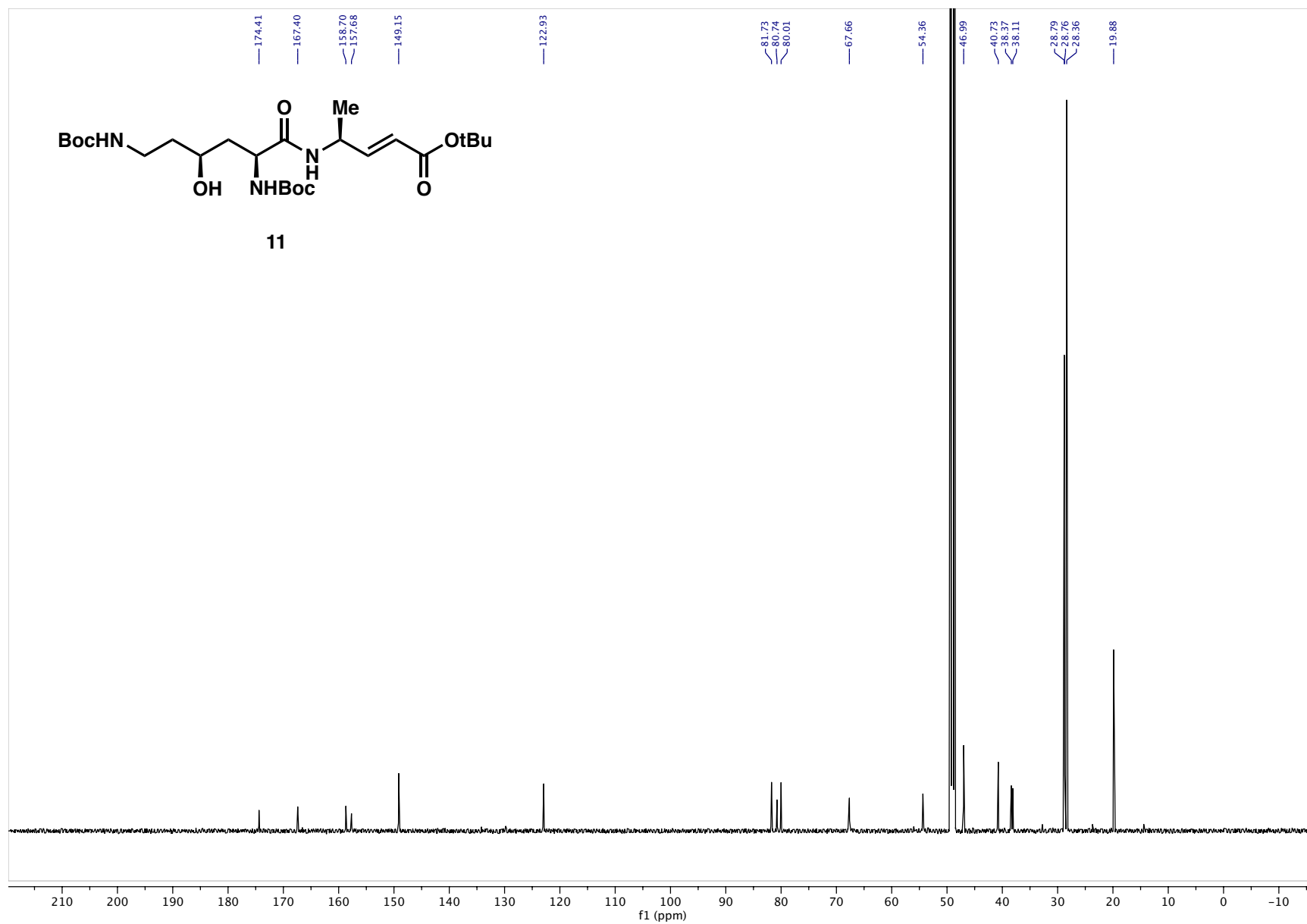


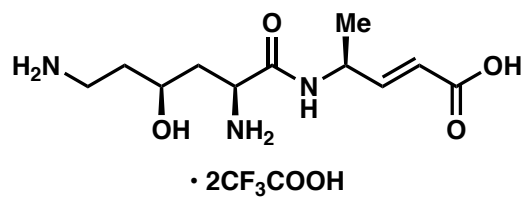




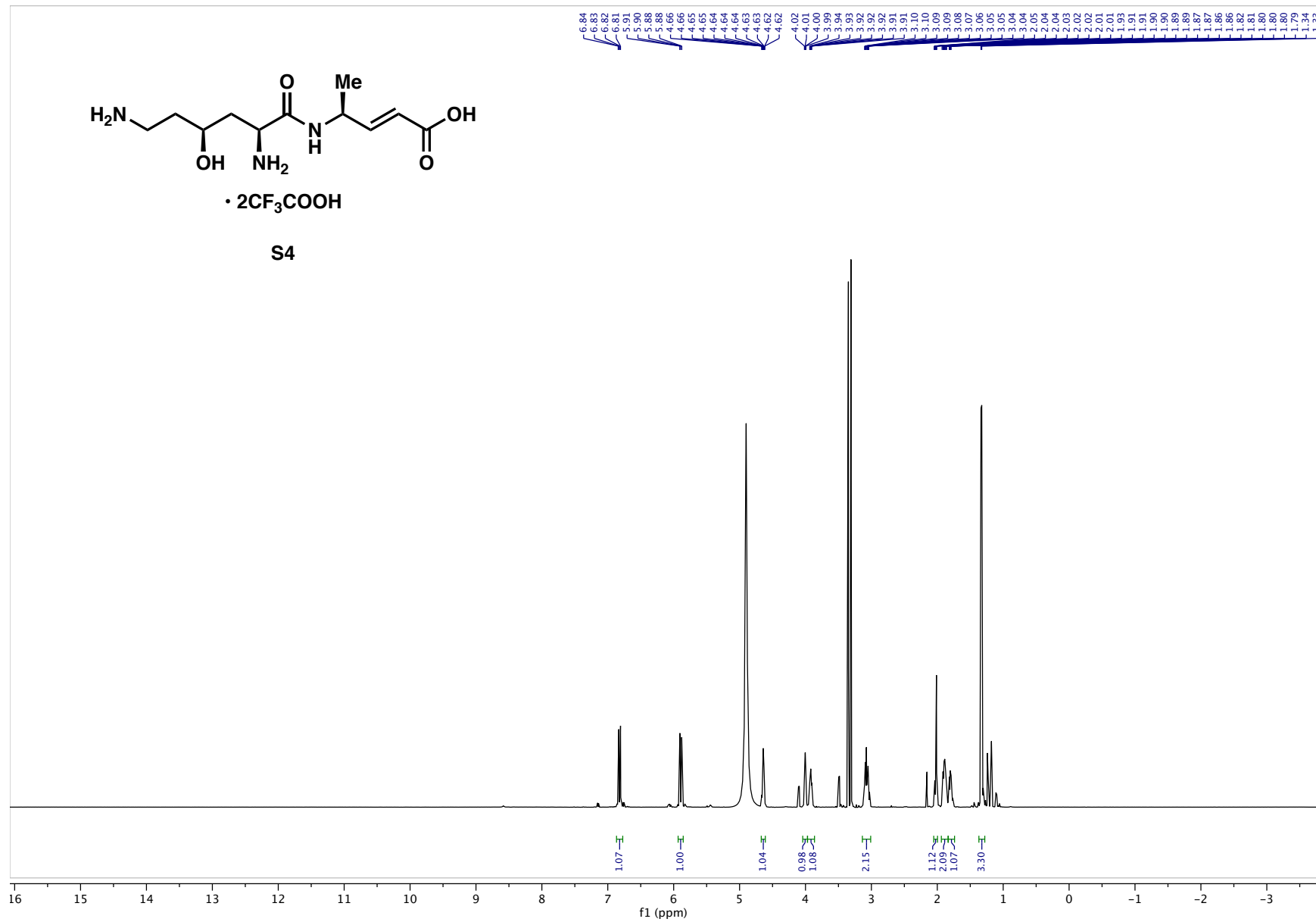


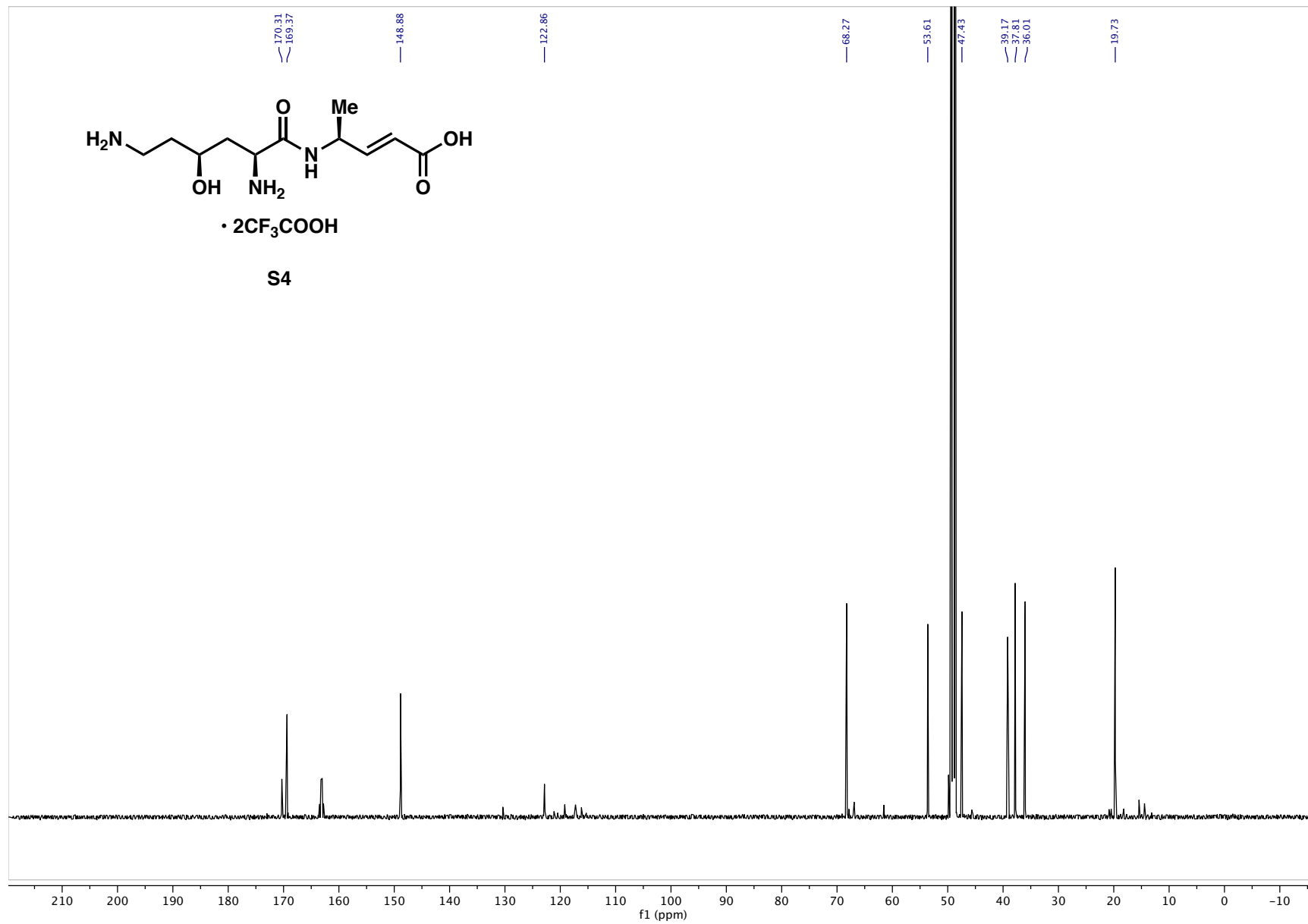


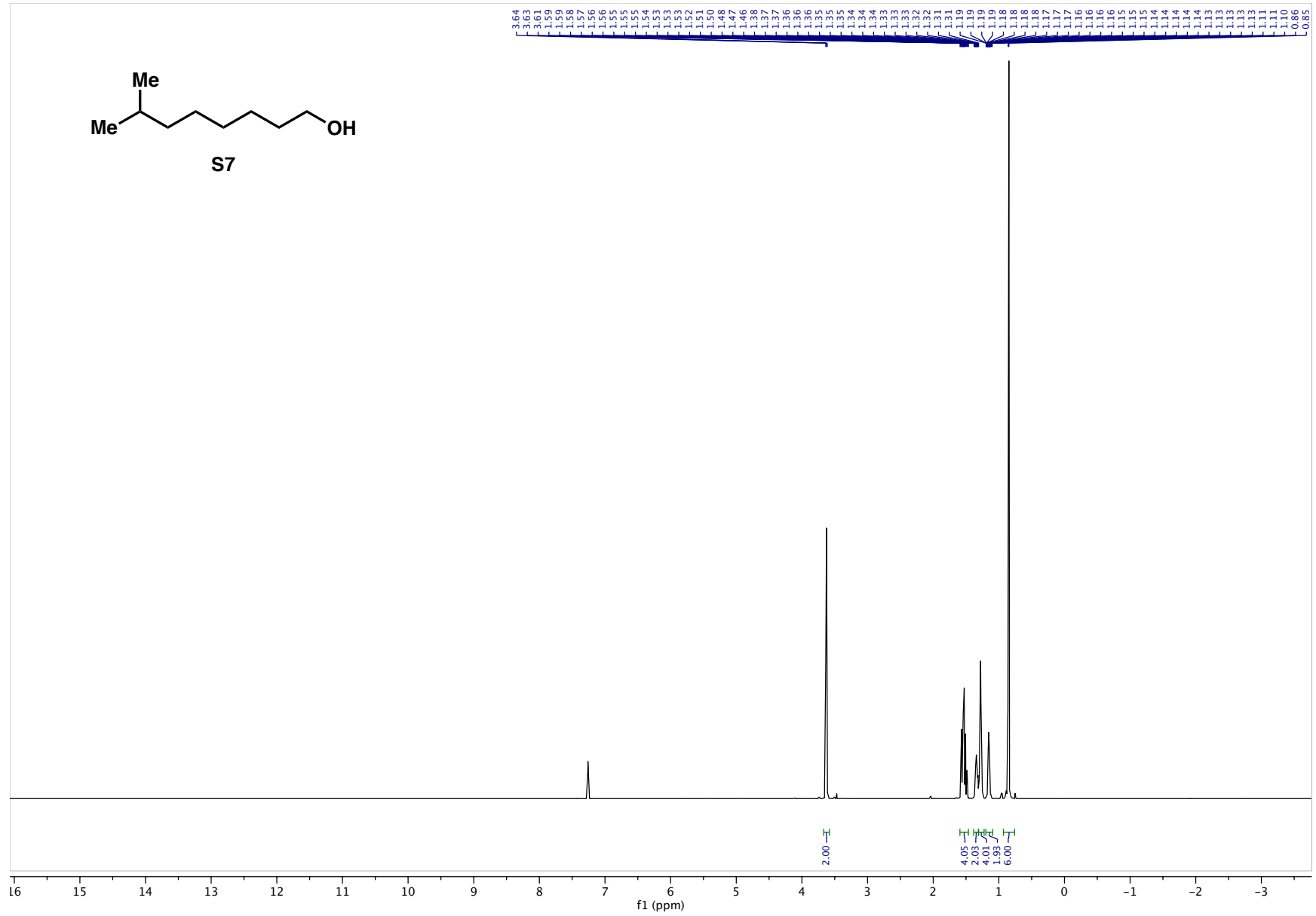


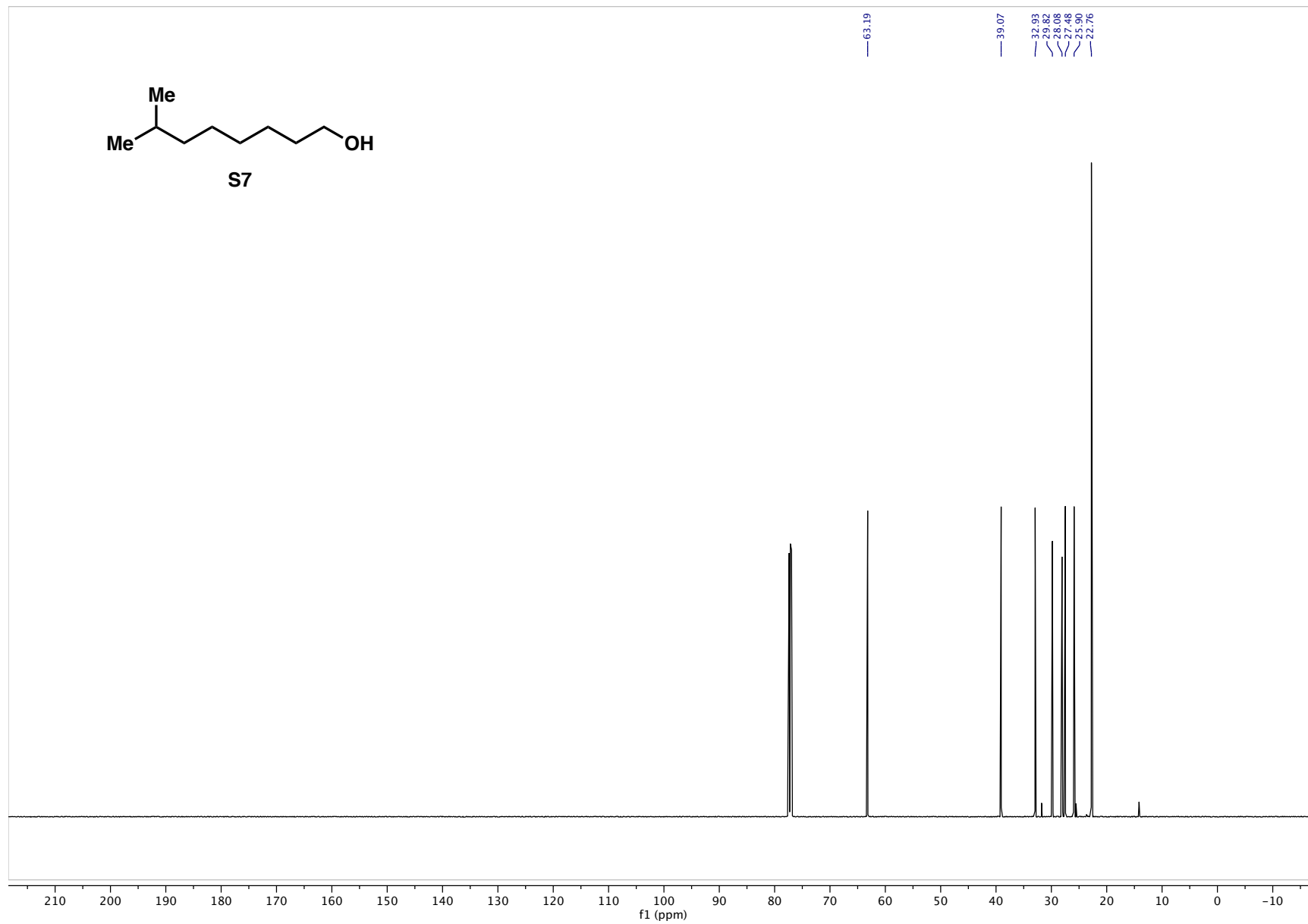


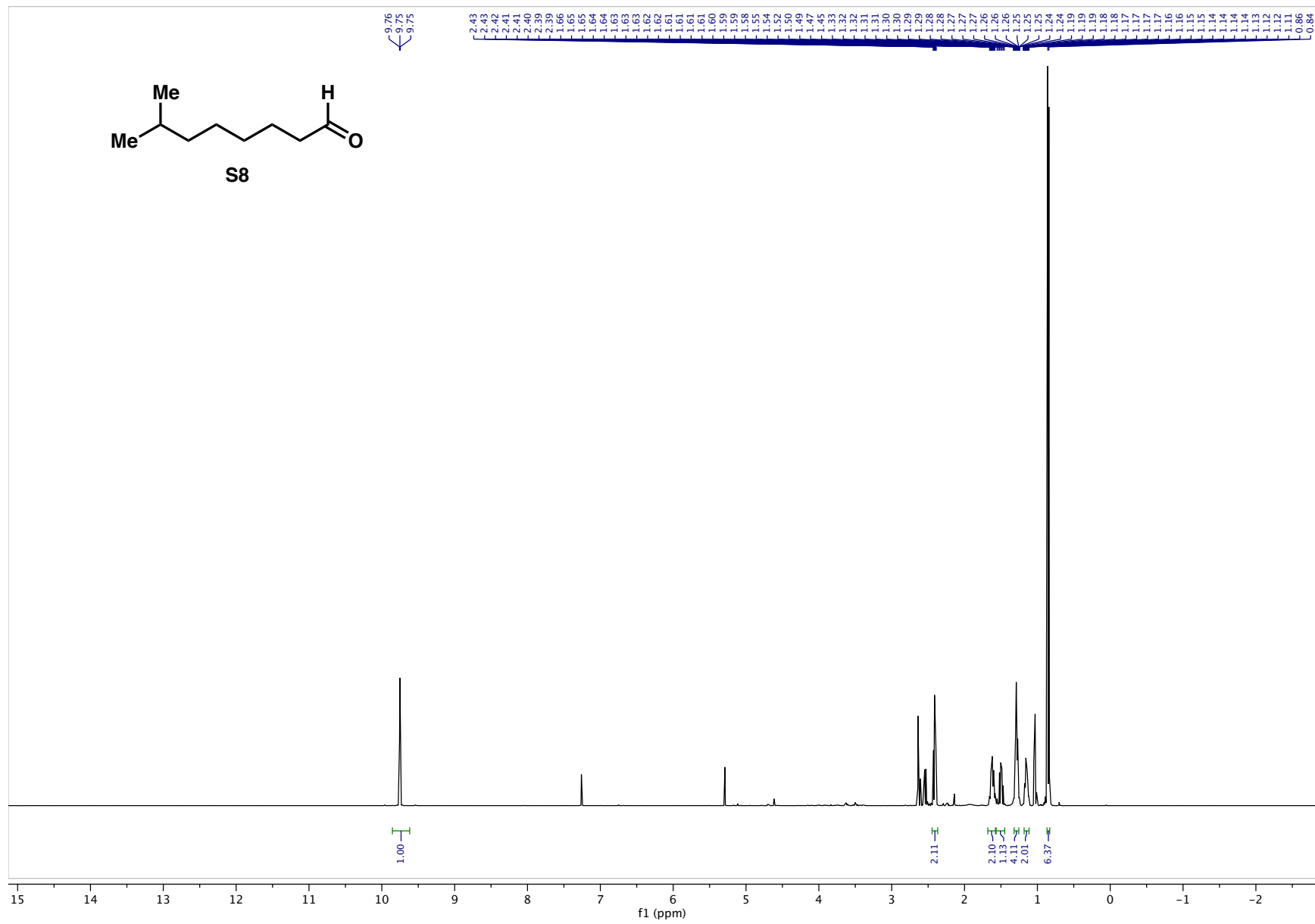
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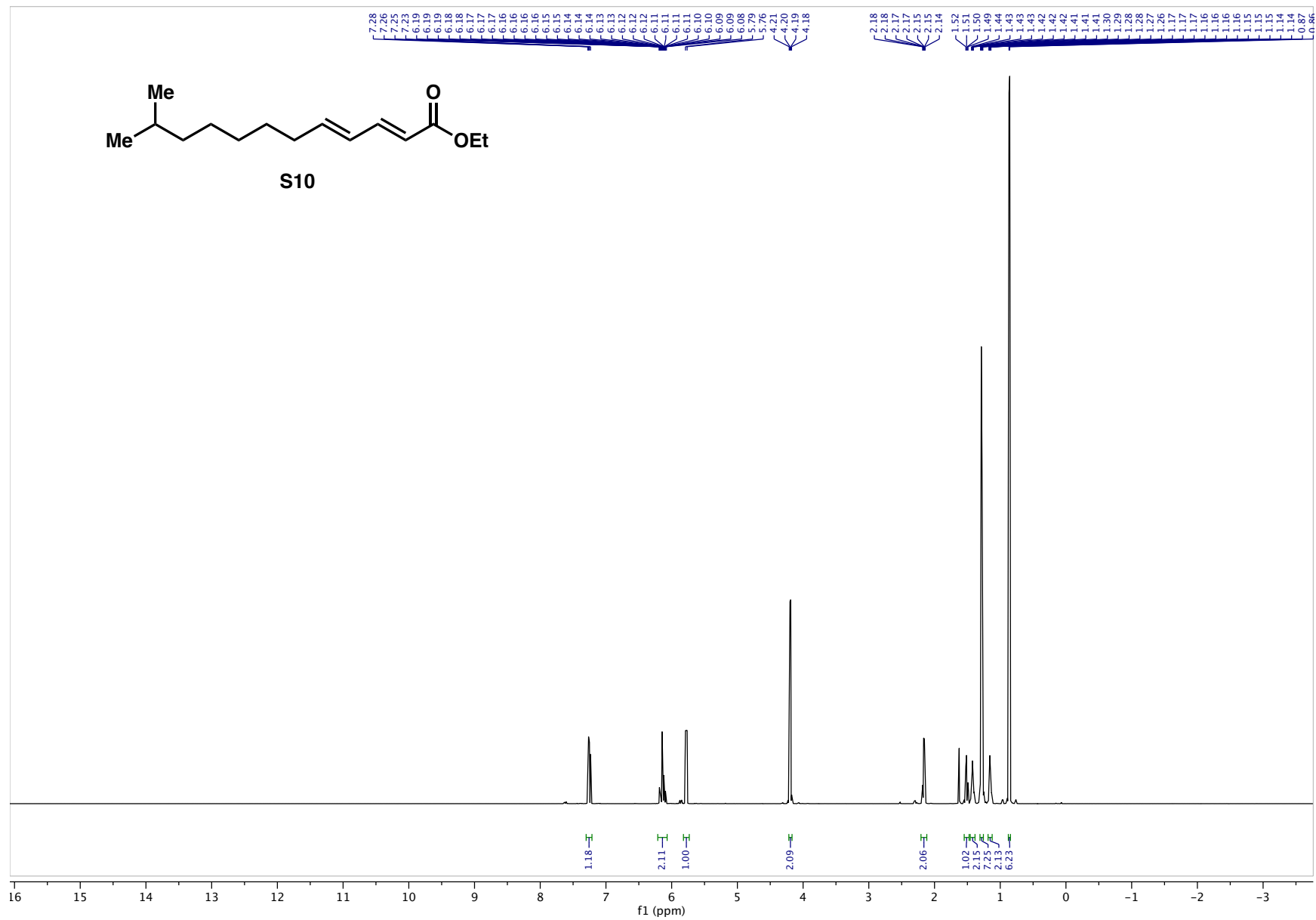


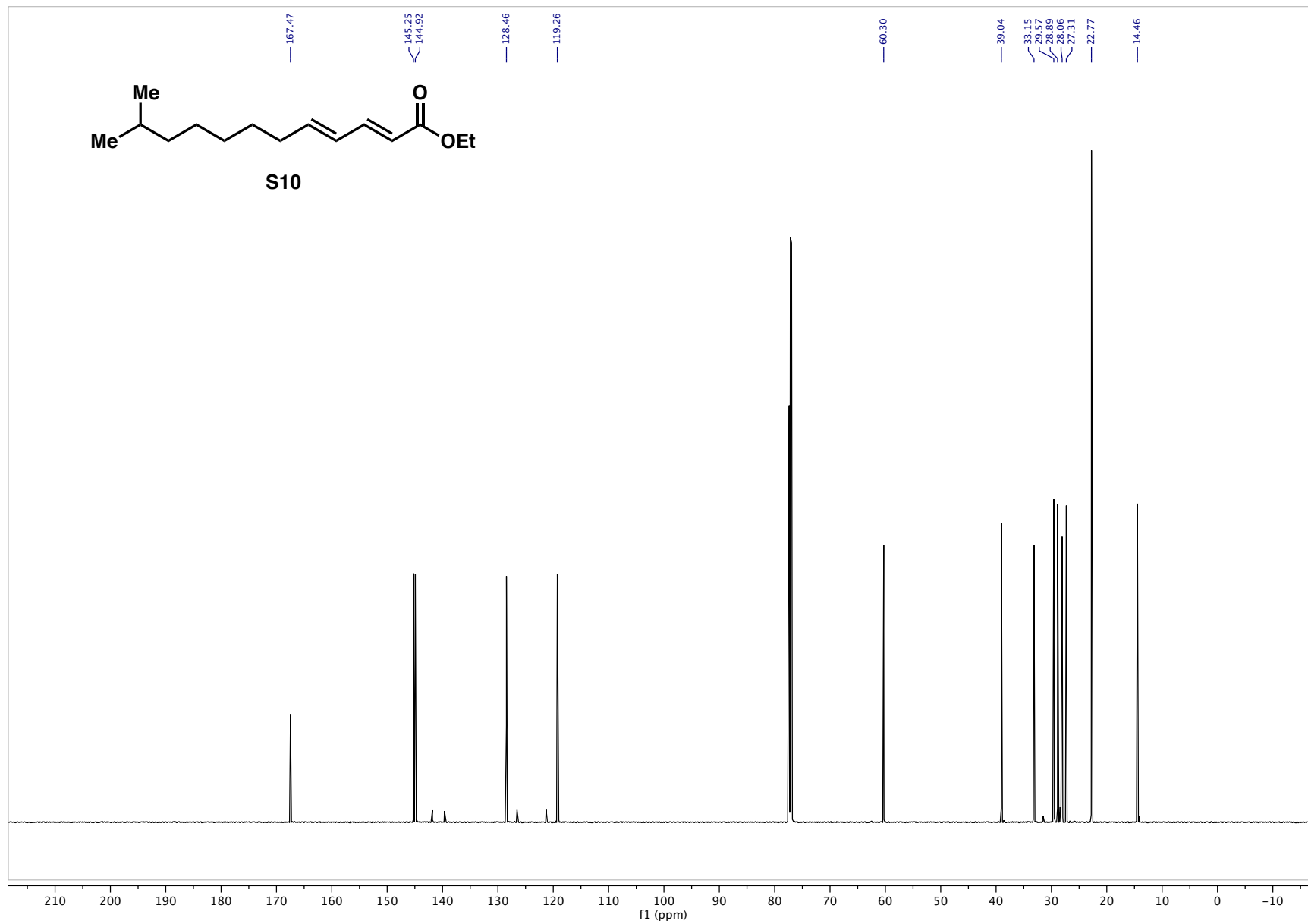


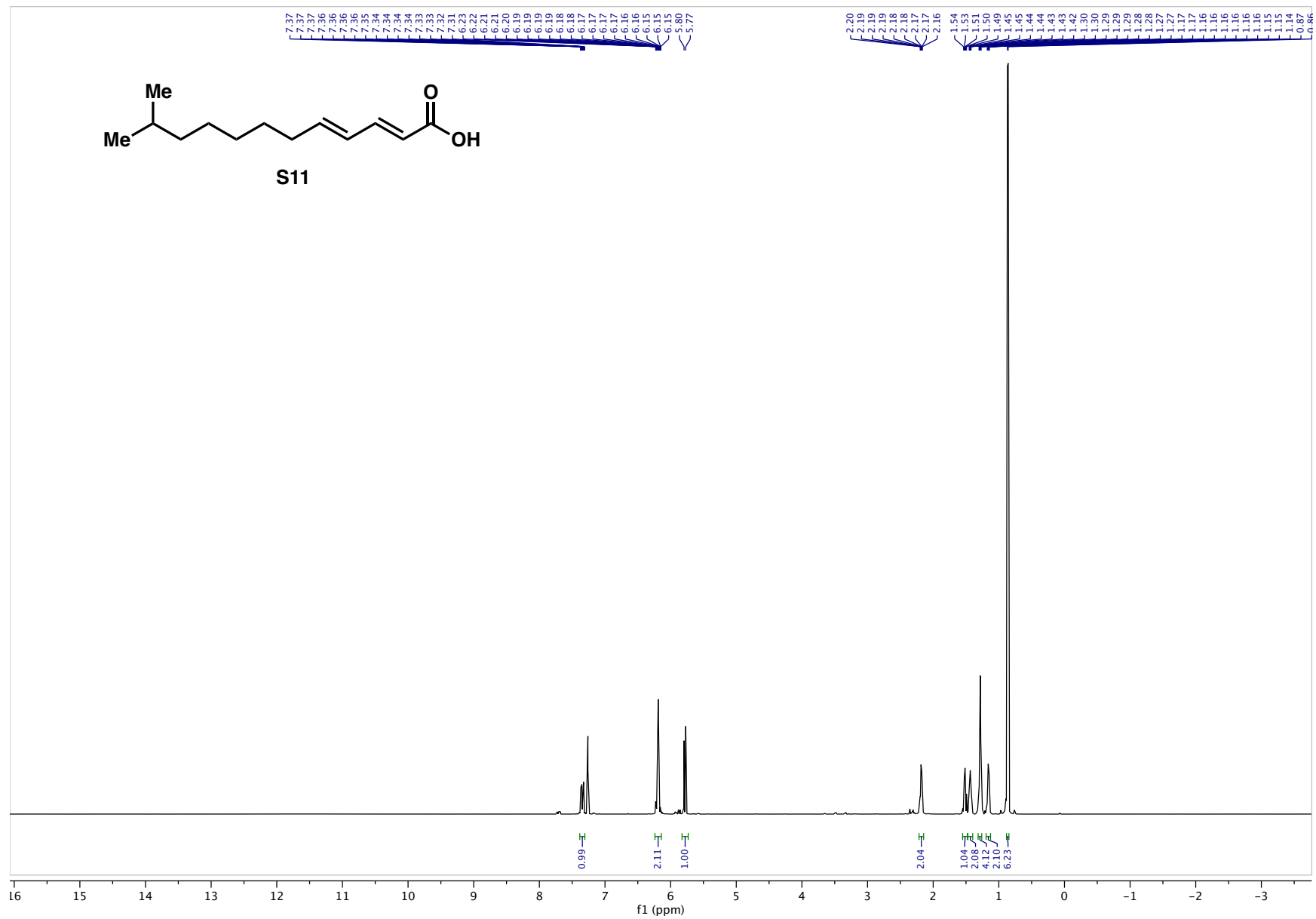


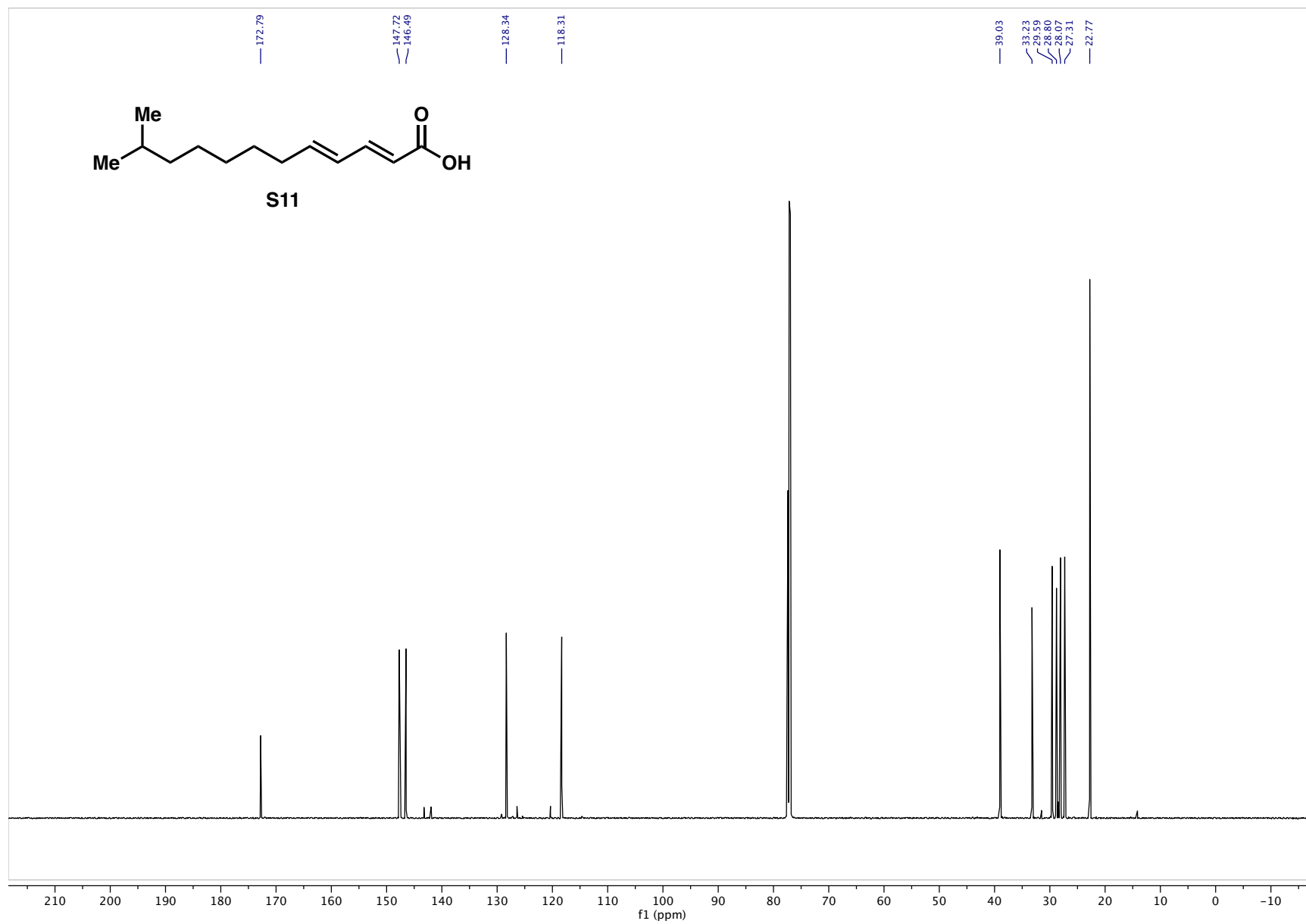


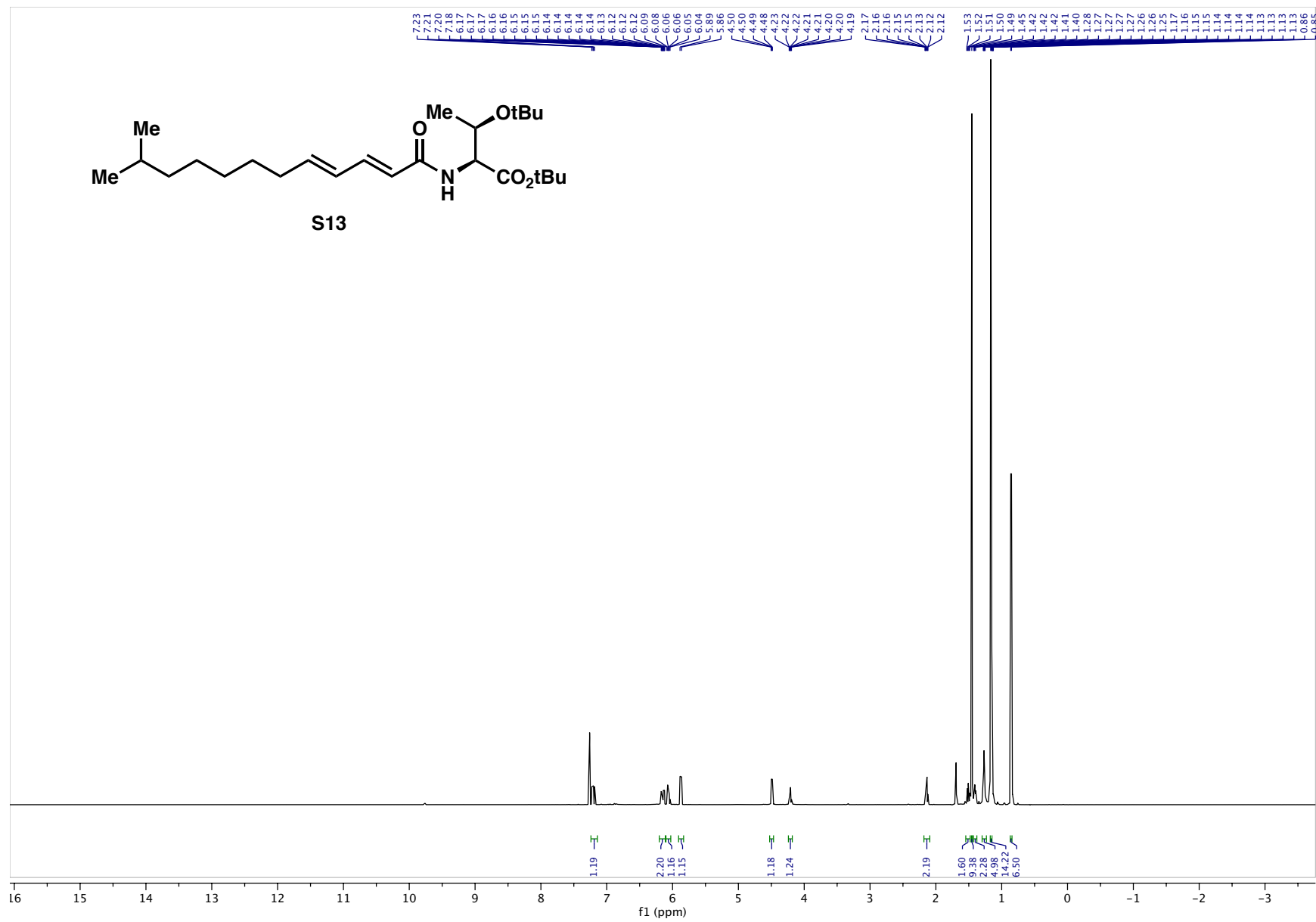


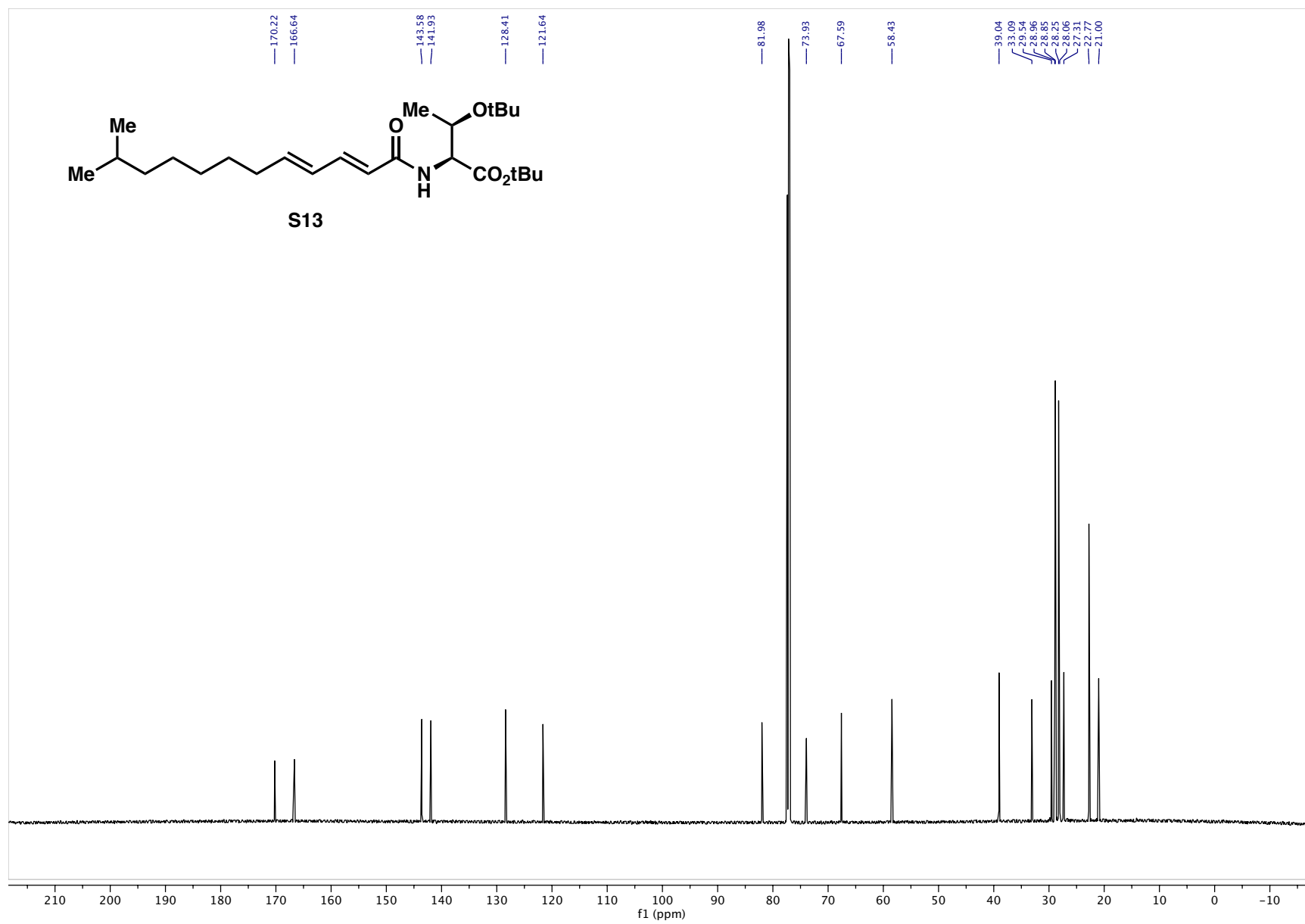


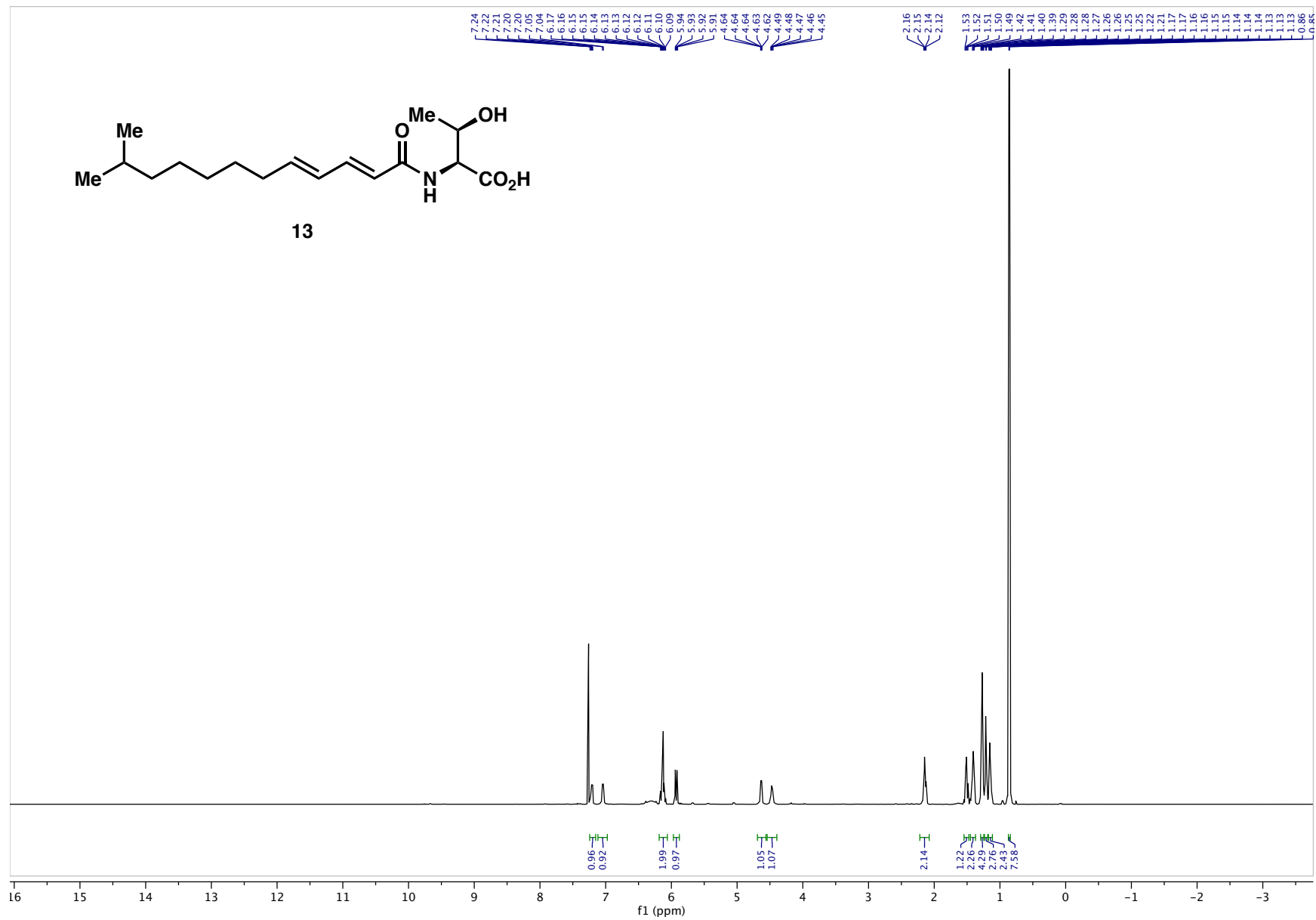


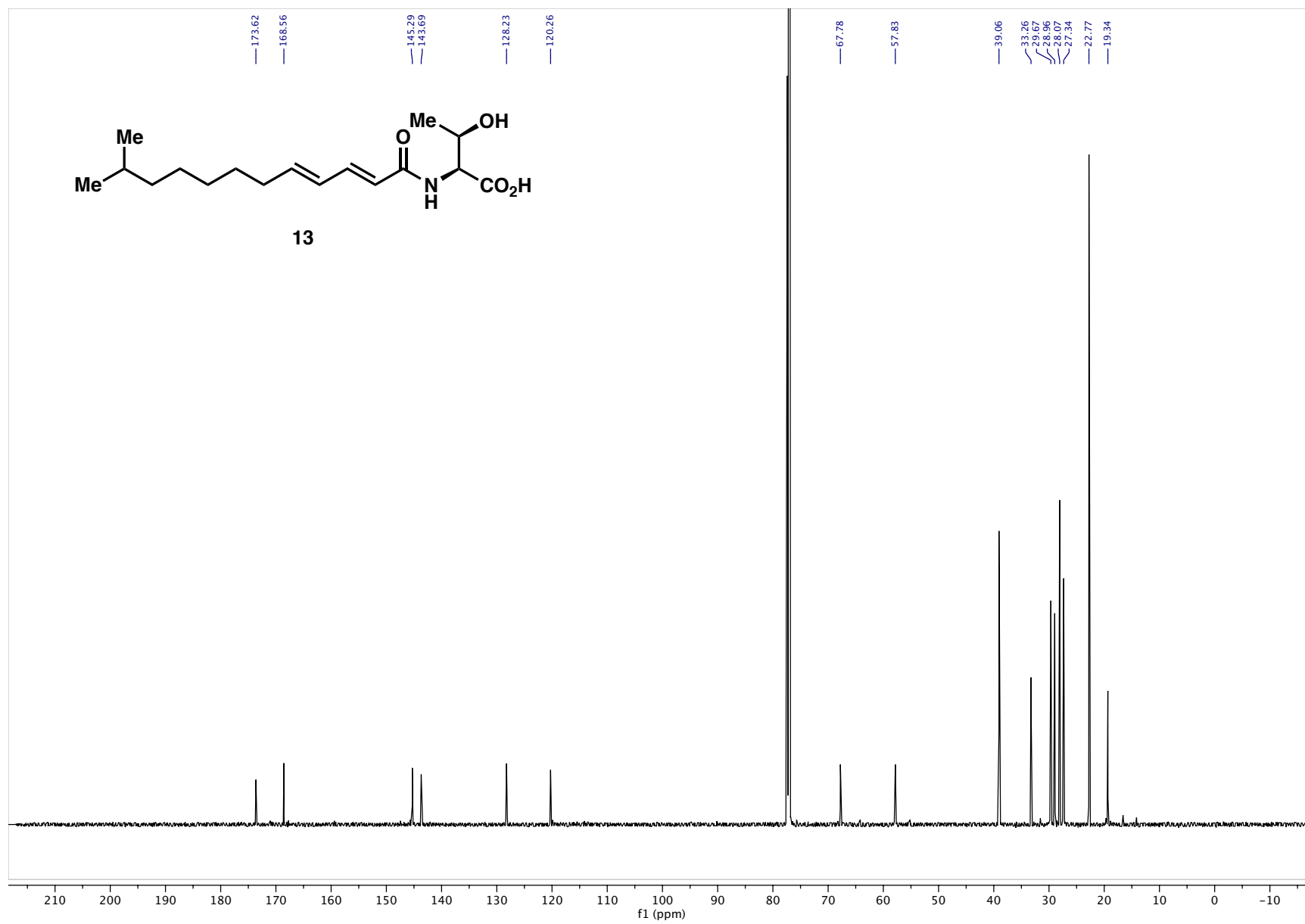


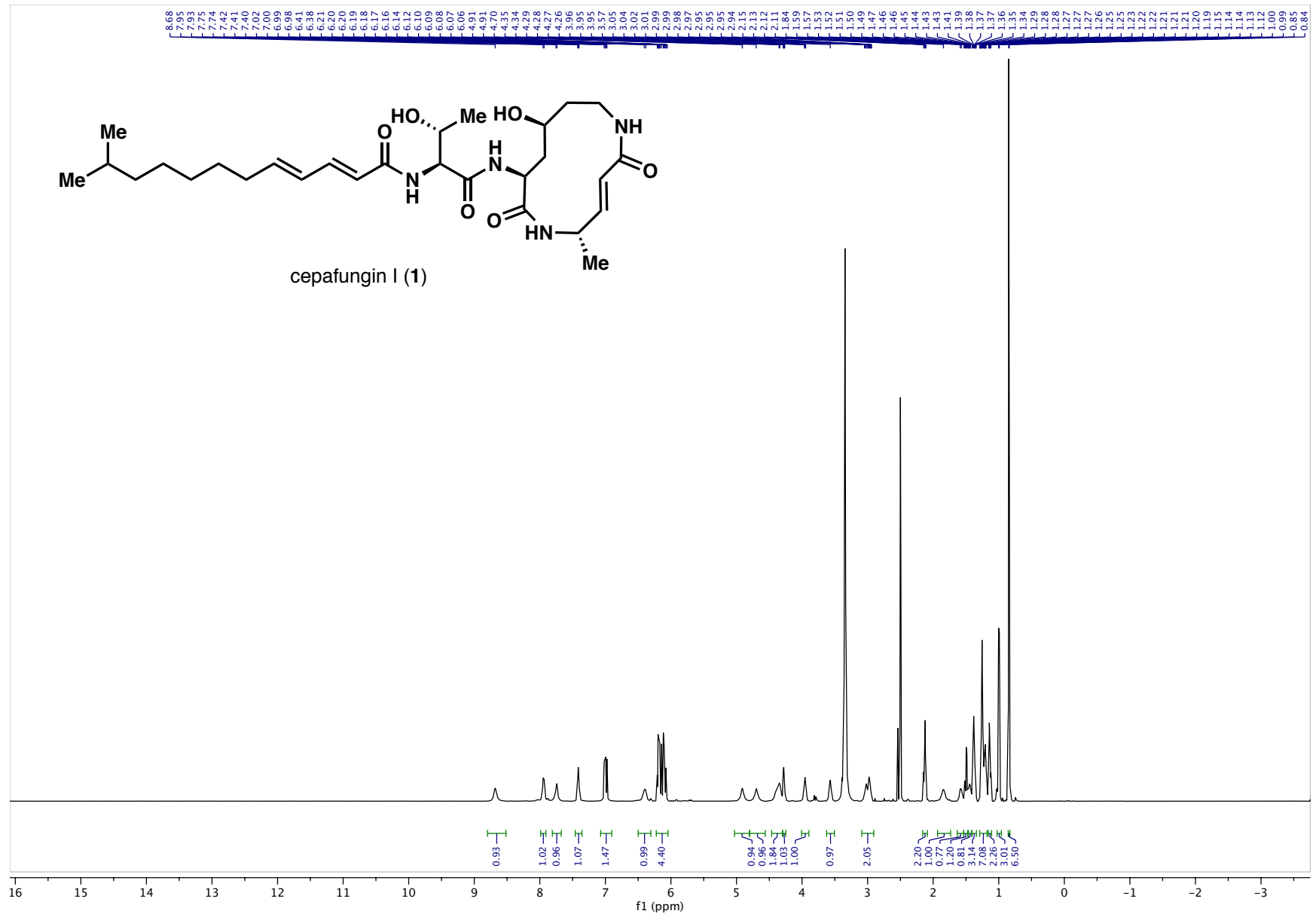


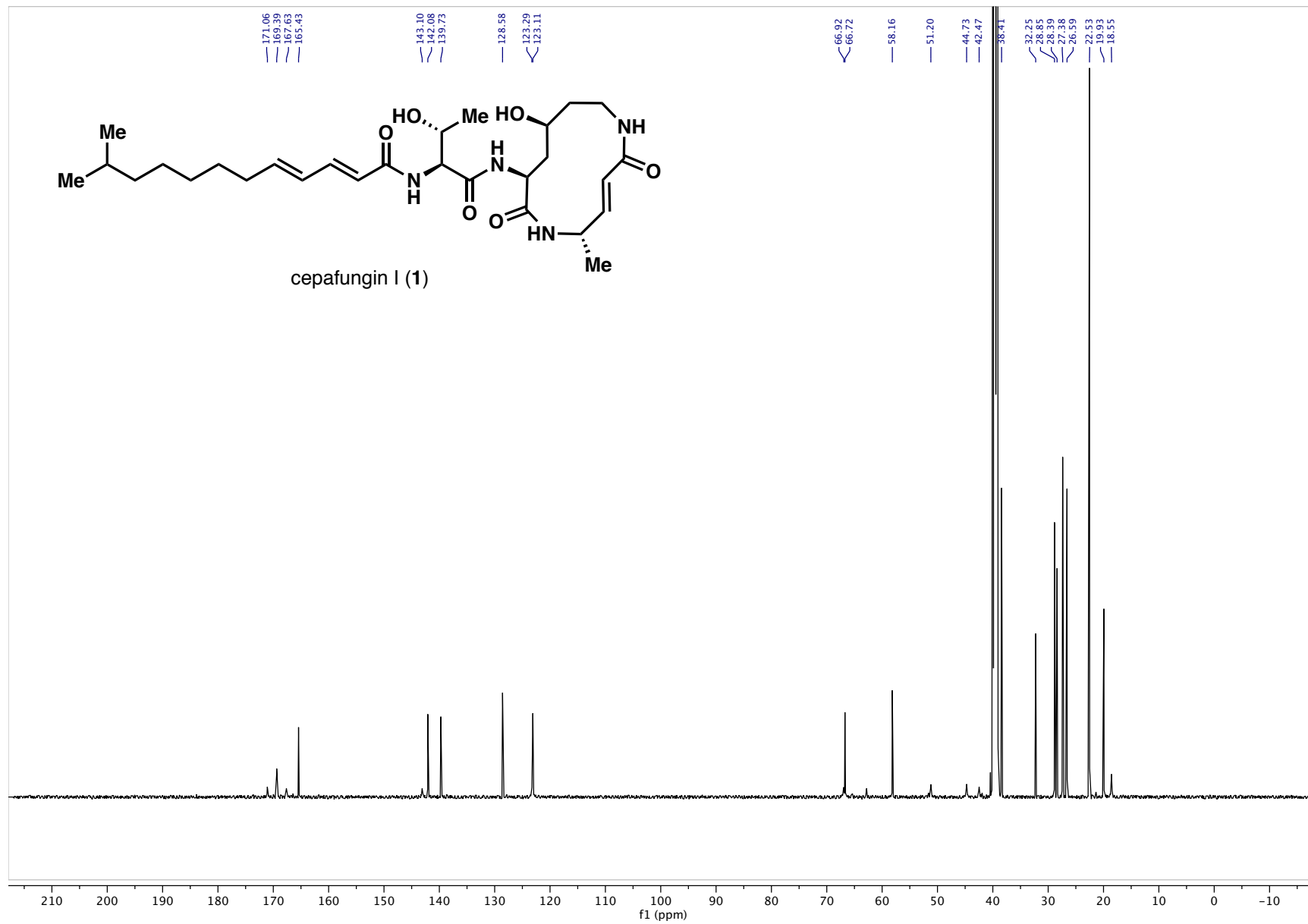


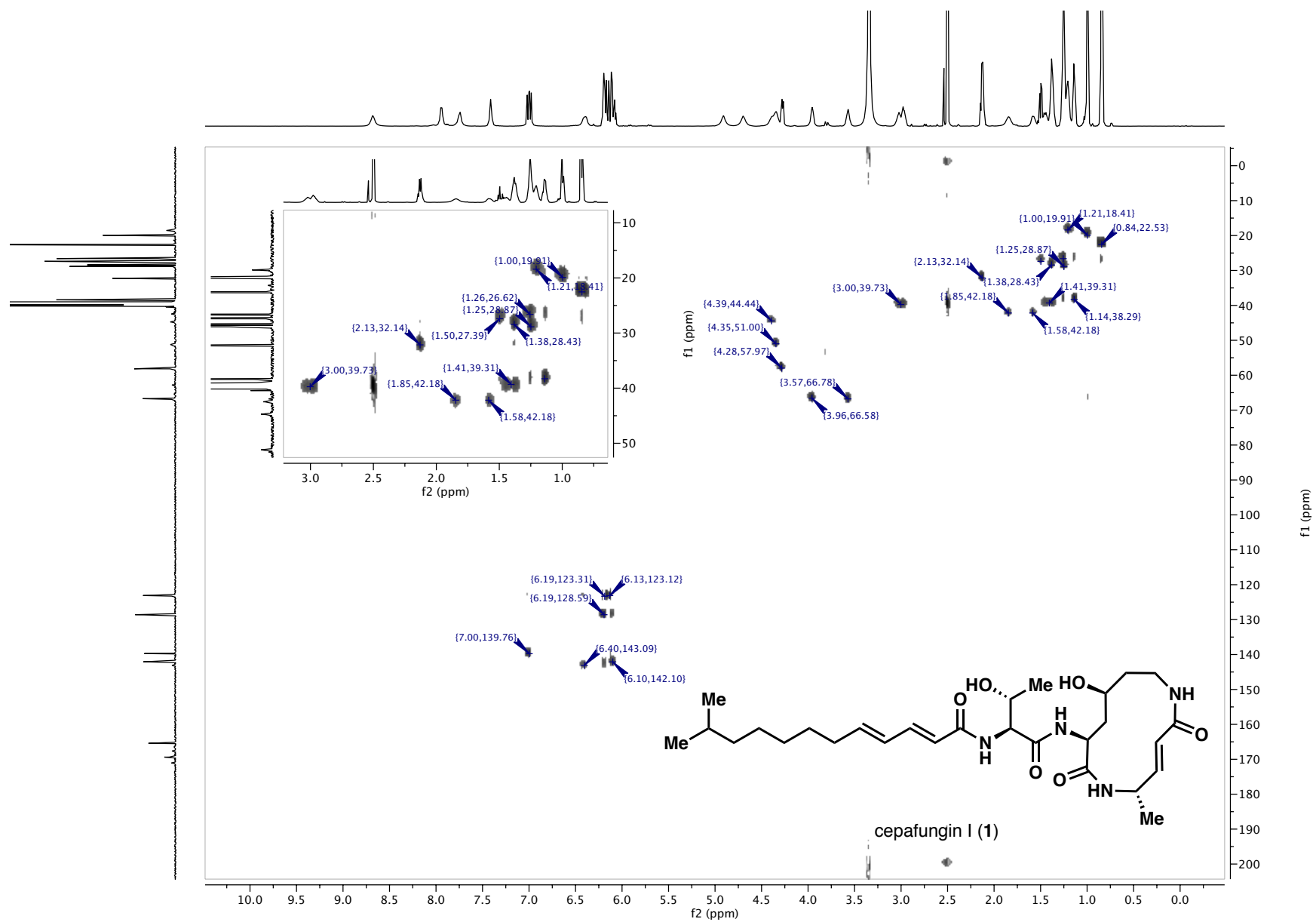


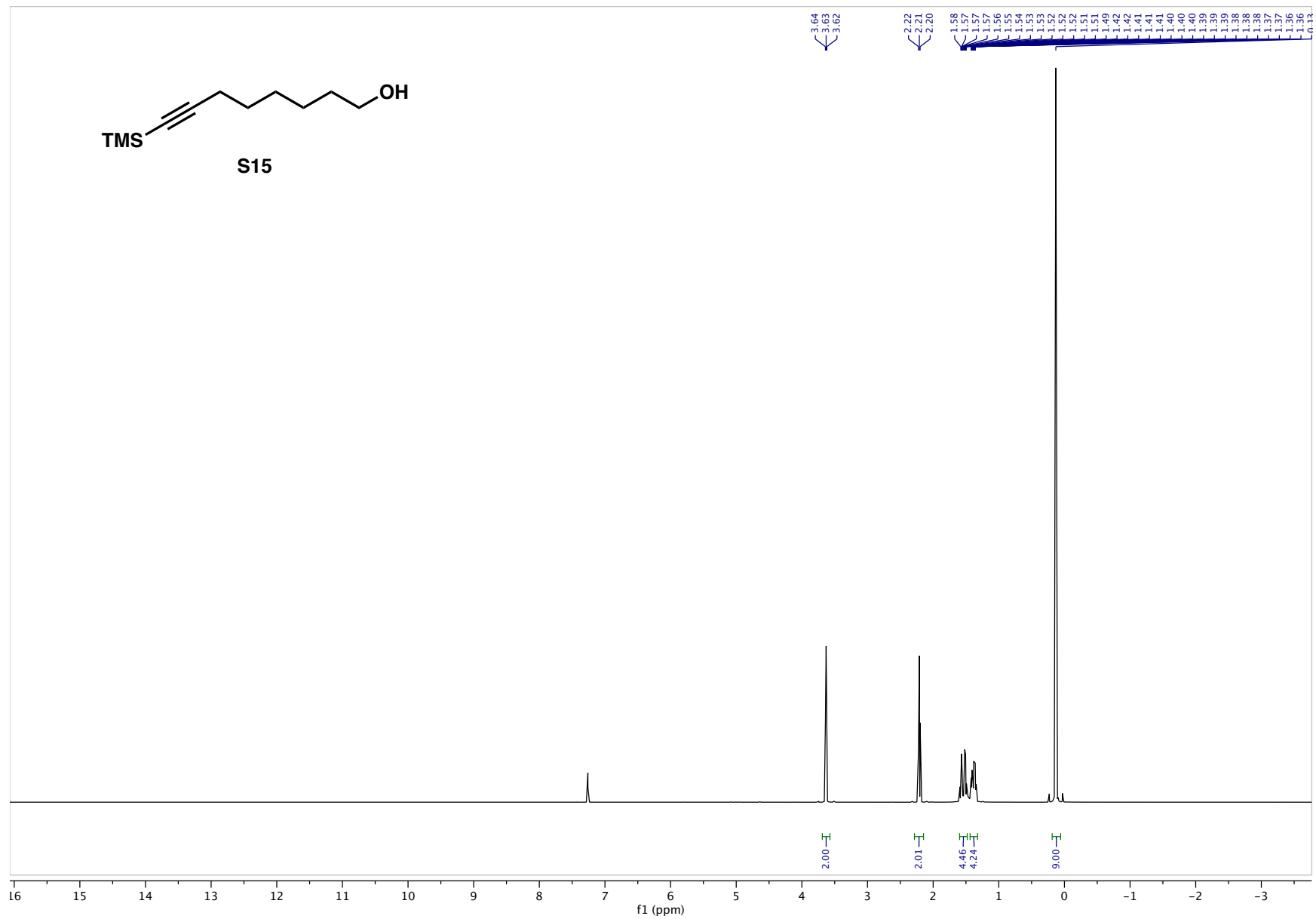


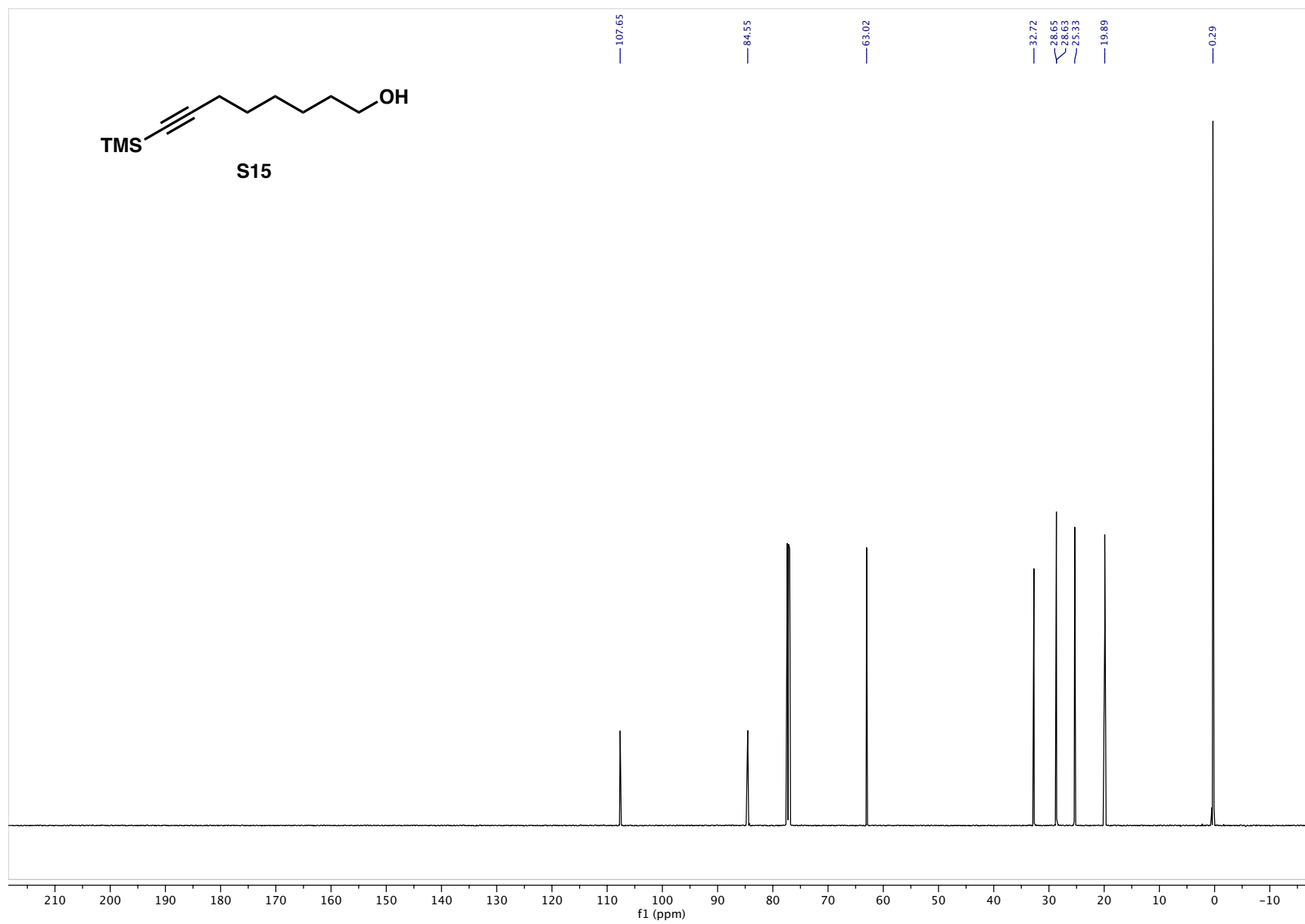


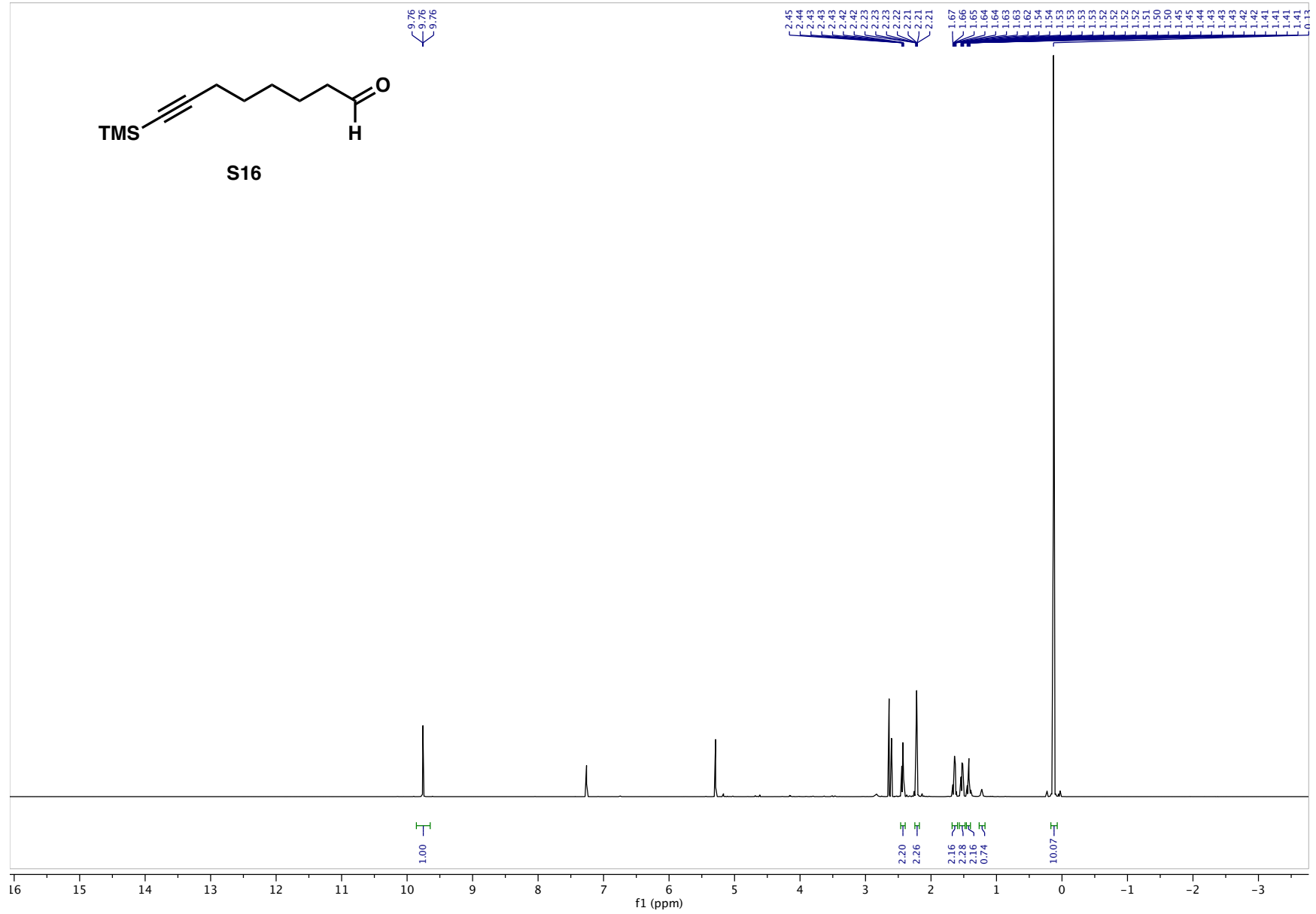


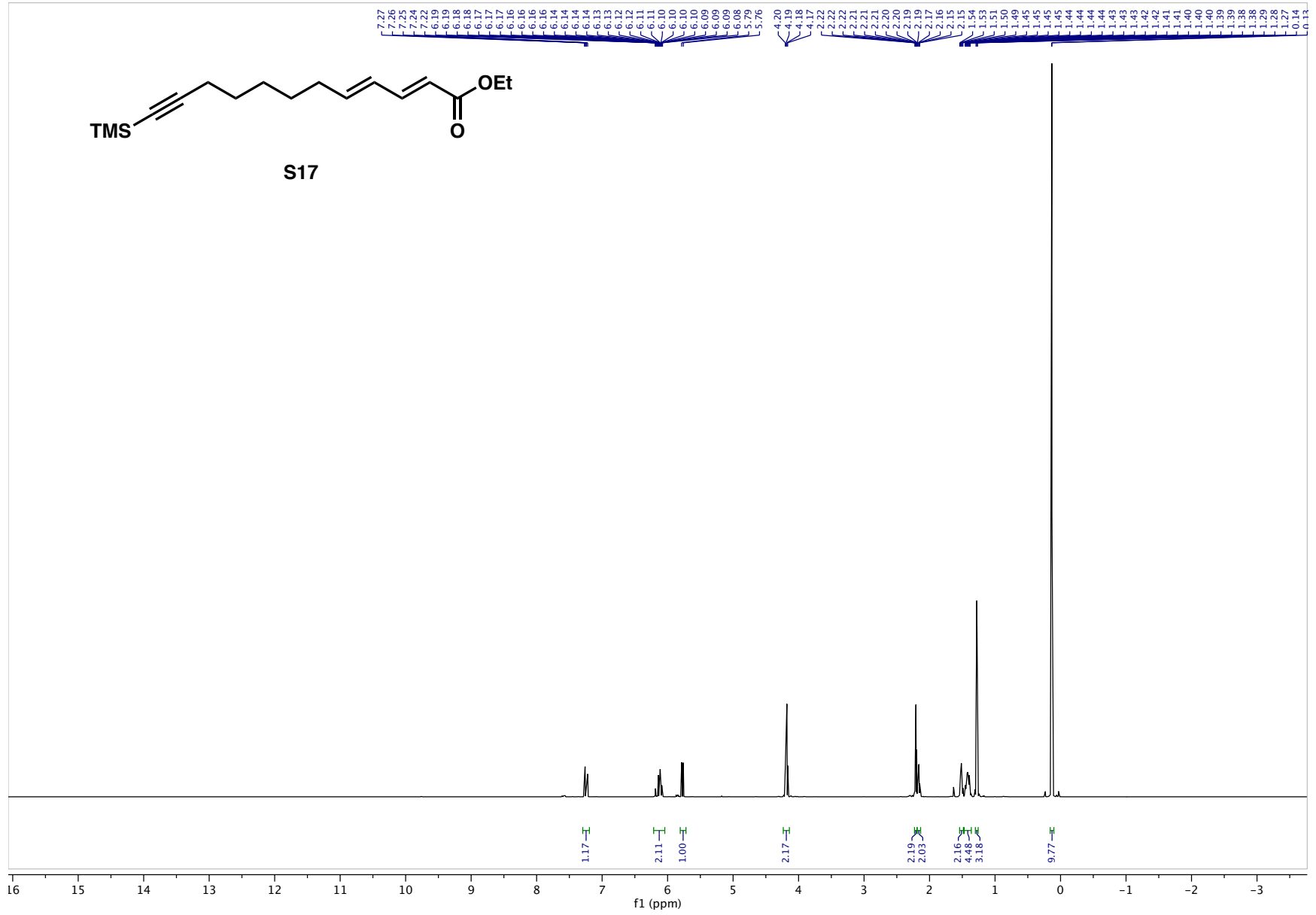


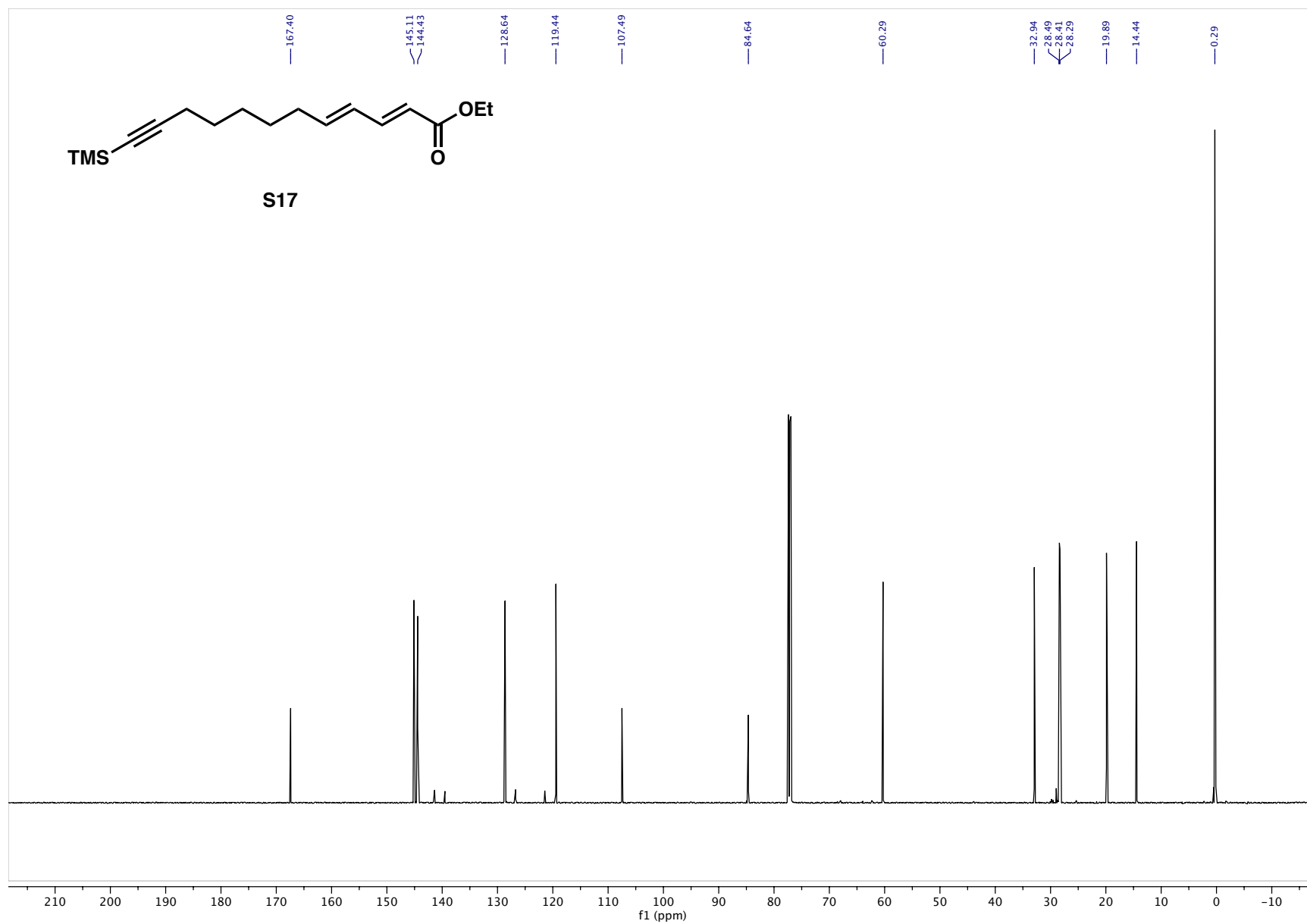


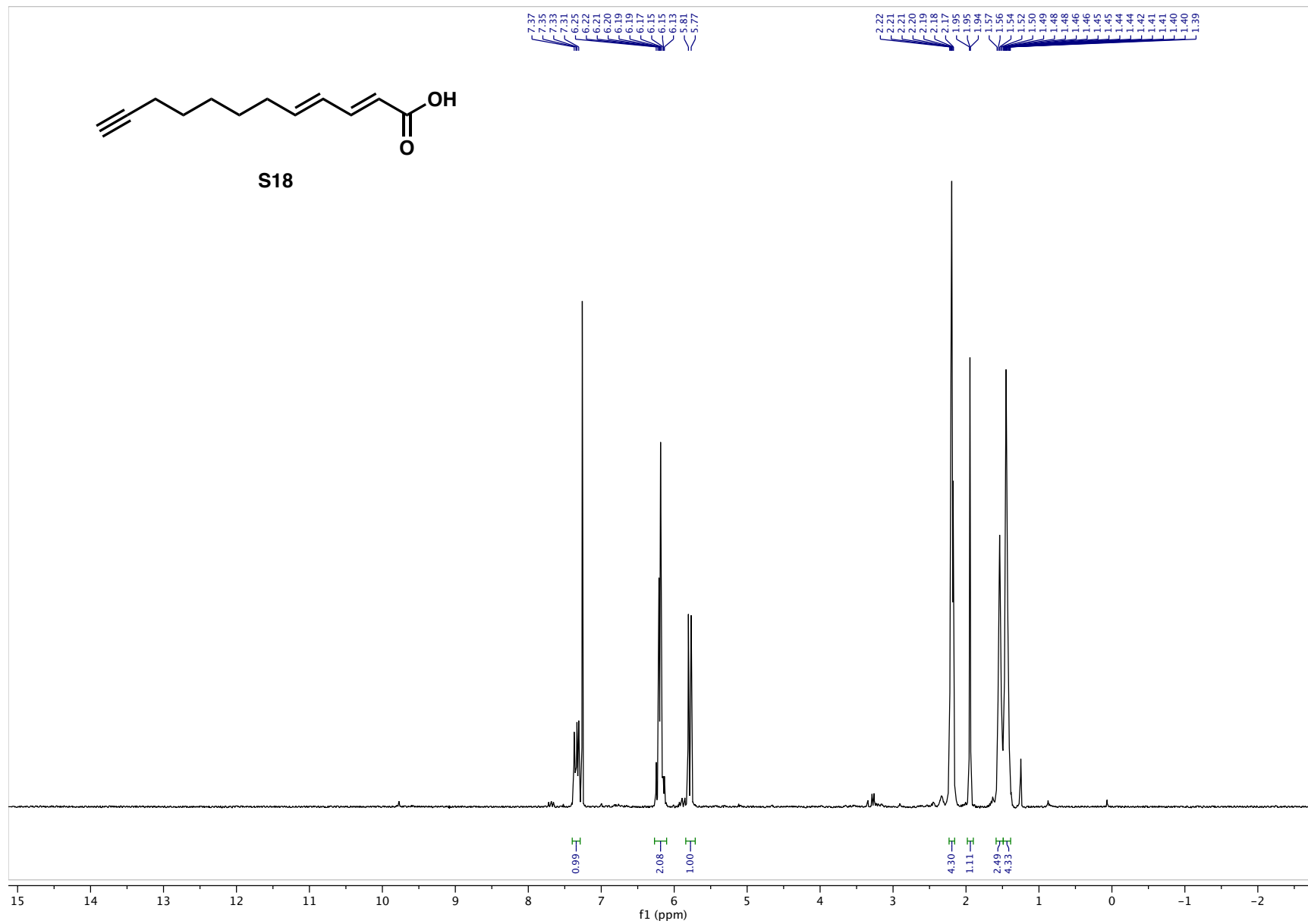


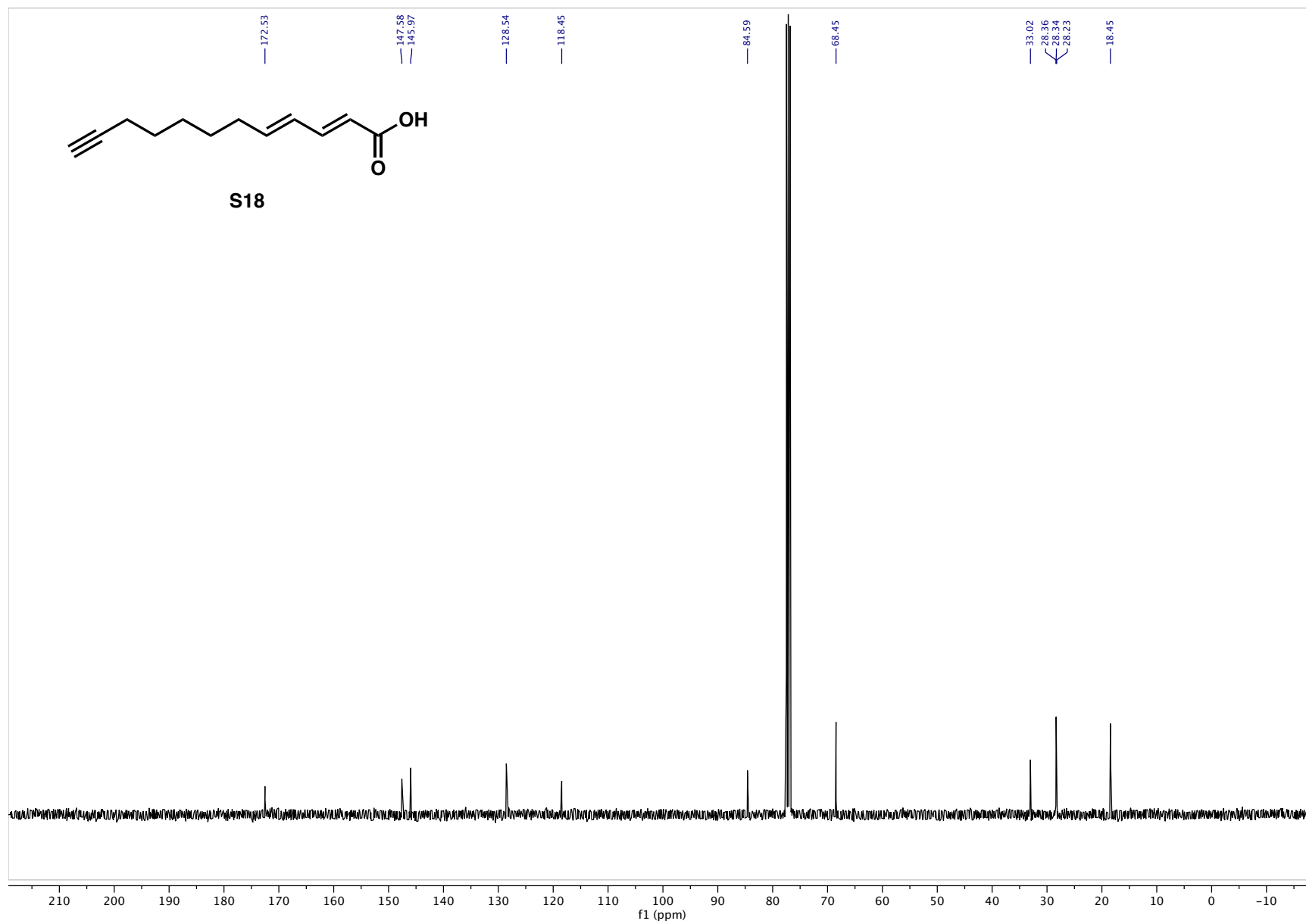


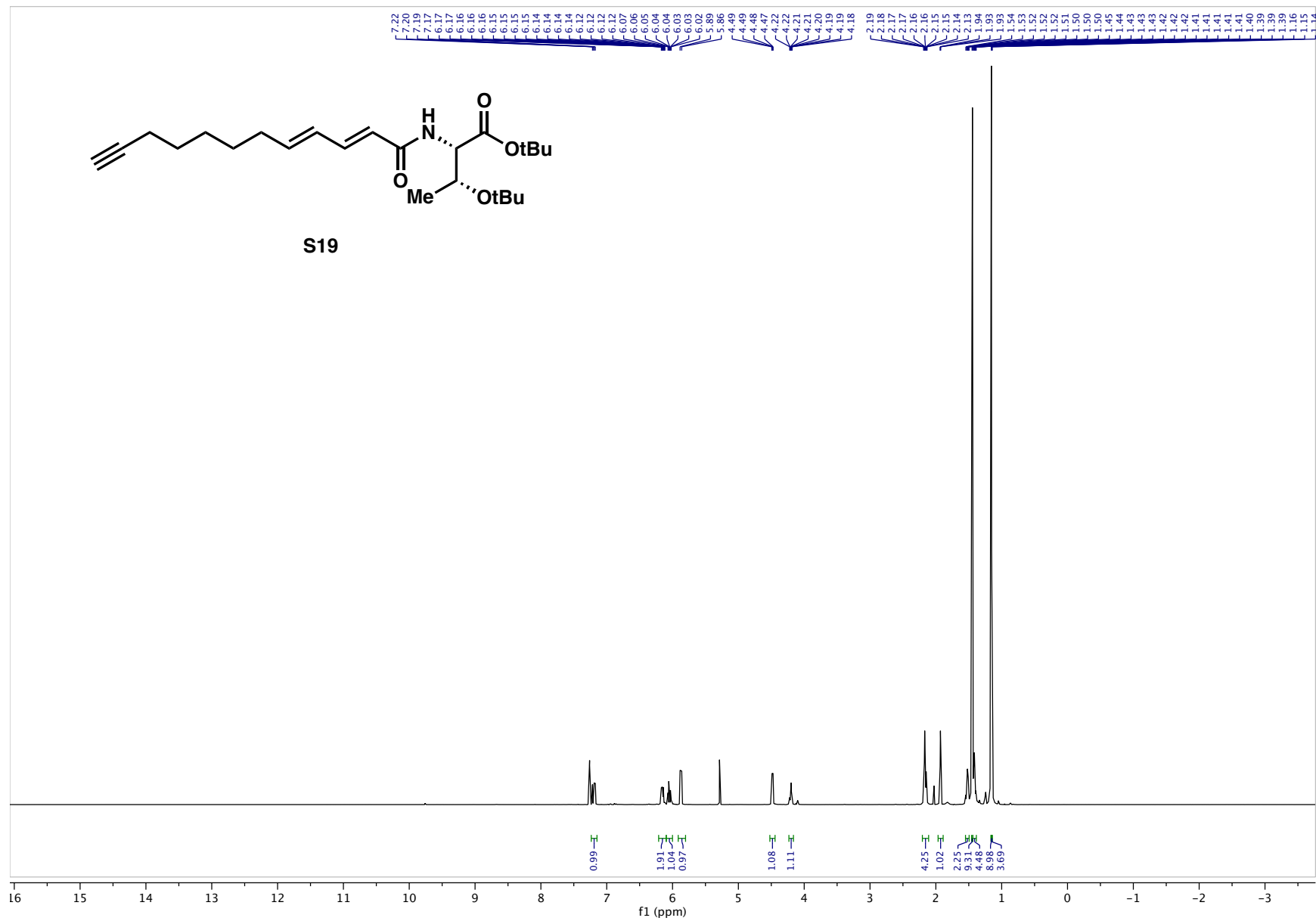


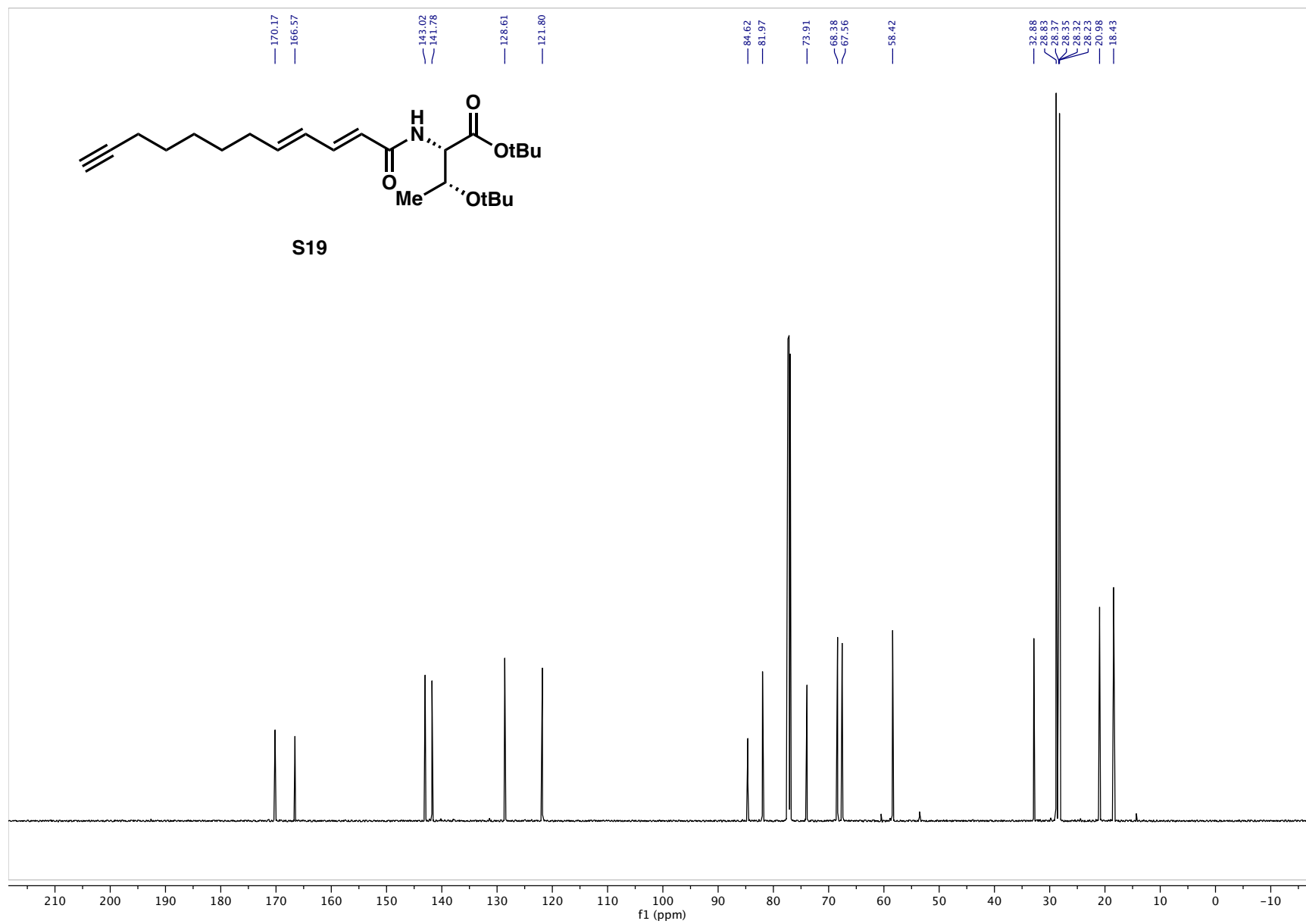


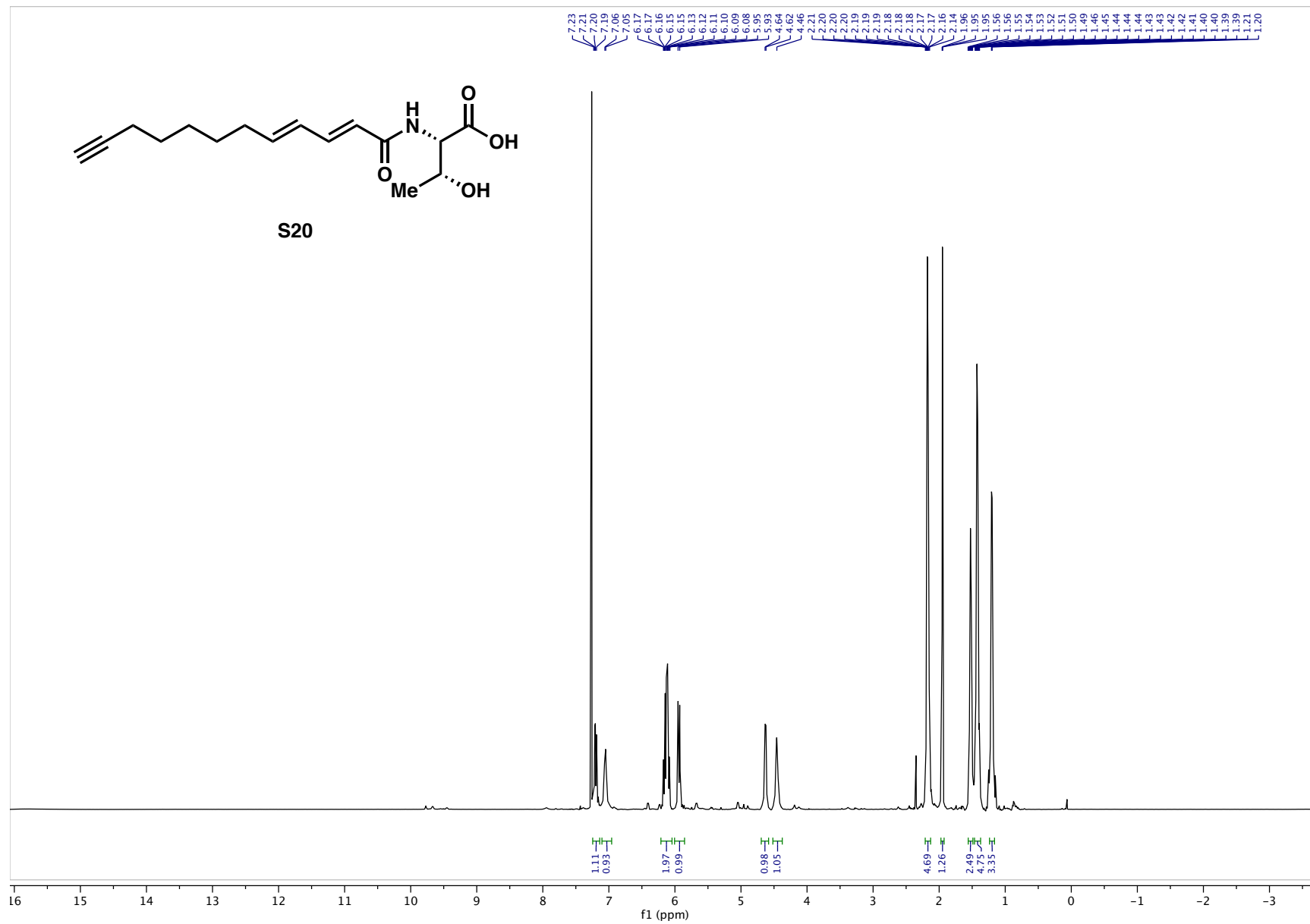


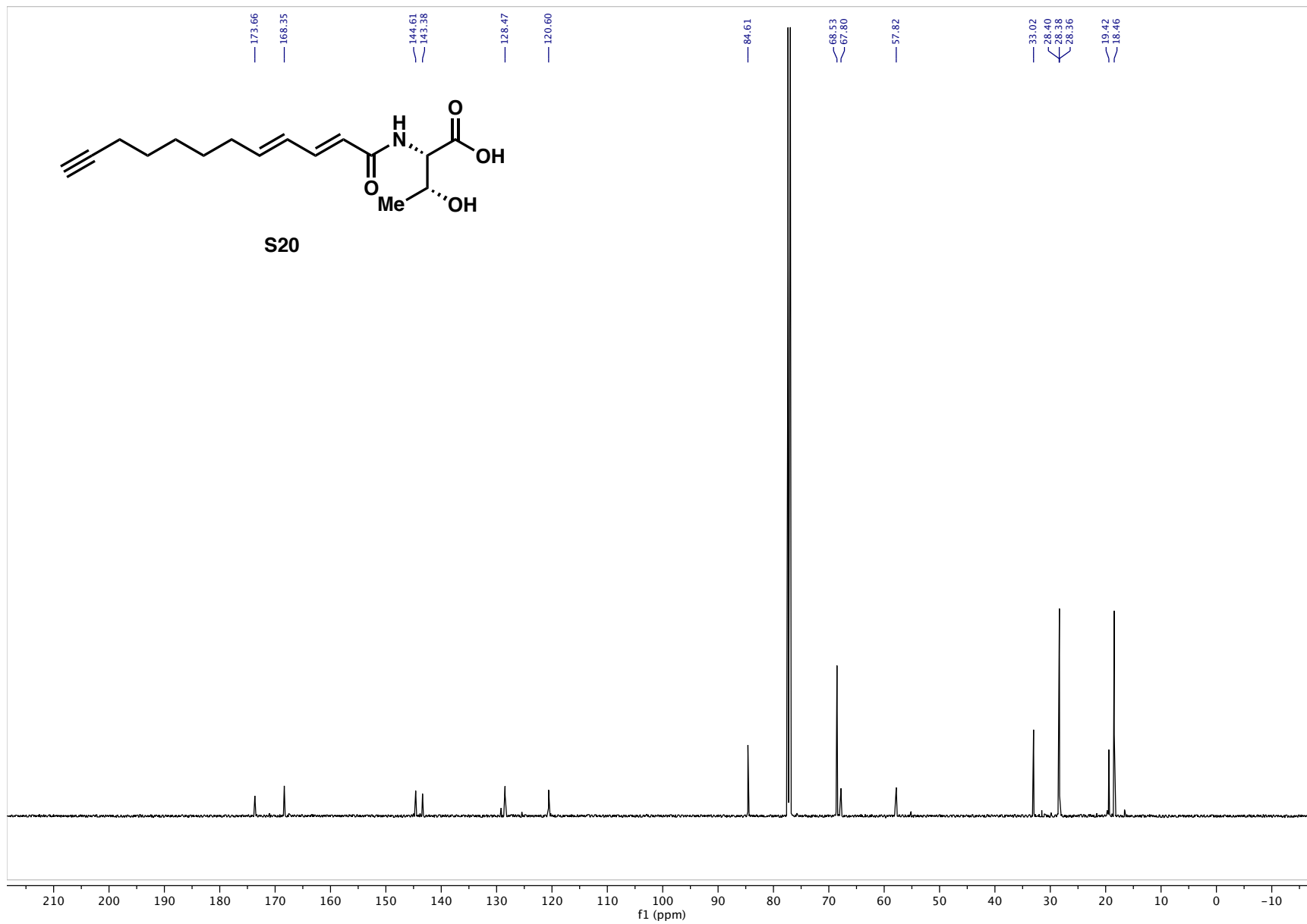


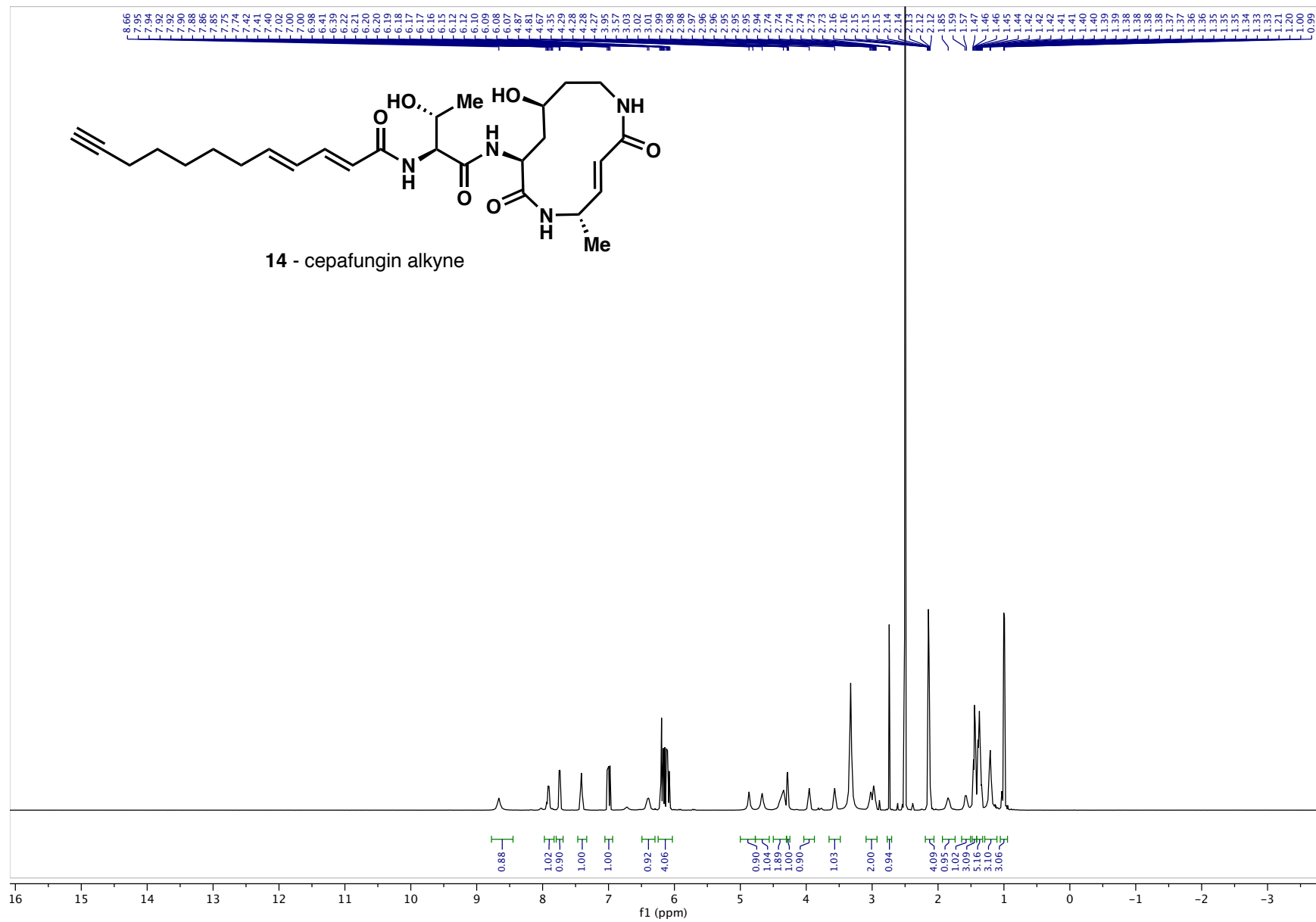


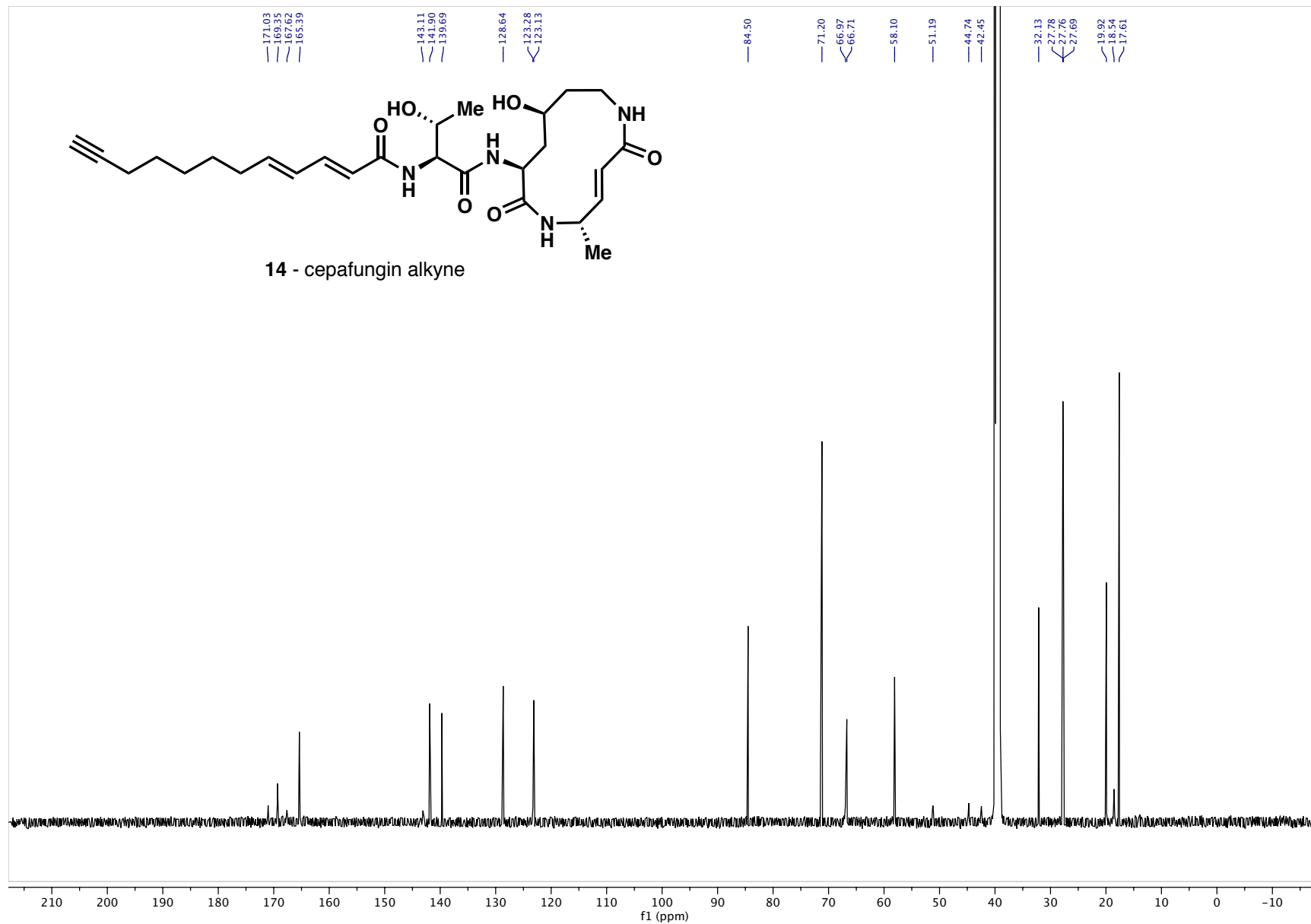


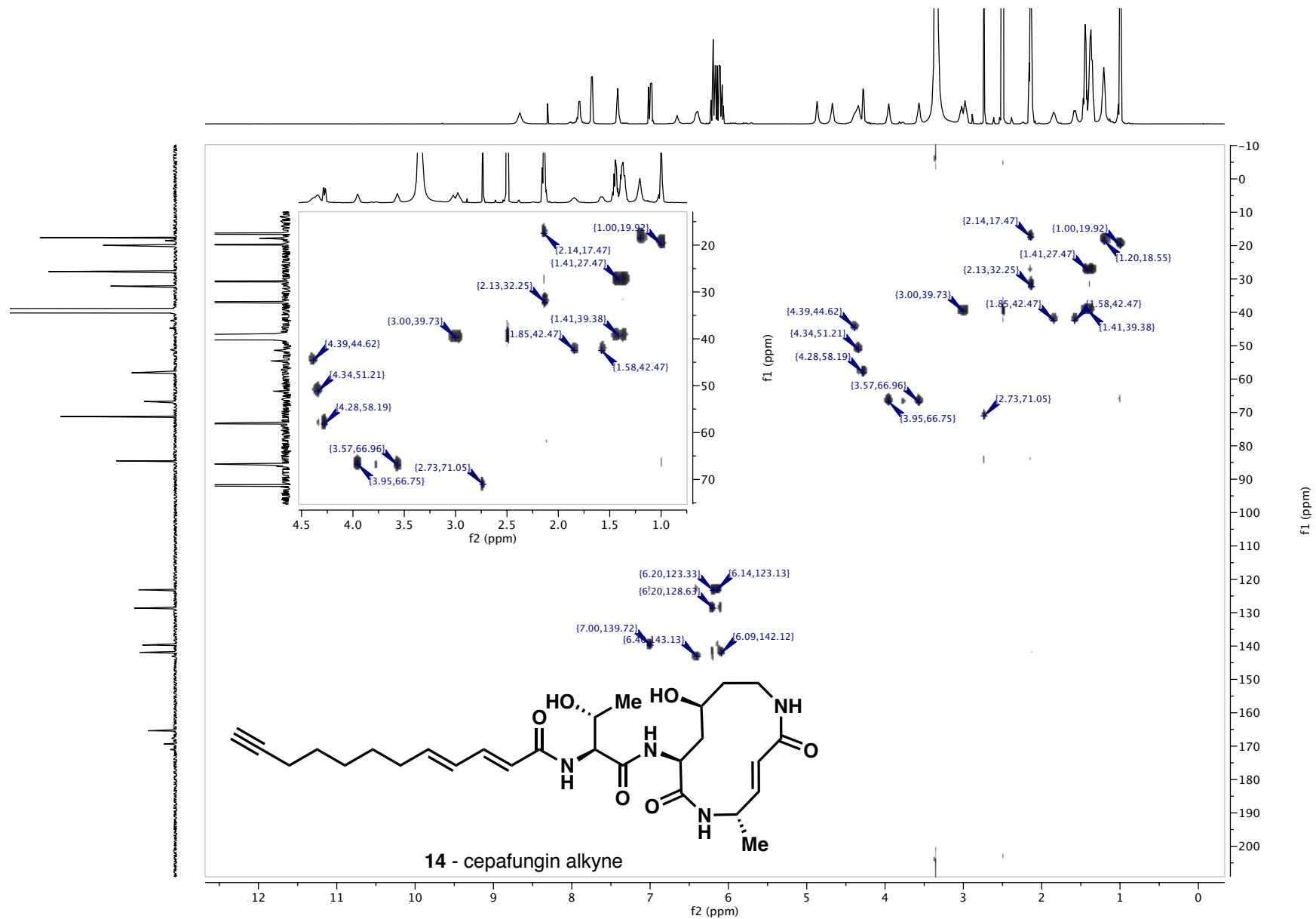


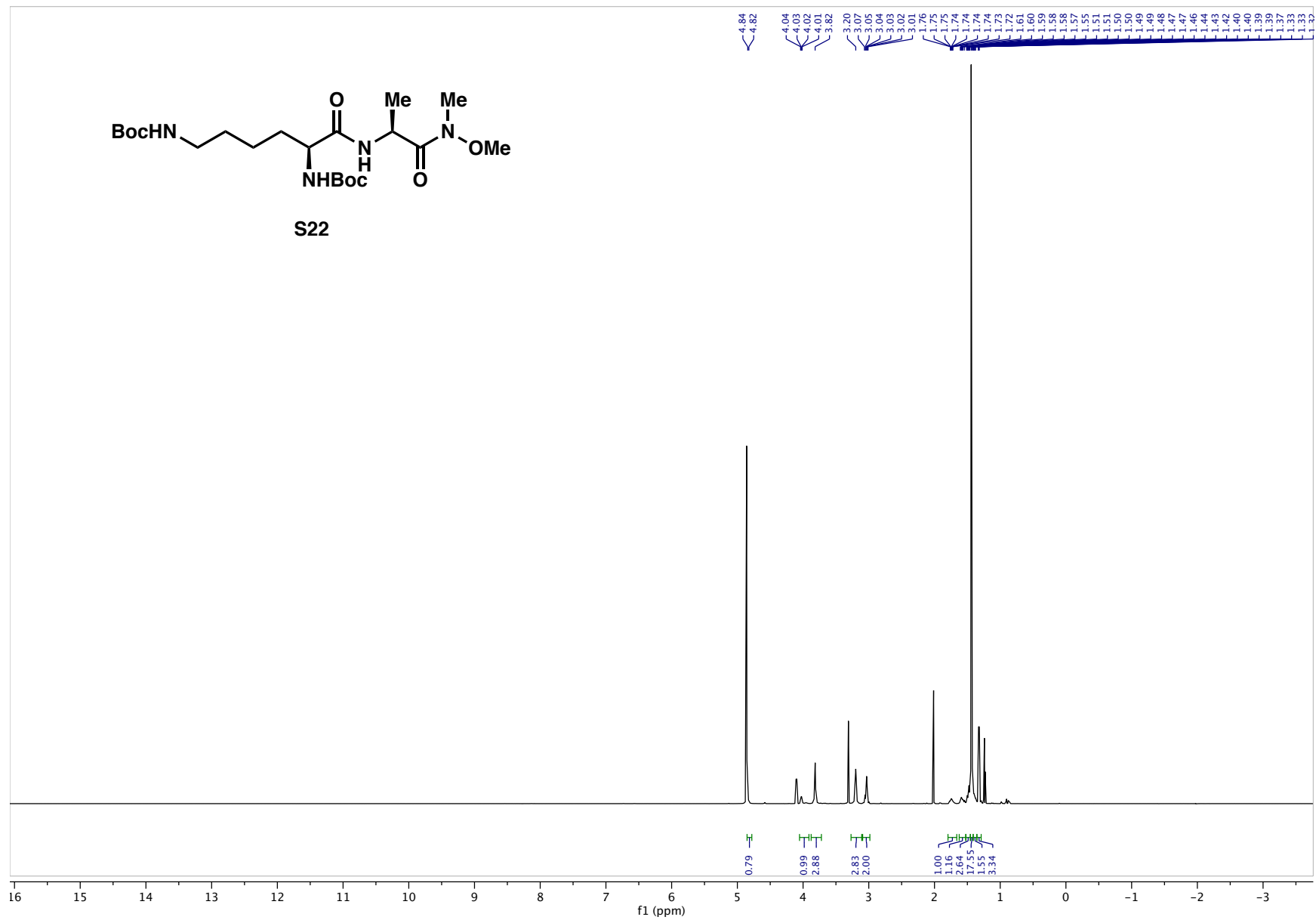


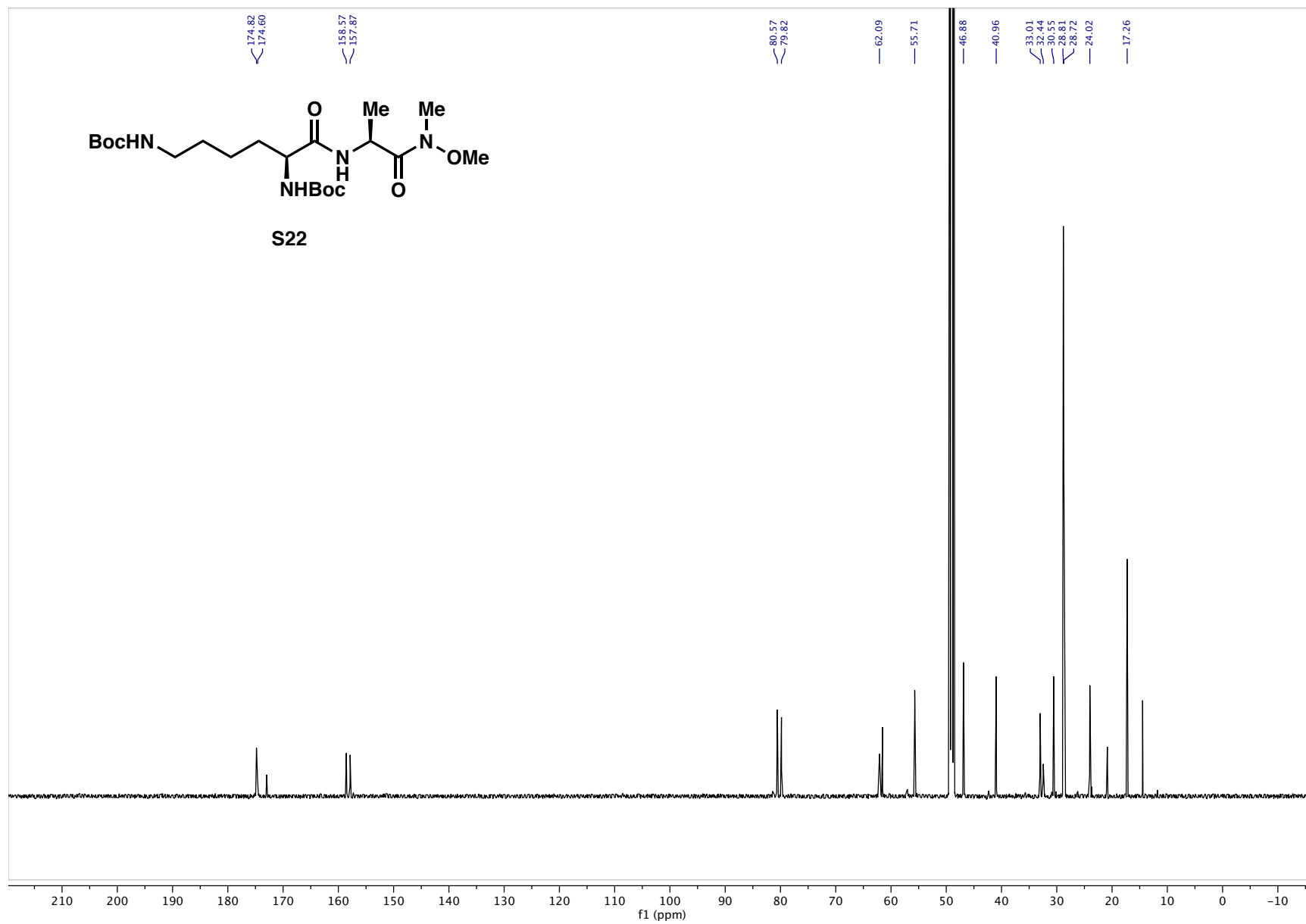


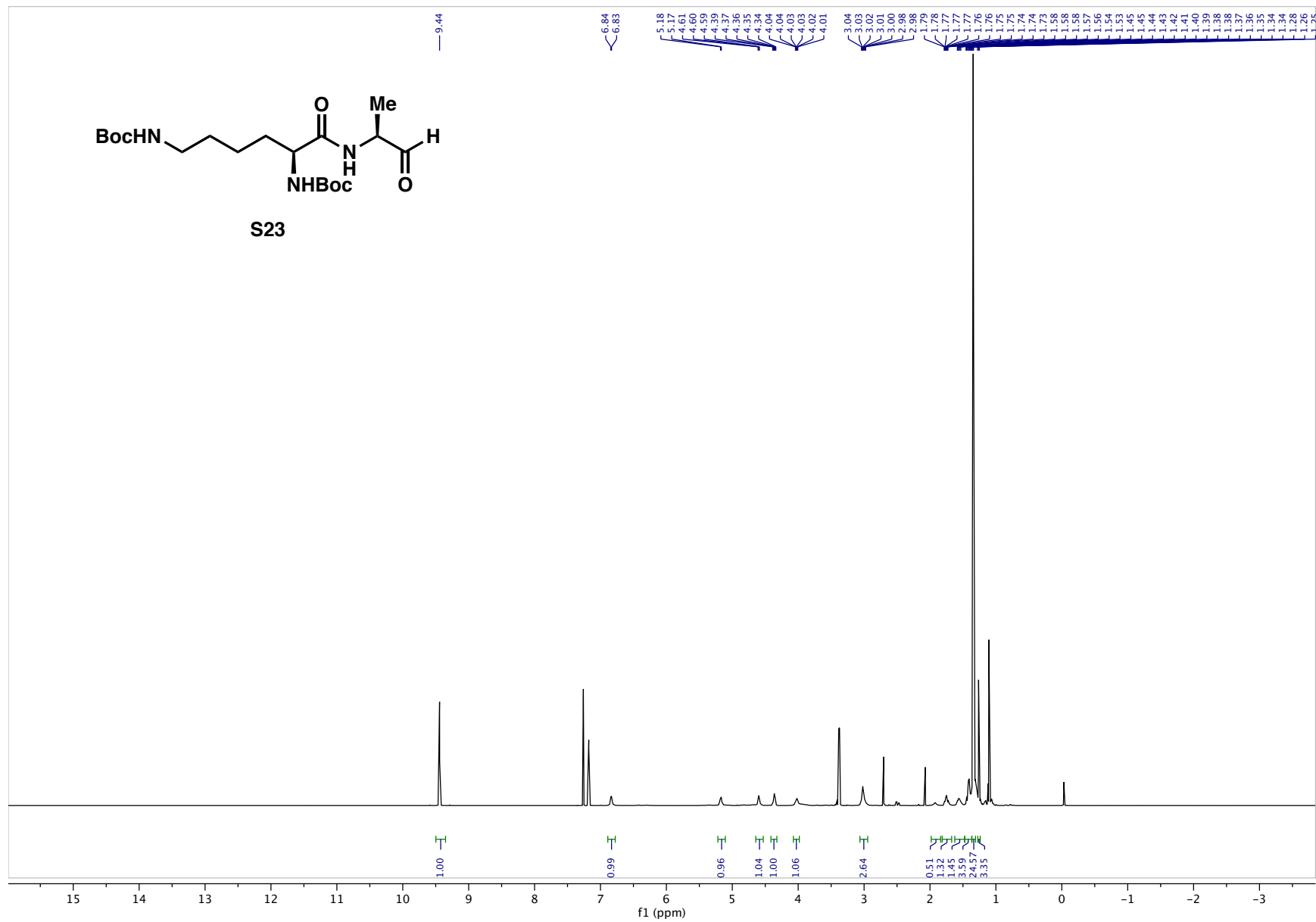


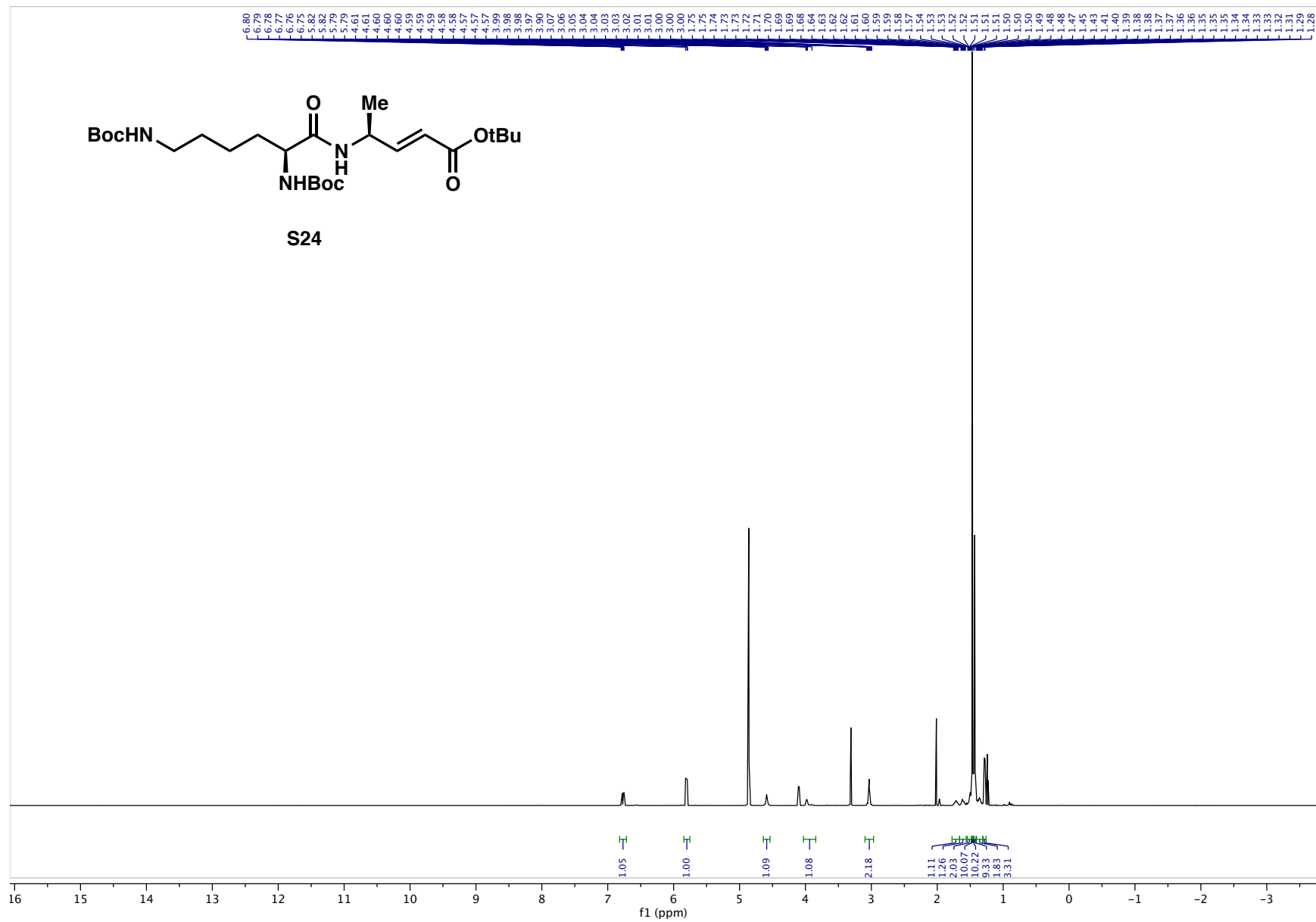


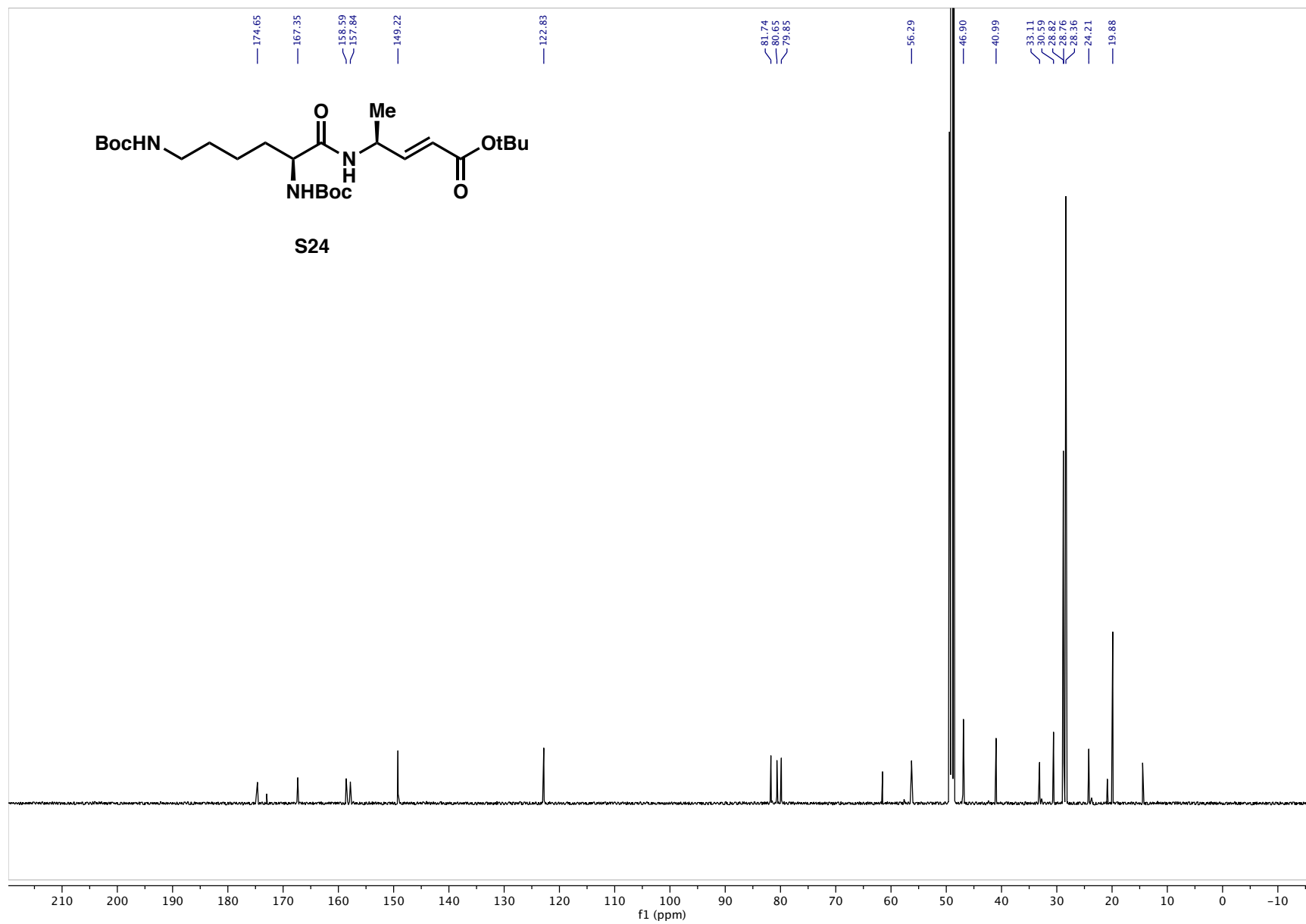


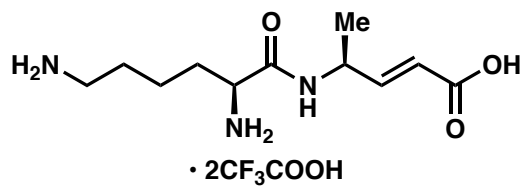




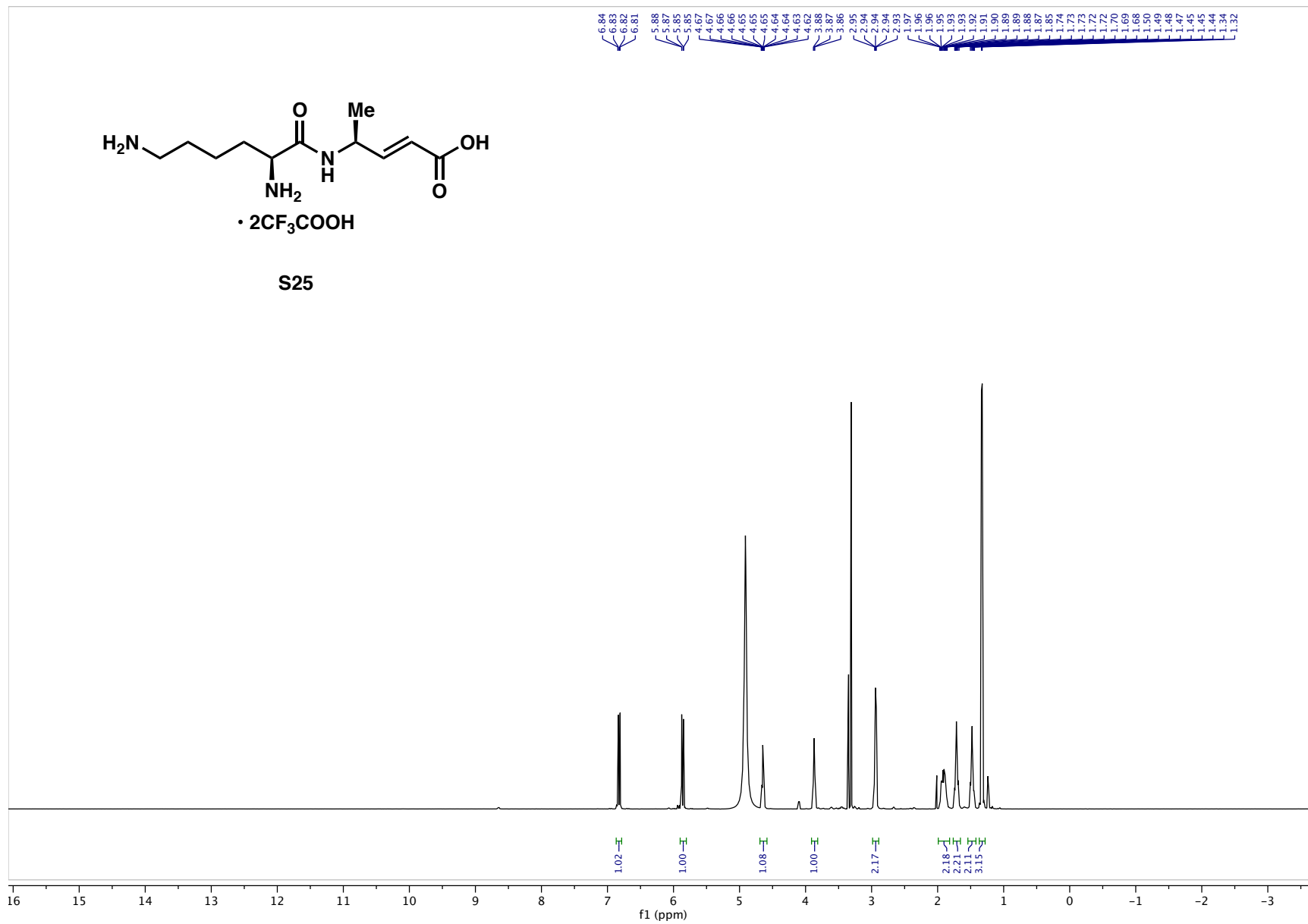


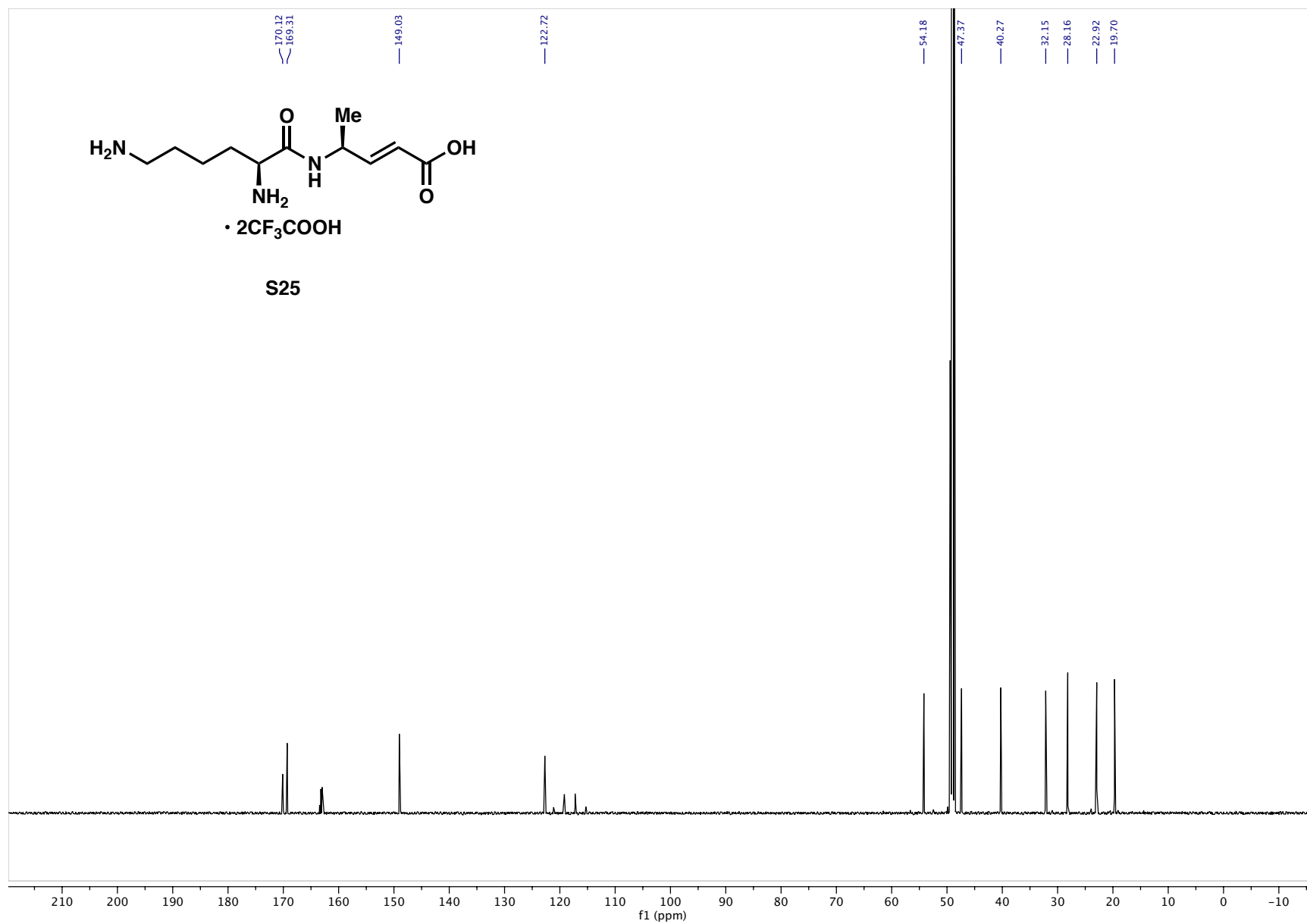


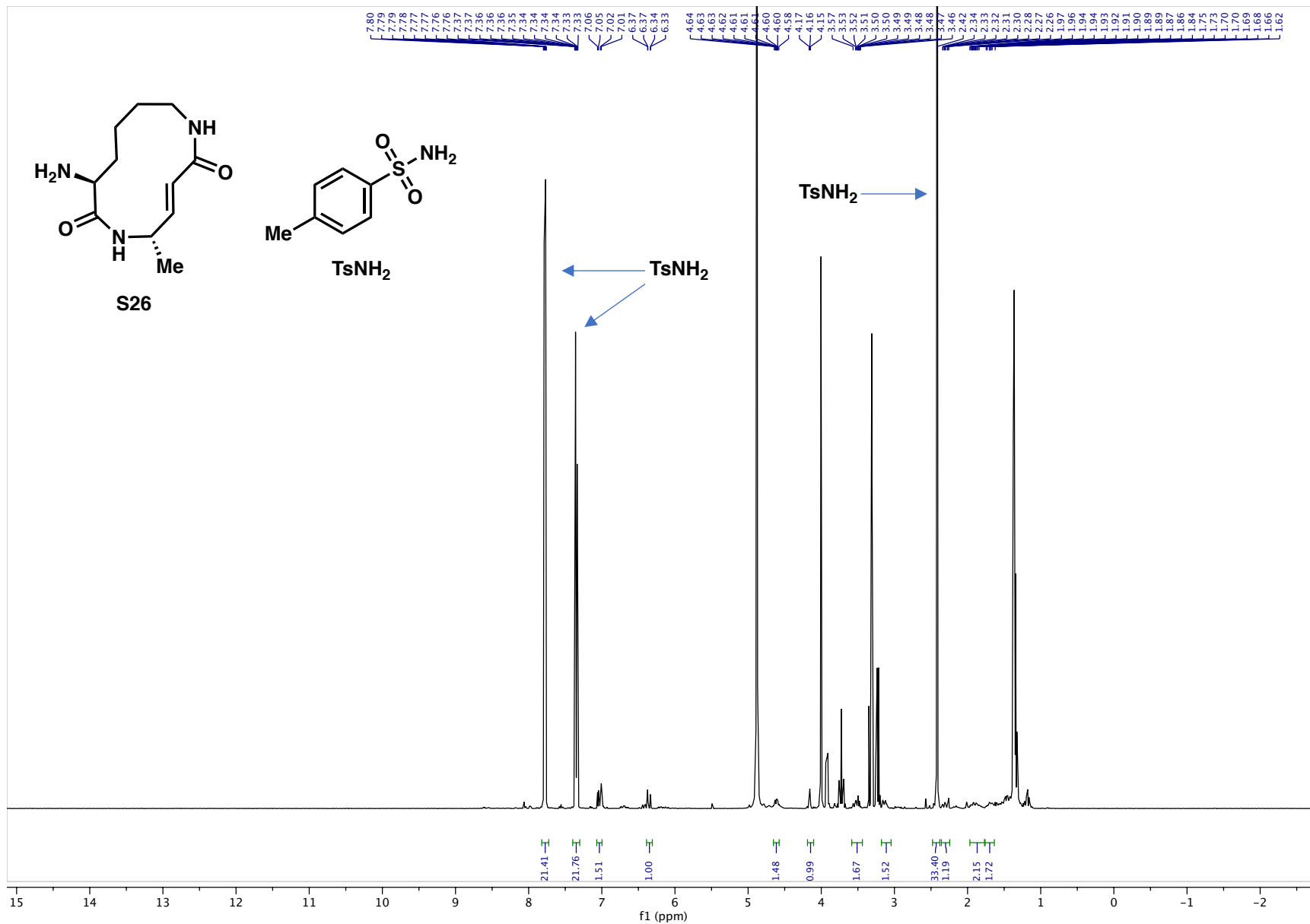


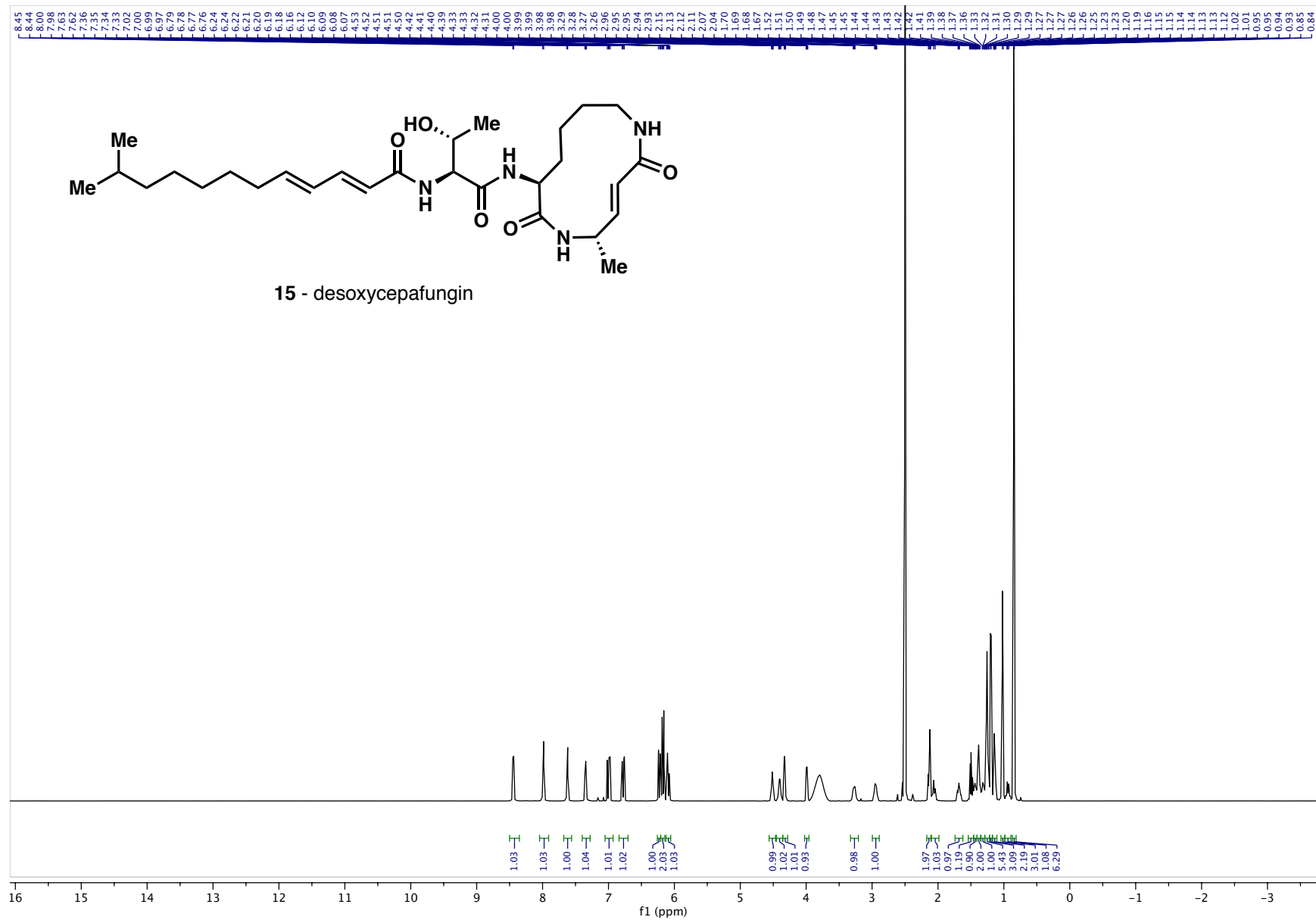


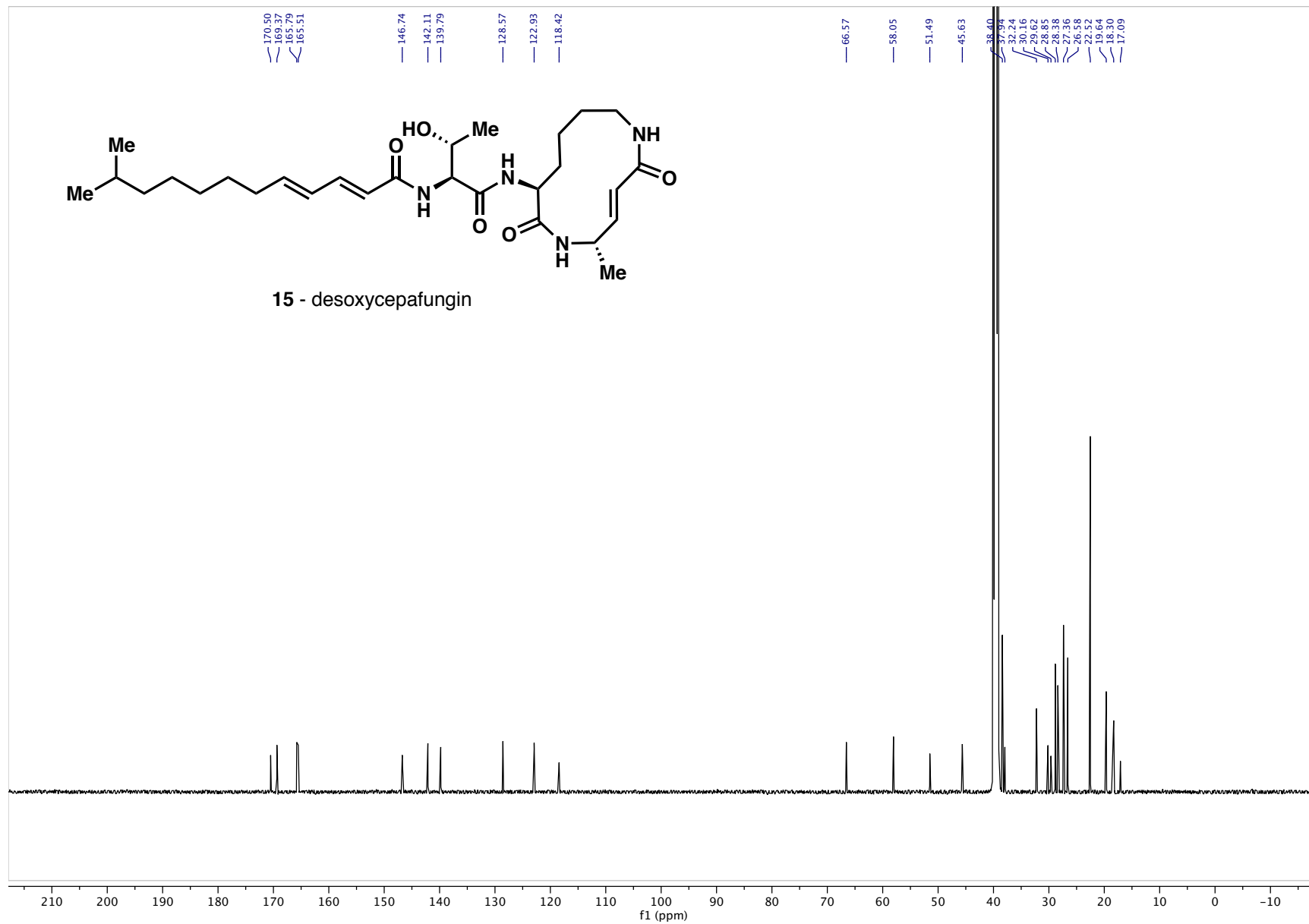
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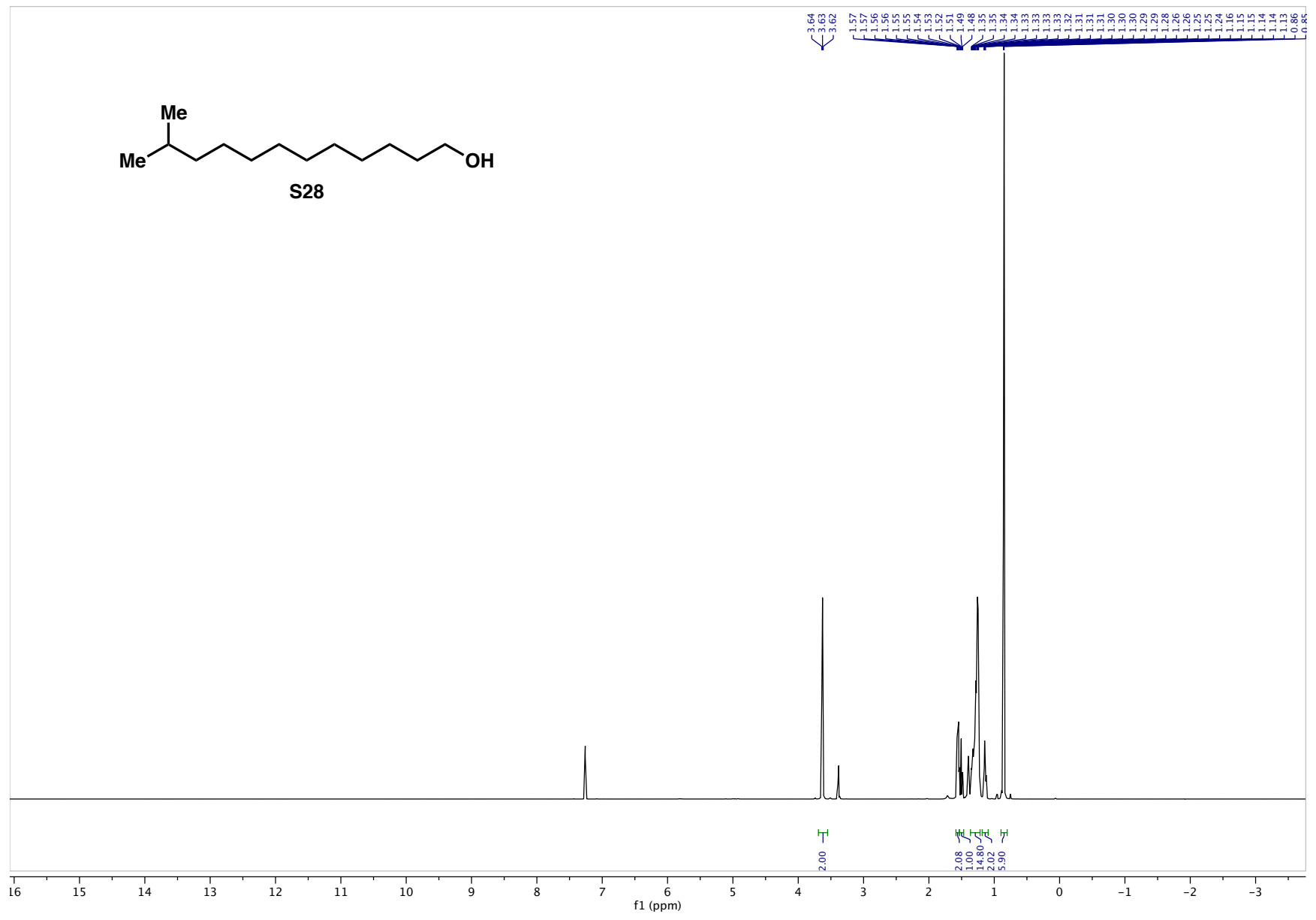
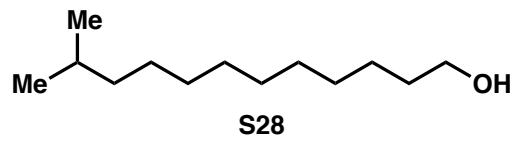


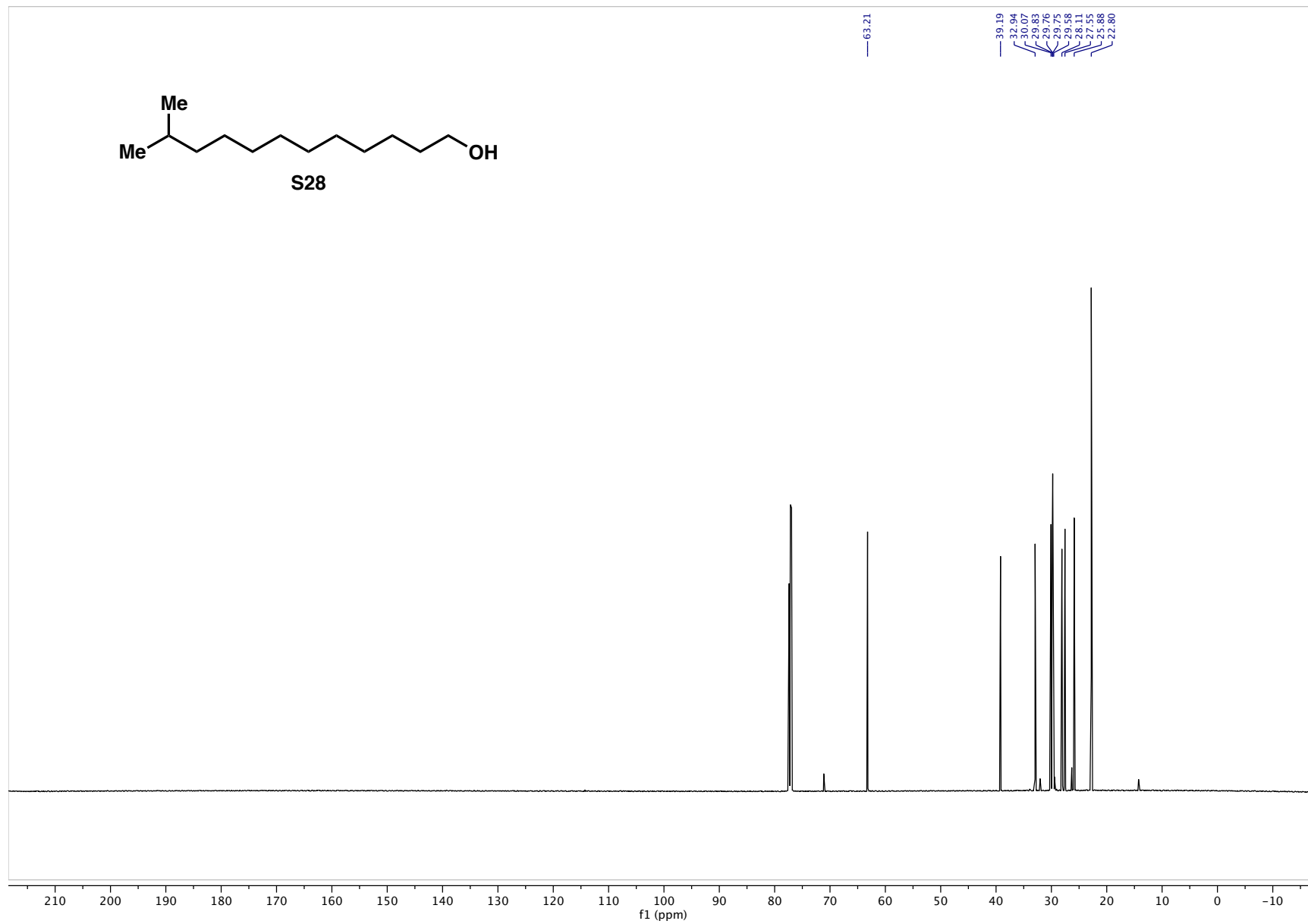


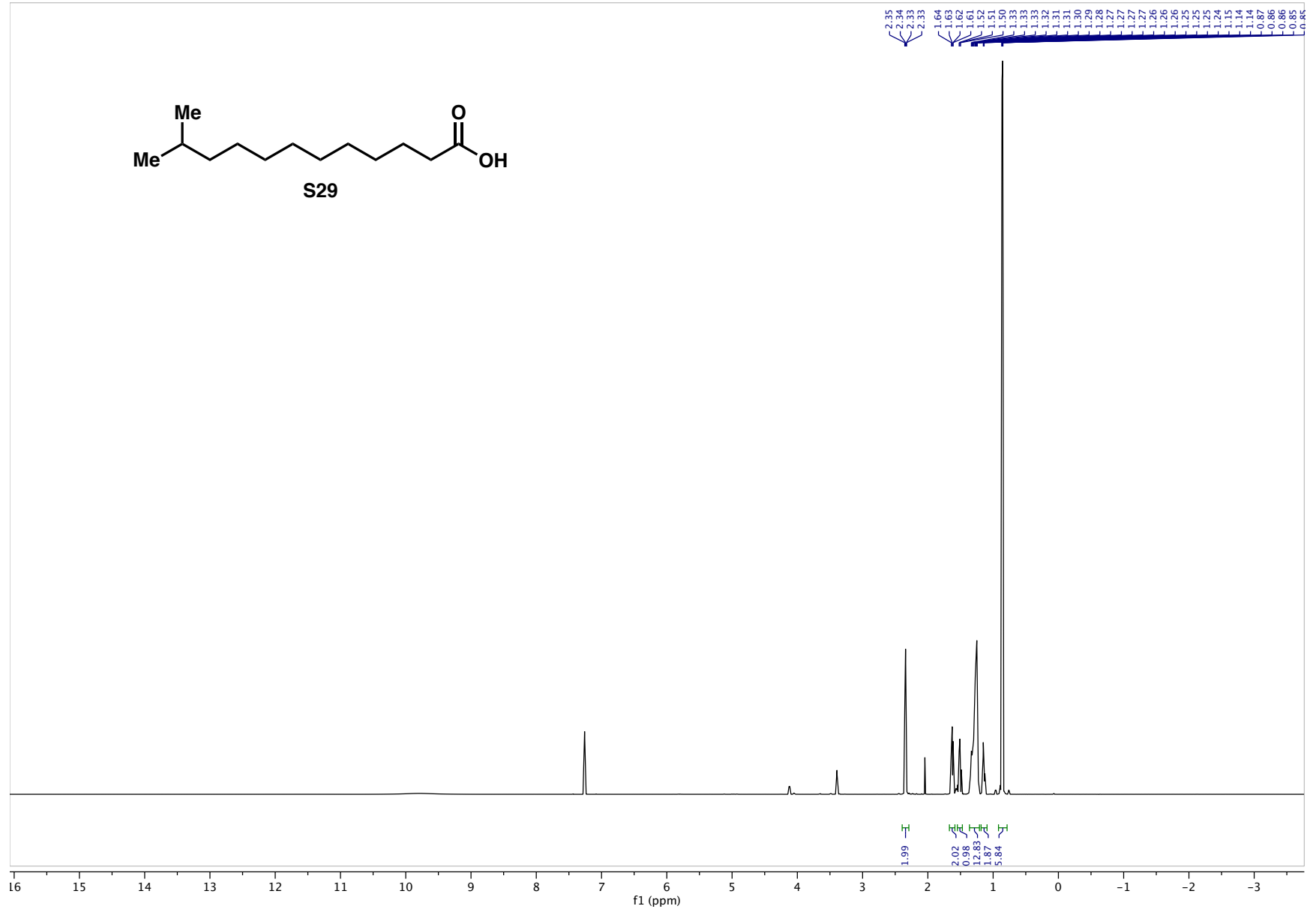


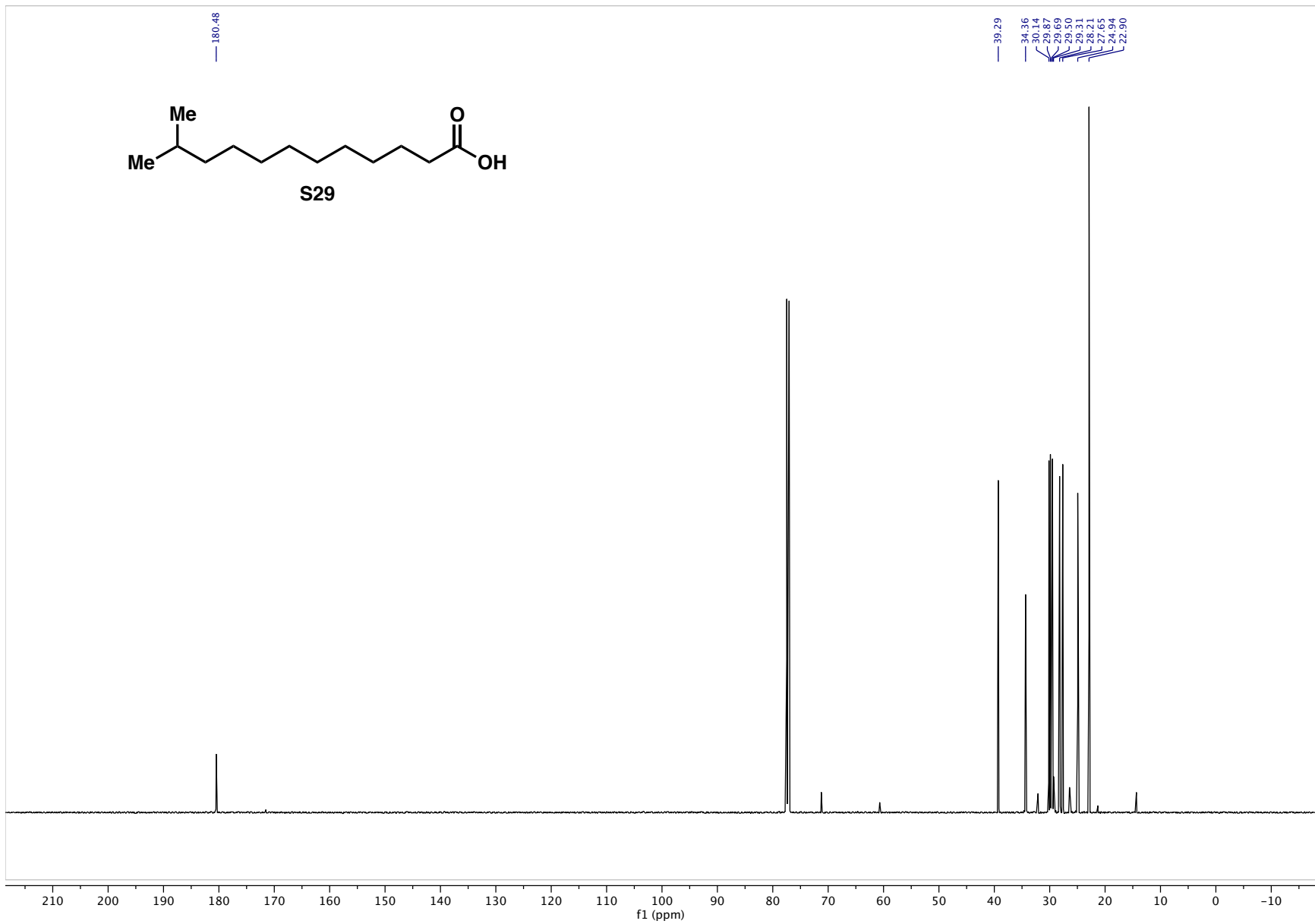


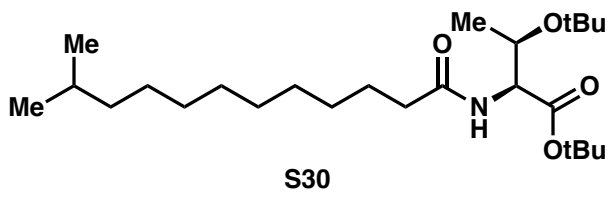


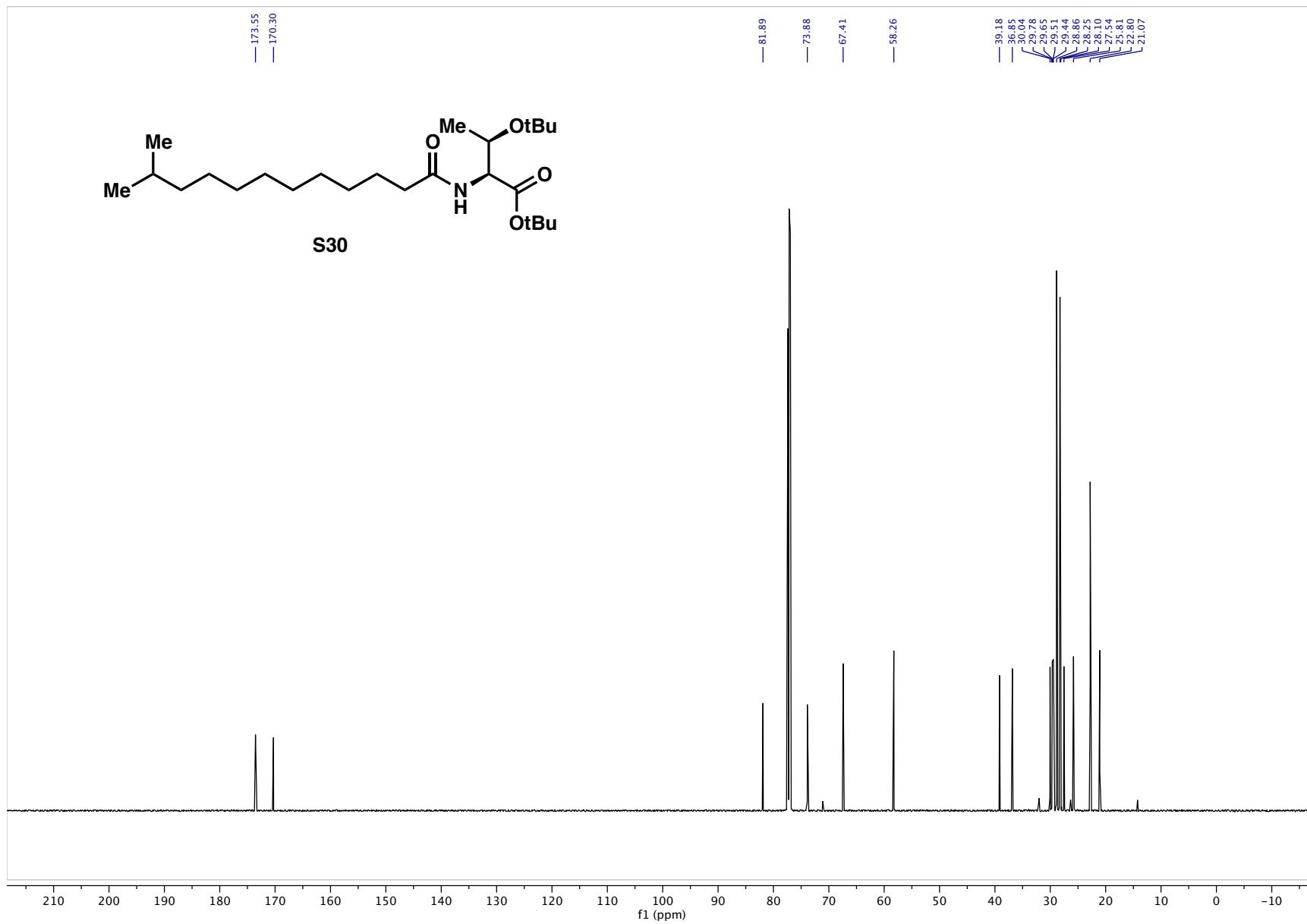


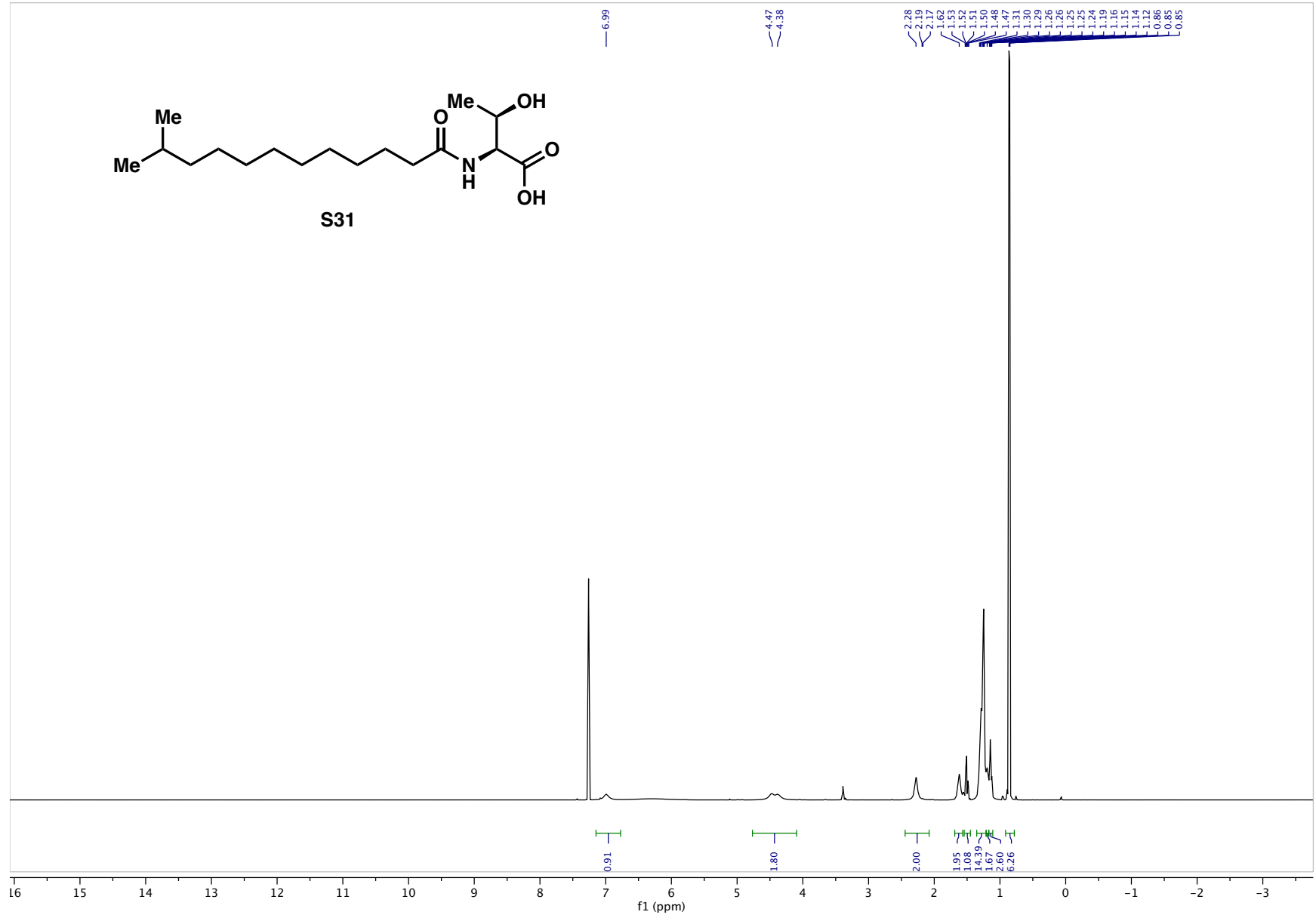


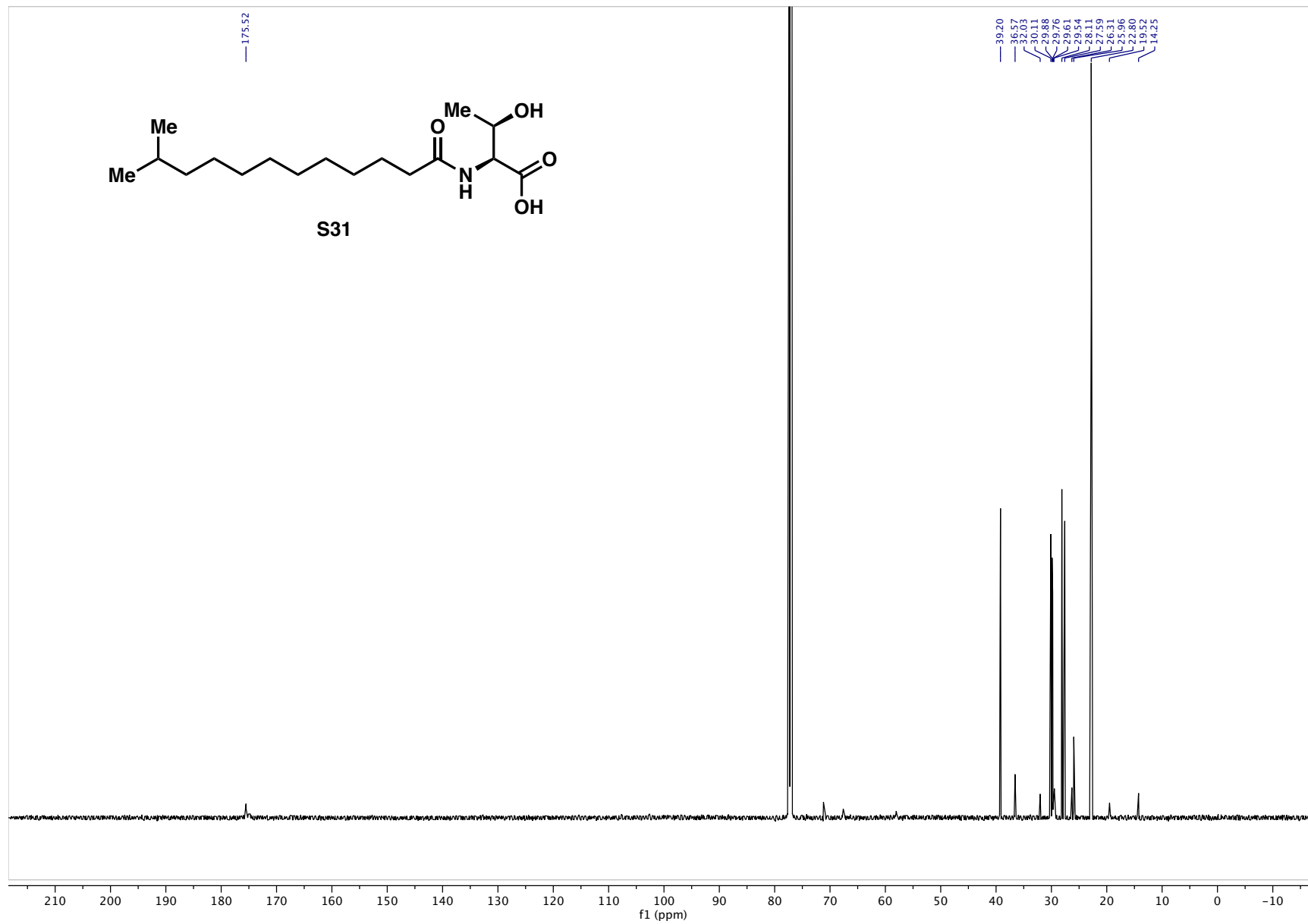


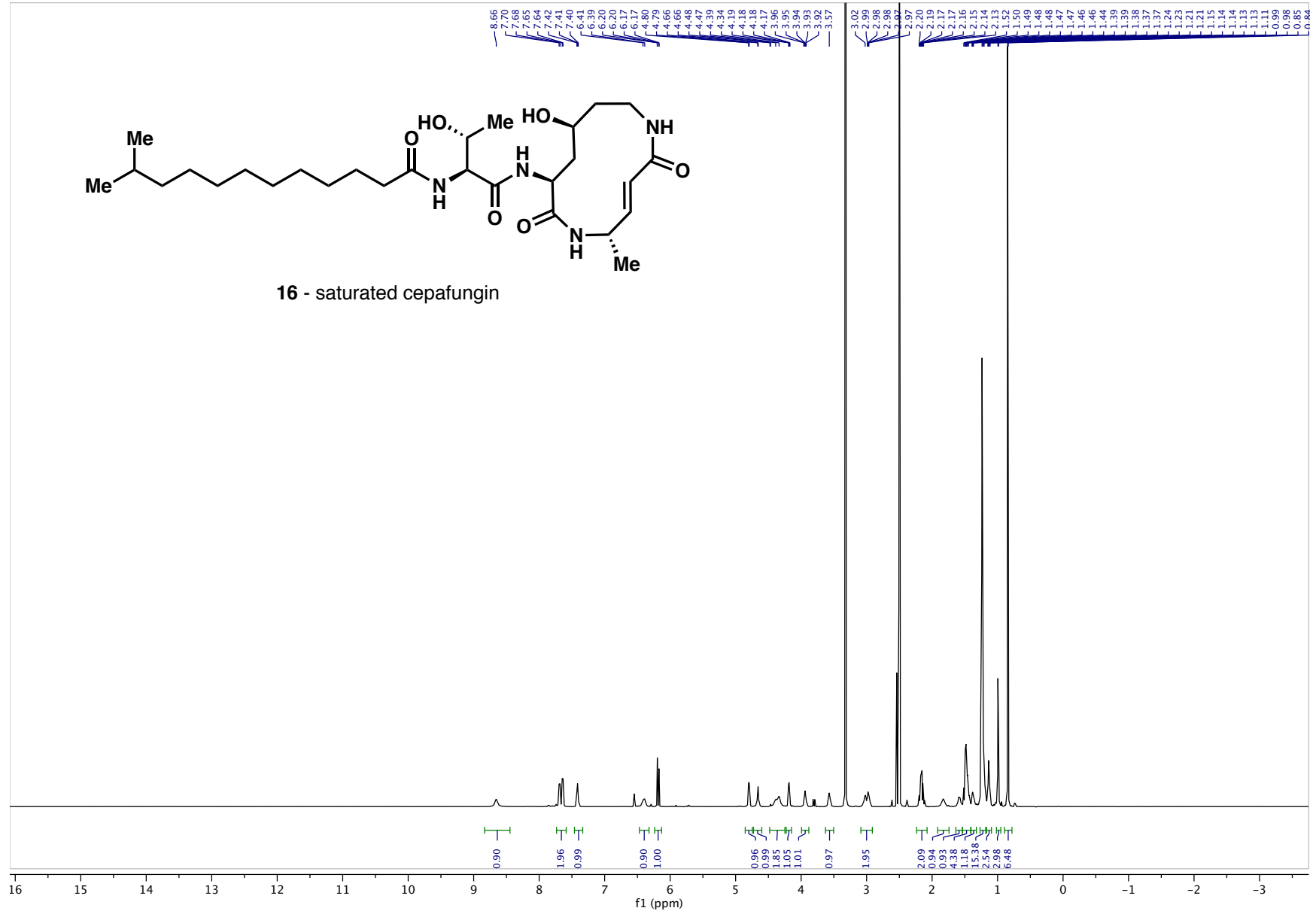


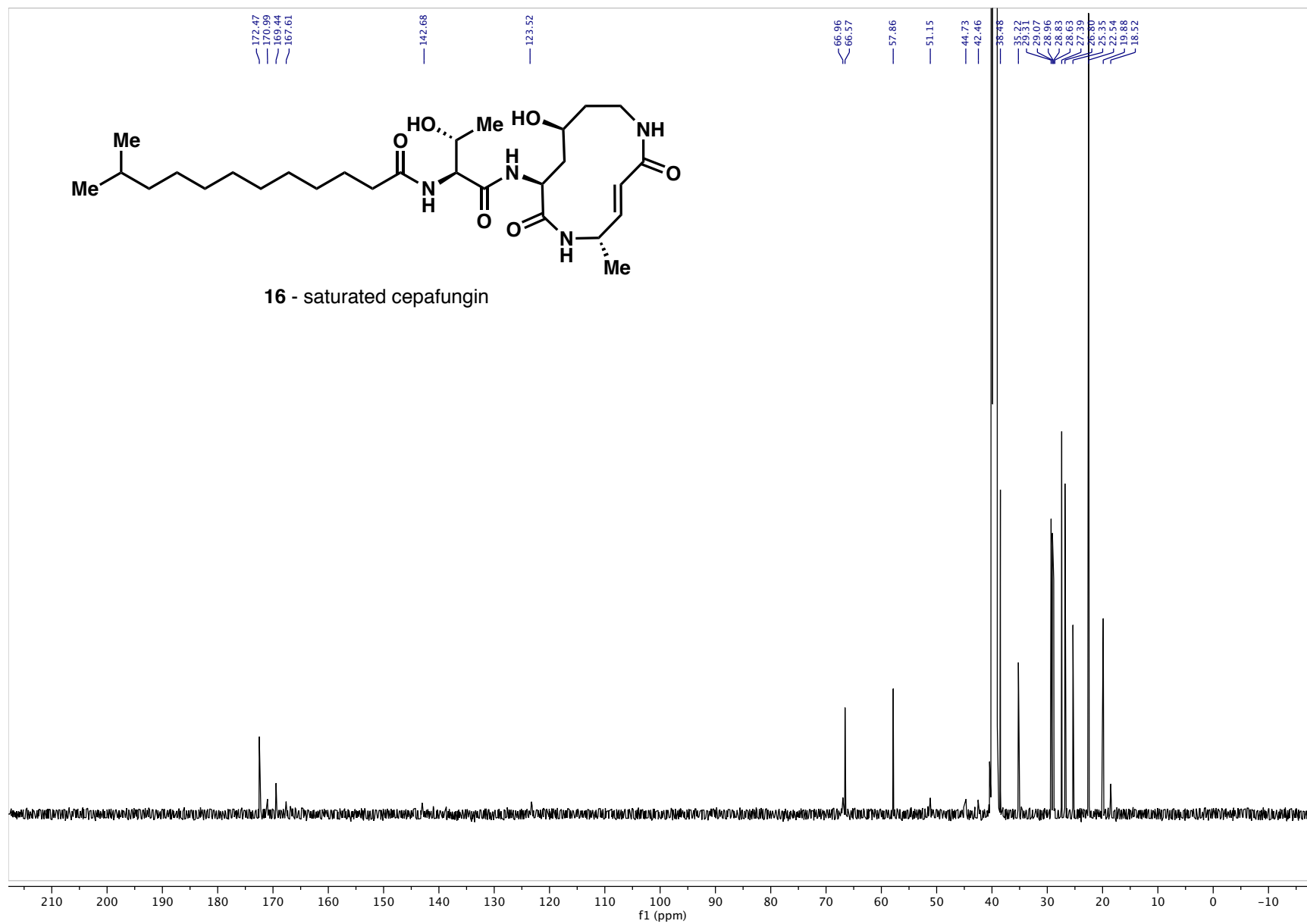


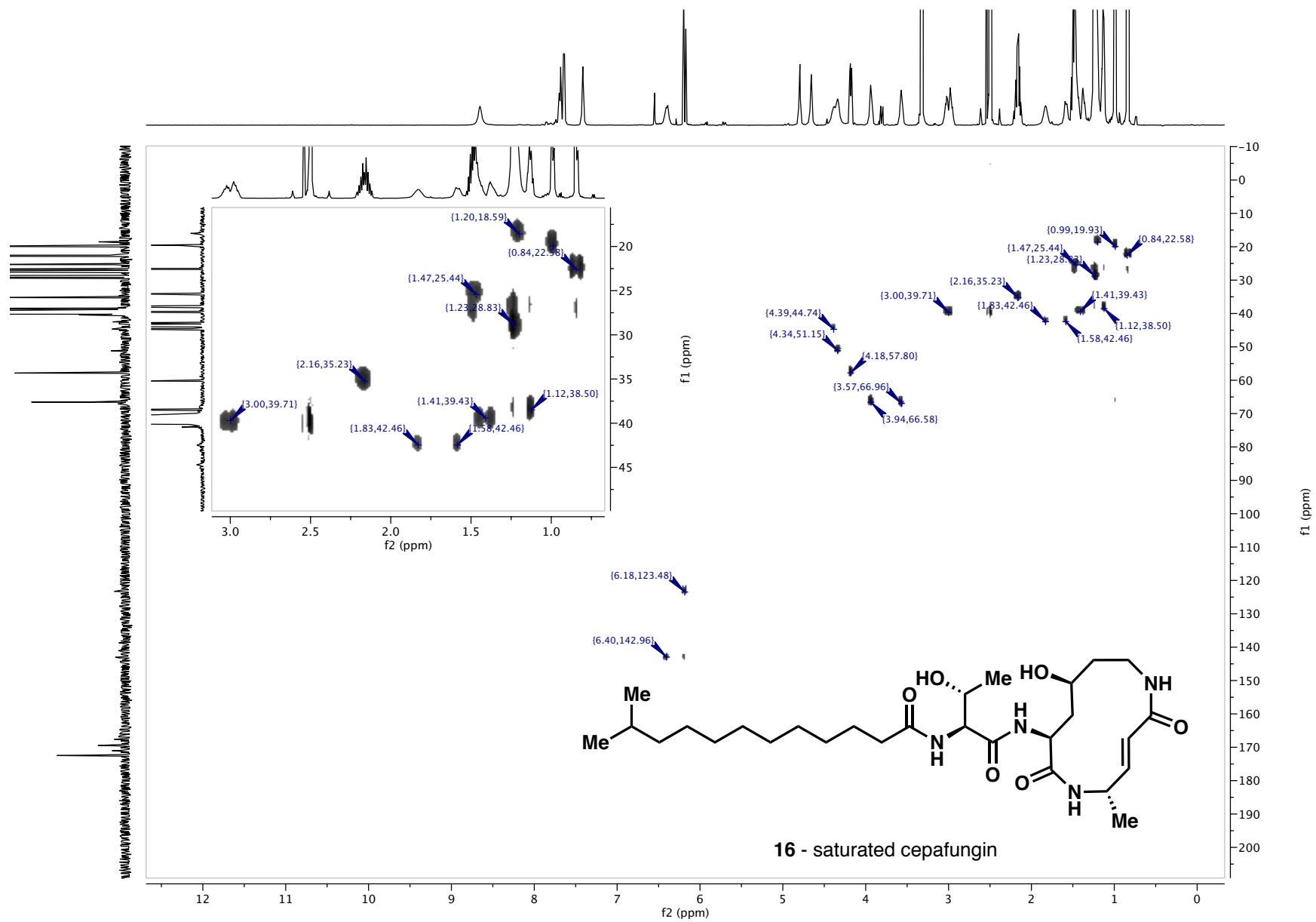


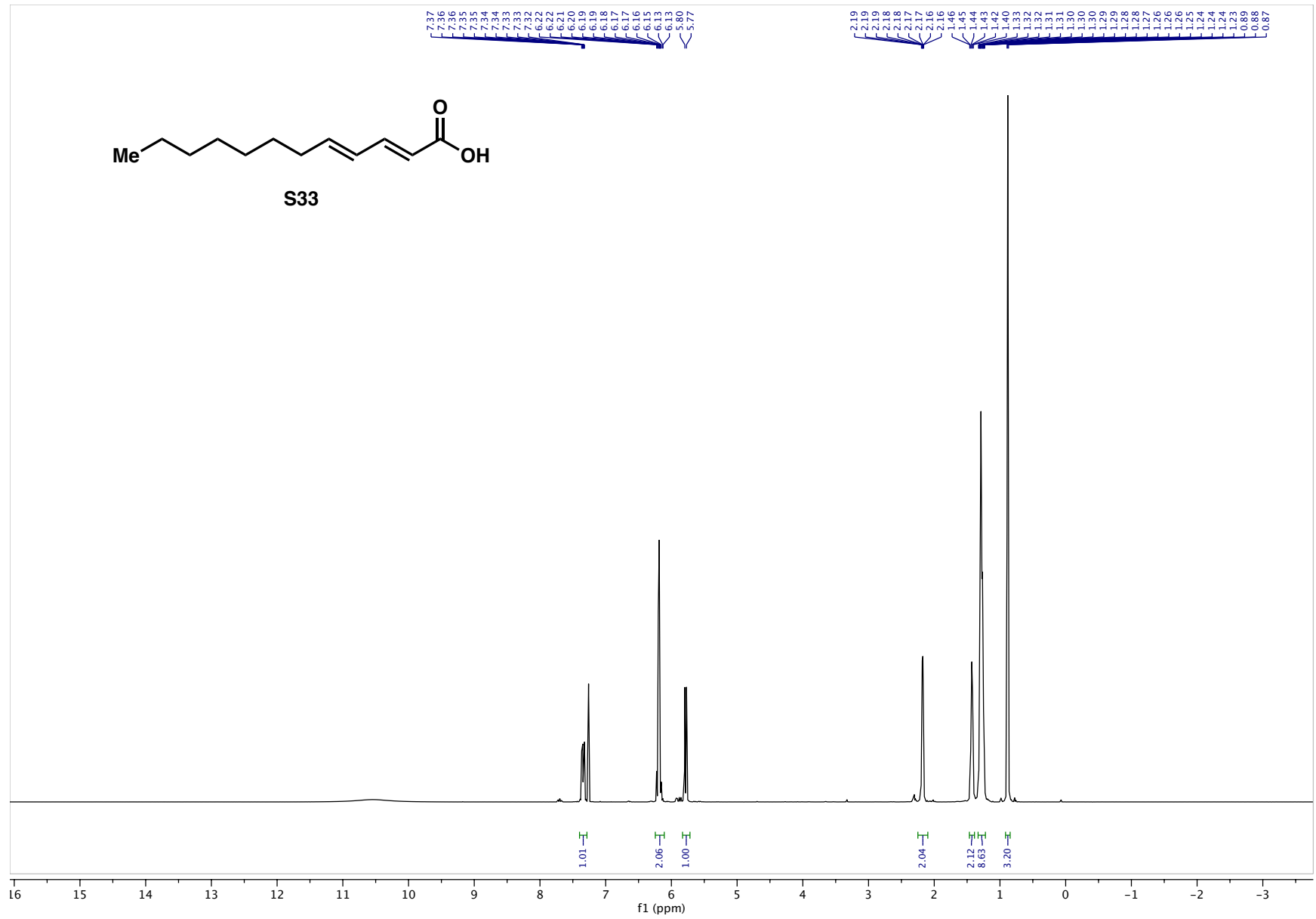


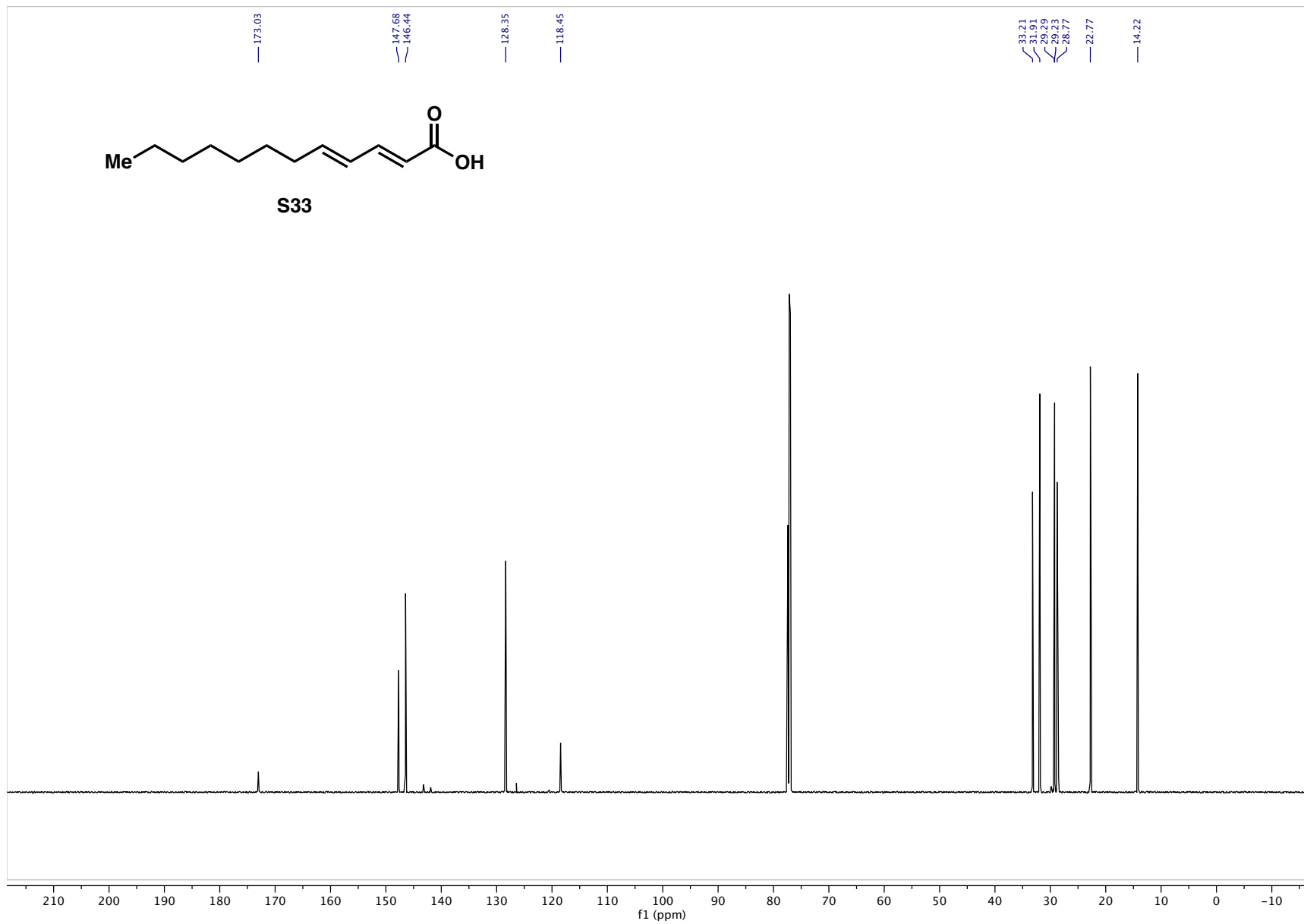


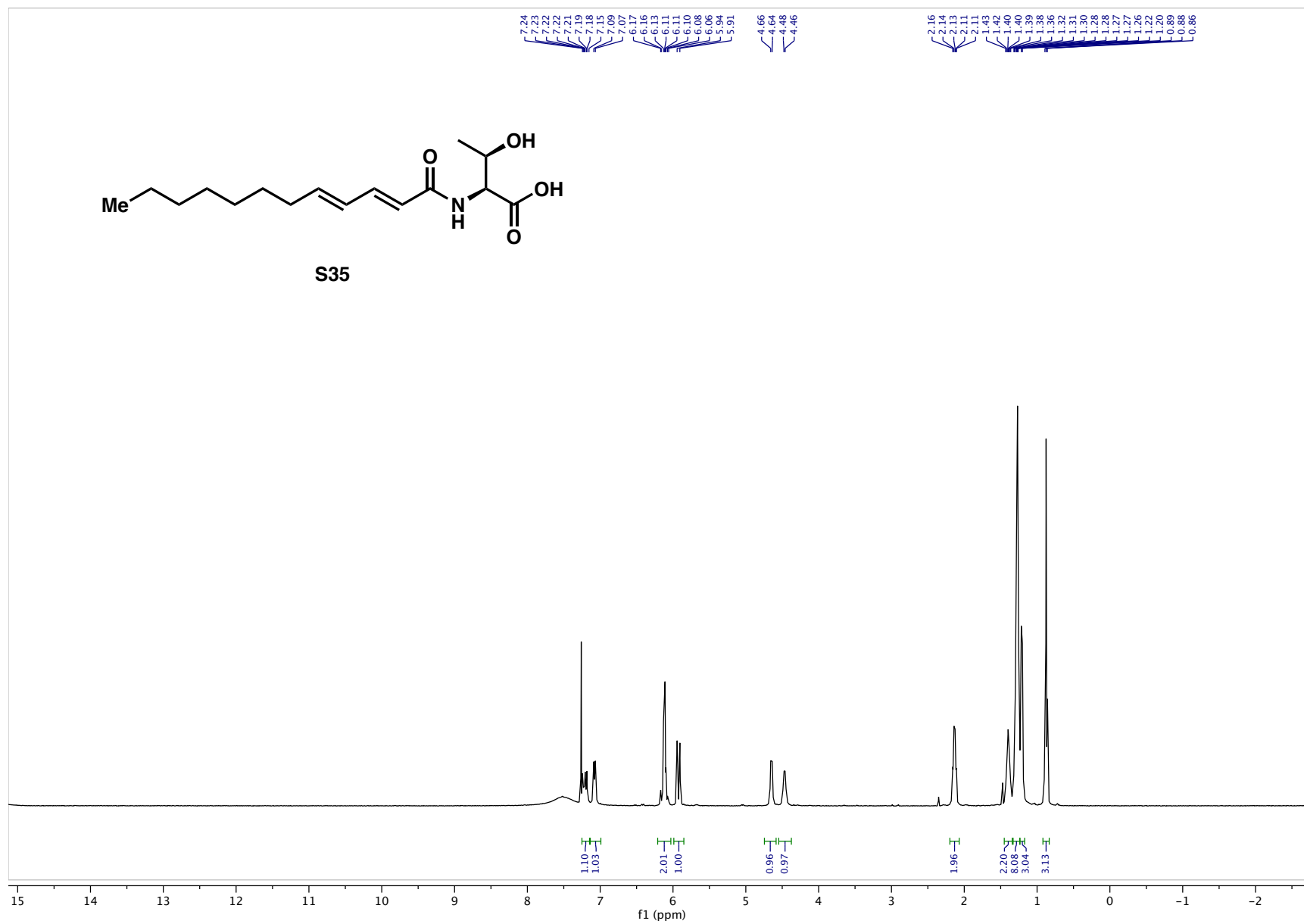


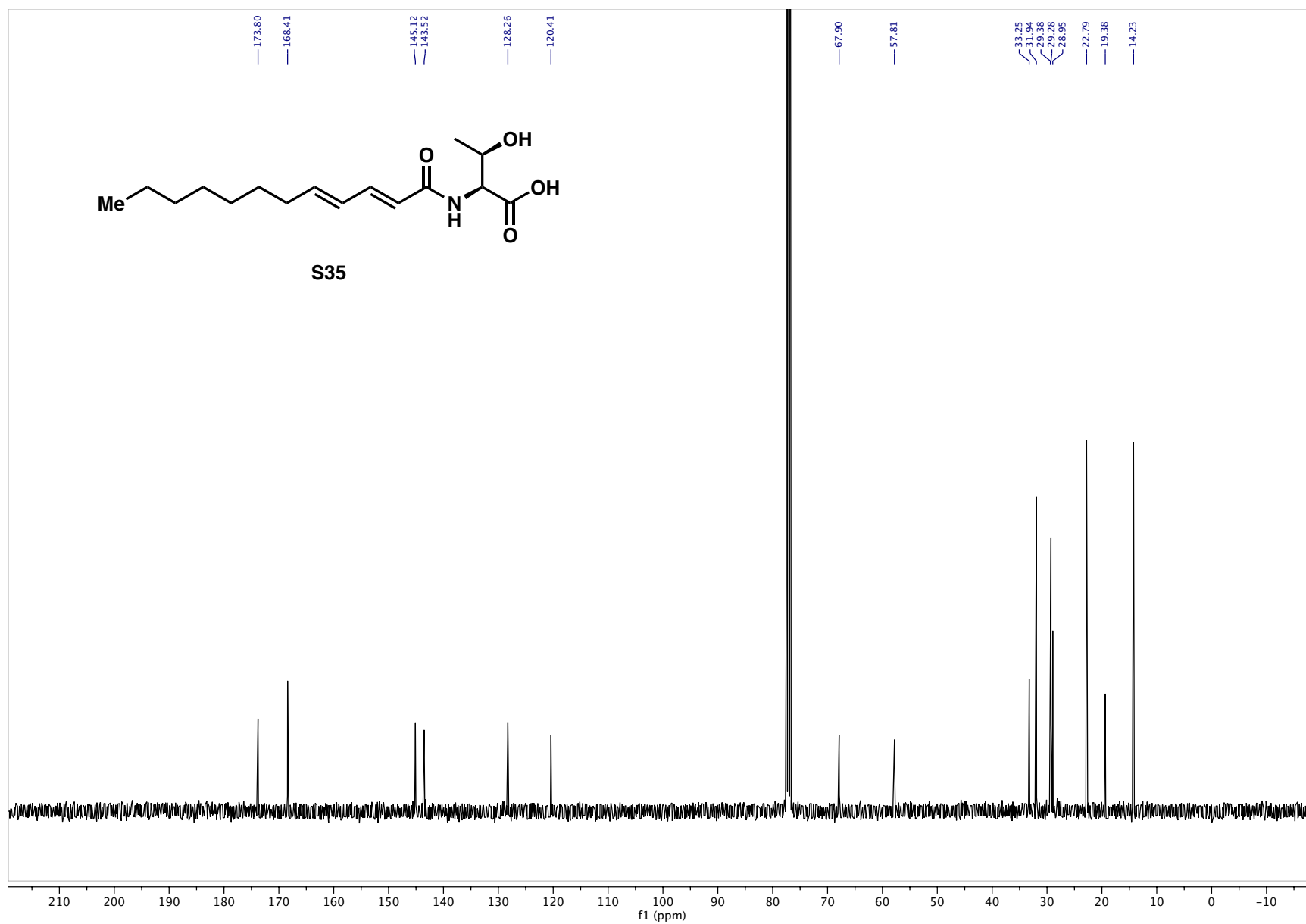


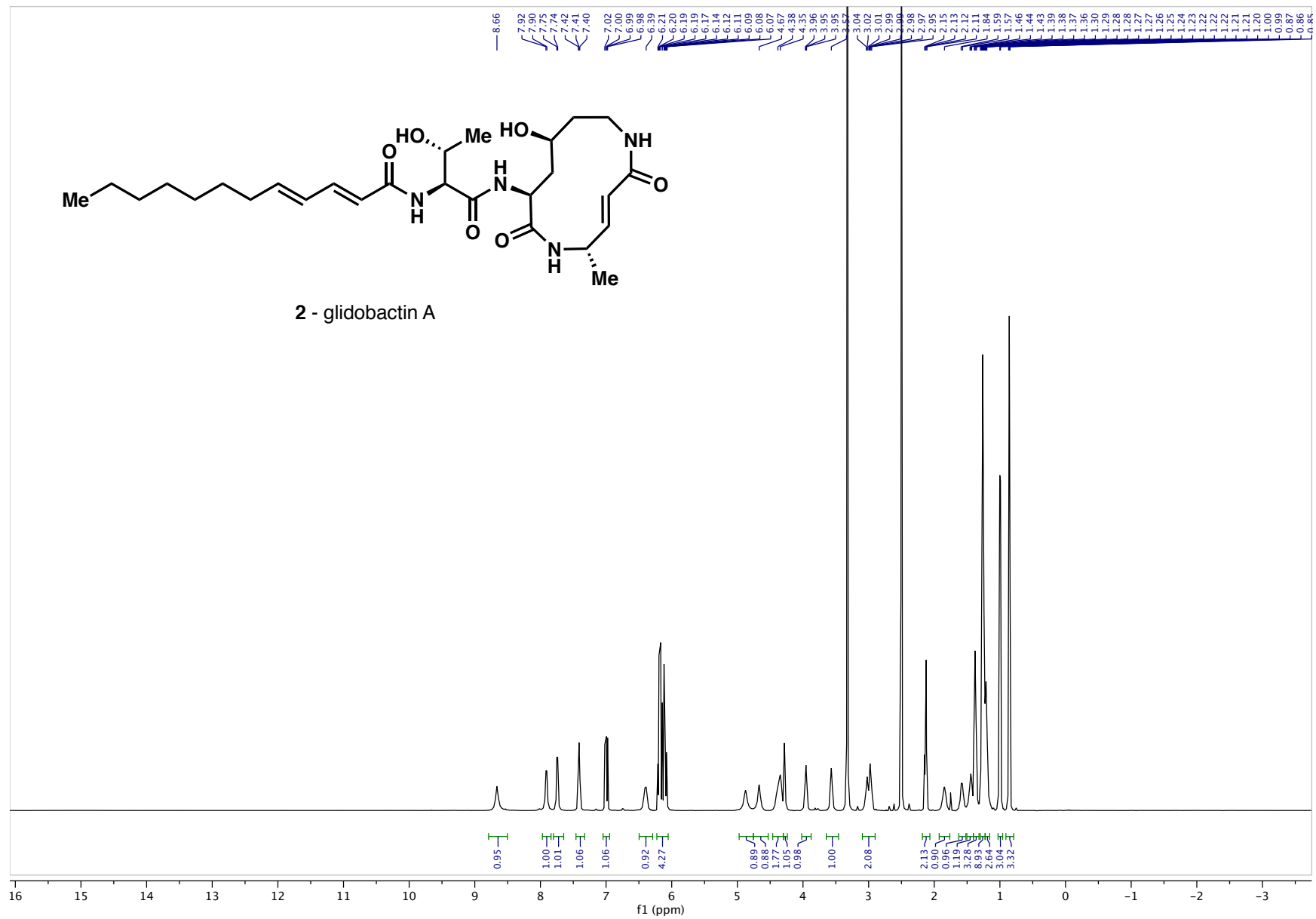


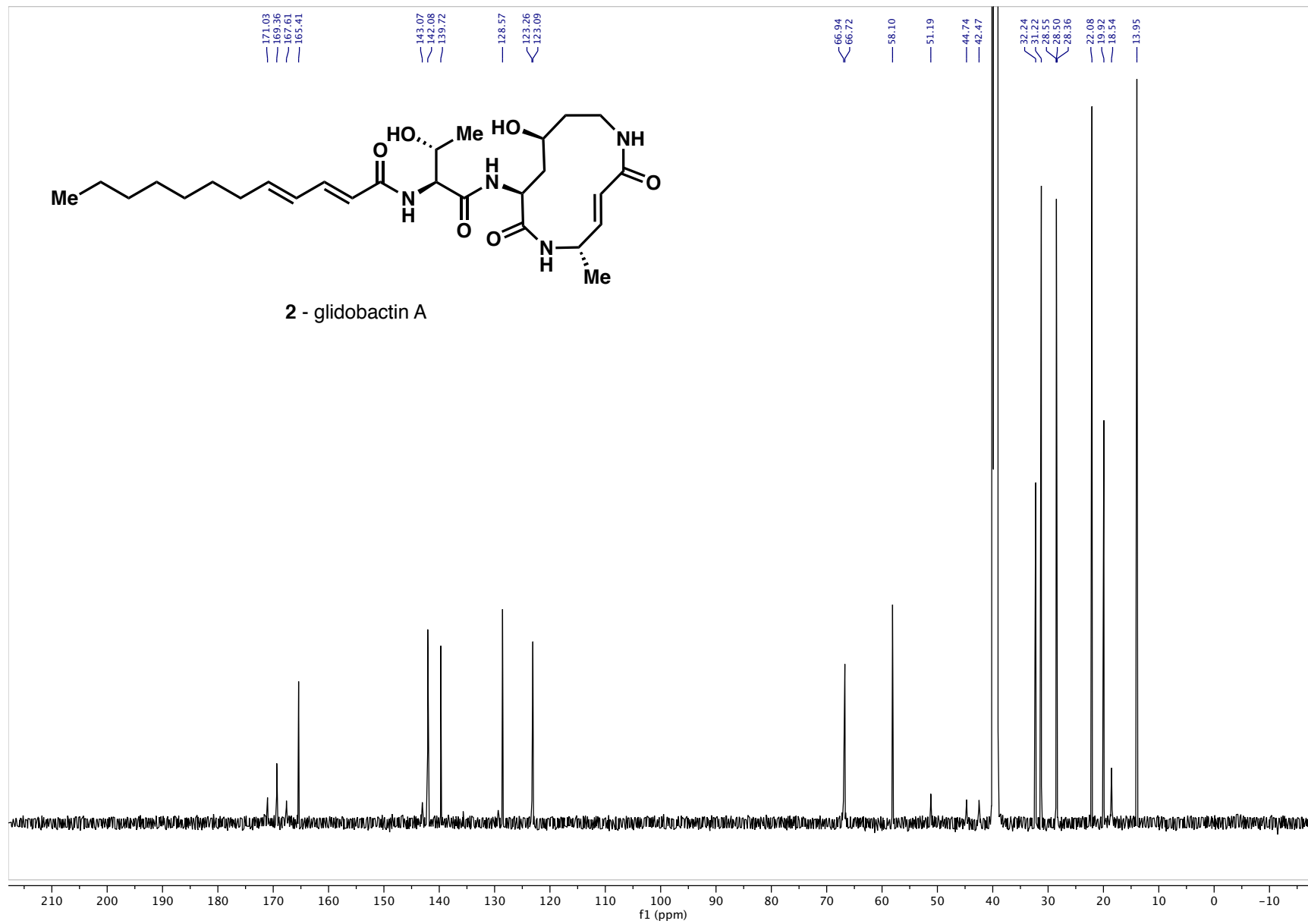


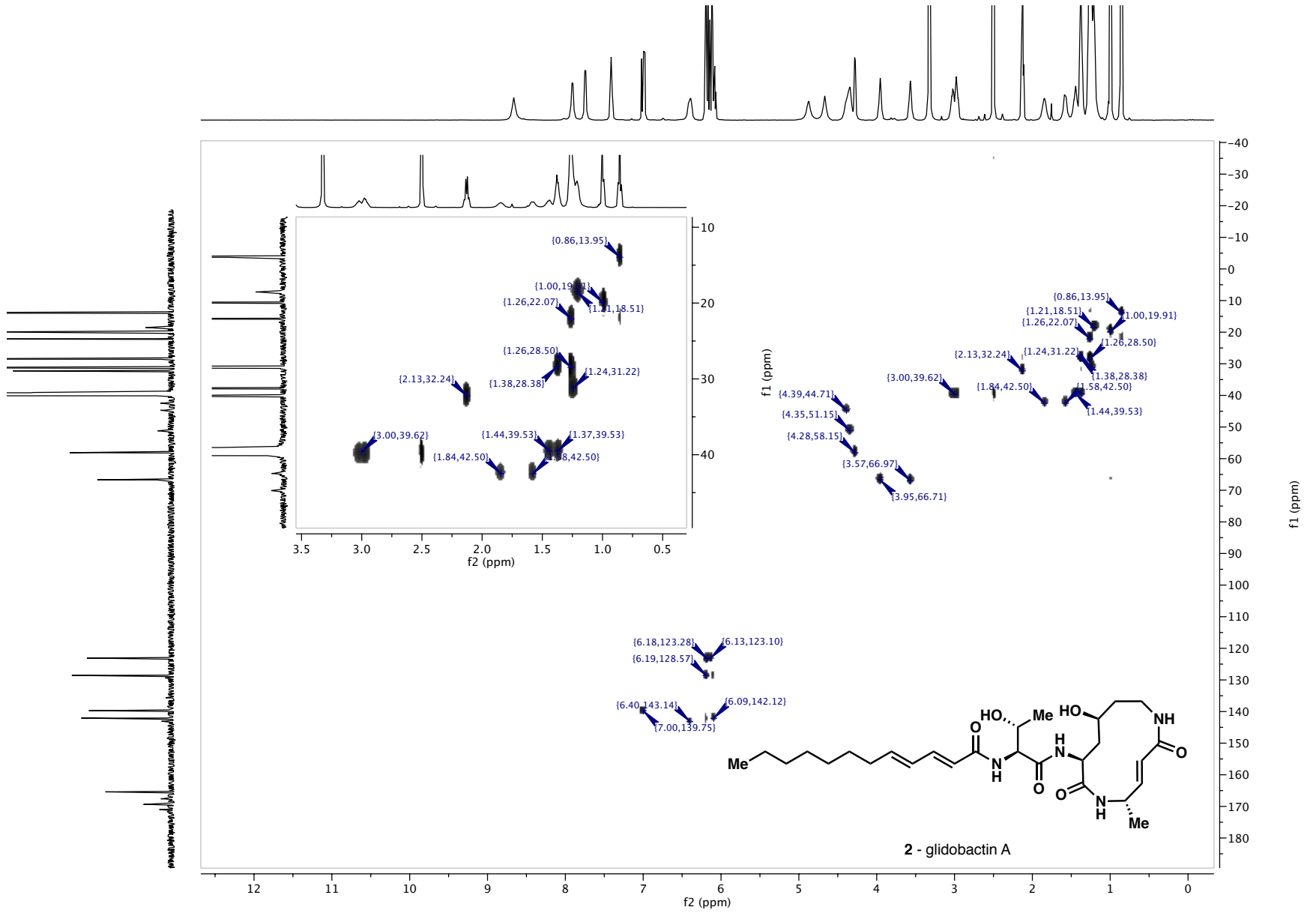












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