

An Introduction to GENI-ACT

[] geni-act

GENI-ACT allows collaborative genome annotation. Researchers or students can collectively suggest changes to an existing genome with supporting evidence. Changes can be ported back to genbank by exporting to a sequin file format.

GENI-ACT also has ported the education components from IMG-ACT. Teachers can assign students work to be completed in a lab notebook that is integrated with the classroom.

2775 genomes available

Sign Up

Login

Browse Genomes

Part of the Vision of GEM:

- Engaging the wider WNY community and increasing its genomic and microbiomic literacy will help promote GEM-relevant science in multiple ways, including building public support for research funding and explaining the importance of public participation in clinical research.
- In tandem with their world-class research on these questions, the GEM faculty will develop new courses to educate both STEM and non-STEM oriented students alike, about these important topical issues. UB students will be involved in K-12 and community outreach GEM activities. By fostering partnerships between Buffalo area school teachers and students and researchers at UB, we will form stronger bonds between the community and the university.

<https://www.buffalo.edu/genomeenvironmentmicrobiome/about-us/our-vision.html>

What is GENI-ACT?

- GENI-ACT is the current version of what initially was the Integrated Microbial Genomes Annotation Collaboration Toolkit (IMG-ACT).
- IMG-ACT was developed by instructors from both research-intensive and predominately undergraduate institutions in collaboration with the Department of Energy-Joint Genome Institute (DOE-JGI) as a means to innovate and update undergraduate education and faculty development in 2008.
- The IMG-ACT program provided a cadre of tools, including access to a clearinghouse of genome sequences, bioinformatics databases, data storage, instructor course management, and student notebooks for organizing the results of their bioinformatic investigations.
- In the process, IMG-ACT made it feasible to provide undergraduate research opportunities to a greater number and diversity of students, in contrast to the traditional mentor-to-student apprenticeship model for undergraduate research, which can be too expensive and time-consuming to provide for every undergraduate.

<http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.1000448>

History of the use of GENI-ACT at UB

- 2008-2011: The Department of BCLS had a workforce development grant to give teachers enrichment training in fields related to clinical laboratory sciences and biotechnology
- 2008-2009: ~96 teachers from several counties came to UB for the enrichment training.
- In January of 2010 Dr. Rama Dey-Rao and Dr. Stephen Koury travel to the JGI to receive training in the use of IMG-ACT.
- Summer of 2010: Teachers come to UB for 1 week of training in the use of GENI-ACT
- Fall of 2010 - Students work with their teachers to annotate genes with guidance from Dr. Dey-Rao and Dr. Koury
- December 2010 - students, teachers and their family come to UB for a Saturday minisymposium to present their findings and hear a talk by Dr. Marc Halfon



Timeline Since 2010:

- 2012- Used the workforce development grant experience as preliminary data for an NSF ITEST (Innovative Technology Experiences for Students and Teachers) Grant - not funded.
- 2013 - Modified the grant for submission to NIH for a SEPA (Scientific Education Partnership Award)
 - One proposal per institution; one other group wanted to submit
 - Upon suggestion from Ken Tramosch, Associate Vice President for Research, we partnered with the NY State AHEC (Area Health Education Center) System, housed in Family Medicine, and their two western NY Centers to revise the proposal
 - ENAHEC - Erie Niagara AHEC
 - Rural AHEC - 12 counties outside of Erie /Niagara
 - Resulted in the formation of the Western New York Genetics in Research and Healthcare Partnership - application submitted and a score was obtained that was likely to be funded.
 - But then came the.....

“United States budget sequestration of 2012”

- SEPA program funds were cut...and the SEPA program in general was threatened with discontinuation
- Program Officer could give no guidance other than to say no awards were going to be given
- Modified the grant as the “Western New York Genetics in Research Partnership” and resubmitted as an NSF ITEST Strategies project
 - Funded in the summer of 2013 for 3 years
- Spring 2014 - SEPA program funds restored with the mandate that all projects that were going to be funded in the previous cycle be funded before another program announcement could be made.
 - June 1 2014 - SEPA award given after modification of the original proposal to make is sufficiently different from the ITEST award; 5 year award.

NSF ITEST AWARD

Project website:

<http://ubwp.buffalo.edu/wnygirp/>

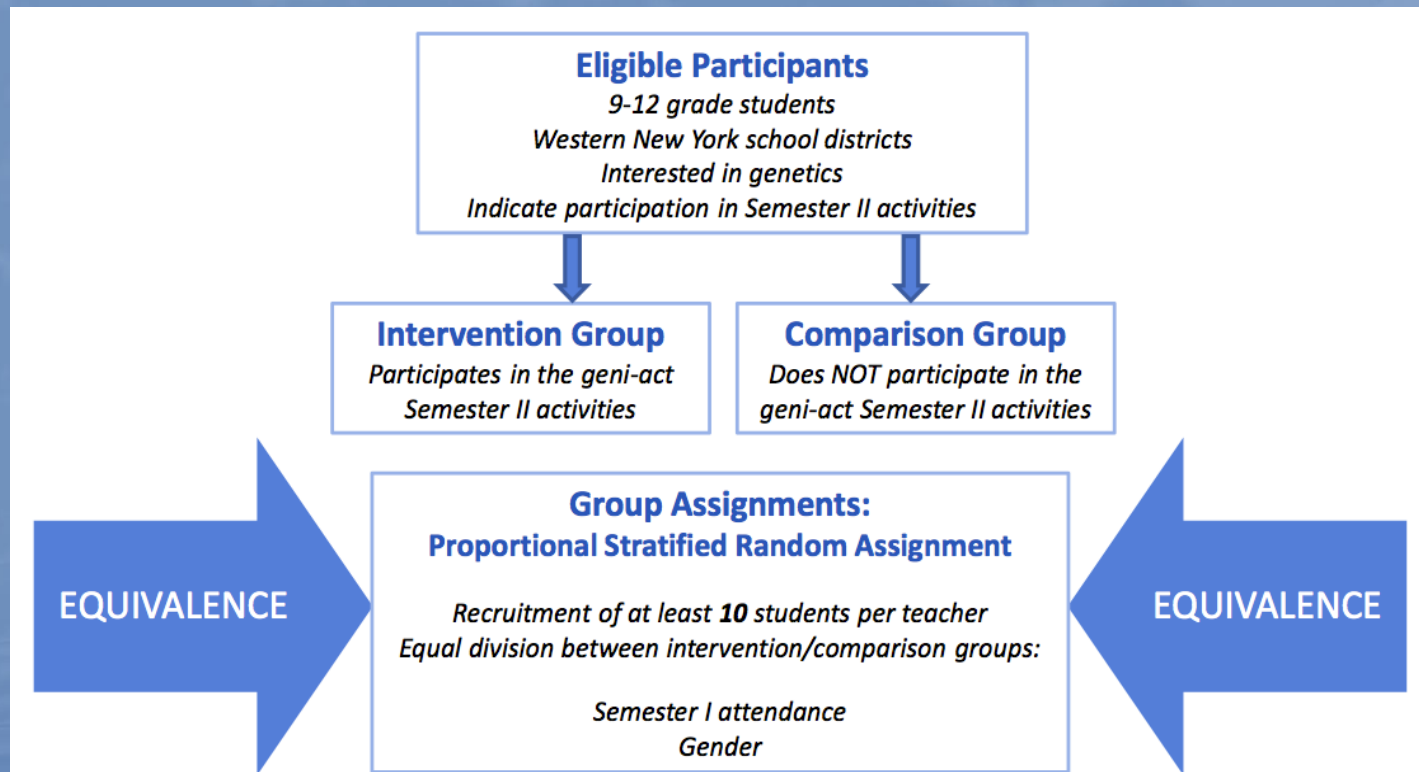
The STEM-related goals of the project are to:

- allow high school students and teachers to participate in scientific research
- stimulate the interest of students in pursuing careers in science and technology through the use of a unique, interactive learning environment combined with intensive support intervention (GENI-ACT)
- encourage teachers to include bioinformatics and genomics in their curriculum.

ITEST Project Overview:

- A week long summer training workshop for teachers (30 per year) to learn the fundamentals of gene annotation using the GENI-ACT system (along with 3 additional subsequent refresher training days).
- 3 fall semester activities to build interest among student participants and to recruit students to participate in the spring semester genome annotation exercises.
- Spring semester teacher guided genome annotation projects for 5 or more students per teacher (150 total per year). A control group of students will be included for comparison.
- A capstone symposium for student and teacher participants to present the results of their genome annotations.

Student Participant Selection



GENI-ACT Overview

[] geni-act

GENI-ACT allows collaborative genome annotation. Researchers or students can collectively suggest changes to an existing genome with supporting evidence. Changes can be ported back to genbank by exporting to a sequin file format.

GENI-ACT also has ported the education components from IMG-ACT. Teachers can assign students work to be completed in a lab notebook that is integrated with the classroom.

2775 genomes available

Sign Up

Login

Browse Genomes

<http://geni-act.org/genomes/browse/>

Signing Up For GENI-ACT

[] geni-act

geni-act :: register

Sign up for an account below. If you are a student in a class, make sure to enter the class-id.

First Name:	<input type="text"/>
Last Name:	<input type="text"/>
Email:	<input type="text"/>
Password:	<input type="password"/>
Password Confirm:	<input type="password"/>
Class Token:	<input type="text"/>
<input type="button" value="Register"/>	

Accounts with a valid class-id are created immediately. Otherwise the account is made as a non-privileged user until validated by an administrator.

If you want to experiment With GENI-ACT you can use this token: GEM_2016

Email me at stvkoury@buffalo.edu after signing up and I will make some gene assignments for you.

Request Course Instructor status from the system administrator, Dr. Brad Goodner at: GoodnerBW@hiram.edu

Workshops can be arranged for any interested faculty.

Profile

Courses

Name	School	Term
<u>MT447/547 - Introduction to Microbial Genome Annotation</u>	University at Buffalo	Spring 2014
<u>MGAN Workshop Genes</u>	University at Buffalo	Spring 2016
<u>Biotechnology Techniques</u>	Westfield Central School	Spring 2016
<u>UB GEM - Try out GENI-ACT</u>	University at Buffalo	Spring 2016

Instructor Course Management

geni-act :: courses :: MT 447/547 Spring 2016

MT 447/547 Spring 2016

Info

Period: Spring 2016
Write Access Date: Not specified.
Course End Date: Not specified.
[Change Course Properties](#)

Change Course Properties

Name

Token

Class Management

[+] Students

[+] Sections

[+] Teaching Assistants

[+] Student Teams

GENI-ACT Modules

Enabled Modules		
Basic Information	ON	Turn OFF
Sequence-based Similarity Data	ON	Turn OFF
Cellular Localization Data	ON	Turn OFF
Alternative Open Reading Frame	ON	Turn OFF
Structure-based Evidence	ON	Turn OFF
Enzymatic Function	ON	Turn OFF
Duplication and Degradation	ON	Turn OFF
Horizontal Gene Transfer	ON	Turn OFF
RNA	ON	Turn OFF
Proposed Annotation	ON	Turn OFF

Available Modules

Basic Information

- **DNA Coordinates:** Use a [GENE Page](#) to enter coordinates
- **Nucleotide Sequence / Length:** Use a [GENE Page](#) to find the Nucleotide Sequence and Length
- **Protein Sequence / Length:** Use a [GENE Page](#) to find the Protein Sequence and Length

Sequence-based Similarity Data

- **BLAST:** Find the top hits in BLAST using NCBI BLAST
- **CCD:** Find COG Results from NCBI BLAST
- **T-Coffee:** Run a multiple sequence alignment using T-Coffee
- **WebLogo:** Find the sequence logo and analyze it

Cellular Localization Data

- **Gram Stain:** Research Pubmed to find the gram stain of the organism
- **TMHMM:** Plot the transmembrane topology
- **SignalP:** Plot the signal peptide graph
- **LipoP:** Predict lipoproteins and signal peptides
- **PSORT-B:** Predict protein localization
- **Phobius:** Plot the phobius posterior probabilities

Alternative Open Reading Frame

- **DNA Coordinates:** Change the DNA Coordinates if the ORF has been incorrectly determined

Structure-based Evidence

- **TIGRFAM:** Search TIGRFAM Hidden Markov Model database for hits
- **Pfam:** Find Pfam families within a sequence
- **PDB:** Align sequences using Protein Data Bank

Enzymatic Function

- **KEGG:** Find the KEGG Pathway and analyze the pathway map
- **MetaCyc:** Find the Metabolic Pathway and analyze
- **EC Number:** Use ExPASy ENZYME to locate the EC number and name

Duplication and Degradation

- **Paralogs:** Use NCBI BLAST to find paralogs
- **Pseudogene:** Research to find if the gene is a pseudogene

Horizontal Gene Transfer

- **Phylogenetic Tree:** Use Phylogeny.fr to plot the phylogenetic tree from sequences
- **Gene Context:** Find the Ortholog Neighborhood Region using IMG
- **Chromosome Viewer GC Heat Map:** Analyze the GC heat map to find the characteristic and average GC%

RNA

- **Rfam:** Find the Rfam number, score and pairwise alignment

Proposed Annotation

- **Note:** Propose a new annotation to be placed in the note section of GENI-ACT and Genbank GBK

Types of Assignments in GENI-ACT

Assignments

[+] Isolate Genome Gene Annotations

[+] Isolate Genome Pathways / Structures

[+] Metagenome Gene Annotations

[+] Metagenome Pathways / Structures

[+] Metagenome Analyses

Ideas for implementation strategies in using GENI-ACT can be found at:

https://sites.google.com/a/augustana.edu/mgan_workshop_ccuri2014/home/implementation-strategies

Organism: Kytococcus sedentarius DSM 20547 CP001686

Locus: Ksed_00010

← The locus tag for the gene under investigation in this notebook

Instructions

Basic Information

Sequence-based Similarity Data

Cellular Localization Data

Alternative Open Reading Frame

Structure-based Evidence

Enzymatic Function

Duplication and Degradation

Horizontal Gene Transfer

RNA

← Basic online module instructions

Clicking on a notebook section opens it for editing

← **[+] Basic Information**

[+] Sequence-based Similarity Data

[+] Cellular Localization Data

[+] Alternative Open Reading Frame

The GENI-ACT Student Notebook

[Locus Tag Links to Gene Page for the gene under investigation](#)

[Detailed Module Instructions Have Been Developed on our Project Websites.](#)

Making Entries in the Lab Notebook


[-] Basic Information

Module Instructions

DNA Coordinates

go to the [Gene Page](#)


Clicking here will open the editor for data to be added to the notebook.


DNA coordinates 



DNA Sequence

go to the [Gene Page](#)

Nucleotide sequence (FASTA format; see module Quick Links for instructions) 

Sequence Length 

DNA Sequence

go to the [Gene Page](#)

Nucleotide sequence (FASTA format; see module Quick Links for instructions)

↶ ↷ Formats ▾ **B** *I* ☰ ☷ ☶ ☵ ☱ ☲ ☳ ☴ ☽ ☿ ♋ ♌ ♍ ♎ ♏ ♐ ♑ ♒ ♓

```
> Ksed_00010 nucleotide sequence
GTGAGCCAGACCCCGACGACCACGCCACCGCCATCTGGCAGGAGGCCATGGTCCACCTCCAGG GAGCAGGCTGGCCCCGCGGACATCGGGGTGCTCCGGCTGGCCACGCTCGTGGGTCTGCTGGA
GGGCACTGCCCTGCTCGCGTGAAGTACGACCACGTCAAGGACGCCGTCGAGGGGCACCTGCGC GAGGACGTGTCCACCCTGGCGGAGTCTTGACCGTGACATCCGGCTGGCCGCTCGGTGG
ACCCCGATGCGGTGAGCGCCGCCAGGAGGAGGCCACCCCGGCCCGTCCCGGCCGATGA GGACGACCCGGCCACAGGTGAGGACCGTTGTCCACAGCTGTGGACGGAGCCGTGGAAAAGCAC
GAGGGAAGCAGTCCGGCACGTGCCGGGAATCGGTGGCGCCGCCACGACGCCAGCCTGACGG CGACAACTCCTCACCCGGTGTGGAGCGGATTACTCCGCGCTGAACCACAAGTACACTTTCGA
CACCTTCGTGCTGGGGTCTGCGAACCGTTTCGCCACGCCGACGCGACCCCGTGGCCGAAGCC CCCGCCGCGCCTACAACCCGCTGTTTCATCTACGGCGGATCAGGTCTGGGCAAGACCCACCTGT
```

Upload Image:

No file selected.

Overview of a filled in notebook and examples of student posters:

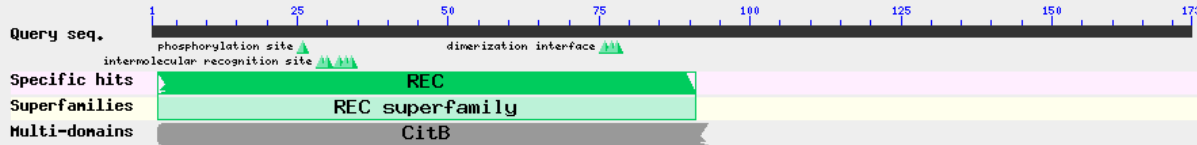
http://www.geni-act.com/lab_notebook/public/8ed2a45227a744df/

<http://ubwp.buffalo.edu/wnygirp/student-research/>

One example of wet lab experiment resulting from annotation results

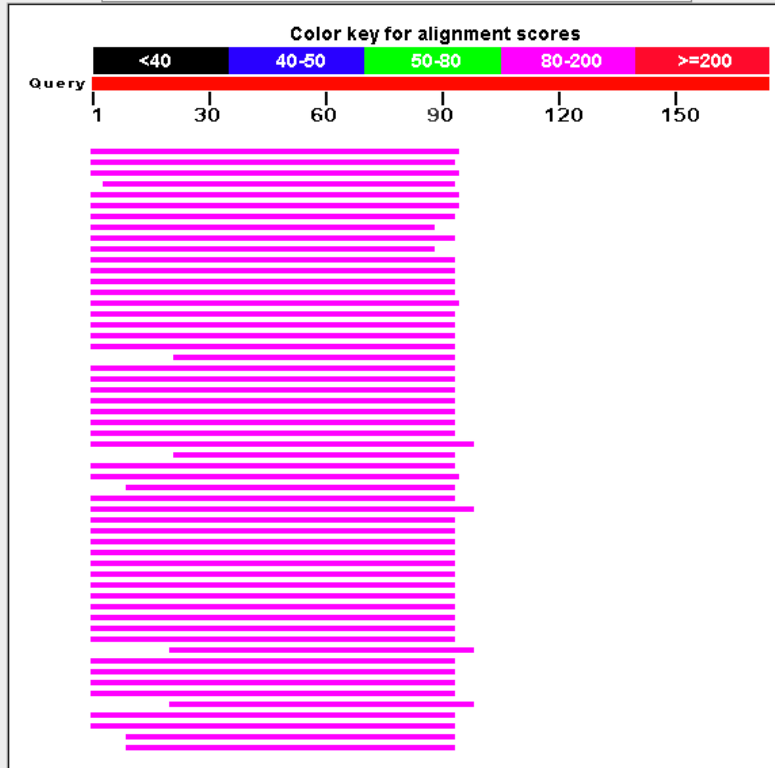
- Illustrates how undergraduate research or MS level project or thesis research studies can be generated from annotation of a genome.
- http://geni-act.org/gene/locus/CP001686/Ksed_02850/

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Ksed_02850:
Example of an
interesting
finding leading
to proposed wet
lab experiments;
annotated as a
pseudogene.

T-Coffee multiple sequence alignment: Incorrect start codon?

Multiple sequence alignment

CLUSTAL W (1.83) multiple sequence alignment

```

Ksed_02850-aa
gi|377537422|dbj|GAB48067.1|-----MFRDALVMLLSMQ
gi|496022179|ref|WP_008746686.1|MTT-----EPAP-AQPVTSRVRVLLADDEHLIRGALAALLALE
gi|502488441|ref|WP_012803990.1|MSPARDSRTSPEPGTSPAQASEPADAALRVILVDDENLIRSALATMLSLE
gi|502715736|ref|WP_012950794.1|M-----IRVLLADDENLIRSALAALLALE
gi|654875439|ref|WP_028327408.1|M-----IRLLLADDENMFRDALATLLGLQ
gi|738384255|ref|WP_036336310.1|M-----IRVLLADDENLVRSAFAALLGLE
gi|739287555|ref|WP_037150275.1|M-----IPVLLADDENLVRTAMAAMDLE
gi|750276589|ref|WP_040562936.1|M-----PIRILIADDETLFRDALATLLDLR
gi|772758607|ref|WP_045317119.1|-----MAALLSLE
gi|820816812|ref|WP_046769457.1|M-----IRVLLADDENLIRSALRALLSLE
    
```

```

Ksed_02850-aa
gi|377537422|dbj|GAB48067.1|----MVRAGSVAEAKAVLR----STEVDVALLDLQLPDGDGIDLAVHL
gi|496022179|ref|WP_008746686.1|DDLEVVAQAASGPEAMALAR----AHEFDVALLDLQMPGADGIAVAETI
gi|502488441|ref|WP_012803990.1|EDLEVVAEAASGAEALAMAR----ARTPDVAVLDLQMPDGDGVSVATAL
gi|502715736|ref|WP_012950794.1|ADLDVRGEAATVADGLCLAE----AVQPDVAVLDLQLPDGDGLELAARI
gi|654875439|ref|WP_028327408.1|EDLEVVAQAASGAEALAMAR----AHIPDVAVLDLQMPDRDGISVAGEL
gi|738384255|ref|WP_036336310.1|EDLLVVAQAASGPEAIAMAC----SHEVDVAVLDLQMPGADGIAVAESL
gi|739287555|ref|WP_037150275.1|DDLEVVAQAASSGAEALAMAR----AHAPDVAVLDLQMPDRDGISVAGEL
gi|750276589|ref|WP_040562936.1|TDIDVIADVESGEDLIAIWRRRVDRGESAAVAVIDLQMPGIDGIDTAIEL
gi|772758607|ref|WP_045317119.1|DDLHVVAQAASGPEAVAMAR----AHRPDVALLDLQMPGQDGIETAIAL
gi|820816812|ref|WP_046769457.1|DDLEVVAQAATGAEALATAR----VVRPDVAVIDLQMPDLDGVSVAQAL
DGIEVVAEAATADEALAMAR----SFSPDVAVLDLQLPDRDGIALAAEL
          : . : : .          **: : ** : * :
    
```

Alternate Open Reading Frame Viewer – IMG/EDU

hint:

- █ indicates potential start codon region
- █ indicates possible Shine-Dalgarno region
- blue line is the GC content graph

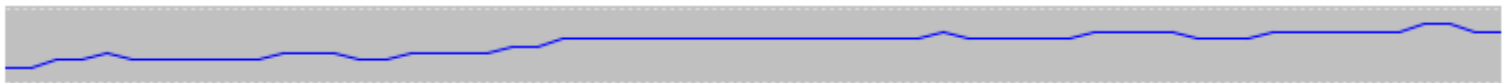
2 potential upstream start codons, but with no Shine-Dalgarno

F1	P	V	T	P	D	S	P	I	R	I	S	L	C	L	V	S	E	R	D	E	R	T	L	I	S	R	E				
F2	P	P	V	P	T	P	A	P	H	S	A	S	C	W	S	R	G	T	R	D	R	A	D	P	R	G					
F3	R	D	R	Q	P	H	P	H	P	V	G	R	G	T	R	D	A	D	P	R	G										
GC	66	64	63	64	64	65	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	66	65	64	64	66	65



277737	CCC	GTG	ACCG	ACAG	CC	CCAT	CCGC	ATCCT	GTT	GGT	CGAG	GACG	AGAC	GCT	GAT	CCG	CGAG																		
277737	GGG	CACT	GGCT	GTC	GGG	GTAG	GGCG	TAGG	ACAA	CCAG	CTCCT	GCTCT	GCG	ACTAG	GGC	GCTC																			
GC	34	36	37	36	36	35	34	34	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	35	36	36	35	36	34	35
F6		T	V	S	L	G	M	R	M	R	N	T	S	S	V	S	I	R	S																
F5	R	S	R	C	A	G	W	G	C	G	T	P	R	L	P	S	R	A	S	G	R														
F4	G	H	G	V	A	G	D	A	D	Q	Q	D	L	V	L	R	Q	D	A	L															

F1	A	L	A	S	L	L	A	P	L	E	D	D	L	E	V	V	V	R	A	G	S																			
F2	P	S	P	P	C	L	W	P	L	W	R	T	T	S	R	W	S	V	S	A	P	R	A	L	R															
F3	P	R	L	P	A	A	G	P	G	P	R	G	R	G	G	R	P	R	R	L	G																			
GC	64	64	66	66	66	66	66	66	66	66	68	68	68	66	66	68	68	68	68	68	70	70	72	72	72	72	72	72	72	72	74	74	74	74	74	74	76	76	74	74



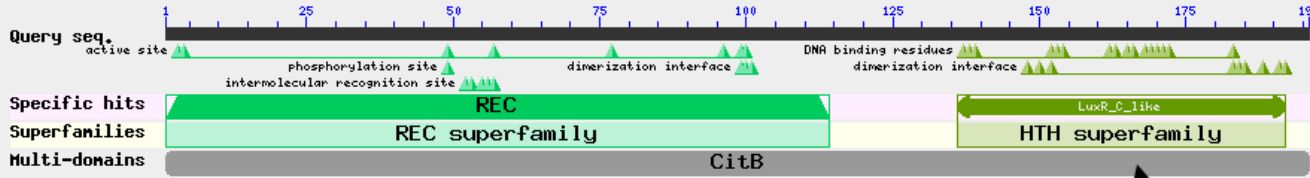
277797	GCC	CTCG	CCTC	CGCT	GCTG	GG	CCCTGG	AGG	ACG	ACCTCG	AG	GTGG	TCGT	CCG	CGC	CGC	GGCTCG																							
277797	CGG	GAGC	GGA	GGG	ACGA	CCG	GGAC	CTCCT	GCTGG	AGCT	CAC	CCAG	CAAG	GCC	CGC	CGC	GAGC																							
GC	36	36	34	34	32	32	32	34	34	32	32	32	30	30	28	28	28	28	28	28	28	28	28	28	28	28	26	26	26	26	28	28	26	26	26	26	26	24	26	26
F6	A	R	A	E	R	S	A	R	S	S	R	S	T	T	T	R	A	P	E																					
F5	P	A	R	R	E	G	A	P	A	G	P	S	R	G	R	L	H	D	D	A	G	A	R																	
F4	G	E	G	G	Q	Q	G	Q	L	V	V	E	L	H	D	D	A	G	A	R																				

Obtained the translation from the upstream in frame start codon from the text output of the AORF viewer

>645946474_1_ORF1 Translation of 645946474 in frame 1, ORF 1, threshold 80,206aa

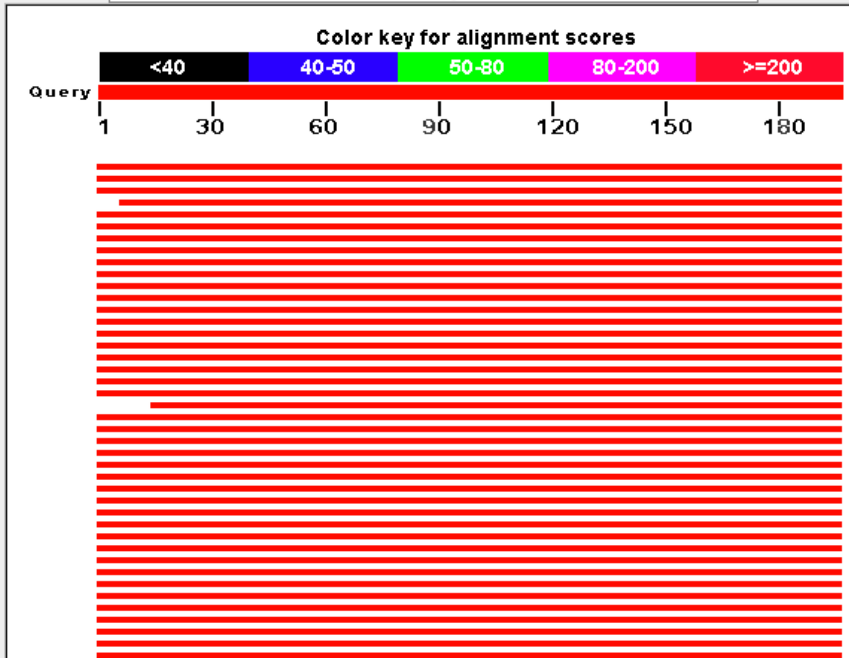
LVEDETLIREALASLLALEDDLEVVRAGSVAEAKAVLRSTEV DVALL
DLQLPDGDGIDLAVHLGEVQPQAASLIITSHGRPGY LKRALESGVRG
FLPKTVGRRALGEAVRTLAEGGRYVDQELAADALAAGASPLSAREA
DVLELSADAAPVEEIAQRAHLSAGTVRNYLSAAVAKTGTSNRHEAAR
VARSKGWI

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



A "new" C-terminal CDD appears, even though we thought we were only adding amino terminal amino acids

Blast of first upstream start codon sequence: unexpected result!

This led to an align two sequences experiment in blast: frame shift “mutation” detected

 Download v [Graphics](#)

645946474_1_ORF1 Translation of 645946474 in frame 1, ORF 1, threshold 80, 206aa
 Sequence ID: lcl|Query_240543 Length: 196 Number of Matches: 1

Range 1: 24 to 183 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
187 bits(476)	1e-64	Compositional matrix adjust.	108/168(64%)	114/168(67%)	12/168(7%)
Query 1		MVVRAGSVAEAKAVLRSTVEDVALLDLQLPDGDGIDLAVHLGEVQPQAASLIITSHGRPG			60
Sbjct 24		+VVVRAGSVAEAKAVLRSTVEDVALLDLQLPDGDGIDLAVHLGEVQPQAASLIITSHGRPG			83
Query 61		YLKRALESGVRGFLPKTVGRRALGEAVRTLAEAGAGTWTRSWRPTPWPLAPPRSAPGRPTC			120
Sbjct 84		YLKRALESGVRGFLPKTVGRRALGEAVRTLAEAG-----RYVDQELAADALAAG-ASP			135
Query 121		WSSRPTPRRWRSPSGPTCRPAR----CATTCTRRPWRRPAPPTGTRPR		164	
Sbjct 136		LSAREADVLELSADAAPVEEIAQRAHLSAGTVRNYLSAAVAKTGTSNR		183	

Download v [Graphics](#)

Alt_Ksed_02850 DNA sequence consisting of 522 bases

Sequence ID: lcl|Query_142477 Length: 522 Number of Matches: 1

Range 1: 1 to 522 [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
957 bits(518)	0.0	521/522(99%)	1/522(0%)	Plus/Plus
Query 1		GTGGTTCGTCCGCGCCGGCTCGGTGGCCGAGGCGAAGGCCGTGCTGCGCTCCACCGAGGTG		60
Sbjct 1		GTGGTTCGTCCGCGCCGGCTCGGTGGCCGAGGCGAAGGCCGTGCTGCGCTCCACCGAGGTG		60
Query 61		GACGTCGCCCTGCTGGACCTGCAGCTGCCGGACGGCGACGGCATCGACCTCGCGGTGCAC		120
Sbjct 61		GACGTCGCCCTGCTGGACCTGCAGCTGCCGGACGGCGACGGCATCGACCTCGCGGTGCAC		120
Query 121		CTGGGTGAGGTGCAGCCGCAGGCGGCGAGCCTCATCATCACCAGCCACGGGCGCCCCGGG		180
Sbjct 121		CTGGGTGAGGTGCAGCCGCAGGCGGCGAGCCTCATCATCACCAGCCACGGGCGCCCCGGG		180
Query 181		TACCTGAAGCGGGCGCTGGAGTCCGGCGTCCGGGGGTTCTTGCCCAAGACGGTGGGACGC		240
Sbjct 181		TACCTGAAGCGGGCGCTGGAGTCCGGCGTCCGGGGGTTCTTGCCCAAGACGGTGGGACGC		240
Query 241		CGGGCGCTCGGCGAGGCGGTGCGGACCCTCGCGGA-GGGGGCCGGTACGTGGACCAGGAG		299
Sbjct 241		CGGGCGCTCGGCGAGGCGGTGCGGACCCTCGCGGAGGGGGCCGGTACGTGGACCAGGAG		300
Query 300		CTGGCGGCGGACGCCCTGGCCGCTGGCGCCTCCCGCTCAGCGCCCGGGAGGCCGACGTG		359
Sbjct 301		CTGGCGGCGGACGCCCTGGCCGCTGGCGCCTCCCGCTCAGCGCCCGGGAGGCCGACGTG		360
Query 360		CTGGAGCTCTCGGCCGACGCCGCGCCGGTGGAGGAGATCGCCAGCGGGCCACCTGTCTG		419
Sbjct 361		CTGGAGCTCTCGGCCGACGCCGCGCCGGTGGAGGAGATCGCCAGCGGGCCACCTGTCTG		420
Query 420		GCCGGCACGGTGCGCAACTACCTGTTCGGCGGCCGTGGCGAAGACCGGCACCTCCAACCGG		479
Sbjct 421		GCCGGCACGGTGCGCAACTACCTGTTCGGCGGCCGTGGCGAAGACCGGCACCTCCAACCGG		480
Query 480		CACGAGGCCGCGCGGGTTCGCCCCGGTCCAAGGGCTGGATCTGA	521	
Sbjct 481		CACGAGGCCGCGCGGGTTCGCCCCGGTCCAAGGGCTGGATCTGA	522	

Wet Lab Experiments Initiated –

- *Kytococcus sedentarius* DSM20547 obtained from ATCC
- Genomic DNA isolated
- PCR primers designed to amplify predicted coding region
- Will clone into an expression vector
- mRNA will be isolated to determine if expressed under normal growth conditions
- Further bioinformatic / wet lab studies to help narrow down potential function for testing in rescuing mutants

Collaborators:

Shannon Carlin-Menter, PhD

Danise Wilson, MPH

Rama Dey-Rao, PhD

Norma Nowak, PhD

Patricia Masso-Welch, PhD

Karen Liermo, MS

Lon Knappenberger, MS

Oak Ridge Affiliated Universities - evaluation team

Brad Goodner, PhD - Hiram College

Microbial Genome Annotators Network (MGAN)

Links of Interest:

GENI-ACT: www.geni-act.org

Video Tutorials: <http://geni-act.blogspot.com/p/welcome-to-geni-act-teaching-resources.html>

WNY Genetics in Research Partnership:
<http://ubwp.buffalo.edu/wnygirp/>

WNY Genetics in Research and Health Care Partnership:
<http://ubwp.buffalo.edu/wnygirahcp/>

GENI-ACT Manuals can be found at either of the above websites under Educational Resources