



# Software Engineering

*A Report on Gene Sequence*

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# Task 1

## Goals:

1. Create an interface to upload a fasta file.
2. Validate the file with the given checks:
  - a. The information line starts with a '>' symbol only.
  - b. The information is contained in one single line and is not continued to the next line.
  - c. There is no blank line between the information line and gene sequence.
  - d. Gene sequence contains only four characters, A,T,G and C.
3. If validated, display the file contents as an output file.

## Requirements, Design and Implementation:

### Requirements:

- Fasta file
- Python 2.7

### Design and Implementation:

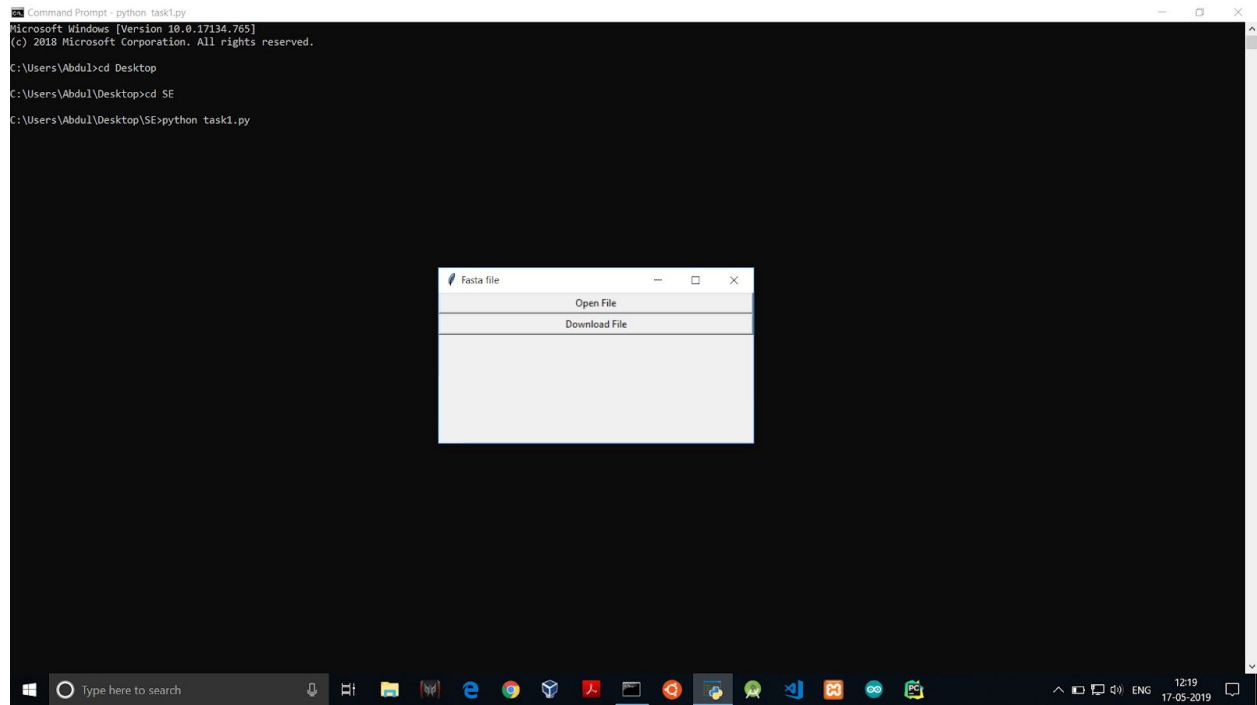
- We took the fasta file as input and parsed the input into different elements.
- The gene info sequence was checked to be single line only and that it started with > symbol, the gene sequence was checked to contain only A, T, G, C.
- The output was formatted into the required form as stated in the task.

## Testing Techniques Used and Bugs Found:

We used Black Box testing and found out the following bugs:

- The loop was running infinitely while checking for blank lines between information line and gene sequence.
- Even if there was a blank line between information line and gene sequence, the output was validated.

## Screenshots:



## Task 2

### Goals:

1. Connect the GUI to the database
2. Information that is contained in the database are:  
Sl.no, gene information, gene sequence, count\_A,count\_T,count\_G,count\_C,length  
(G+C)%

### Requirements, Design and Implementation:

#### Requirements:

- Fasta file
- Python 2.7
- MySQL database

#### Design and Implementation:

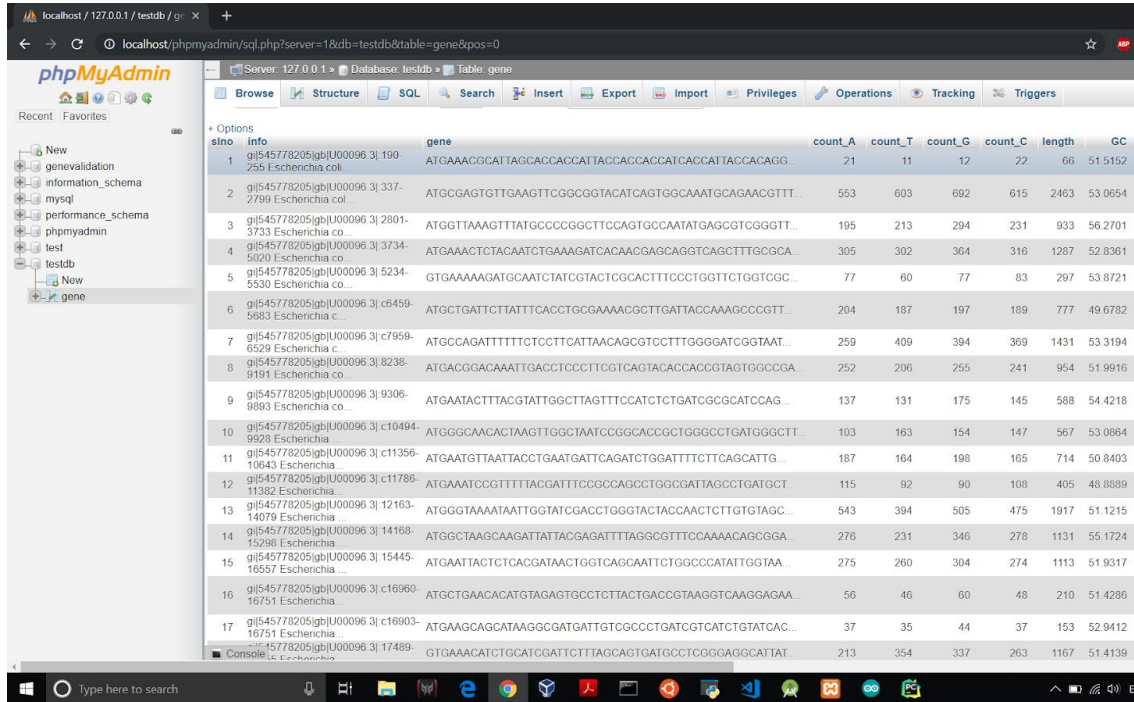
- We took the fasta file as input and parse it into the required components.
- Calculated the count\_A,count\_T,count\_G,count\_C,length,(G+C)%
- Designed the GUI and connected to the database.
- Inserted the values to the database.

### Testing Techniques Used and Bugs Found:

We used Black Box testing and found out the following bugs:

- The database insertion was not correct in the initial attempts.
- Some data was left out in the first attempt, which required reconsideration.

## Screenshots:



localhost / 127.0.0.1 / testdb / g...  
localhost/phpmyadmin/sql.php?server=1&db=testdb&table=gene&pos=0

phpMyAdmin

Recent Favorites

Database: testdb Table: gene

Options

gene

sldno	info	gene	count_A	count_T	count_G	count_C	length	GC
1	gi545778205.gb U00096.3 190-755 Escherichia coli	ATGAAACGCATTAGCACCACCATTACACCACCATTACCAATACCAAGG...	21	11	12	22	66	51.5152
2	gi545778205.gb U00096.3 337-2799 Escherichia coli	ATGCGAGTGTGAAGTTCGGCGGTACATCAGTGGCAATGCAGAACGTTT...	553	603	692	615	2463	53.0654
3	gi545778205.gb U00096.3 2801-3733 Escherichia coli	ATGGTTAAAGTTTATGCCCGGCTTCCAGTGGCAATATGAGCGTCGGGTT...	195	213	294	231	933	56.2701
4	gi545778205.gb U00096.3 3734-5020 Escherichia coli	ATGAAACTCTACAATCTGAAAGATCACAAAGAGCAGGTGAGCTTTGCGCA...	305	302	364	316	1287	52.8361
5	gi545778205.gb U00096.3 5234-5530 Escherichia coli	GTGAAAAGATGCAATCTATCGTACTGGCAGCTTCCCTGGTTCTGGTCGC...	77	60	77	83	297	53.8721
6	gi545778205.gb U00096.3 c6459-5683 Escherichia coli	ATGCTGATTCTTATTTACCTGCGAAACGGCTTATTACCAAAGCCCGTT...	204	187	197	189	777	49.6782
7	gi545778205.gb U00096.3 c7959-6529 Escherichia coli	ATGCCAGATTTTTTCTCCTTATTAACAGCGCTCTTTGGGGATCGGTAAT...	259	409	394	369	1431	53.3194
8	gi545778205.gb U00096.3 8238-9191 Escherichia coli	ATGACGGACAAATGACCTCCCTTCGTACGACACCGTAGTGCCGCA...	252	206	255	241	954	51.9916
9	gi545778205.gb U00096.3 9306-9893 Escherichia coli	ATGAATCTTTACGATTGGCTTAGTTTCCATCTCTGATCGCGCATCCAG...	137	131	175	145	588	54.4218
10	gi545778205.gb U00096.3 c10494-9928 Escherichia coli	ATGGGCAACACTAAGTTGGCTAATCCGGCACCGCTGGGCTGATGGGCTT...	103	163	154	147	567	53.0864
11	gi545778205.gb U00096.3 c11356-10643 Escherichia coli	ATGAATGTTAATTACCTGAATGATTGATCTGGATTTTCTTACGACATTG...	187	164	198	165	714	50.8403
12	gi545778205.gb U00096.3 c11786-11382 Escherichia coli	ATGAAATCGTTTTTACGATTTCCGCCAGCCTGGCGATTAGCGTGATGCT...	115	92	90	108	405	48.8889
13	gi545778205.gb U00096.3 12163-14079 Escherichia coli	ATGGCTAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTGTAGC...	543	394	505	475	1917	51.1215
14	gi545778205.gb U00096.3 14168-15298 Escherichia coli	ATGGCTAAGCAAGATTATACGAGATTTAGGCGTTTCCAAAACAGCGGA...	276	231	346	278	1131	55.1724
15	gi545778205.gb U00096.3 15445-16557 Escherichia coli	ATGAATTACTCTCACGATAACTGGTCAGCAATTCTGGCCCATATTGGTAA...	275	260	304	274	1113	51.9317
16	gi545778205.gb U00096.3 c16960-16751 Escherichia coli	ATGCTGAACACATGTAGATGCGCTCTTACTGACCGTAAGGTCAAGGAGAA...	56	46	60	48	210	51.4286
17	gi545778205.gb U00096.3 c16903-16751 Escherichia coli	ATGAAGCAGCATAAGGCGATGATTGTGCGCCTGATGTCATCTGTATCAC...	37	35	44	37	153	52.9412
	gi545778205.gb U00096.3 17489-...	GTGAAACATCTGCATCGATTCTTTAGCAGTGATGCTCGGGAGGCATAT...	213	354	337	263	1167	51.4139

Console

## Task 3

### Goals:

1. Add all the fields given in the gene detail list to the database.

Checks:

- If the location field of a gene in a gene sequence file contains:

- a. 1798....1800,1919....2020

If there is a comma-separated location then we can ignore this gene and not add to your database.

- b. c1666...17000

Here c means that the gene is present in the complementary strand, the location starting with c will be stored 17000...1666 in the gene detail list. While checking, check it in the reverse order.

### Requirements, Design and Implementation:

Requirements:

- Fasta file
- Python 2.7
- MySQL database

Design and Implementation:

- We took GeneDetails.txt file as input and created a dictionary to store the information.
- If the location field in the gene sequence file has the values 1798....1800,1919....2020 then remove that entry from the database.
- Inserted the updated values to the database.

### Testing Techniques Used and Bugs Found:

We used Black Box testing and bugs were found in the syntax of the SQL code. However, some gene sequence having a comma in them got included in the database, which we had to remove again by reconsidering all the possible errors.

## Screenshots:

The screenshot displays the phpMyAdmin interface for a MySQL database named 'testdb'. The 'gene' table is selected, and its structure is shown. The table has 14 columns: count\_A, count\_T, count\_G, count\_C, length, GC, location, strand, pid, geneshort, synonym, code, cog, and product. The data is displayed in a table format with 14 rows of gene sequences and their associated metadata.

	count_A	count_T	count_G	count_C	length	GC	location	strand	pid	geneshort	synonym	code	cog	product
CATTAGCACCACCATTACCACCACCATTACCACAGG...	21	11	12	22	66	51.5152	190.255	+	1786182	thrL	b0001	-	-	thr operon leader peptide
GTTGAAGTTCGGGGTACATCAGTGGCAATGCAGAACGTT...	553	603	692	615	2463	53.0654	337.2759	+	1786183	thrA	b0002	-	-	Bifunctional aspartokinase/homoserine dehydrogenas...
AGTTTATGCCCCGGCTTCAGTGCCAATATGAGCGTCGGGT...	195	213	294	231	933	56.2701	2801.3733	+	1786184	thrB	b0003	-	-	homoserine kinase
CTACAATCTGAAGATCACACGAGCAGGTGAGCTTTGCGCA...	305	302	364	316	1287	52.8361	3734.5020	+	1786185	thrC	b0004	-	-	L-threonine synthase
GATCAACTATCGTACTCGGCACTTCCCTGTTCTGTTGCG...	77	60	77	83	297	53.8721	5234.5530	+	1786186	yaaX	b0005	-	-	DUF2502 family putative periplasmic protein
TCTATTACCTCGGAAACGCTTGATTACAAAGCCGCTT...	204	187	197	189	777	49.6782	5683.6459	-	1786187	yaaA	b0006	-	-	peroxide resistance protein, lowers intracellular
TTTTTTCCTTCATTACACGCTGCTTTGGGGATCGGTAAT...	259	409	394	369	1431	53.3194	6529.7859	-	1786188	yaaJ	b0007	-	-	putative transporter
CAATTGACCTCCCTTGGTCAGTACACCGGTAGTGGCGCA...	252	206	255	241	954	51.9916	8238.9191	+	1786189	talB	b0008	-	-	transaldolase B
TTACGTAITGGCTTAGTTTCATCTCTGATCGGCAATCCAG...	137	131	175	145	588	54.4218	9306.9893	+	1786190	mog	b0009	-	-	molybdochelatase incorporating molybdenum into mol...
CACATAAGTTCGCTAATCCGGCACCCTGGGCTGATGGGCT...	103	163	154	147	567	53.0884	9928.10494	-	1786191	satP	b0010	-	-	succinate-acetate transporter
TAATTACCTGAATGATTGAGTCTGGATTCTTCAGCATG...	187	164	198	165	714	50.8403	10643.11356	-	1786193	yaaW	b0011	-	-	UFFF0174 family protein
CGTTTTACGATTTCCGGCAGCTGGCGATTAGCCTGATGCT...	115	92	90	108	405	48.8889	11382.11786	-	1786195	yaaI	b0013	-	-	UFFF0412 family protein
AATAATTGGTATCGACCTGGGTACTACCACTCTTGTGTAGC...	543	394	505	475	1917	51.1215	12163.14079	+	1786196	dnaK	b0014	-	-	chaperone Hsp70, with co-chaperone DnaJ
SCAAGATTATAGAGATTATAGGGTTTCCAAACACGGCGA...	276	231	346	278	1131	55.1724	14168.15298	+	1786197	dnaJ	b0015	-	-	chaperone Hsp40, DnaK co-chaperone
CTCTCAGTAACCTGGTCAGCAATCTGGCCCATATTGGTAA...	275	260	304	274	1113	51.9317	15445.16557	+	1786198	insL1	b0016	-	-	IS186 transposase
CACATGTAGAGTGCCTTACTGACCGTAAGGTCAAGGAGAA...	56	46	60	48	210	51.4286	16751.16960	-	1786200	mokC	b0018	-	-	regulatory protein for HokC, overlaps CDS of hokC
GCATAAGCGCATGATTGTGGCCTGATCGTCTGTATCAC...	37	35	44	37	153	52.9412	16751.16903	-	48994874	hokC	b4412	-	-	toxic membrane protein, small
TCGTGATCGATTCTTTAGCAGTGATGCTCGGGAGGCATAT...	213	354	337	263	1167	51.4139	17489.18655	+	1786201	nhaA	b0019	-	-	sodium-proton antiporter
GTCTCATATCAATTACAACCACTGTATTACTTCTGGCATGT...	233	243	227	203	906	47.4614	18715.19620	+	1786202	nhaR	b0020	-	-	transcriptional activator of nhaA
CAACAGCGCGCATATGGCGCTTGGCCTCAACACGATTTC...	122	107	149	126	504	54.5635	19811.20314	-	1786203	insB1	b0021	-	-	IS1 transposase B
TGTTTCTATCAGCTGTCCCTCTGTTTCAAGTACTGACGGGT...	65	65	66	80	276	52.8986	20233.20508	-	1786204	insA	b0022	-	-	IS1 repressor TnpA
Console:GCTAAGAGCGCGCCATTGAGTCTGAAAGGC...	89	52	57	66	264	46.5909	20815.21078	-	1786206	rpsT	b0023	-	-	30S ribosomal subunit

## Task 4

### Goals:

1. Convert the gene sequence into protein sequence.

Checks:

- If any stop codon appears within a gene sequence, the generate a warning message stating "Stop codon found in gene gene\_name". gene\_name you will get from Task 3.

### Requirements, Design and Implementation:

Requirements:

- Fasta file
- Python 2.7
- MySQL database

Design and Implementation:

- We took the GeneDetails.txt as input then scanned the input file and sequentially converted it to protein sequence.
- We have shown the output of the conversion into protein sequence in the database table by creating one new attribute for it.

### Testing Techniques Used and Bugs Found:

We used Black Box testing and bugs were found in the syntax of the SQL code, some codons remain unspotted, without stating the warning message.



## Screenshots:

localhost / 127.0.0.1 / testdb / g/ X

localhost/phpmyadmin/sql.php?server=1&db=testdb&table=gene&pos=0

Server: 127.0.0.1 Database: testdb Table: gene

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- genevalidation
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- New
- gene

count_T	count_G	count_C	length	GC	location	strand	pid	geneshort	synonym	code	cog	product	protein
11	12	22	66	51.5152	190.255	+	1786182	thrL	b0001	-	-	thr operon leader peptide	MMKRSTTTTTTTTTTTGNGAGStop
603	652	615	2463	53.0654	337.2799	+	1786183	thrA	b0002	-	-	Bifunctional aspartokinase/homoserine dehydrogenase	MMRVLKFGGTSVANAERFLRVADILESNAHQGGQVATVLSAPAKITNHLVA
213	294	231	933	56.2701	2801.3733	+	1786184	thrB	b0003	-	-	homoserine kinase	MMVKVYAPASSANMSVGFVDLGAANTPDGALLGDVVTVEAAETFSLNIL...
302	364	316	1287	52.8361	3734.5020	+	1786185	thrC	b0004	-	-	L-threonine synthase	MMKLYNLKDHNEQVSFAQAVTQGLGNQGLFFPHDLPEFSLTEIDEMLKL...
60	77	83	297	53.8721	5234.5530	+	1786186	yaaX	b0005	-	-	DUF2502 family putative periplasmic protein peroxide resistance	VVQKMQSIVLALSLVLVAPMAAAEITLPSVKLQIGDRNRGYYWDGG...
187	197	189	777	49.6782	5683.6459	-	1786187	yaaA	b0006	-	-	protein, lowers intracellular	MMILISPAKTLDYQSPLTTTRYTLPELLDNSQQLIHEARKLTPPQISTL...
409	394	369	1431	53.3194	6529.7959	-	1786188	yaaJ	b0007	-	-	putative transporter	MMPDFFFSINSLVWGSVMYLLFGAGCWTFRTGFVQFVRYRQFGKSLKN...
206	255	241	954	51.9916	8238.9191	+	1786189	talB	b0008	-	-	transaldolase B	MMTDKLTSLRQYTTVADTGDIAAMKLYGQDATTNPSIULNAAQIPEYR...
131	175	145	588	54.4218	9306.9893	+	1786190	mog	b0009	-	-	molybdochelatase incorporating molybdenum into mol...	MMNTLRIGLVSSDRASSGVYQDKGIPEALEEWLTSAITPFELETRUPD...
163	154	147	567	53.0864	9928.10494	-	1786191	satP	b0010	-	-	succinate acetate transporter	MMGNTKLANPAPLGLMGFCMTITLLNLINVGYYALDQILAMQIFYGIA...
164	198	165	714	50.8403	10643.11356	-	1786193	yaaW	b0011	-	-	UPF0174 family protein	MMNVNVLNDSLDLQHCSEELANFARLLTHNEKGKRLSSVLMRNEFL...
92	90	108	405	48.8889	11382.11796	-	1786195	yaaI	b0013	-	-	UPF0412 family protein	MMKSVFTISASLALSMLCCTAQANDHKLGAIAMPRNENDLAKLPVC...
394	505	475	1917	51.1215	12163.14079	+	1786196	dnaK	b0014	-	-	chaperone Hsp70, with co-chaperone DnaJ	MMGKIIGDLGTTNSCAVMDGTTPRVLENAEGDRTFSPHAYQDGETL...
231	346	278	1131	55.1724	14168.15298	+	1786197	dnaJ	b0015	-	-	chaperone Hsp40, DnaK co-chaperone	MMAKQDYIEILGVSKTAEEERIKAYKRLAMKYHPDRNQGDKEAEAKFE...
260	304	274	1113	51.9317	15445.16557	+	1786198	insL1	b0016	-	-	IS186 transposase	MMNYSHDNWSAILAHIGKPEELDTARNAGALTRRREIRDAATLLRLGLA...
46	60	48	210	51.4286	16751.16960	-	1786200	mkcC	b0018	-	-	regulatory protein for hokC, overlaps CDS of hokC	MMMLNCRVPLTRDKVKEKRAMKQHKAMIVALVICITAVAAALYTRKDL...
35	44	37	153	52.9412	16751.16903	-	48994874	hokC	b4412	-	-	toxic membrane protein, small	MMKQHKAMIVALVICITAVAAALYTRKDLCEVHRTQQTVEAVFTAYES...
354	337	263	1167	51.4139	17489.18655	+	1786201	nhaA	b0019	-	-	sodium-proton antiporter	VVQHLHRTSSDASGGIILIAILAMIMANSATSGWYHDFLETPVQLR...
243	227	203	906	47.4614	18715.19620	+	1786202	nhaR	b0020	-	-	transcriptional activator of nhaA	MMMSHINYNYLHYFWHYKYGSVVGAEALYLPQTITGQIRALEERLQ...
107	149	126	504	54.5635	19811.20314	-	1786203	insB1	b0021	-	-	IS1 transposase B	MMPGNSPHYGRWPQHDFTSLLKLRPQSVTSRIQPSQSDVVCAMDEQWGY...
65	66	80	276	52.8966	20233.20508	-	1786204	insA	b0022	-	-	IS1 repressor TnpA	VVASVSSISCPSCSATDGVARNKGSAGHGRYLCHCRKWTWOLQFTYASQ...
Console	57	66	264	46.5909	20815.21078	-	1786206	rpsT	b0023	-	-	30S ribosomal subunit protein S20	LLANKSAKKRAVQSEAKRKHNASRSMRRTFKKVVAAEAGDKAAVQK...

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## Task 5

### Goals

Calculate the effective number of codons for each Gene sequence and store them into the database.

### Requirements, Design and Implementation:

Requirements:

- Fasta file
- Python 2.7
- MySQL database

Design and Implementation:

- We took the GeneDetails.txt as input then scanned the input file and counted and stored the effective number of codons.
- We have shown the stored number of codons in one new attribute in the database.

### Testing Techniques Used and Bugs Found:

We used Black Box testing and found out that the number of codons was being incorrectly inserted into the database because of a error we made while declaring the data type for the number of codons(nc) field.

## Screenshots:

localhost / 127.0.0.1 / testdb / g: X +

localhost/phpmyadmin/sql.php?server=1&db=testdb&table=gene&pos=0

phpMyAdmin

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New

Server: 127.0.0.1 Database: testdb Table: gene

Browse

Structure

SQL

Search

Insert

Export

Import

Privileges

Operations

Tracking

Triggers

count	g	count_c	length	GC	location	strand	pid	gene	synonym	code	cog	product	protein	nc
12	22	66	51152	190.255	+	1786182	thrL	b0001	-	-	-	thr operon leader peptide	MMKRISITITITITITITGNGAGStop	10.6807
692	615	2463	53.0654	337.2799	+	1786183	thrA	b0002	-	-	-	Bifunctional aspartokinase/homoserine dehydrogenase	MMVRVLFGGTSGVANAERLRVADILESNAHQGVATVLSAPAKTNHLVA	46.846
294	231	933	56.2701	2801.3733	+	1786184	thrB	b0003	-	-	-	homoserine kinase	MMVKVYAPASSANMSVDFGLDAVPTVDGALLGDWTVAAETSLNLL	47.5021
364	316	1287	52.8361	3734.5020	+	1786185	thrC	b0004	-	-	-	L-threonine synthase	MMKILYNKDHNEQSFQAVTQGLKNGGVPFHDLPEFLSTEIDEMLLK	43.2397
77	83	297	43.8721	5234.5530	+	1786186	yaaX	b0005	-	-	-	DUF2502 family putative periplasmic protein	VWKMOSVLAISLVVAPHAQAQAEITVPSVKLGQDRDNRYWVGG	38.15
197	189	777	49.6782	5683.6459	+	1786187	yaaA	b0006	-	-	-	peroxide resistance protein, lowers intracellular	MMLLISPAKTLDYGSPILTRYTLPEELLNDSQILHEARKTLTPQISLT	40.1647
394	369	1431	53.3194	6529.7959	+	1786188	yaaJ	b0007	-	-	-	putative transporter	MMPPDFSFNSVLWGSVMYLLFAGCOWFTFRVGFQFRRYRQFGKSLKN	46.6498
255	241	954	51.9916	8238.8191	+	1786189	talB	b0008	-	-	-	transaldolase B	MMTKLTSRLQYTTVADTGDIAAMKLYQPDQATNPISLIINAQOIFEYR	36.8684
175	145	588	54.4218	9306.8893	+	1786190	mog	b0009	-	-	-	molybdochelataase incorporating molybdenum into mol...	MMNTLRGLVSLDRASSGVYQDKGFPALEEWTSALTTPFELETRLP...	43.8857
154	147	567	53.0894	9928.10494	+	1786191	satP	b0010	-	-	-	succinate oxidase	MMNGKICANPAPLGLMGFTMTILLNLHNWGYFALDGLIAMGFYGGBA	36.6805
198	165	714	50.8403	10043.11356	+	1786193	yaaW	b0011	-	-	-	UPF0174 family protein	MMNVNLYNDSLOFLHCCEQLEAFARLITLNEKGKTRLSVLMRNEFL	45.8997
90	108	405	48.8899	11332.11786	+	1786195	yaaI	b0013	-	-	-	UPF0412 family protein	MMKSVFTISALISLMLCTGAQANDHKLGAAMPNRETNDIALKIPVC	37.9354
505	475	1917	51.1215	12163.14079	+	1786196	dnaK	b0014	-	-	-	chaperone Hsp70, with co-chaperone DnaJ	MMKQIKGIDGLTNSVAMIDGTPRVLNAEQDRTTSPHAIYQDGETL	34.2894
364	278	1131	55.1724	14168.15298	+	1786197	dnaJ	b0015	-	-	-	chaperone Hsp40, DnaK co-chaperone	MMNAQZDYVYGSKTAEIEREKAYRMLKPTDNRNGQKEAEAFKE	40.5902
304	274	1113	51.9317	15445.16557	+	1786198	insL1	b0016	-	-	-	IS156 transposase	MMNYSCHDWASAILHAGKPEELDTSARNAGALTRRREIDATLRLGLA	52.4563
60	48	210	51.4286	16751.19690	+	1786200	mocK	b0018	-	-	-	regulatory protein for H <sub>2</sub> O <sub>2</sub> , overlaps CDS of hokC	MMMLNCRVLPTDRKYKEKRAMKQKHAMVALMVICATAVAALVTRKDL	31.5189
44	37	153	52.9412	16751.16903	+	4898474	hokC	b4412	-	-	-	toxic membrane protein, small	MMKQKHAMVALVICATAVAALVTRKDLCEVHRTQGEVATFAYTES	27.3562
337	263	1167	51.4139	17489.18655	+	1786201	rhaA	b0019	-	-	-	sodium-proton antiporter	VWKLHRRFSSQSGGILIAALIMANSQATSGWYHDLFTPVQLR	48.6066
227	203	906	47.4614	18715.19620	+	1786202	rhaR	b0020	-	-	-	transcriptional activator of rhaA	MMMSHSHYNLYHFHYHYKESVSGAAEALYLPQTITGQIRALEERLQ	48.4964
149	126	504	54.5635	19811.20314	+	1786203	insB1	b0021	-	-	-	IS1 transposase B	MMPNQSPHNGRWQPHDTLSKLKRPJRSITRQPSDSVIVCAEMDEQWY	41.7449
66	80	276	52.8966	20233.20508	+	1786204	insA	b0022	-	-	-	IS1 repressor TnpA	VVASNSICPSCSADTGVRNKGSTAGHORYLCSHCKRTWQLQFTEYTA	38.7559
■ Console	66	264	46.5909	20815.21078	+	1786206	rpsT	b0023	-	-	-	30S ribosomal subunit	LLNINKSAQRN/QSEKARG-NASRISMRITFRKQYVAIE/GDKAAQIK	27.8612

Type here to search

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