

A Guide to



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What Manatee Is

- Manatee is a web-based manual annotation tool for accessing and editing annotation data
- Manatee draws information from an underlying database for its displays
- Manatee sends information entered by annotators to the underlying database for storage
- Multiple users can access the same database from different computers when Manatee is run on a server

Getting started with Manatee

- Start Mozilla or Firefox on your computer
 - other browsers work fine too, but Manatee is optimized for Firefox.
- To log into Manatee one must have an account and password.
- Each student will have their own account with the format “training#”
- When logging into Manatee, one must enter a user account name, a password, and the name of the database on which you wish to work.
- For this class we will be using a training version of the *Shewanella oneidensis* genome database
 - the db name is “cgsp”

Finding Manatee

On the internet:

go to http://manatee.igs.umaryland.edu/tigr-scripts/chado_prok_manatee/shared/login.cgi.

To download:

go to <http://manatee.sourceforge.net>



The image shows a web form titled "Manatee Login". The form has a blue header with the title in white. Below the header, there are three input fields: "user_name:" with the value "training#", "password:" with the value "training#", and "database:" with the value "cgsp". A "Submit" button is located below the input fields.

Manatee Login	
user_name:	<input type="text" value="training#"/>
password:	<input type="text" value="training#"/>
database:	<input type="text" value="cgsp"/>
<input type="button" value="Submit"/>	

“Welcome to Manatee”

After logging into Manatee, you come to the “Welcome to Manatee” page. Here you will find several menu and search options to choose from.

I will discuss the menu options in more detail in following slides. You can search using a gene id to access a curation page for that gene; you can search by a keyword in a protein name; and if you are working with more than one database you can shift to another database.

In the upper right hand corner of every Manatee page is a navigation bar:

- The “Home” link takes you back to the “Welcome to Manatee” page, from where ever you are within the Manatee tool.
- This area also shows you which database you are logged into, and who is logged in. Clicking on the login name will take you back to the login page.
- The “Help” link should go to page specific documentation. However, these pages are still under development.

BLAST options

You can BLAST a sequence of interest against the predicted set of genes (nucleotide or protein) or against the entire genome sequence.

Data download options:

At the bottom of the Welcome page are several options for downloading text files containing annotation information. Some of these take a long time to query and load so please be patient. Simply click on the line of interest and the download process will begin.

Welcome to Manatee

Home | Help | Logout | Logged into [cgsp] a
organism: Shewanella oneidensis MR-1

This is the main menu page for the Manatee tool. One can access genes directly (with gene's id number or name) or link to additional menus with more options.

ACCESS LISTINGS

- ▶ Annotation Tools
- ▶ Genome Summary
- ▶ Genome Viewer

ACCESS GENE CURATION PAGE

▶ gene_id:

SEARCH GENES BY PROTEIN NAME

▶ protein name:

CHANGE ORGANISM DATABASE

▶ database:

BLASTN BLASTP TBLASTN

▶ Paste nucleotide or protein sequence below:

▶ Run against NCBI databases: *NCBI Blast*

Data file downloads (potentially long download times)

- ▶ GO Dumper (Tab delimited file of GO annotation)
- ▶ Nucleotide Sequence Dumper (Multifasta File)
- ▶ Protein Sequence Dumper (Multifasta File)
- ▶ Annotation Dumper (Tab delimited file of annotation)
- ▶ Genbank Dumper (For use in Artemis, BioPerl, etc.)
- ▶ GFF3 Dumper (For use in GBrowse, JBrowse, etc.)
- ▶ TBL Dumper (For submission to NCBI, along with the nucleotide FASTA)

“Genome Summary”

The Genome Summary section provides summary information about the annotation content of the entire genome.

Get there by clicking “Genome Summary” on the “Welcome to Manatee” page.

Welcome to Manatee [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] : organism: *Shewanella oneidensis* MR-1

This is the main menu page for the Manatee tool. One can access genes directly (with gene's id number or name) or link to additional menus with more options.

ACCESS LISTINGS

- ▶ **Annotation Tools**
- ▶ **Genome Summary**
- ▶ **Genome Viewer**

ACCESS GENE CURATION PAGE

▶ gene_id:

SEARCH GENES BY PROTEIN NAME

▶ protein name:

CHANGE ORGANISM DATABASE

▶ database:

BLASTN **BLASTP** **TBLASTN**

▶ Paste nucleotide or protein sequence below:

▶ Run against NCBI databases: *NCBI Blast*

Data file downloads (potentially long download times)

- ▶ **GO Dumper** (Tab delimited file of GO annotation)
- ▶ **Nucleotide Sequence Dumper** (Multifasta File)
- ▶ **Protein Sequence Dumper** (Multifasta File)
- ▶ **Annotation Dumper** (Tab delimited file of annotation)
- ▶ **Genbank Dumper** (For use in Artemis, BioPerl, etc.)
- ▶ **GFF3 Dumper** (For use in GBrowse, JBrowse, etc.)
- ▶ **TBL Dumper** (For submission to NCBI, along with the nucleotide FASTA)

submit

reset

The "Genome Summary" page

Genome Summary

[Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as :
 organism: *Shewanella oneidensis* MR-1

The Genome Summary information page displays specific information concerning the selected genome. From here the user can view the following information : ORF counts, Role category information, genes of interest, HMM and paralogous family information, membrane protein information, frameshift information, and annotation progress.

Home
Annotation Tools
Genome Summary

SUMMARY LISTS

- ▶ Genome Calculations
- ▶ Role Category Breakdown

start sites	number	percent
▶ ATG:	4037 (2887)	83.3% (85.8%)
▶ GTG:	501 (323)	10.3% (9.6%)
▶ TTG:	311 (156)	6.4% (4.6%)
▶ OTHER:	0	0.0% (0.0%)

Numbers in parentheses do not include hypothetical proteins

feature name	feature count	feature type
▶ transcript	4849	transcript
▶ tRNA	101	tRNA

Information Table

▶ sequence id:	cgsp.assembly.2
▶ type:	chromosome
▶ molecule length:	161613 bp
▶ GC content:	43.7%
▶ base frequencies:	(A) (C) (G) (T) 28.2% 21.4% 22.3% 28.1%
▶ funny characters:	
▶ ORF count:	170
▶ average gene length:	734 nt
▶ percent coding:	77.2%
▶ percent coding OR tRNA, rRNA, or repeat:	77.2%

Information Table

▶ sequence id:	cgsp.assembly.1
	chromosome
	4969803 bp
	46%
	(A) (C) (G) (T) 27.0% 23.0% 23.0% 27.0%
	R Y 2 6
	4679
	904 nt
	85.2%
	85.2%

▶ ORF Summary		
Total ORFs:	4930	100.0 %
assigned function	2521	51.1 %
conserved hypothetical	871	17.7 %
unknown function	378	7.7 %
hypothetical proteins	1162	23.6 %

▶ Role Breakdown				
role id	name	number	complete	%
main	Unclassified	2	0	0.04%
185	Role category not yet assigned	2	0	0.04%
main	Amino acid biosynthesis	91	0	1.85%
70	Aromatic amino acid family	17	0	0.34%
71	Aspartate family	24	0	0.49%
73	Glutamate family	21	0	0.43%
74	Pyruvate family	13	0	0.26%
75	Serine family	8	0	0.16%
161	Histidine family	8	0	0.16%
69	Other	0	0	0.00%
main	Purines, pyrimidines, nucleosides, and nucleotides	63	0	1.28%
123	2'-Deoxyribonucleotide metabolism	8	0	0.16%
124	Nucleotide and nucleoside interconversions	11	0	0.22%

“Annotation Tools”

The Annotation Tools section contains most of the tools used during the process of manual annotation.

Get there by clicking “Annotation Tools” on the “Welcome to Manatee” page.

The screenshot shows the Manatee web interface. At the top, there is a navigation bar with links for Home, Help, Logout, and a user login status: "Logged into [cgsp] : organism: Shewanella oneidensis MR-1". Below this is a sub-header: "Welcome to Manatee". A grey box below the sub-header contains the text: "This is the main menu page for the Manatee tool. One can access genes directly (with gene's id number or name) or link to additional menus with more options." The main content area is divided into several sections. The first section is "ACCESS LISTINGS", which contains three items: "Annotation Tools", "Genome Summary", and "Genome Viewer". The "Annotation Tools" item is highlighted with a red rectangular box. Below this section are three radio button options: "ACCESS GENE CURATION PAGE", "SEARCH GENES BY PROTEIN NAME", and "CHANGE ORGANISM DATABASE". Each option has a corresponding input field: "gene_id:" for the first, "protein name:" for the second, and "database:" for the third. To the left of these input fields are "submit" and "reset" buttons. Below the "CHANGE ORGANISM DATABASE" section are three radio button options: "BLASTN", "BLASTP", and "TBLASTN". Below these is a text area labeled "Paste nucleotide or protein sequence below:". Below the text area is a link: "Run against NCBI databases: NCBI Blast". The final section is "Data file downloads (potentially long download times)", which contains a list of tools: "GO Dumper", "Nucleotide Sequence Dumper", "Protein Sequence Dumper", "Annotation Dumper", "Genbank Dumper", "GFF3 Dumper", and "TBL Dumper".

Annotation Tools Page: “Search Genes By: gene_id /locus”

This option will take you directly to a page containing gene specific information called the “Gene Curation Page” or “GCP” for short. The GCP displays most of what knowledge we have about a given protein - you will be seeing this page in much more detail later. For now just know that you can reach this page by entering either a gene_id or locus id (e.g. ghi_1234, xyz_23) into this box and then clicking “submit”. The gene_ids displayed in Manatee will be locus ids if those are available, or they will be internal tracking ids that are used prior to locus id assignments. Locus ids (loci) are assigned to proteins sequentially from the origin of replication of the genome (if it can be identified). Loci are unique accessions and are used for public release and display of the proteins.

Annotation Tools [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: *Shewanella oneidensis* MR-1

The ann_tools.cgi script generates the Annotator Tools webpage, which is the entry point for accessing the Submit webpage for all ORFs in a genome, as well a resource for locating general properties of the genome and determining the progress made in the Annotation of the genome of interest.

Home **Annotation Tools** Genome Summary Gene Naming and Annotation

ACCESS GENE LISTS

▶ molecule:

all genes, ordered by role category

main role category

single role category

SEARCH GENES BY:

gene_id / locus:

protein name:

gene symbol:

EC number:

ACCESS GENES BY COORDINATE RANGE

▶ end5: end3:

OTHER TOOLS

▶ PubMed Organism Search

Annotation Tools Page

Search genes by: protein name or gene symbol

This is a keyword-based search for the common names and gene symbols that have been given to the genes/proteins

Whatever keyword you enter will be treated as though it has wildcards flanking it. This means that you will get results that include names with your keyword as an individual word and names with words that contain your keyword.

For example, if you search with “kinase”

you could get these:

“adenylate kinase”

“protein kinase”

“sensor histidine kinase”

as well as these:

“glutamate 5-kinase”

“phosphoenolpyruvate carboxykinase”

“ribose-phosphate pyrophosphokinase”

The results will be in the form of a table containing additional information and links to other pages - this table format will be described later.

Annotation Tools [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: Shewanella oneidensis MR-1

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Home Annotation Tools Genome Summary Gene Naming and Annotation

ACCESS GENE LISTS

▶ molecule: All molecules

all genes, ordered by role category

main role category: Unclassified

single role category: role_id

SEARCH GENES BY:

gene_id / locus:

protein name:

gene symbol:

EC number:

ACCESS GENES BY COORDINATE RANGE

▶ end5: end3:

OTHER TOOLS

▶ PubMed Organism Search

submit reset

Annotation Tools Page

Search Gene By: EC number

The Enzyme Commission maintains a database of enzymatic reactions which are each assigned an accession number of this format:

1.17.3.2

this is the id number for xanthine oxidase

Each position in the number indicates an additional level of specificity, a four position number is the most specific level and identifies a specific enzyme.

For more information go to:
www.chem.qmul.ac.uk/iubmb

For the search, enter an EC number to see a list of all genes in the genome that have been annotated with that particular EC number.

Annotation Tools [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: *Shewanella oneidensis* MR-1

The ann_tools.cgi script generates the Annotator Tools webpage, which is the entry point for accessing the Submit webpage for all ORFs in a genome, as well a resource for locating general properties of the genome and determining the progress made in the Annotation of the genome of interest.

Home **Annotation Tools** Genome Summary Gene Naming and Annotation

ACCESS GENE LISTS

▶ molecule: All molecules

all genes, ordered by role category

main role category: Unclassified

single role category: role_id

SEARCH GENES BY:

gene_id / locus:

protein name:

gene symbol:

EC number:

ACCESS GENES BY COORDINATE RANGE

▶ end5: end3:

OTHER TOOLS

▶ PubMed Organism Search

submit reset

Annotation Tools Page

“Access genes by coordinate range” search:

Input a coordinate range and you will get a list of genes whose coordinates fall anywhere in that range.

If the genome consists of more than one molecule results from all molecules will be shown

The screenshot shows the 'Annotation Tools' web interface. The 'ACCESS GENES BY COORDINATE RANGE' section is highlighted with a red box. It includes input fields for 'end5:' and 'end3:'. Other sections include 'ACCESS GENE LISTS' with filters for molecule, role category, and search options like 'gene_id / locus', 'protein name', 'gene symbol', and 'EC number'. There are 'submit' and 'reset' buttons.

▶ List of all genes found between 10000 - 20000

A	C	gene id	locus	end5	end3	role id	gene name	gene symbol	ec
		ORF02375	SO0017	22090	18941	156	conserved hypothetical protein		
		ORF02378	SO0016	18279	18854	132	DNA-3-methyladenine glycosidase I	tag	3.2.2.20
		ORF02379	SO0015	18161	17256	137	glycyl-tRNA synthetase, alpha subunit	glyQ	6.1.1.14
		ORF02381	SO0014	17246	15180	137	glycyl-tRNA synthetase, beta subunit	glyS	6.1.1.14
		ORF02382	SO0013	14311	15111		hypothetical protein		
		ORF02383	SO0012	13791	13129	96 102,	glutathione S-transferase family protein		
		ORF02385	SO0011	10638	13055	132	DNA gyrase, B subunit	gyrB	5.99.1.3
		ORF02386	SO0010	9539	10621	132	DNA replication and repair protein RecF	recF	
		ORFA00005	SOA0024	20332	19523	154	ISSo1, transposase OrfB		
		ORFA00006	SOA0023	19154	19453	94 186,	proteic killer suppressor protein	higA	
		ORFA00007	SOA0022	18774	19079	94 186,	proteic killer active protein	higB	
		ORFA00008	SOA0021	18235	18462	154 270,	ISSo1, transposase OrfB, truncation		
		ORFA00009	SOA0020	17414	18154	154 270,	transposase family protein, truncation		
		ORFA00011	SOA0019	16733	17290	132 154,	TnSon1, resolvase		
		ORFA00012	SOA0018	16362	16739	154 156,	TnSon1, conserved hypothetical protein		
		ORFA00013	SOA0017	16075	16365	703	TnSon1, nucleotidyltransferase domain protein		
		ORFA00014	SOA0016	15911	12945	154	TnSon1, transposase		
		ORFA00015	SOA0015	12878	12732		hypothetical protein		
		ORFA00016	SOA0014	12332	12427		hypothetical protein		
		ORFA00017	SOA0013	11739	11335	132	umuD protein	umuD	3.4.-.-
		ORFA00019	SOA0012	11334	10078	132	umuC protein	umuC	

“Annotation Tools”: “Access Gene Lists” section

This tool will create a table of genes chosen according to the options in the red box at right. This tool allows one to view the genes organized by TIGR role category.

The first option to select in this section is which molecule you wish to annotate. Some genomes consist of just one chromosome and nothing else, while others can have multiple chromosomes and/or one or more plasmids. If multiple DNA molecules exist for the genome in question, the pull down menu at the top of this section will list them along with their id number. The default selection is “All molecules”. To choose just one of the molecules, simply select it from the pull-down menu.

Next, choose one of the 3 options for which role categories you want to see genes from with the toggle buttons: first you can choose all role categories, second you can choose one particular main role category, and third you can choose one particular sub-role category. All of the mainrole categories are listed in the pull-down menu in the main role category selection, to choose one, simply highlight it. In order to select a particular sub-role category you must enter into the box next to “single role category” the id number of the sub-role category. There is a listing of all of the TIGR role categories and their id numbers on the next two pages of this tutorial.

Once you have chosen your desired options, click submit to see a list of the genes that fit your selections.

Annotation Tools [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: *Shewanella oneidensis* MR-1

The ann_tools.cgi script generates the Annotator Tools webpage, which is the entry point for accessing the Submit webpage for all ORFs in a genome, as well as a resource for locating general properties of the genome and determining the progress made in the Annotation of the genome of interest.

Home Annotation Tools Genome Summary Gene Naming and Annotation

ACCESS GENE LISTS

▶ molecule: All molecules

all genes, ordered by role category

main role category: Unclassified

single role category: role_id

SEARCH GENES BY:

gene_id / locus:

protein name:

gene symbol:

EC number:

ACCESS GENES BY COORDINATE RANGE

▶ end5: end3:

OTHER TOOLS

▶ PubMed Organism Search

submit

reset

14

TIGR Role Categories - Page 1

Unclassified (the automated program was unable to assign a role to these)

185 Role category not yet assigned

Amino acid biosynthesis

- 70 Aromatic amino acid family
- 71 Aspartate family
- 73 Glutamate family
- 74 Pyruvate family
- 75 Serine family
- 161 Histidine family
- 69 Other

Purines, pyrimidines, nucleosides, and nucleotides

- 123 2'-Deoxyribonucleotide metabolism
- 124 Nucleotide and nucleoside interconversions
- 125 Purine ribonucleotide biosynthesis
- 126 Pyrimidine ribonucleotide biosynthesis
- 127 Salvage of nucleosides and nucleotides
- 128 Sugar-nucleotide biosynthesis and conversions
- 122 Other

Fatty acid and phospholipid metabolism

- 176 Biosynthesis
- 177 Degradation
- 121 Other

Biosynthesis of cofactors, prosthetic groups, and carriers

- 77 Biotin
- 78 Folic acid
- 79 Heme, porphyrin, and cobalamin
- 80 Lipoate
- 81 Menaquinone and ubiquinone
- 82 Molybdopterin
- 83 Pantothenate and coenzyme A
- 84 Pyridoxine
- 85 Riboflavin, FMN, and FAD
- 86 Glutathione
- 162 Thiamine
- 163 Pyridine nucleotides
- 191 Chlorophyll
- 707 Siderophores
- 76 Other

Central intermediary metabolism

- 100 Amino sugars
- 698 One-carbon metabolism
- 103 Phosphorus compounds
- 104 Polyamine biosynthesis
- 106 Sulfur metabolism
- 179 Nitrogen fixation
- 160 Nitrogen metabolism
- 709 Electron carrier regeneration
- 102 Other

Energy metabolism

- 108 Aerobic
- 109 Amino acids and amines
- 110 Anaerobic
- 111 ATP-proton motive force interconversion
- 112 Electron transport
- 113 Entner-Doudoroff
- 114 Fermentation
- 116 Glycolysis/gluconeogenesis
- 117 Pentose phosphate pathway
- 118 Pyruvate dehydrogenase
- 119 Sugars
- 120 TCA cycle
- 159 Methanogenesis
- 105 Biosynthesis and degradation of polysaccharides
- 164 Photosynthesis
- 180 Chemoautotrophy
- 184 Other

Transport and binding proteins

- 142 Amino acids, peptides and amines
- 143 Anions
- 144 Carbohydrates, organic alcohols, and acids
- 145 Cations and iron carrying compounds
- 146 Nucleosides, purines and pyrimidines
- 182 Porins
- 147 Other
- 141 Unknown substrate

TIGR Role Categories - Page 2

DNA metabolism

132	DNA replication, recombination, and repair
183	Restriction/modification
131	Degradation of DNA
170	Chromosome-associated proteins
130	Other

Transcription

134	Degradation of RNA
135	DNA-dependent RNA polymerase
165	Transcription factors
166	RNA processing
133	Other

Protein synthesis

137	tRNA aminoacylation
158	Ribosomal proteins: synthesis and modification
168	tRNA and rRNA base modification
169	Translation factors
136	Other

Protein fate

97	Protein and peptide secretion and trafficking
140	Protein modification and repair
95	Protein folding and stabilization
138	Degradation of proteins, peptides, and glycopeptides
189	Other

Regulatory functions

261	DNA interactions
262	RNA interactions
263	Protein interactions
264	Small molecule interactions
129	Other

Signal transduction

699	Two-component systems
700	PTS
710	Other

Cell envelope

91	Surface structures
89	Biosynthesis and degradation of murein sacculus and peptidoglycan
90	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
88	Other

Cellular processes

93	Cell division
188	Chemotaxis and motility
702	Cell adhesion
702	Conjugation
96	Detoxification
98	DNA Transformation
705	Sporulation and Germination
94	Toxin production and resistance
187	Pathogenesis
149	Adaptations to atypical conditions
706	Biosynthesis of natural products
92	Other

Mobile and extrachromosomal element functions

186	Plasmid functions
152	Prophage functions
154	Transposon functions
708	Other

Unknown

703	Enzymes of unknown specificity
157	General

Hypothetical

156	Conserved
704	Domain
856	General

Disrupted reading frame

270	NULL
-----	------

Gene List: The results of your selection from the Access Listings tool are displayed in a gene list containing gene id number, locus (if available), coordinates of the gene (end5, end3), common name of the gene/protein, gene_sym, EC number, and other roles for the protein. Not all of these fields will be populated for every gene. The genes are organized by role category (if your selection included more than one.) There are many features of the gene list, and much information displayed - text describing a feature is boxed in the same color as the feature itself.

Gene List [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as 1
organism: Shewanella oneidensis MR-1

This List contains ORFs which are currently assigned to TIGR microbial role categories. It is sorted by role category.

[All categories](#)
[Unclassified](#)
[Amino acid biosynthesis](#)
[Purines, pyrimidines, nucleosides, and nucleotides](#)
[Fatty acid and phospholipid metabolism](#)
[Biosynthesis of cofactors, prosthetic groups, and carriers](#)
[Central intermediary metabolism](#)
[Energy metabolism](#)
[Transport and binding proteins](#)
[DNA metabolism](#)
[Transcription](#)
[Protein synthesis](#)
[Protein fate](#)
[Regulatory functions](#)
[Signal transduction](#)
[Cell envelope](#)
[Cellular processes](#)
[Mobile and extrachromosomal element functions](#)
[Unknown function](#)
[Hypothetical proteins](#)
[Disrupted reading frame](#)
[Viral functions](#)
[Glimmer rejects](#)

Amino acid biosynthesis

Aromatic amino acid family Role id: 70

A	C	seq id	gene id	locus	end5	end3	gene name	gene symbol	ec	other roles	start_edit
		cgsp.assembly.1	cgsp_196		3559863	3559588	trp operon repressor	trpR		261	
		cgsp.assembly.1	cgsp_4549		1415682	1416773	3-deoxy-7-phosphoheptulonate synthase		2.5.1.54		

Amino acid biosynthesis

Aspartate family Role id: 71

A	C	seq id	gene id	locus	end5	end3	gene name	gene symbol	ec	other roles	start_edit
		cgsp.assembly.1	cgsp_650		4487553	4486089	aspartate aminotransferase	lysA	4.1.1.20		
		cgsp.assembly.1	cgsp_872		1974639	1975523	aspartate hydroxylase	dapA	4.2.1.52		
		cgsp.assembly.1	cgsp_2588		4124415	4123060	aspartate kinase, monofunctional class		2.7.2.4		
		cgsp.assembly.1	cgsp_3091		1180790	1181590	aspartate hydroxylase	dapB	1.3.1.26		

Amino acid biosynthesis

Glutamate family Role id: 73

A	C	seq id	gene id	locus	end5	end3	gene name	gene symbol	ec	other roles	start_edit
		cgsp.assembly.1	cgsp_886		284611	285978	argininosuccinate lyase	argH	4.3.2.1		
		cesn.assembly.1	cesn_2045		3498002	3498820	pyruvate carboxylase	proC	6.4.1.3		

A pink dot will appear in the "C" column once an annotator has finished annotation for the gene and marked it "complete".

Link to role notes for this category

Click on the gene_id (feat_name) link to see the Gene Curation Page for each gene. Click on "GV" for Genome Viewer.

Clicking on the blue names of any mainrole category takes you to a gene list for that category.

The ORFs can be ordered according to any of the blue headers by clicking on that header.

Gene list link: Role information page:

TIGR annotators expert in particular role categories have written “role notes” to aid new annotators and annotators unfamiliar with the category in the annotation process. These notes contain information on what genes belong in the category and what genes don't, on the pathways found in particular categories, and on the TIGR naming conventions for proteins within the category.

The utility of these documents has diminished as metabolic pathway reconstruction tools and the Gene Ontology have become more prominent in the annotation process.

Shewanella oneidensis MR-1 | **Role Information For Role_id 77**

The role_info.cgi script is executed from the Submit web display page and directs the user to a web display page that contains Single Role Category.

Role 77 Biosynthesis of cofactors, prosthetic groups, and carriers - Biotin

Role Info:

```
Genes involved in the synthesis of biotin.

pathway from 6-carboxyhexanoyl-CoA plus L-alanine to biotin:
step  gene
1      8-amino-7-oxononanoate synthase (bioF)
TIGR00858: bioF
2      adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(bioA)
TIGR00508: bioA
3      dethiobiotin synthetase (bioD)
TIGR00347: bioD
4      biotin synthase (bioB)
TIGR00433: bioB
Other genes also involved:

BirA bifunctional protein (birA)
    acts as operon repressor, synthesizes corepressor, activates
biotin,
    and transfers activated biotin to proteins
biotin synthesis protein BioC (bioC)
    involved in an early, undefined step in biotin synthesis
biotin sulfoxide reductase (bisZ)
    changes biotin sulfoxide back to biotin, scavenging reaction
TIGR01738 bioH protein (bioH)
    in early steps of biotin biosynthesis
TIGR01204 bioW protein = 6-carboxyhexanoate--CoA ligase
    found in Bacillus and Methanoccus, involved in biotin
synthesis
    BioW plus BioF of Bacillus can replace bioC and bioH of E.
coli
    (says PMID:2110099)

In many, but by no means all, organisms most of these genes can be
found in an operon.

mioC protein: MioC is a flavodoxin thought to function as an electron
transporter (role_id=112) and in biotin biosynthesis (role_id=77).
mioC neighbors oriC in E. coli. Early studies on mioC expression
demonstrate a dramatic effect on initiation of chromosome duplication
at oriC on minichromosomes. This role has not been demonstrated in
duplication of the wild type chromosome. Additionally, the
minichromosome is not necessarily a valid model for chromosomal
replication. Because of this dubious association with chromosomal
```

Update Role Note For 77

Gene Curation Page

The Gene Curation Page (GCP) is likely the most important page within Manatee, it is certainly the one that annotators spend the bulk of their time looking at and working with.

This page can be accessed within Manatee from many places:

any gene list, the “Access Gene Curation Page” option on the Genome Summary/Annotation Tools pages, Genome Viewer, and more.

The GCP is a very complex page so we will look at it in sections. I will try to organize the descriptions of each section in roughly the same order that the concepts behind each section were reviewed in the Annotation Overview.

cgsp_4048 - Shewanella oneidensis MR-1 [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: Shewanella oneidensis MR-1

GENE CURATION INFORMATION

cgsp_4048 () ▶ View BER Searches (long load time) asmb_id: cgsp.assembly.1 ▶ Reload Page	end5/end3: 2856763 / 2855711 gene length: 1053 protein length: 350	database: cgsp feat_name / locus: <input type="text"/> <input type="button" value="New Gene"/>
Select Display <input type="button" value="v"/>		

GENE IDENTIFICATION

gene name:

gene_sym:

EC number(s):
 

EC GO suggestions:
▶ [GO:0004076](#) biotin synthase activity (molecular_function)

private comment:

public comment:

Gene Curation Page

Gene Curation Information

This section contains basic identifying information about the gene and some search and display options.

The [gene_id](#) of the gene is listed at the top of the page. The gene_id is followed in parentheses by the [locus name](#) (final loci are assigned to genes at the end of a project, once annotation is complete, but they may get temporary loci during the course of the project).

The [blue link](#) under these names is a link to a file containing the BER search results for this gene (see later slide). There is another link to this page further down the orf info page (will be seen in a later slide).

To the right of the ORF names is a box containing [coordinates, length, and molecular weight \(if available\)](#). “end5” is the 5’ coordinate for the beginning of the coding sequence, “end3” is the 3’ coordinate for the end of the coding sequence.

Finally on the extreme right is a box allowing you to move to another ORF info page by typing in the feat_name or locus in the box and clicking “[new gene](#)”. One can also change to an orf in a different genome by [changing the database](#) in the database box, typing in the new orf number and clicking “new gene”.

If you want to reload the GCP, use the “[Reload Page](#)” link in this section. Do not use the browser’s reload button.

cgsp_4048 - Shewanella oneidensis MR-1		Home Help Logout Logged into [cgsp] : organism: Shewanella oneidensis MR-1
GENE CURATION INFORMATION		
cgsp_4048 () View BER Searches (long load time) asmb_id: cgsp.assembly.1 Reload Page	end5/end3: 2856763 / 2855711 gene length: 1053 protein length: 350	database: cgsp feat_name / locus: <input type="text"/> <input type="button" value="New Gene"/>
Select Display <input type="button" value="v"/>		

GENE IDENTIFICATION		<input type="button" value="submit"/>
gene name: <input type="text" value="biotin synthase"/>		
gene_sym: <input type="text" value="bioB"/>		
EC number(s): <input type="text" value="2.8.1.6"/>	EC GO suggestions: GO:0004076 <input type="button" value="add"/> biotin synthase activity (molecular_function)	
private comment: <input type="text"/>	public comment: <input type="text"/>	

Gene Curation Page

Gene Identification

Initial information for this section comes from AutoAnnotate. The manual annotation then confirms or changes the information.

gene name: the descriptive name given to the protein

gene sym: the gene symbol for the protein (in this case bioB) (we default to E. coli gene symbols when possible and B. subtilis for Gram + specific things)

EC#: If the protein is an enzyme, we store the Enzyme Commission number. See later slides for info on ECGO term suggestions.

private comment: a field for annotators to note information for later reference by themselves or other annotators. A good place to keep notes.

public comment: comments meant to go out with our public accessions .

cgsp_4048 - Shewanella oneidensis MR-1 [Home](#) | [Help](#) | [Logout](#) | Logged into [cgsp] as organism: Shewanella oneidensis MR-1

GENE CURATION INFORMATION

<p>cgsp_4048 ()</p> <p>▶ View BER Searches (long load time)</p> <p>asmbld_id: cgsp.assembly.1</p> <p>▶ Reload Page</p>	<p>end5/end3: 2856763 / 2855711</p> <p>gene length: 1053</p> <p>protein length: 350</p>	<p>database: cgsp</p> <p>feat_name / locus: <input type="text"/></p> <p><input type="button" value="New Gene"/></p>
<p>Select Display <input type="button" value="v"/></p>		

GENE IDENTIFICATION

[submit](#) |

gene name:

gene_sym:

EC number(s):
 

private comment:

EC GO suggestions:
 ▶ [GO:0004076](#) biotin synthase activity (molecular_function)

public comment:

Gene Curation Page - BER Skim and Characterized Match

The characterized match section is where we enter the accession of a match gene whose function has been characterized in the lab (as opposed to having received its name based on sequence similarity.) This is stored as a piece of annotation evidence. This accession will pop into the go with_evidence field in the proper format if you click on “Add to GO Evidence”. (more on GO data later)

The BTAB SKIM section shows the top hits from the BER search file (see Annotation Overview presentation for more information on BER searches). The first column is the accession of the match protein (from various databases), the second is the percent similarity of the match, the third is the length of the match (in nucleotides), the fourth is the name of the match protein and finally, the P score from the BLAST search.

The color of the background for each entry in the skim indicates whether it is in the characterized table and at what confidence level: **green**=high confidence; **red**=automated process; **sky blue**=partial characterization; **olive**=trusted, used when multiple extremely good lines of evidence exist for function but no experiment has been done; **blue-green**=fragment/domain has been characterized; **fuzzy gray**=void, used to indicate that something that was originally thought to be characterized really is not; **gray**=omnium only

Clicking on the **blue accession number** will automatically populate the field in the characterized match section with that accession which can then be used as GO evidence. Clicking on the **blue names of the proteins** in the skim will take you to a page with just the alignment to that protein. The blue “**View BER searches**” link at the top of the skim section will take you to a file of all of the pairwise alignments from the BER search (see later slide).

BER SKIM				
			View BER Searches	search date: Wed Oct 23 12:59:20 2002
accession	%sim	length	description	p-value
OMNI:SO2740	100.0	349	biotin synthase (Shewanella oneidensis MR-1)	1.5e-176
SP:P36569	80.7	340	Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (Serotia	2.5e-119
SP:P12996	79.7	342	Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (Escherich	7.2e-120
GP:145425	79.7	342	biotin synthetase (Escherichia coli)	1.5e-119
GP:12620127	79.4	342	biotin synthase BioB (uncultured bacterium pCosHE2)	1.5e-119
OMNI:NTL03EC0855	79.4	342	biotin synthetase (Escherichia coli O157:H7 VT2-Sakai)CGP13	5.1e-119
OMNI:NTL01YP1094	81.0	340	biotin synthase (Yersinia pestis CO92)COMNIINTL02YP2986 biot	8.3e-119
GP:12620099	79.5	340	BioB-like protein (uncultured bacterium pCosFS1)	9.5e-118
OMNI:NTL02EC0848	79.1	342	biotin synthesis, sulfur insertion? (Escherichia coli O157:H	2.2e-118
SP:Q47862	79.2	339	Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (Erwinia h	3.6e-118
SP:P12678	78.6	344	Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (Salmonell	5.1e-119
OMNI:VC1112	81.8	348	biotin synthase (Vibrio cholerae El Tor N16961)CGP9655583g	5.1e-119
OMNI:NTL03ST0726	78.6	344	biotin synthetase (Salmonella enterica serovar Typhi CT18)CG	1.1e-118
OMNI:NTL03PA00501	78.9	348	biotin synthase (Pseudomonas aeruginosa PAO1)CGP9946364gbl	7.7e-116
GP:12407614	76.8	339	biotin synthase BioB (uncultured bacterium pCosAS1)	9.1e-113
OMNI:NTL01XC0388	79.2	311	biotin synthase (Xanthomonas campestris pv. campestris ATCC3	2.8e-111
OMNI:NTL01XA0388	78.5	311	biotin synthase (Xanthomonas axonopodis pv. citri 306)CGP21	6.6e-110
OMNI:NTL02BA0265	77.0	340	biotin synthase (Buchnera aphidicola Sg)CGP12623185gblAAM6	1.4e-109
OMNI:NTL01XF00065	79.4	309	biotin synthase (Xylella fastidiosa 9a5c)CGP19104834gblAAF8	8.4e-110
OMNI:NTL01RS0266	79.5	306	PROBABLE BIOTIN SYNTHASE PROTEIN (Ralstonia solanacearum GMI	4.7e-109
SP:P57378	77.3	342	Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (Buchnera	1.1e-107
GP:15419053	79.1	328	biotin synthase (Acinetobacter calcoaceticus)	1.6e-106
OMNI:CC3521	76.2	339	biotin synthase (Caulobacter crescentus CB15)CGP13425251gbl	3.0e-105
OMNI:NTL01BMA0776	79.8	311	BIOTIN SYNTHASE (Brucella melitensis 16M)CGP17984969gblAAL	6.3e-105

BER Alignment detail: Boxed Header

66.0/79.7% over 343aa	<i>Escherichia coli</i>
<ul style="list-style-type: none"><li data-bbox="220 329 1923 609">• SP P12996BIOB_ECOLI Biotin synthase (EC 2.8.1.6) (Biotin synthetase). (exp=1; wgp=-1; cg=-1; closed=-1; pub=1; rf_status=;)RF NP_415296.1 16128743 NC_000913 biotin synthase {Escherichia coli K12;} (exp=0; wgp=1; cg=1; closed=1; pub=1; rf_status=provisional;)RF AP_001406.1 89107626 AC_000091 biotin synthase {Escherichia coli W3110;} (exp=0; wgp=1; cg=1; closed=1; pub=1; rf_status=provisional;)RF YP_309738.1 74311319 NC_007384 biotin synthesis	

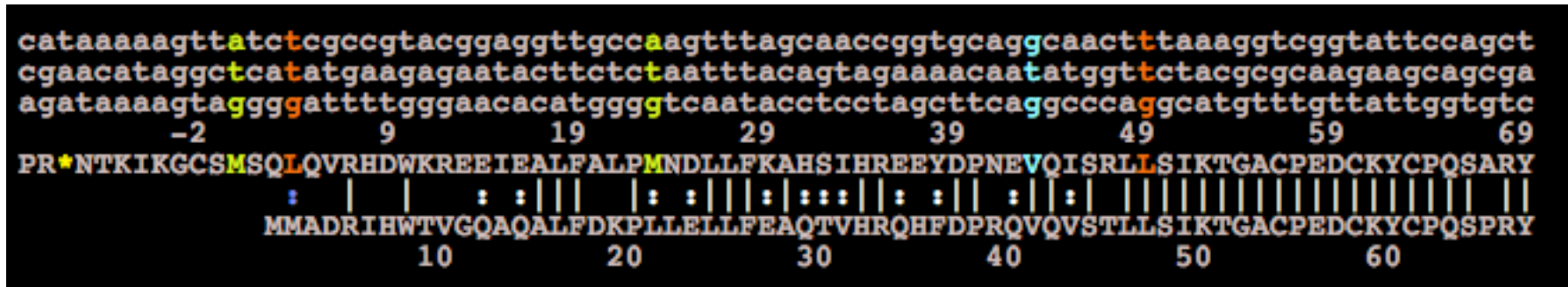
- The background color of this box will be gold if the protein is in the characterized table and grey if it is not.
- The top bar lists the percent identity/similarity and the organism from which the protein comes (if available).
- The bottom section lists an accession numbers and names for instances of the match protein from the search databases. The accession numbers are links to pages for the match protein in the source databases.
- A particular entry in the list will have colored text (the color corresponding to its characterized status) if that is believed to have experimental evidence - this tells the annotators which link they should follow to find experimental characterization information. Only one accession for the match protein need be characterized for the header to turn gold.

BER Alignment detail: alignment header

```
ORF04813( 7 - 348 of 351 aa)  
SP|P36569|BIOB SERMA(5 - 345 of 346) Biotin synthase (EC 2.8.1.6) (Biotin synthetase).  
%Identity = 67.5 %Similarity = 80.7  
Gaps = 2 InDels = 9 Frame Shifts = 0  
Primary Frame = 1 [340, 0, 0]
```

- It is most important to look at the range over which the alignment stretches and the percent identity
- The top line show the amino acid coordinates over which the match extends for our protein
- The second line shows the amino acid coordinates over which the match extends for the match protein, along with the name and accession of the match protein
- The last line indicates the number of amino acids in the alignment found in each forward frame for the sequence as defined by the coordinates of the gene. The primary frame is the one starting with nucleotide one of the gene. If all is well with the protein, all of the matching amino acids should be in frame 1.
- If there is a frameshift in the alignment (see overview) the phrase “Frame Shifts = #” will flash and indicate how many frameshifts there are.

BER Alignment detail: alignment of amino acids



- In these alignments the codons of the DNA sequence read down in columns with the corresponding amino acid underneath.
- The numbers refer to amino acid position. Position 1 is the first amino acid of the protein. The first nucleotide of the codon coding for amino acid 1 is nucleotide 1 of the coding sequence. Negative amino acid numbers indicate positions upstream of the predicted start of the protein.
- Vertical lines between amino acids of our protein and the match protein (bottom line) indicate exact matches, dotted lines (colons) indicate similar amino acids.
- Start sites are color coded: ATG is green, GTG is blue, TTT is red/orange
- Stop codons are represented as asterisks in the amino acid sequence. An open reading frame goes from an upstream stop codon to the stop at the end of the protein, while the gene starts at the chosen start codon.

Swiss-Prot entry - slide #1 - top of page

SwissProt is an incredibly useful database for manual annotation. All of the genes in SwissProt have been manually annotated by an experienced knowledgeable staff. In addition, along with each protein's annotation is stored additional information on references that describe the protein, cross referenced databases in which the protein can be found, motifs which the protein contains, and coordinates of any known features in the protein (and much more.)

accession and
version
information

name, EC#
gene_symbol
taxonomy

references with
links to
abstracts (click
on NCBI to see
a PubMed
abstract of the
paper)

NiceProt View of Swiss-Prot: [P12996](#)

[Printer-friendly view](#) [Submit update](#) [Quick BlastP search](#)

[\[Entry info\]](#) [\[Name and origin\]](#) [\[References\]](#) [\[Comments\]](#) [\[Cross-references\]](#) [\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the corresponding entry document.

Entry information

Entry name	BIOB_ECOLI
Primary accession number	P12996
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 13, January 1990
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 44, July 2004

Name and origin of the protein

Protein name	Biotin synthase
Synonyms	EC 2.8.1.6
Gene name	Name: bioB
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria ; Proteobacteria ; Gammaproteobacteria ; Enterobacteriales ; Enterobacteriaceae ; Escherichia .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=89066784;PubMed=3058702 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]
[Otsuka A.J.](#), [Buoncrisiani M.R.](#), [Howard P.K.](#), [Flamm J.](#), [Johnson O.](#);
"The Escherichia coli biotin biosynthetic enzyme sequences predicted from the nucleotide sequence of the bio operon.";
[J. Biol. Chem.](#) 263:19577-19585(1988).
- [2] SEQUENCE FROM NUCLEIC ACID.
[Pearson B.M.](#), [McKee R.A.](#);
"Genetic material for expression of biotin synthetase enzymes.";
Patent number [GB2216530](#), 11-OCT-1989.
- [3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=K 12 / MG1655;
MEDLINE=97426617;PubMed=9278503 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]
[Blattner F.R.](#), [Plunkett G. III](#), [Bloch C.A.](#), [Perna N.T.](#), [Burland V.](#), [Riley M.](#), [Collado-Vides J.](#), [Glasner J.D.](#), [Rode C.K.](#), [Mayhew G.F.](#), [Gregor J.](#), [Davis N.W.](#), [Kirkpatrick H.A.](#),
[Goeden M.A.](#), [Rose D.J.](#), [Mau B.](#), [Shao Y.](#);
"The complete genome sequence of Escherichia coli K-12.";
[Science](#) 277:1453-1474(1997).
- [4] CHARACTERIZATION.
PubMed=8142361 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]
[Sanval I.](#), [Cohen G.](#), [Flint D.H.](#);
"Biotin synthase: purification, characterization as a [2Fe-2S] cluster protein, and in vitro activity of the Escherichia coli bioB gene product.";
[Biochemistry](#) 33:3625-3631(1994).
- [5] MUTAGENESIS OF CYSTEINE RESIDUES.
MEDLINE=21547100;PubMed=11686025 [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]

Link to Enzyme Commission page
(see later slide)

Swiss-Prot entry - slide #2 - middle of page

useful
functional
information

links to
other dbs
where the
protein is
found or to
motif
clusters or
protein
families
which this
protein is a
member of

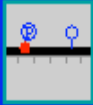
Comments	
	<ul style="list-style-type: none"> • CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin. • COFACTOR: Binds a 4Fe-4S cluster coordinated with 3 cysteines and an exchangeable S-adenosyl-L-methionine, and a 2Fe-2S cluster coordinated with 3 cysteines and 1 arginine. • PATHWAY: Biotin biosynthesis; last step. • SUBUNIT: Homodimer. • SIMILARITY: Belongs to the biotin and lipoic acid synthetases family.
Copyright	
	<p>This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch)</p>
Cross-references	
EMBL	J04423; AAA23515.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] A11530; CAA00965.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AE000180; AAC73862.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	JC2517 ; SYECBB.
PDB	1R30; 13-JAN-04 [Expasy / RCSB / EBI]
ECO2DBASE	E038.6 ; 6TH EDITION.
EchoBASE	EB0116 ; -.
EcoGene	EG10118 ; bioB.
EcoCyc	EG10118 ; bioB.
CMR	P12996 ; b0775.
InterPro	IPR010722 ; BATS. IPR002684 ; Biotin_synth. IPR006638 ; Elp3/MiaB/NifB. IPR007197 ; Radical_SAM. Graphical view of domain structure.
Pfam	PF06968 ; BATS; 1. PF04055 ; Radical_SAM; 1. Pfam graphical view of domain structure.
SMART	SM00729 ; Elp3; 1.
TIGRFAMs	TIGR00433 ; bioB; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P12996 .
ProtoNet	P12996 .
ProtoMap	P12996 .
PRESAGE	P12996 .
DIP	P12996 .
ModBase	P12996 .
SMR	P12996 ; 550A7899A2DF6082.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Swiss-Prot entry - slide #3 - bottom of page

keywords and sequence features with coordinates

Keywords
[2Fe-2S](#); [3D-structure](#); [4Fe-4S](#); [Biotin biosynthesis](#); [Complete proteome](#); [Iron-sulfur](#); [Transferase](#).

Features



[Feature table viewer](#)

Key	From	To	Length	Description
METAL	53	53		Iron-sulfur 1 (4Fe-4S).
METAL	57	57		Iron-sulfur 1 (4Fe-4S).
METAL	60	60		Iron-sulfur 1 (4Fe-4S).
METAL	97	97		Iron-sulfur 2 (2Fe-2S).
METAL	128	128		Iron-sulfur 2 (2Fe-2S).
METAL	188	188		Iron-sulfur 2 (2Fe-2S).
METAL	260	260		Iron-sulfur 2 (2Fe-2S).
CONFLICT	63	63		S -> T (in Ref. 1).

sequence features

Sequence information

Length: **346 AA** Molecular weight: **38648 Da** CRC64: **550A7899A2DF6082** [This is a checksum on the sequence]

```

10      20      30      40      50      60
|       |       |       |       |       |
MAGRPRTWLS QVTELFKPL LDLLFPAQV HQQHFDPQV QVSTLLSIKT GACPEDCKYC

70      80      90      100     110     120
|       |       |       |       |       |
PQSSRYKTGL EAERLMEVQ VLESARKAKA AGSTRICMGA AWKNPHEEDM FYLEQWQGV

130     140     150     160     170     180
|       |       |       |       |       |
KAMGLEACMT LGTLESQQAQ KLANAGLDYY NBNLDTSPF YGNIITRTY QERLDTLEKY

190     200     210     220     230     240
|       |       |       |       |       |
RDAGIKVCSG GIVGLGTYK DRAGLLQLA NLPDPPEVY INPLVKVKGK PLADNDVDA

250     260     270     280     290     300
|       |       |       |       |       |
EDFIRTIAWA RIMPTSYR LSAGREQME QTQAMCMAG ANSIFYGCKL LPTNPPEEDK

310     320     330     340
|       |       |       |
DLQLFKLGL NPQQTAVLAG DNEQQRLQ ALPTDTEY YNAAL
    
```

P12996 in [FASTA format](#)

View of EC number info page from Swiss Institute of Bioinformatics site

NiceZyme View of ENZYME: EC [2.8.1.6](#)

Official Name	
Biotin synthase.	
Alternative Name(s)	
Biotin synthetase.	
Reaction catalysed	
Dethiobiotin + sulfur <=> biotin	
Cofactor(s)	
Iron-sulfur.	
Comments	
<ul style="list-style-type: none"> The sulfur donor has been unidentified to date - it is not elemental sulfur or an iron-sulfur cluster. 	
Cross-references	
BRENDA	2.8.1.6
EMP/PUMA	2.8.1.6
WIT	2.8.1.6
Kyoto University LIGAND chemical database	2.8.1.6
IUBMB Enzyme Nomenclature	2.8.1.6
IntEnz	2.8.1.6
MEDLINE	Find literature relating to 2.8.1.6
Swiss-Prot	P54967 , BIOB_ARATH ; P19206 , BIOB_BACSH ; P53557 , BIOB_BACSU ; P57378 , BIOB_BUCAI ; Q8K9P1 , BIOB_BUCAP ; Q89AK5 , BIOB_BUCBP ; P12997 , BIOB_CITFR ; P46396 , BIOB_CORGL ; P12996 , BIOB_ICOLI ; Q47862 , BIOB_ERWHE ; P44987 , BIOB_HAEIN ; Q92JK8 , BIOB_HELPJ ; Q25956 , BIOB_HELPY ; Q58692 , BIOB_METWA ; P94966 , BIOB_METSK ; P46715 , BIOB_MYCLE ; Q06601 , BIOB_MYCTU ; P12678 , BIOB_SALTY ; Q59778 , BIOB_SCHPO ; P36569 , BIOB_SERMA ; P73538 , BIOB_SYMYS ; P32451 , BIOB_YEAST ;

[View entry in original ENZYME format](#)

[All Swiss-Prot entries referenced in this entry](#), with possibility to download in different formats, align etc.

Link to official Enzyme Commission site

View of information page for an EC number at IUBMB site

The Enzyme Commission (EC) is part of the IUBMB and is charged with maintaining the database of enzyme classifications. In the EC system, each reaction is assigned a 4 part accession number with each part consisting of an integer, where the numbers are separated by periods. As one moves from the first number to the second to the third to the fourth the nature of the reaction becomes more specific. For example: EC2.-.- = “transferase”, 2.8.-.- = “transferase, transferring sulfur-containing groups”, 2.8.1.- = “sulfurtransferases”, and finally 2.8.1.6 = “biotin synthase” (a specific sulfurtransferase, which is a specific class of transferases that transfer sulfur-containing groups). One can see the breakdown of all of the classes within each EC first number (they only go up to 6) by clicking on the home page for each number (see below).

IUBMB Enzyme Nomenclature

EC 2.8.1.6

Common name: biotin synthase

Reaction: dethiobiotin + sulfur = biotin

Systematic name: dethiobiotin:sulfur sulfurtransferase

Comments: an iron-sulfur enzyme. The sulfur donor has been unidentified to date - it is not elemental sulfur or an iron-sulfur cluster.

Links to other databases: [BRENDA](#), [EXPASY](#), [KEGG](#), [ERGO](#), [PDB](#), CAS registry number: 80146-93-6 (204794-88-7, 179608-56-1, 209603-31-6, 153554-27-9, 174764-24-0 and 215108-34-2)

References:

1. Shiuan, D., Campbell, A. Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons. *Gene* 67 (1988) 203-211. [Medline UI: [89006280](#)]
2. Zhang, S., Sanyal, I., Bulboaca, G.H., Rich, A., Flint, D.H. The gene for biotin synthase from *Saccharomyces cerevisiae*: cloning, sequencing, and complementation of *Escherichia coli* strains lacking biotin synthase. *Arch. Biochem. Biophys.* 309 (1994) 29-35. [Medline UI: [94161552](#)]

[EC 2.8.1.6 created 1999]

Return to [EC 2.8.1 home page](#)
Return to [EC 2.8 home page](#)
Return to [EC 2 home page](#) → Click here to see all the classifications within EC #2 (the transferases).
Return to [Enzymes home page](#)
Return to [IUBMB Biochemical Nomenclature home page](#)

Gene Curation page - HMM hits scoring above noise

(Text describing the features of the HMM section is boxed in the same color as each feature.)

The blue id numbers for each HMM link to an info page for that HMM.

Key information is the isology type and the “total” and “cutoff” scores.

The “Add To GO Evidence” link automatically fills the HMM information into the “with” field in the GO term entry box.

GO terms assigned to each HMM are listed under the HMM (if any). Clicking on the “Add” button here adds not only the GO term id, but also the HMM evidence.

The “Add To Annotation” link will automatically copy the annotation from the HMM to the protein.

Click to see hits below noise

HMM submit all hmms

▶ [TIGR00433: biotin synthase](#) gene_sym: bioB ec#: 2.8.1.6 role_id: 77 tc_num: none [Add To Annotation]

Isology: equivalog
Total score: 564.1 Trusted cutoff: 300.0 Gathering cutoff: 300.0 Noise cutoff: 50.0 Total expect: 2e-166
Trusted cutoff2: 300.0 Gathering cutoff2: 300.0 Noise cutoff2: 50.0

Coords	HMM Coords	Score	Expect	Curation	[Add To GO Evidence]
17-313	17-313 / 350				

▶ [GO:0004076](#) add biotin synthase activity (F)
▶ [GO:0009102](#) add biotin biosynthetic process (P)

HMM report page - to get to this page click on an HMM accession number almost anywhere in Manatee

At the top is information about the HMM including HMM name, associated annotation (gene symbol, EC#, TIGR role, etc.) and comments from the authors.

Below is a list of all genes in the organism which hit the HMM and the scores they received. The row with the gold background is the protein of interest. Rows with a green background have scores below the trusted cutoff, rows with a purple background have scores below the noise cutoff.

Shewanella oneidensis MR-1 | TIGR00433 HMM Report for ORF04813 | [Home](#) | Logged into [gsp] as mlgwinn

This page displays information about a specific HMM accession as it relates to the ORF being annotated. General information about the model is presented, as well as an alignment of the model to the ORF and a list of all hits of this model to the genome. The user can follow links to more information about the model and other proteins that the model hits.

accession and name	TIGR00433: biotin synthase				
expanded name	biotin synthetase				
gene symbol	bioB	EC number	2.8.1.6	HMM length	350
model type	equivalog	trusted cutoff	300.00	noise cutoff	50.00
author	Loftus BJ	created	04/20/99	last modified	09/23/03
related accession	IPR002684	accession type	InterPro assignment		
role category	77: Biosynthesis of cofactors, prosthetic groups, and carriers, Biotin				
gene ontology	GO:0004076 (function): biotin synthase activity GO:0009102 (process): biotin biosynthesis				
comment	Catalyzes the last step of the biotin biosynthesis pathway.				
private comment					

[Edit HMM Annotation](#)
[HMM Inter Link Editor](#)
[All DB Hits to TIGR00433](#)

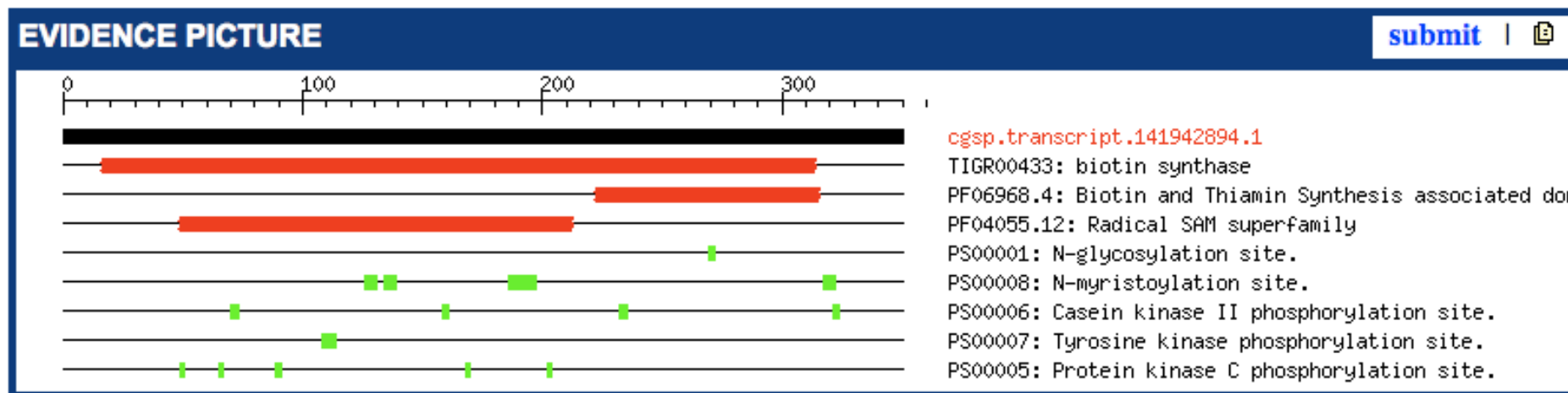
color key

- ▶ Protein of Interest.
- ▶ Scores below trusted cutoff (< 300.00).
- ▶ Scores below noise cutoff (< 50.00).

feat_name	role_id	EC number	gene region	HMM region	score	gene name
ORF04813	77	2.8.1.6	18-313	1-350	564.1	biotin synthase
ORF03390	157	-	34-331	1-350	-168.2	biotin synthase family protein
ORF01034	80	-	76-296	1-350	-178.3	lipoic acid synthetase
ORF03392	162	-	62-370	1-350	-187.3	thiH protein, putative

Gene Curation Page - Evidence Picture - ORF04813

All of the evidence stored for an ORF is displayed in this graphic. The black bar represents the ORF in question. Green bars represent HMMs which hit the ORF above trusted cutoff. Green HMM bars indicate above trusted score, orange indicates above noise but below trusted, red indicates below noise and is generally not shown unless an annotator has decided that the HMM should be included as evidence by toggling the curation box. The pink bar represents the characterized match to this ORF. Characterized matches are shown in different colors that at this time have no meaning. Also shown here is a secondary structure prediction (not run on all genomes). Clicking on the colored bars in the graphic opens windows with additional information on that piece of evidence. To get additional cog info, you must click on the very skinny bar all the way to the left of the cog row. The evidence picture for ORF04813 does not contain all of the possible evidence types, so later slides will show some evidence pictures from other genes.

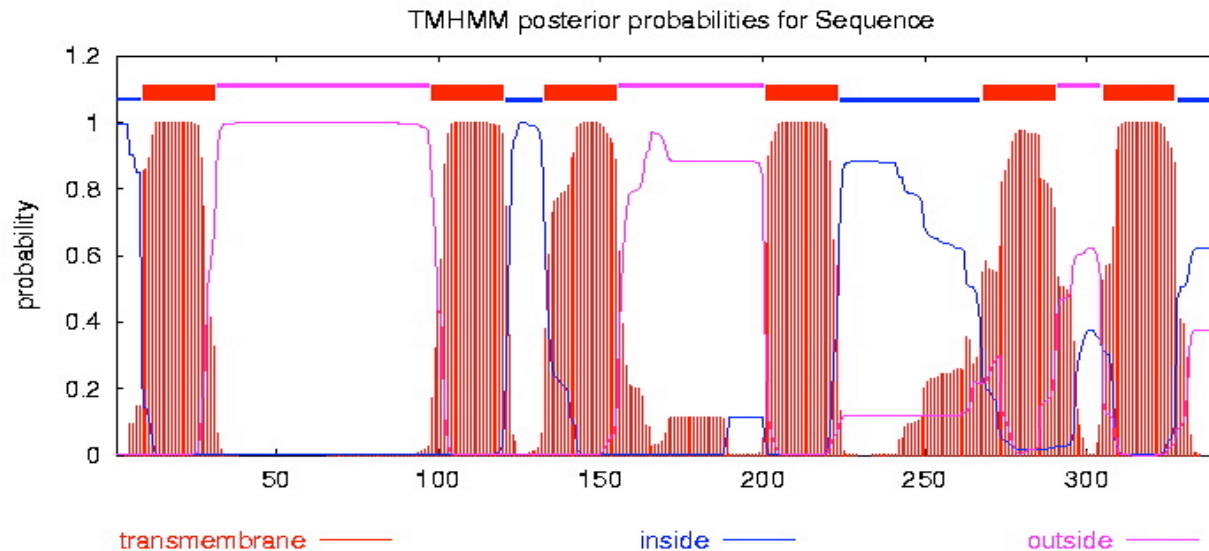


NOTE: this display is for ORF03779

TMHMM result

[HELP](#) with output formats

```
# Sequence Length: 343
# Sequence Number of predicted TMHs: 6
# Sequence Exp number of AAs in TMHs: 139.48261
# Sequence Exp number, first 60 AAs: 20.99155
# Sequence Total prob of N-in: 0.99734
# Sequence POSSIBLE N-term signal sequence
Sequence      TMHMM2.0      inside      1      8
Sequence      TMHMM2.0      TMhelix     9      31
Sequence      TMHMM2.0      outside     32     97
Sequence      TMHMM2.0      TMhelix     98    120
Sequence      TMHMM2.0      inside    121    132
Sequence      TMHMM2.0      TMhelix    133    155
Sequence      TMHMM2.0      outside    156    200
Sequence      TMHMM2.0      TMhelix    201    223
Sequence      TMHMM2.0      inside    224    267
Sequence      TMHMM2.0      TMhelix    268    290
Sequence      TMHMM2.0      outside    291    304
Sequence      TMHMM2.0      TMhelix    305    327
Sequence      TMHMM2.0      inside    328    343
```



[plot](#) in postscript, [script](#) for making the plot in gnuplot, [data](#) for plot

Gene Curation Page - PROSITE and Signal P sections on the GCP

NOTE: this display is for a different protein

Click here to see info on PROSITE motif.

PROSITE [submit](#) |

[PS01039](#): Bacterial extracellular solute-binding proteins, family 3 signature.
Match sequence: **GFDIELAKQIAKDA**

Coords	Precision	Recall	Curation	
52/65	0.76	0.93	<input checked="" type="checkbox"/>	[Add To GO Evidence]

ATTRIBUTES [submit](#) |

No Frameshifts Detected.

SIGNAL_P [submit](#) |

SignalP-2.0 Results: [\[Graphical Display\]](#) [\[Raw output for SP-HMM/NN\]](#)

SignalP-2.0 HMM

Prediction Curated

Signal peptide probability 0.984

Signal anchor probability

Max cleavage site probability 0.340

Click here to see output in graphical form.

The Korean ExPASy site, kr.expasy.org, is temporarily not available.

Search for Go Clear

PROSITE page at ExPASy

NiceSite View of PROSITE: [PDOC00798](#) NOTE: this display is for ORF01166 (documentation)

Bacterial extracellular family 3 signature

PROSITE cross-reference(s)

[PS01039: SBP BACTERIAL 3](#)

Documentation

Bacterial high affinity transport solutes across the cytoplasmic traffic systems include one or two membrane-associated ATP-binding proteins (e.g. [PDOC00185](#)) and a high affinity substrate transfer it to a complex of proteins in the cytoplasm.

In gram-positive bacteria which are surrounded by a single membrane and have therefore no periplasmic region the equivalent proteins are bound to the membrane via an N-terminal lipid anchor. These homolog proteins do not play an integral role in the transport process per se, but probably serve as receptors to trigger or initiate translocation of the solute through the membrane by binding to external sites of the integral membrane proteins of the efflux system.

In addition at least some solute-binding proteins function in the initiation of sensory transduction pathways.

On the basis of sequence similarities, the vast majority of these solute-binding proteins can be grouped into eight families of clusters which generally correlate with the

- Family 3 groups together proteins and a periplasmic h
- Histidine-binding protein of *Bacteroides nodosus*
 - Lysine/arginine/ornithine binding protein of *Escherichia coli* and related bacteria
 - Glutamine-binding protein of *Stearothermophilus*
 - Glutamate-binding protein of *Escherichia coli*
 - Arginine-binding proteins of *Escherichia coli*
 - Nopaline-binding protein of *Bacillus subtilis*
 - Octopine-binding protein of *Bacillus subtilis*
 - Major cell-binding factor of *Bacteroides nodosus*
 - Cyclohexadienyl/arogenate periplasmic enzyme which is involved in the biosynthesis of cyclohexadienyl derivatives
 - *Escherichia coli* protein
 - *Vibrio harveyi* protein
 - *Escherichia coli* hypothetical protein
 - *Bacillus subtilis* hypothetical protein
 - *Bacillus subtilis* hypothetical protein

The signature pattern is located

Description of pattern(s) and/or profile(s)	
Consensus pattern	G-[FYIL]-[DE]-[LIVMT]-[DE]-[LIVMF]-x(3)-[LIVMA]-[VAGC]-x(2)-[LIVMAGN]
Sequences known to belong to this class detected by the pattern	ALL.
Other sequence(s) detected in Swiss-Prot	23.
Last update	
November 1997 / Pattern and text revised.	
References	
[1] Tam R., Saier M.H. Jr. Microbiol. Rev. 57:320-346(1993).	
Copyright	
This PROSITE entry is copyright by the Swiss Institute of Bioinformatics (SIB). There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or email to license@isb-sib.ch).	

[View entry in original PROSITE document format](#)
[View entry in raw text format \(no links\)](#)

Gene Curation Page (ORF04813) - Gene Ontology Display

Current GO term assignments are listed in table.

- Click id # to see term in tree.
- Click box for GO term to be deleted.
- Click “add” to add additional evidence rows. (or click delete and add to completely redo evidence)
- Click “edit” to edit evidence.
- ”Make ISS”(not seen in this example) can be used when the GO term and evidence assigned by AutoAnnotate are correct, clicking this button marks the old association for deletion and automatically puts in the new info for insertion.

These pull downs have commonly used GO terms. If you choose the unknown terms from any pull-down, the evidence will automatically fill in (since it is always the same.)

Fill in the fields in this section to add or change GO term assignments. These columns are detailed on later slides.

Link to GO suggestions

Link to GO search tool

[submit](#) | [go sug](#) | [search](#) | [L](#)

delete	go id	assigned	date	evidence	
<input type="checkbox"/>	GO:0004076 [add] [edit]	(F) biotin synthase activity	mlgwin	07/29/04	ISS: PMID:12368813 with TIGR_TIGRFAMS:TIGR00433
<input type="checkbox"/>	GO:0009102 [add] [edit]	(P) biotin biosynthesis	mlgwin	07/29/04	ISS: PMID:12368813 with TIGR_TIGRFAMS:TIGR00433

function	process	component
▼	▼	▼

add go id	ev code	reference	with	qualifier
	ISS ▼	TIGR_CM:annotation ▼	▼	▼
	ISS ▼	TIGR_CM:annotation ▼	▼	▼
	ISS ▼	TIGR_CM:annotation ▼	▼	▼
	ISS ▼	TIGR_CM:annotation ▼	▼	▼
	ISS ▼	TIGR_CM:annotation ▼	▼	▼

GO data entry columns:

The format for all GO data is carefully controlled by the GO. Manatee knows all of the formatting rules and will format the data for you whenever you use the “add” or suggestions buttons. (more on this later)

GO id - the format is GO:#####.

ev code - pick an evidence code from the pull down.

reference - identifier for publication or other accessible text that describes experiments, methods, or SOPs as appropriate for the annotation being made. Format is DB:identifier (e.g. PMID:1234567)

with - used with ISS, IPI, IGI, IC, IGC. Format is DB:identifier. (e.g. UniProt:P12345)

qualifier - only used with some annotations. contributes_to is only used when annotating function to a subunit of a complex

GENE ONTOLOGY submit | go sug | search |

delete	go id		assigned	date	evidence
<input type="checkbox"/>	GO:0004076 [add] [edit]	(F) biotin synthase activity	mlgwin	07/29/04	ISS: PMID:12368813 with TIGR_TIGRFAMS:TIGR00433
<input type="checkbox"/>	GO:0009102 [add] [edit]	(P) biotin biosynthesis	mlgwin	07/29/04	ISS: PMID:12368813 with TIGR_TIGRFAMS:TIGR00433

function	process	component
<input type="text"/>	<input type="text"/>	<input type="text"/>

add go id	ev code	reference	with	qualifier
<input type="text"/>	ISS <input type="text"/>	TIGR_CM:annotation <input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	ISS <input type="text"/>	TIGR_CM:annotation <input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	ISS <input type="text"/>	TIGR_CM:annotation <input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	ISS <input type="text"/>	TIGR_CM:annotation <input type="text"/>	<input type="text"/>	<input type="text"/>
<input type="text"/>	ISS <input type="text"/>	TIGR_CM:annotation <input type="text"/>	<input type="text"/>	<input type="text"/>

Gene Curation Page - GO suggestions and Auto-fill-ins

GO term suggestions and auto-fill-in buttons are located in several places on the Gene Curation Page:

- GO terms assigned to [HMMs](#) are listed under HMM hits (if any have been assigned - see the HMM slide for how these look). These are often excellent sources for GO terms. Clicking the “Add” button next to a GO term under an HMM adds both the term id and the evidence to the appropriate fields in the GO entry section. Clicking the “Add to GO evidence” button adds just the HMM accession into the “with” field in the GO entry section.
- GO terms corresponding to [EC numbers](#) are listed next to the EC box (for enzymes). Clicking the “add” button will put the GO term id into the “add go id” fields in the GO entry section.
- “Add to GO evidence” buttons are also available for [Prosites](#) hits, this populates the “with” field with the Prosite accession. Available when a protein has matches to Prosite.
- “Add to GO evidence” is also available for the [characterized match accession](#), this will put the accession of the characterized matching protein into the “with” field entry box.

See next page for screen shots.

GO terms and evidence

Auto Fill-ins

Follow the arrows to see which fields are filled in by clicking the various GO "evidence" and "add" buttons around the GCP

add go id	ev code	reference	with	qualifier
	ISS	TIGR_CM:annotation		
	ISS	TIGR_CM:annotation		
	ISS	TIGR_CM:annotation		
	ISS	TIGR_CM:annotation		
	ISS	TIGR_CM:annotation		

EC GO suggestions:

▶ GO:0004076 biotin synthase activity (function)

HMM submit | all hms |

▶ TIGR00433: biotin synthase gene_sym: bioB ccf: 2.8.1.6 role_id: 77 tc_num: none [Add To Annotation]

Isology: equiolog
Total score: 54.1 Trustd cutoff: 300.00 Gathering cutoff: 300.00 Noise cutoff: 50.00 Total expect: 2e-166
Trimmed cutoff: 300.00 Gathering cutoff2: 300.00 Noise cutoff2: 50.00

Coords HMM Coords Score Expect Curation

17-313 7-313 / 1-6

▶ GO:0004076 biotin synthase activity (F)

▶ GO:0009102 biotin biosynthetic process (P)

[Add To GO Evidence]

CHARACTERIZED MATCH submit | history |

Add accession: ▶ Add To GO Evidence

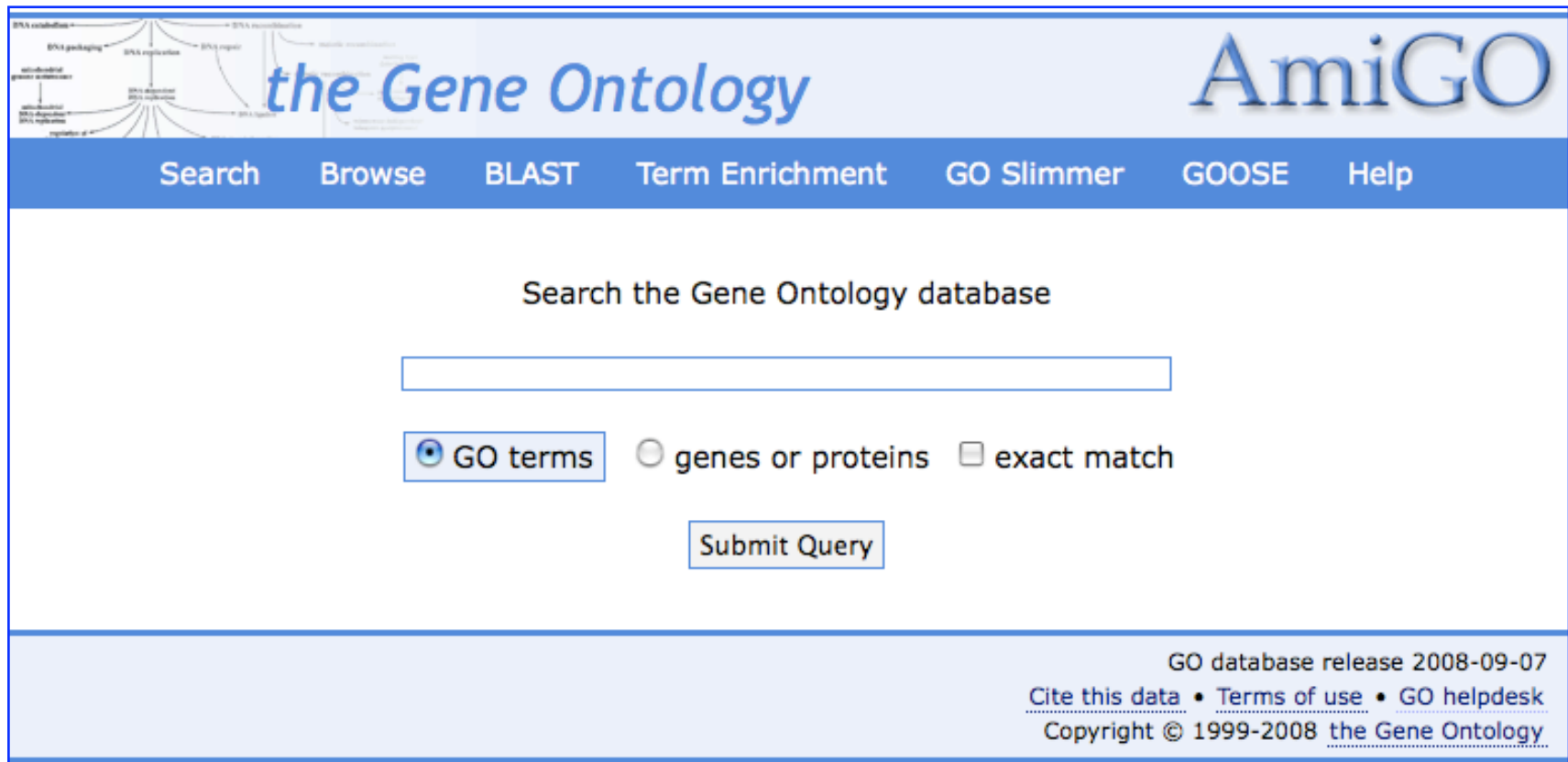
BER SKIM submit |

Alignment not found View BER Searches (log load time) search date: Thu Sep 4 16:09:24 2008

accession	cl	length	description	p-value	OMNI accession
GB_AA55798.1	100.0	349	biotin synthase (Shewanella oneidensis MR-1)	3.20e-185	SO_2740
GB_ABK4748.1	98.0	349	biotin synthase	1.00e-181	
GB_ABP5066.1	97.1	349	biotin synthase (Shewanella putrefaciens CN-32)	2.70e-181	
GB_ABN1261	95.7	349	biotin synthase (Shewanella halica DS155) [e]	1.50e-178	
GB_AB11327.1	86.0	349	biotin synthase (Shewanella frigidimarina NCIM)	2.00e-162	
GB_ABES5942.1	85.8	356	biotin synthase (Shewanella denitrificans OK2)	3.30e-160	NTL04SD1658
GB_ABQ2596.1	82.9	349	biotin synthase (Shewanella loihica PV-4) [ex]	5.50e-158	
GB_ABQ5945.1	83.4	352	biotin synthase (Shewanella amazonensis SB2B)	3.50e-156	
GB_ABK9458.1	70.3	342	biotin synthase (Aeromonas hydrophila subsp. 3)	9.10e-133	
GB_ABQ9889.1	69.8	342	biotin synthase (Aeromonas salmonicida subsp.)	1.20e-130	
GB_ABK3340.1	69.3	349	biotin synthase (Halobacterium salinarum R1)	9.70e-129	NTL01HC5119
GB_AAV3254.1	68.9	342	biotin synthase (Moraxella bovis L278)	3.80e-127	NTL01L1320
GB_ABG40773.1	67.8	345	biotin synthase (Pseudomonas fluorescens Pf-0)	5.00e-125	NTL06P42557
GB_AB118021.1	66.8	347	biotin synthase (Moraxella bovis L278)	3.90e-125	
GB_CALT7968.1	67.1	347	biotin synthase (Akkermansia muciniphila M2)	2.20e-124	NTL01AD2220
GB_ABK2796.1	66.6	343	biotin synthase (Saccharophagus degradans 2-40)	6.80e-123	NTL01SD2139
GB_CALT2943.1	67.4	342	biotin synthase (Yersinia enterocolitica subsp.)	3.80e-122	
SPF9569	67.5	340	biotin synthase (Yersinia enterocolitica subsp.)	7.50e-122	
GB_ABQ6988.1	66.0	342	biotin synthase (Escherichia coli 556) [exp-0]	2.50e-121	NTL12EC0774
GB_AA79328.1	66.0	342	biotin synthase	3.30e-121	
PDB:1R3V_A	66.0	342	Chain A, The Crystal Structure Of Biotin Synthase, An S- Ad	6.80e-121	
SPF1296	66.0	342	biotin synthase (Yersinia enterocolitica subsp.)	6.80e-121	
GB_ABH0113.1	66.0	342	biotin synthase (Shigella dysenteriae Sd197)	6.80e-121	NTL02SD00795
GB_AA42115.1	65.7	342	biotin synthase (Escherichia coli) [exp-0] wgp	1.40e-120	
GB_ABH0341.1	66.0	342	biotin synthase (Shigella boydii Sd227) [exp]	1.40e-120	NTL02SD0030
GB_AA25022.1	65.1	342	biotin synthase (Pseudomonas syringae pv. phaseolicola)	6.80e-121	PSPH1_4721
GB_AAY30743.1	65.1	342	biotin synthase (Pseudomonas syringae pv. syringae)	6.80e-121	NTL04P54667
GB_CAG2714.1	63.8	349	putative biotin synthase (Photobacterium profundum)	2.50e-121	NTL01P2259
RFP_NF_35403.1	65.7	342	biotin synthase, sulfur insertion (Shigella)	1.40e-120	
GB_BAB34276.1	65.7	342	biotin synthase (Escherichia coli O157:H7)	4.80e-120	NTL01EC0855
GB_CAB062.1	64.8	345	biotin synthase, contains an iron-sulfur cluster and PLP Pa	2.90e-120	NTL02P01568
AB01408-000000.1	64.4	349	biotin synthase (Pseudomonas fluorescens Pf-0)	1.40e-120	

Searching for GO terms: the AmiGO search tool:

In many cases the GCP will not have a suggested GO term that meets an annotators needs. In that situation the annotator can click on “Search GO” in the header of the search section and use AmiGO to find terms.



The image shows the AmiGO search interface. At the top left is a small diagram of the Gene Ontology hierarchy. The main header features the text "the Gene Ontology" and "AmiGO". Below the header is a navigation bar with links: Search, Browse, BLAST, Term Enrichment, GO Slimmer, GOOSE, and Help. The main content area is titled "Search the Gene Ontology database" and contains a search input field. Below the input field are three radio buttons: "GO terms" (selected), "genes or proteins", and "exact match". A "Submit Query" button is located below the radio buttons. At the bottom right of the page, there is a footer with the text: "GO database release 2008-09-07", "[Cite this data](#) • [Terms of use](#) • [GO helpdesk](#)", and "Copyright © 1999-2008 the Gene Ontology".

<http://amigo.geneontology.org/>

Gene Curation Page - TIGR roles

Click here to view/edit role notes

Click here to enter this role into the "Delete" box

Click on the name of the main role or sub role to take you to a page with the gene list for that main/sub role.

TIGR ROLES				submit	role help	history
role_id	delete	main role		sub role		
77	<input type="button" value="del"/>	Biosynthesis of cofactors, prosthetic groups, and carriers		Biotin		

Add role_ids (separate with spaces):

Delete role_ids (click on ids above):

Add or delete role ids with these boxes.

Click here for a list of TIGR roles.

Gene Curation Page - How to get the data into the database: The “Submit” buttons

SUBMIT DATA

- ▶ Start confidence not calculated.
- Start Site Curated:
- Completed:

Submit Reset

Click this button when you have completed annotation for this gene. With this toggle we know that this gene is finished.

Clicking this button indicates that you have reviewed the start site and either found it to be fine or edited it to the correct (or at least what we hope is correct) position.

Click here to submit your entries to the database. You can also do this by clicking on any of the “submit” buttons in the upper right of each section on the page. Clicking “submit” anywhere on the page submits data from all fields (not just the section from which you clicked the button.)

This button resets the page to the state it was when originally opened.

Gene Curation Page - The pull down menu

If you click on the pull down menu you will get a selection of options. Each of these when selected will generate a new page with the desired information. (Later slides show examples of some of these.)

The image shows two screenshots of a web interface for gene curation. The top screenshot displays 'GENE CURATION INFORMATION' for 'cgsp_4048 ()'. It includes fields for 'end5/end3', 'gene length', and 'protein length', along with a 'Reload Page' button and a 'Select Display' dropdown menu. The bottom screenshot shows a 'GENE' form with a 'submit' button, a 'gene name' field containing 'biotin synthase', and a 'gene_sym' field containing 'bioB'. A dropdown menu is open over the 'gene name' field, listing options: 'Select Display', 'Genome Viewer', 'View Sequences', '3rd Position GC Skew', and 'Signal Peptide Prediction'.

GENE CURATION INFORMATION		
cgsp_4048 () ▶ View BER Searches (long load time) asmbld_id: cgsp.assembly.1 ▶ Reload Page	end5/end3: 2856763 / 2855711 gene length: 1053 protein length: 350	database: cgsp feat_name / locus: <input type="text"/> <input type="button" value="New Gene"/>
<input type="text" value="Select Display"/>		

GENE	
gene name: <input type="text" value="biotin synthase"/>	<input type="button" value="submit"/>
gene_sym: <input type="text" value="bioB"/>	
EC number(s):	EC GO suggestions:

Genome Viewer

Access Genome Viewer from the Welcome to Manatee page or the pull down on the Gene Curation page. Genome Viewer provides a linear view of the coding genes and other features along the DNA molecule and provides a tool for gene model curation.

The screenshot displays the Manatee Genome Viewer interface. On the left, a navigation menu under "ACCESS LISTINGS" includes "Annotation Tools", "Genome Summary", and "Genome Viewer" (highlighted with a red box). A green arrow points from this menu item to the main viewer area. The main area shows a linear view of the genome with a scale from 1.261 Mb to 1.270 Mb. Several genes are represented by colored arrows: *cgsp_1637* (green), *cgsp_3113* (green), *cgsp_4448* (orange), *cgsp_417* (orange), *cgsp_800* (orange), *cgsp_2867* (orange), *cgsp_355* (pink), and *cgsp_309* (grey). Below the gene models, a detailed view of the transcript *cgsp.transcript.141930837.1* is shown, displaying a multi-segmented sequence with various colored blocks representing different features or annotations.

Gene Model Curation in Manatee: Genome Viewer

Genome Viewer
Shewanella onedensis MR-1 ()
Find Orf | Coord Search

logged into [gsp] as mlqwlwn
Search For ORF [] Go
chromosome (7974)

ORF02395 ORF02394 ORF02392 ORF02391 ORF08000

ORF02393 (C)
Coordinates: 3962 - 2589
Locus: SO_0003
Gene sym: trmE
Common Name: tRNA modification
GTPase TrmE
EC number:
Role ID: 168
Property: tRNA U34
carboxymethylaminomethyl
modification

ORF02393
Go to ORFInfo page
Edit this gene

Click

The arrows represent the predicted gene set. They are color-coded according to TIGR role id. The small arrows on the top represent the entire molecule along one scroll bar. The larger arrows depict a zoomed in view of one area of the genome. Mousing over the arrows brings up a box with info on the protein. Clicking on a small arrow will focus the zoom view onto that gene. Clicking on the info box in the zoomed view pops up a new box with links to other tools/pages. Underneath the zoomed view of the predicted genes is a graphical representation of a 6-frame translation of that region of DNA.

Genome Viewer - Gene Edit Page

ORF 02394

ORF 02395

ORF 02392

ORF 02393

ORF 02390

ORF 02391

ORF 08000

Gene Model

Name

End 5:

End 3:

Open reading frame

End 5:

End 3:

```

:CGGCGGAAAGGAAATCTACTAACTATCTATAAATTACCCATAAAGGCACTGTTGACTGTGATAGCACCGTGCCGGTGGCGGGGCCTG
 A A K E K L H N S L Y K I P I E T V V S V I T A C A V A G P
 P R R K R * I I Q Y I N L P Y K R S L Q C * R P V P W R A R V
 Q G G K G K S S K I S I * H T N G H C S V S D H C L G G R G S
;GCCGCCTTTCCCTTTAGATGATTTGATAGATATTTAATGGGTATTTCCGTGACAACTGACACTATCGTGGCACAGGCCACCGCGCCCGGAC
i R L F L * M I * * I F N G Y F R D N * H Y R G T G H R A R T
 P P F P L D D L I D I * M V F P * Q L T L S W H R P P R P D
 A A F S F R * F D R Y L H G I S V T T O T I V A Q O T R P G R
  
```

Choosing to edit a gene brings up this view. Two boxes with coordinates for the predicted gene and for the ORF in which it resides are displayed. At the bottom is a text version of a six frame translation of the sequence in the area. Predicted genes are highlighted. Start sites are color-coded. Clicking on a “start” in the sequence will bring up a box asking you to confirm the change.

Links from the Gene Curation Page - View sequence

This page shows the nucleotide and protein sequences in fasta format.

CDS

```
>cgs_p_4048
ATGTCGCAGTTGCAAGTTCGTCATGATTGGAAGCGGGAAGAAATCGAAGCCTTATTTGCG
CTGCCGATGAATGACTTATTATTTAAAGCCACAGTATCCACCGTGAAGAGTACGATCCT
AACGAAGTGCAGATCAGCCGCTTATTGTTCGATCAAACTGGGGCTTGTCTGAGGATTGT
AAATATTGTCCGAGAGTGGCGTTACGACACTGGCCTTGAAAAAGAGCGTCTCTTAGCG
ATGGAACCGTGCTCACCGAAGCGGTAGCGGAAAGCGGGCGCTTCGCGTTCTGT
ATGGGCGCCGCTTGGCGTAACCCGAAAGATAAAGATATGCCATACCTCAAGCAAATGGTG
CAAGAGGTGAAAGCCCTCGGCATGGAAACCTGTATGACCTTAGGGATGTTAAGTGCCGAG
CAAGCCAATGAGTTGGCCGAAGCAGGCCTTGACTATTACAACCACAATTTAGATACCTCG
CCTGAATACTACGGCGATGTGATCACCACCGTACCTATCAAAACCGCTTAGATACCTTA
AGCCATGTGCGCGCATCGGGCATGAAAGTTTGCTCTGGCGGCATGTGCGGCATGGGCGAG
AAGGCTACTGACAGAGCCGGTTTATTACAACAACCTGGCTAATTTACCCCAAGCATCCGGAT
TCTGTGCCGATCAATATGTTAGTCAAAGTAGCGGGTACCCCTTTGAAAACTTGATGAT
TTAGATCCACTCGAGTTTGTCCGAACCATCGCCGTGGCGCGTATTTAATGCCACTGTGCG
CGGTGCGTTTATCCGCAAGCCGTGAAAATATGAGCGATGAAGTGCAGGCCATGTGTTTC
TTTGGCGGGCGGAACTCGATTTTTTACGGCTGTAAGTTACTGACCACGCCCAACCCCGAA
GAAAGTGATGATATGGGGTTGTTCCGTCGCCTGGGTTTACGCCCTGAGCAGGGCGCAGCC
GCCTCTATTGATGATGAGCAAGCGGTATTAGCTAAAGCTGCGGCTTATCAAGATAAAGCT
TCAGCTCAGTTTTTATGATGCGGGCGGCACTATAA
```

Protein

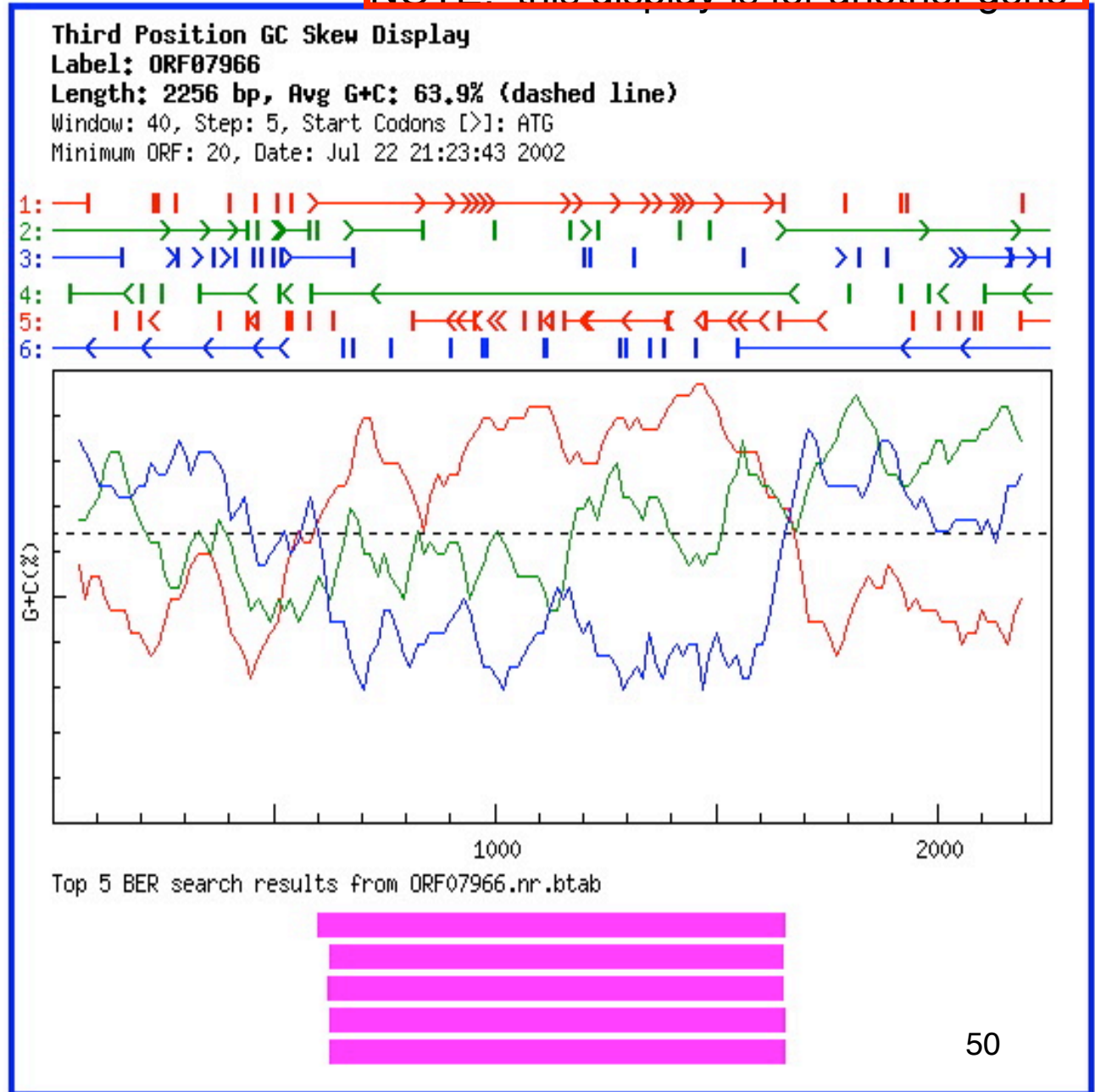
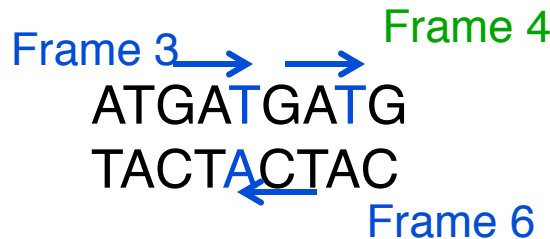
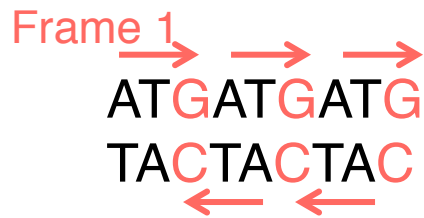
```
>cgs_p_4048
MSQLQVRHDWKREEIEALFALPMNDLLFKAHSIHREEYDPNEVQISRLLSIKTGACPEDC
KYCPQSARYDTGLEKERLLAMETVLTEARSAKAAGASRFCMGAAWRNPKDKDMPYLKQMV
QEVKALGMETCMTLGMLSAEQANELAEAGLDYYNHNLDTSP EYGDVITTRTYQNRLDTL
SHVRASGMKVCSSGGIVGMGEKATDRAGLLQQLANLPQHPDSVPINMLVKVAGTPFEKLDD
LDPLEFVRTIAVARILMPLSRVRLSAGRENMSDELQAMCFAGANSIFYGKLLTTPNPE
ESDDMGLFRRLGLRPEQGAASIDDEQAVLAKAAAYQDKASAQFYDAAAL
```

Links from the Gene Curation Page - Third position GC skew

NOTE: this display is for another gene

In organisms whose DNA has a high GC content it can sometimes be helpful to look at third position GC skew to help resolve overlaps.

Due to the nature of the genetic code, the third position is the least constrained of a codon and therefore will be able to reflect the higher GC content of the overall genome. Therefore one should see a markedly higher GC content in the third position of the correct frame.



Manual Annotation Checklist

- Look for HMM hits
 - evaluate what the HMMs are telling you - exact function? family membership? domain?
- Look at BER results
 - looking for proteins in the skim which are characterized (colored backgrounds)
 - many proteins are characterized but not marked so in our tables - may need to check proteins with white backgrounds to see if they are characterized
 - color coding does not indicate quality of match only that the match protein has been experimentally characterized
 - evaluate the alignment - what percent ID over what length? active sites? binding sites?
 - fill in characterized match accession number (by clicking on the accession in left column)
- Check Genome Viewer to view neighboring genes - annotate all genes in an operon together
- Look at TMHMM, SignalP, Prosite, region, etc.
- Decide what you think the protein should be named
- Fill in appropriate fields for common name, gene symbol, EC#, comment as needed.
- Decide what GO terms you need
 - find them on the Gene Curation Page (HMMs, EC number) or with the GO search tool AmiGO
 - change/remove any IEA GO annotations
 - add GO evidence from HMMs, BER, Prosite, etc.
- Review TIGR role and change as needed
- Check start site
 - Look at several BER matches, here you want to look at the best hits regardless of whether they are experimentally characterized
 - adjust if necessary – using Genome Viewer
 - check start site box when finished curation
- Check “complete”, click “submit” and your done!