

# Basic Local Alignment Search Tool

[NCBI/ BLAST/ blastn suite/](#) Formatting Results - 3YWPU43M014

▶ [Formatting options](#)

▶ [Download](#)

[Blast report description](#)

Nucleotide Sequence (1437 letters)

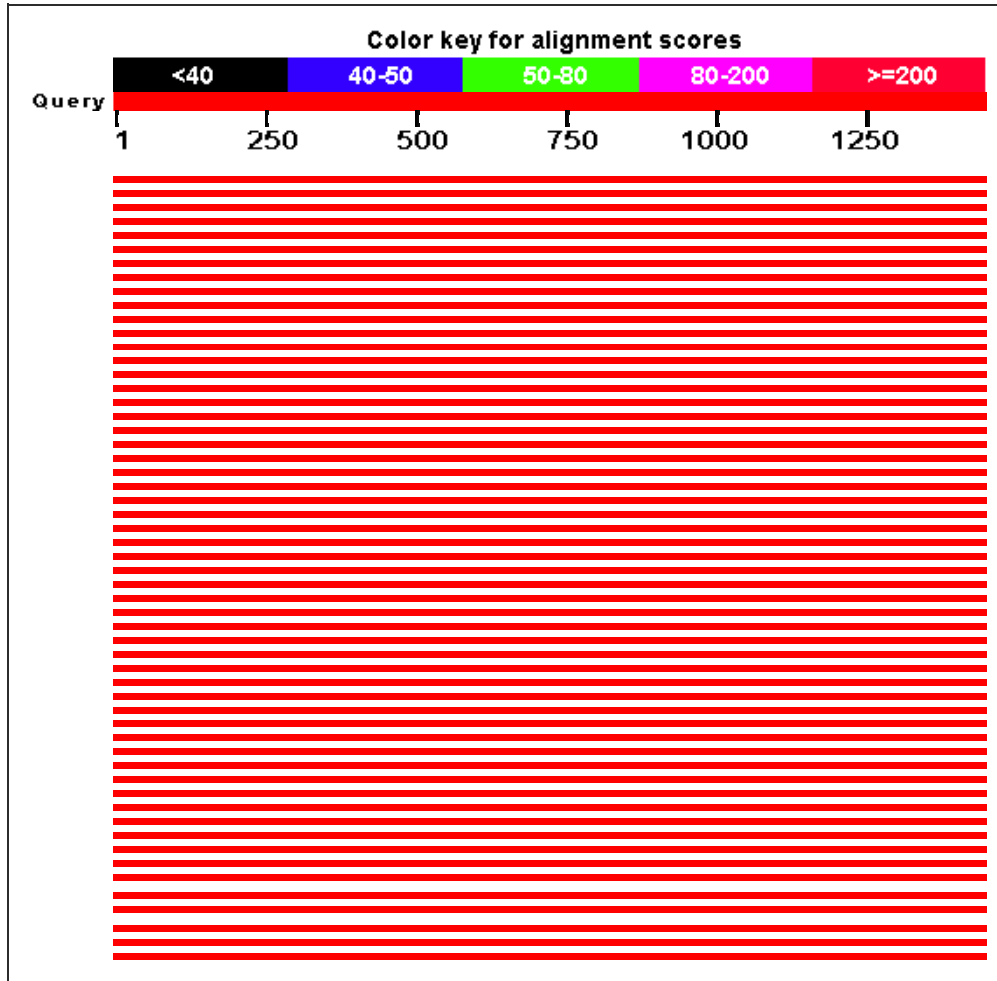
RID [3YWPU43M014](#) (Expires on 10-17 15:25 pm)

Query ID |cl|11067  
Description None  
Molecule type nucleic acid  
Query Length 1437

Database Name chromosome  
Description NCBI Chromosome Sequences  
Program BLASTN 2.2.30+

## Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



## ☰ Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Escherichia coli str. K-12 substr. MG1655 strain K-12 chromosome, whole genome shotgun sequence, complete genome	2592	2592	100%	0.0	100%	<a href="#">NZ_AKBV01000001.1</a>
Escherichia coli str. K-12 substr. MG1655 strain K-12 chromosome, whole genome shotgun sequence, complete genome	2592	2592	100%	0.0	100%	<a href="#">NZ_AKVX01000001.1</a>
Escherichia coli str. K-12 substr. MG1655 strain K-12 ctg718000000002_quiver, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_APIN01000002.1</a>
Escherichia coli str. K-12 substr. MG1655 strain K-12 cont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_AYEK01000001.1</a>
Escherichia coli str. K-12 substr. MG1655, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_000913.3</a>
Escherichia coli LY180, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_022364.1</a>
Escherichia coli UMEA 3609-1 acYAw-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE702425.1</a>
Escherichia coli UMEA 3240-1 acYxP-supercont1.3, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE702179.1</a>
Escherichia coli HVH 221 (4-3136817) acYAh-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE701070.1</a>
Escherichia coli HVH 164 (4-5953081) acYwz-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE700471.1</a>
Escherichia coli KTE132 acHaT-supercont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE137261.1</a>
Escherichia coli KTE71 acHaR-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE137100.1</a>
Escherichia coli KTE198 acHaY-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE136920.1</a>
Escherichia coli KTE34 acHbo-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE136741.1</a>
Escherichia coli KTE14 acHbn-supercont1.19, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE136655.1</a>
Escherichia coli KTE35 acHbr-supercont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KE136604.1</a>
Escherichia coli KTE197 acASN-supercont1.4, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB733185.1</a>
Escherichia coli KTE154 genomic						

scaffold acASW-supercont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB733130.1</a>
Escherichia coli KTE42 acATg-supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB733011.1</a>
Escherichia coli KTE171 acEnC-supercont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB732958.1</a>
Escherichia coli KTE161 acEof-supercont1.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB732934.1</a>
Escherichia coli KTE156 acEuf-supercont1.3, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB733421.1</a>
Escherichia coli KTE111 acEnT-supercont1.5, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB732931.1</a>
Escherichia coli KTE77 acEnw-supercont1.3, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_KB732820.1</a>
Escherichia coli str. K-12 substr. MDS42 DNA, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_020518.1</a>
Escherichia coli H730 supercont1.2, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_JH768585.1</a>
Escherichia coli str. K-12 substr. W3110, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_007779.1</a>
Escherichia coli BL21(DE3) chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_012971.2</a>
Escherichia coli BL21(DE3), complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_012892.2</a>
Escherichia coli DH1, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_017638.1</a>
Escherichia coli ETEC H10407, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_017633.1</a>
Escherichia coli M919 supercont2.1, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_JH659569.1</a>
Escherichia coli KO11FL chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_017660.1</a>
Escherichia coli UMNK88 chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_017641.1</a>
Escherichia coli DH1 chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_017625.1</a>
Escherichia coli KO11FL chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_016902.1</a>
Escherichia coli str. K-12 substr. MG1655star strain K-12 chromosome, whole genome shotgun sequence	2592	2592	100%	0.0	100%	<a href="#">NZ_CM000960.1</a>
Escherichia coli B str. REL606 chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_012967.1</a>
Escherichia coli 'BL21-Gold(DE3)pLysS AG' chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_012947.1</a>
Escherichia coli BW2952 chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_012759.1</a>
Escherichia coli str. K-12 substr. DH10B chromosome, complete genome	2592	2592	100%	0.0	100%	<a href="#">NC_010473.1</a>
Escherichia coli KTE212 acEnm-						

supercont1.3, whole genome shotgun sequence	2587	2587	100%	0.0	99%	<a href="#">NZ_KB732530.1</a>
Escherichia coli KTE210 acEoo-supercont1.4, whole genome shotgun sequence	2569	2569	100%	0.0	99%	<a href="#">NZ_KB732522.1</a>
Escherichia coli W chromosome, complete genome	2569	2569	100%	0.0	99%	<a href="#">NC_017664.1</a>
Escherichia coli W chromosome, complete genome	2569	2569	100%	0.0	99%	<a href="#">NC_017635.1</a>
Escherichia coli HVH 36 (4-5675286) addTA-supercont1.2, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KI538666.1</a>
Escherichia coli KTE102 acHaG-supercont1.3, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KE137162.1</a>
Escherichia coli KTE100 acHbl-supercont1.1, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KE137155.1</a>
Escherichia coli KTE64 acHbq-supercont1.3, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KE137028.1</a>
Escherichia coli KTE29 acATr-supercont1.3, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KB733016.1</a>
Escherichia coli KTE142 acEnG-supercont1.5, whole genome shotgun sequence	2560	2560	100%	0.0	99%	<a href="#">NZ_KB732916.1</a>
Escherichia coli IA11 chromosome, complete genome	2560	2560	100%	0.0	99%	<a href="#">NC_011741.1</a>
Escherichia coli SE11 chromosome, complete genome	2560	2560	100%	0.0	99%	<a href="#">NC_011415.1</a>
Shigella boydii CDC 3083-94 chromosome, complete genome	2560	2560	100%	0.0	99%	<a href="#">NC_010658.1</a>
Escherichia coli KTE101 acASP-supercont1.4, whole genome shotgun sequence	2556	2556	100%	0.0	99%	<a href="#">NZ_KB733078.1</a>
Escherichia coli KTE48 acASU-supercont1.2, whole genome shotgun sequence	2556	2556	100%	0.0	99%	<a href="#">NZ_KB733034.1</a>
Shigella sonnei 53G, complete genome	2556	2556	100%	0.0	99%	<a href="#">NC_016822.1</a>
Shigella boydii Sb227 chromosome, complete genome	2556	2556	100%	0.0	99%	<a href="#">NC_007613.1</a>
Shigella sonnei Ss046 chromosome, complete genome	2556	2556	100%	0.0	99%	<a href="#">NC_007384.1</a>
Escherichia coli KTE234 acEnk-supercont1.1, whole genome shotgun sequence	2554	2554	100%	0.0	99%	<a href="#">NZ_KB732598.1</a>
Escherichia coli UMEA 3355-1 acYzd-supercont1.2, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KE702386.1</a>
Escherichia coli HVH 150 (4-3258106) acYAv-supercont1.4, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KE700264.1</a>
Escherichia coli HVH 82 (4-2209276) acYwv-supercont1.1, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KE699566.1</a>
Escherichia coli KTE222 acHbh-supercont1.1, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KE136972.1</a>

Escherichia coli KTE13 acHbv-supercont1.6, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KE136600.1</a>
Escherichia coli KTE203 acATn-supercont1.2, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KB733201.1</a>
Escherichia coli KTE184 acASO-supercont1.4, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KB733172.1</a>
Escherichia coli KTE135 acASy-supercont1.1, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KB733086.1</a>
Escherichia coli APEC O78, complete genome	2551	2551	100%	0.0	99%	<a href="#">NC_020163.1</a>
Escherichia coli O104:H4 str. Ec12-0466 supercont1.9, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_KB021454.1</a>
Escherichia coli strain IMT2125 chromosome IMT2125, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_HE964769.1</a>
Escherichia coli O104:H4 str. 2009EL-2050 chromosome, complete genome	2551	2551	100%	0.0	99%	<a href="#">NC_018650.1</a>
Escherichia coli O104:H4 str. 2011C-3493 chromosome, complete genome	2551	2551	100%	0.0	99%	<a href="#">NC_018658.1</a>
Escherichia coli O104:H4 str. 2009EL-2071 chromosome, complete genome	2551	2551	100%	0.0	99%	<a href="#">NC_018661.1</a>
Escherichia coli B799 supercont1.2, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH768572.1</a>
Escherichia coli chi7122 chromosome chi7122, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_HE962388.1</a>
Escherichia coli O104:H4 str. ON2011 scaffold00003, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH648168.1</a>
Escherichia coli O104:H4 str. 11-4632 C4 supercont1.3, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH377991.1</a>
Escherichia coli O104:H4 str. 11-4623 supercont1.3, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH378023.1</a>
Escherichia coli O104:H4 str. 04-8351 supercont1.2, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH378073.1</a>
Escherichia coli O104:H4 str. C227-11 supercont1.5, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_JH378089.1</a>
Escherichia coli O104:H4 str. H112180280 scaffold00001, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_GL988050.1</a>
Escherichia coli 97.0264 scf1125157570047, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_GL878082.1</a>
Escherichia coli 95.0941 scf1127129428402, whole genome shotgun sequence	2551	2551	100%	0.0	99%	<a href="#">NZ_GL878028.1</a>
Escherichia coli 55989 chromosome, complete genome	2551	2551	100%	0.0	99%	<a href="#">NC_011748.1</a>
Escherichia coli E24377A	2551	2551	100%	0.0	99%	<a href="#">NC_009801.1</a>

chromosome, complete genome							
Escherichia coli UMEA 3065-1 acYzx-supercont1.2, whole genome shotgun sequence	2547	2547	100%	0.0	99%	<a href="#">NZ_KE701494.1</a>	
Escherichia coli HVH 195 (3-7155360) acYyq-supercont1.2, whole genome shotgun sequence	2547	2547	100%	0.0	99%	<a href="#">NZ_KE700796.1</a>	
Escherichia coli KTE136 acASw-supercont1.2, whole genome shotgun sequence	2547	2547	100%	0.0	99%	<a href="#">NZ_KB733094.1</a>	
Escherichia coli O104:H4 str. ON2010 scaffold00001, whole genome shotgun sequence	2547	2547	100%	0.0	99%	<a href="#">NZ_JH648165.1</a>	
Escherichia coli HS, complete genome	2547	2547	100%	0.0	99%	<a href="#">NC_009800.1</a>	
Escherichia coli HVH 147 (4-5893887) acYxy-supercont1.2, whole genome shotgun sequence	2529	2529	100%	0.0	99%	<a href="#">NZ_KE700242.1</a>	
Escherichia coli KTE81 acEoj-supercont1.1, whole genome shotgun sequence	2529	2529	100%	0.0	99%	<a href="#">NZ_KB732854.1</a>	
Escherichia coli O157:H7 str. F8092B EcO157F8092B_41, whole genome shotgun sequence	2524	2524	100%	0.0	99%	<a href="#">NZ_AVCD01000005.1</a>	
Escherichia coli BWH 32 addUj-supercont1.3, whole genome shotgun sequence	2524	2524	100%	0.0	99%	<a href="#">NZ_KI535541.1</a>	
Escherichia coli BIDMC 39 addUT-supercont1.2, whole genome shotgun sequence	2524	2524	100%	0.0	99%	<a href="#">NZ_KI535383.1</a>	
Escherichia coli KTE233 acEoc-supercont1.1, whole genome shotgun sequence	2524	2524	100%	0.0	99%	<a href="#">NZ_KB732580.1</a>	
Escherichia coli Xuzhou21 chromosome, complete genome	2524	2524	100%	0.0	99%	<a href="#">NC_017906.1</a>	
Escherichia coli O55:H7 str. RM12579 chromosome, complete genome	2524	2524	100%	0.0	99%	<a href="#">NC_017656.1</a>	
Escherichia coli H30 scf1125115109432, whole genome shotgun sequence	2524	2524	100%	0.0	99%	<a href="#">NZ_GL896790.1</a>	

## Alignments

Escherichia coli str. K-12 substr. MG1655 strain K-12 chromosome, whole genome shotgun sequence, complete genome  
Sequence ID: ref|NZ\_AKBV01000001.1| Length: 4638970 Number of Matches: 1  
Range 1: 4057158 to 4058594

Score	Expect	Identities	Gaps	Strand	Frame
2592 bits(2874)	0.0()	1437/1437(100%)	0/1437(0%)	Plus/Plus	

Features:  
rRNA-23S ribosomal RNAcytochrome C nitrite reductase subunit c552

Query	1	ATGACAAGGATAAAAAATAAACGCACGCCGTATCTTCAGCTTATTGATTCC	tttttcttt	60
Sbjct	4057158	ATGACAAGGATAAAAAATAAACGCACGCCGTATCTTCAGCTTATTGATTCC	TTTTTCTTT	4057217
Query	61	ttCAC TTC GTT CACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTA	AACTGTGGAAGCG	120
Sbjct	4057218	TTCA TTC TGT T CACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTA	AACTGTGGAAGCG	4057277
Query	121	AAGAATGAAACCTTTGCCCCGAGCATCCCGATCAATATCTCTCCTGGAA	AGCCACCTCG	180

```

Sbjct 4057278 AAGAATGAAACCTTTGCCCGCAGCATCCCAGTCAATATCTCTCCTGAAAGCCACCTCG 4057337
Query 181 GAACAGT CAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGATCCTGTGGGCG 240
Sbjct 4057338 GAACAGT CAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGATCCTGTGGGCG 4057397
Query 241 GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTTGCTGTGACCGAT 300
Sbjct 4057398 GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTTGCTGTGACCGAT 4057457
Query 301 GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAAACGCTGAAGATGGTCCGCTACCGATG 360
Sbjct 4057458 GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAAACGCTGAAGATGGTCCGCTACCGATG 4057517
Query 361 GCATGCTGGAGTTGTA AAAAGCCCGGATGTGGCGCTCTGATCCAGAAAGACGGCGAAGAT 420
Sbjct 4057518 GCATGCTGGAGTTGTA AAAAGCCCGGATGTGGCGCTCTGATCCAGAAAGACGGCGAAGAT 4057577
Query 421 GGCTACTTCCACGGTAAATGGGCGCGCGGCGTCCGGAAATCGTCAACAACCTTAGGTTGT 480
Sbjct 4057578 GGCTACTTCCACGGTAAATGGGCGCGCGGCGTCCGGAAATCGTCAACAACCTTAGGTTGT 4057637
Query 481 GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCGGAGTTAACCTT 540
Sbjct 4057638 GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCGGAGTTAACCTT 4057697
Query 541 TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGAGAAAGCCGGA 600
Sbjct 4057698 TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGAGAAAGCCGGA 4057757
Query 601 CGTTTCGACCAGCAATCGATGGTTTGGCGTCAAGTGCATGTGGAGTATTACTTCGACGGC 660
Sbjct 4057758 CGTTTCGACCAGCAATCGATGGTTTGGCGTCAAGTGCATGTGGAGTATTACTTCGACGGC 4057817
Query 661 AAAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG 720
Sbjct 4057818 AAAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG 4057877
Query 721 TATTACGACAAAATTGCCTTCTCTGACTGGACTAACTCCCTGTGAAAACGCCAATGCTG 780
Sbjct 4057878 TATTACGACAAAATTGCCTTCTCTGACTGGACTAACTCCCTGTGAAAACGCCAATGCTG 4057937
Query 781 AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGTAAAAACAACGTG 840
Sbjct 4057938 AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGTAAAAACAACGTG 4057997
Query 841 ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAAGGCAAACCTTACACCGAC 900
Sbjct 4057998 ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAAGGCAAACCTTACACCGAC 4058057
Query 901 CATAAAAATTGGTAAATCCGTTTGATAACTTCGCCCAGACTTGTGCGAACTGCCATACCCAG 960
Sbjct 4058058 CATAAAAATTGGTAAATCCGTTTGATAACTTCGCCCAGACTTGTGCGAACTGCCATACCCAG 4058117
Query 961 GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGCAGTCGATTAACGACCTGAAA 1020
Sbjct 4058118 GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGCAGTCGATTAACGACCTGAAA 4058177
Query 1021 ATCAAGGTTGAAGATCAACTGGTTACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA 1080
Sbjct 4058178 ATCAAGGTTGAAGATCAACTGGTTACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA 4058237
Query 1081 GGCGCGACGGAAAGCTGAAATGAAGCCAATTACAGGACGATATCCGTATGCCAGTGGCGC 1140
Sbjct 4058238 GGCGCGACGGAAAGCTGAAATGAAGCCAATTACAGGACGATATCCGTATGCCAGTGGCGC 4058297
Query 1141 TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGAAGAAGGTTTACGG 1200
Sbjct 4058298 TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGAAGAAGGTTTACGG 4058357
Query 1201 ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAACCTGGCGGCCTGCTG 1260
Sbjct 4058358 ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAACCTGGCGGCCTGCTG 4058417
Query 1261 GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAAGCC 1320
Sbjct 4058418 GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAAGCC 4058477
Query 1321 CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA 1380
Sbjct 4058478 CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA 4058537
Query 1381 ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTA AAAACGGTCTGTTAAGCCAATAA 1437
Sbjct 4058538 ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTA AAAACGGTCTGTTAAGCCAATAA 4058594

```

Escherichia coli str. K-12 substr. MG1655 strain K-12 chromosome, whole genome shotgun sequence, complete genome  
Sequence ID: ref|NZ\_AKVX01000001.1| Length: 4638970 Number of Matches: 1  
Range 1: 4285193 to 4286629

Score	Expect	Identities	Gaps	Strand	Frame
2592 bits(2874)	0.0()	1437/1437(100%)	0/1437(0%)	Plus/Plus	

Features:  
cytochrome C nitrite reductase subunit c552

Query	1	ATGACAAGGATAAAAAATAAACGCACGCCGATCTTCAGCTTATTGATTCC	60
Sbjct	4285193	ATGACAAGGATAAAAAATAAACGCACGCCGATCTTCAGCTTATTGATTCC	4285252
Query	61	TTTACCTTCTGTTTACCGTGAACAAACGGCTGCTCCCGCAAAACCTGTA	120
Sbjct	4285253	TTTACCTTCTGTTTACCGTGAACAAACGGCTGCTCCCGCAAAACCTGTA	4285312
Query	121	AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCTCTG	180
Sbjct	4285313	AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCTCTG	4285372
Query	181	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGT	240
Sbjct	4285373	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGT	4285432
Query	241	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTT	300
Sbjct	4285433	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTT	4285492
Query	301	GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAAACGCTGAAGATGGT	360
Sbjct	4285493	GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAAACGCTGAAGATGGT	4285552
Query	361	GTCATGCTGGAGTTGTAAGGACCGGATGTGGCGCGTCTGATCCAGAA	420
Sbjct	4285553	GTCATGCTGGAGTTGTAAGGACCGGATGTGGCGCGTCTGATCCAGAA	4285612
Query	421	GGCTACTTCCACGGTAAATGGGCGCGCGCGGTCCGGAAATCGTCAACA	480
Sbjct	4285613	GGCTACTTCCACGGTAAATGGGCGCGCGCGGTCCGGAAATCGTCAACA	4285672
Query	481	GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCG	540
Sbjct	4285673	GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCG	4285732
Query	541	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTT	600
Sbjct	4285733	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTT	4285792
Query	601	CGTTTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTAT	660
Sbjct	4285793	CGTTTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTAT	4285852
Query	661	AAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAA	720
Sbjct	4285853	AAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAA	4285912
Query	721	TATTACGACAAAATTGCCCTTCTGACTGGACTAACTCCCTGTGAAAA	780
Sbjct	4285913	TATTACGACAAAATTGCCCTTCTGACTGGACTAACTCCCTGTGAAAA	4285972
Query	781	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGT	840
Sbjct	4285973	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGT	4286032
Query	841	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAGGCAA	900
Sbjct	4286033	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAGGCAA	4286092
Query	901	CATAAAATTTGGTAAATCCGTTTATAAATTCGCCAGACTTGTGCGAA	960
Sbjct	4286093	CATAAAATTTGGTAAATCCGTTTATAAATTCGCCAGACTTGTGCGAA	4286152
Query	961	GACAAAGCTGCCCTTGCAAAAGTGGTTCGCGGAACGTAAGCAGTCGA	1020
Sbjct	4286153	GACAAAGCTGCCCTTGCAAAAGTGGTTCGCGGAACGTAAGCAGTCGA	4286212
Query	1021	ATCAAGGTTGAAGATCAACTGGTTTACGCTCACTTCGAAGCGAAAGC	1080
Sbjct	4286213	ATCAAGGTTGAAGATCAACTGGTTTACGCTCACTTCGAAGCGAAAGC	4286272
Query	1081	GGCGCGACGGAAGCTGAAATGAAGCAATTCAGGACGATATCCGTCAT	1140
Sbjct	4286273	GGCGCGACGGAAGCTGAAATGAAGCAATTCAGGACGATATCCGTCAT	4286332
Query	1141	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGA	1200
Sbjct	4286333	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGA	4286392
Query	1201	ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAAC	1260
Sbjct	4286393	ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAAC	4286452
Query	1261	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAAC	1320
Sbjct	4286453	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAAC	4286512
Query	1321	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGC	1380
Sbjct	4286513	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGC	4286572
Query	1381	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTA AAAACGGTCTGTT	1437
Sbjct	4286573	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTA AAAACGGTCTGTT	4286629



Escherichia coli str. K-12 substr. MG1655 strain K-12 ctg718000000002\_quiver, whole genome shotgun sequence  
 Sequence ID: ref|NZ\_APIN0100002.1| Length: 4648564 Number of Matches: 1  
 Range 1: 3087795 to 3089231

Score	Expect	Identities	Gaps	Strand	Frame
2592 bits(2874)	0.0()	1437/1437(100%)	0/1437(0%)	Plus/Plus	

Features:  
 cytochrome C nitrite reductase subunit c552

Query	1	ATGACAAGGATAAAAAATAACGCACGCCGATCTTCAGCTTATTGATTCC	tttttcttt	60
Sbjct	3087795	ATGACAAGGATAAAAAATAACGCACGCCGATCTTCAGCTTATTGATTCC	TTTTTCTTT	3087854
Query	61	ttCACCTCTGTTACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTA	ACTGTGGAAGCG	120
Sbjct	3087855	TTCACTTCTGTTTACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTA	ACTGTGGAAGCG	3087914
Query	121	AAGAATGAAACCTTTGCCCGCAGCATCCCAGTCAATATCTCTCCTG	GAAAGCCACCTCG	180
Sbjct	3087915	AAGAATGAAACCTTTGCCCGCAGCATCCCAGTCAATATCTCTCCTG	GAAAGCCACCTCG	3087974
Query	181	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGT	GATCCTGTGGGCG	240
Sbjct	3087975	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGT	GATCCTGTGGGCG	3088034
Query	241	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCT	TTTTGCTGTGACCGAT	300
Sbjct	3088035	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCT	TTTTGCTGTGACCGAT	3088094
Query	301	GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAACGCTGAAGATGGT	CCGCTACCGATG	360
Sbjct	3088095	GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAACGCTGAAGATGGT	CCGCTACCGATG	3088154
Query	361	GCATGCTGGAGTTGTA AAAAGCCGGATGTGGCGCGTCTGATCCAG	AAGACGGCGAAGAT	420
Sbjct	3088155	GCATGCTGGAGTTGTA AAAAGCCGGATGTGGCGCGTCTGATCCAG	AAGACGGCGAAGAT	3088214
Query	421	GGCTACTTCCACGGTAAATGGCGCGCGGGCGTCCGAAATCGTCA	CAACTTAGGTTGT	480
Sbjct	3088215	GGCTACTTCCACGGTAAATGGCGCGCGGGCGTCCGAAATCGTCA	CAACTTAGGTTGT	3088274
Query	481	GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAA	ACCGGAGTTAACCTT	540
Sbjct	3088275	GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAA	ACCGGAGTTAACCTT	3088334
Query	541	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCT	TTTTGAGAAAGCCGGA	600
Sbjct	3088335	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCT	TTTTGAGAAAGCCGGA	3088394
Query	601	CGTTTCGACCAGCAATCGATGGTTTGGCGTCAAGTCCATGTGG	AGTATTACTTCGACGGC	660
Sbjct	3088395	CGTTTCGACCAGCAATCGATGGTTTGGCGTCAAGTCCATGTGG	AGTATTACTTCGACGGC	3088454
Query	661	AAAAACAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTC	GAAAATATGGAGCAG	720
Sbjct	3088455	AAAAACAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTC	GAAAATATGGAGCAG	3088514
Query	721	TATTACGACAAAATGCGTTCTCTGACTGGACTAACTCCCTGT	GAAAACGCCAATGCTG	780
Sbjct	3088515	TATTACGACAAAATGCGTTCTCTGACTGGACTAACTCCCTGT	GAAAACGCCAATGCTG	3088574
Query	781	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATT	CACGGTAAAAACAACGTG	840
Sbjct	3088575	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATT	CACGGTAAAAACAACGTG	3088634
Query	841	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGA	AGGCAAACCTTACACCGAC	900
Sbjct	3088635	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGA	AGGCAAACCTTACACCGAC	3088694
Query	901	CATAAAATGGTAAATCCGTTTGATAACTTCGCCAGACTTGT	GCGAACTGCCATACCCAG	960
Sbjct	3088695	CATAAAATGGTAAATCCGTTTGATAACTTCGCCAGACTTGT	GCGAACTGCCATACCCAG	3088754
Query	961	GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGC	AGTCGATTAACGACCTGAAA	1020
Sbjct	3088755	GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGC	AGTCGATTAACGACCTGAAA	3088814
Query	1021	ATCAAGGTTGAAGATCAACTGGTTACGCTCACTTCGAAGCG	AAAAGCAGCGCTGGATGCA	1080
Sbjct	3088815	ATCAAGGTTGAAGATCAACTGGTTACGCTCACTTCGAAGCG	AAAAGCAGCGCTGGATGCA	3088874
Query	1081	GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATAT	CCGTCATGCCAGTGGCGC	1140
Sbjct	3088875	GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATAT	CCGTCATGCCAGTGGCGC	3088934
Query	1141	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGC	ACCCGGAAGGTTTACGG	1200
Sbjct	3088935	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGC	ACCCGGAAGGTTTACGG	3088994
Query	1201	ATGCTCGGTACGGCGATGGATAAAGCGCGGATGCACGC	ACCAAACGGCGCCTGCTG	1260
Sbjct	3088995	ATGCTCGGTACGGCGATGGATAAAGCGCGGATGCACGC	ACCAAACGGCGCCTGCTG	3089054
Query	1261	GCGACCAAAGGCATCACCCATGAAATCCAGATCCC	GGATATCTCAACCAAAGAGAAAGCC	1320
Sbjct	3089055	GCGACCAAAGGCATCACCCATGAAATCCAGATCCC	GGATATCTCAACCAAAGAGAAAGCC	3089114

```

Query 1321 CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA 1380
Sbjct 3089115 CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA 3089174

Query 1381 ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA 1437
Sbjct 3089175 ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA 3089231

```

Escherichia coli str. K-12 substr. MG1655 strain K-12 cont1.1, whole genome shotgun sequence  
Sequence ID: ref|NZ\_AYEK0100001.1| Length: 4638920 Number of Matches: 1  
Range 1: 4285032 to 4286468

Score	Expect	Identities	Gaps	Strand	Frame
2592 bits(2874)	0.0()	1437/1437(100%)	0/1437(0%)	Plus/Plus	

Features:  
cytochrome C nitrite reductase subunit c552

```

Query 1 ATGACAAGGATAAAAAATAACGCACGCCGATCTTCAGCTTATTGATTCCtttttcttt 60
Sbjct 4285032 ATGACAAGGATAAAAAATAACGCACGCCGATCTTCAGCTTATTGATTCCtttttcttt 4285091

Query 61 ttCACCTTCTGTTACAGCTGAACAAACGGCTGCTCCCGAAAACCTGTAAGTGTGGAAGCG 120
Sbjct 4285092 TTCACCTTCTGTTACAGCTGAACAAACGGCTGCTCCCGAAAACCTGTAAGTGTGGAAGCG 4285151

Query 121 AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCCTGGAAAGCCACCTCG 180
Sbjct 4285152 AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCCTGGAAAGCCACCTCG 4285211

Query 181 GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGTATCCTGTGGGCG 240
Sbjct 4285212 GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGTATCCTGTGGGCG 4285271

Query 241 GGGTATCCCTTCTCGCGCGATTACAACAAAGCCGCGTGGACATGCTTTTGTGTGACCGAT 300
Sbjct 4285272 GGGTATCCCTTCTCGCGCGATTACAACAAAGCCGCGTGGACATGCTTTTGTGTGACCGAT 4285331

Query 301 GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAACGCTGAAGATGGTCCGCTACCGATG 360
Sbjct 4285332 GTGCGTGAAACCTGCGTACCGGTGCGCCGAAAACGCTGAAGATGGTCCGCTACCGATG 4285391

Query 361 GCATGCTGGAGTTGTA AAAAGCCGGATGTGGCGCTCTGATCCAGAAAGACGGCGAAGAT 420
Sbjct 4285392 GCATGCTGGAGTTGTA AAAAGCCGGATGTGGCGCTCTGATCCAGAAAGACGGCGAAGAT 4285451

Query 421 GGCTACTTCCACGGTAAATGGGCGCGGGCGTCCGGAAATCGTCAACAACTTAGGTTGT 480
Sbjct 4285452 GGCTACTTCCACGGTAAATGGGCGCGGGCGTCCGGAAATCGTCAACAACTTAGGTTGT 4285511

Query 481 GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCGGAGTTAACCTT 540
Sbjct 4285512 GCCGATTGCCATAACACCGCCTCTCCAGAGTTCGCCAAAGGCAAACCGGAGTTAACCTT 4285571

Query 541 TCCCGTCCGATGCGGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGAGAAAGCCGGA 600
Sbjct 4285572 TCCCGTCCGATGCGGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGAGAAAGCCGGA 4285631

Query 601 CGTTTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTATTACTTCGACGGC 660
Sbjct 4285632 CGTTTCGACCAGCAATCGATGGTTTGCGGTCAGTGCCATGTGGAGTATTACTTCGACGGC 4285691

Query 661 AAAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG 720
Sbjct 4285692 AAAAAACAAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG 4285751

Query 721 TATTACGACAAAATGCTTCTCTGACTGGACTAACTCCCTGTGAAAACGCCAATGCTG 780
Sbjct 4285752 TATTACGACAAAATGCTTCTCTGACTGGACTAACTCCCTGTGAAAACGCCAATGCTG 4285811

Query 781 AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGCAATTCACGGTAAAAACAACGTG 840
Sbjct 4285812 AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGCAATTCACGGTAAAAACAACGTG 4285871

Query 841 ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAGGCAAACCTACACCGAC 900
Sbjct 4285872 ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCGAAGGCAAACCTACACCGAC 4285931

Query 901 CATAAAATTTGGTAAATCCGTTTGATAACTTCGCCAGACTTGTGCGAACTGCCATACCCAG 960
Sbjct 4285932 CATAAAATTTGGTAAATCCGTTTGATAACTTCGCCAGACTTGTGCGAACTGCCATACCCAG 4285991

Query 961 GACAAAGCTGCCTTGCAAAAAGTGGTGCAGAACGTAAGCAGTCGATTAACGACCTGAAA 1020
Sbjct 4285992 GACAAAGCTGCCTTGCAAAAAGTGGTGCAGAACGTAAGCAGTCGATTAACGACCTGAAA 4286051

Query 1021 ATCAAGGTTGAAGATCAACTGGTTTACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA 1080
Sbjct 4286052 ATCAAGGTTGAAGATCAACTGGTTTACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA 4286111

Query 1081 GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATATCCGTATGCCAGTGGCGC 1140
Sbjct 4286112 GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATATCCGTATGCCAGTGGCGC 4286171

```

Query	1141	TGGGATCTGGCGATCGCTTCCACGGCATTTCATATGCACGCACCGGAAGAAGGTTTACGG	1200
Sbjct	4286172	TGGGATCTGGCGATCGCTTCCACGGCATTTCATATGCACGCACCGGAAGAAGGTTTACGG	4286231
Query	1201	ATGCTCGGTACGGCGATGGATAAAGCGGGCGATGCACGCACCAAACGGCGCGCTGCTG	1260
Sbjct	4286232	ATGCTCGGTACGGCGATGGATAAAGCGGGCGATGCACGCACCAAACGGCGCGCTGCTG	4286291
Query	1261	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAAGCC	1320
Sbjct	4286292	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAAGCC	4286351
Query	1321	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA	1380
Sbjct	4286352	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA	4286411
Query	1381	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA	1437
Sbjct	4286412	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA	4286468

Escherichia coli str. K-12 substr. MG1655, complete genome

Sequence ID: ref|NC\_000913.3| Length: 4641652 Number of Matches: 1

Range 1: 4287764 to 4289200

Score	Expect	Identities	Gaps	Strand	Frame
2592 bits(2874)	0.0()	1437/1437(100%)	0/1437(0%)	Plus/Plus	

Features:  
nitrite reductase, formate-dependent, cytochrome

Query	1	ATGACAAGGATAAAAAATAACGCACGCGGTATCTTCAGCTTATTGATTCCtttttcttt	60
Sbjct	4287764	ATGACAAGGATAAAAAATAACGCACGCGGTATCTTCAGCTTATTGATTCCTTTTTCTTT	4287823
Query	61	ttCACTTCTGTTACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTAACGTGGAAGCG	120
Sbjct	4287824	TTCACTTCTGTTACGCTGAACAAACGGCTGCTCCCGCAAAACCTGTAACGTGGAAGCG	4287883
Query	121	AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCCTGGAAAGCCACCTCG	180
Sbjct	4287884	AAGAATGAAACCTTTGCCCGCAGCATCCCGATCAATATCTCTCCTGGAAAGCCACCTCG	4287943
Query	181	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGATCCTGTGGGCG	240
Sbjct	4287944	GAACAGTCAGAGCGTGTGACGCCCTGGCGGAAGATCCACGGCTGGTGATCCTGTGGGCG	4288003
Query	241	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTTGTGTGACCGAT	300
Sbjct	4288004	GGGTATCCCTTCTCGCGCGATTACAACAAGCCGCGTGGACATGCTTTTGTGTGACCGAT	4288063
Query	301	GTGCGTGAAACCTTGCCTACCGGTGCGCCGAAAAACGCTGAAGATGGTCCGCTACCGATG	360
Sbjct	4288064	GTGCGTGAAACCTTGCCTACCGGTGCGCCGAAAAACGCTGAAGATGGTCCGCTACCGATG	4288123
Query	361	GCATGCTGGAGTTGTAAGGCCGGATGTGGCGCGTCTGATCCAGAAAGACGGCGAAGAT	420
Sbjct	4288124	GCATGCTGGAGTTGTAAGGCCGGATGTGGCGCGTCTGATCCAGAAAGACGGCGAAGAT	4288183
Query	421	GGCTACTTCCACGGTAAATGGCGCGCGGGCGTCCGGAAATCGTCAACAACCTTAGGTTGT	480
Sbjct	4288184	GGCTACTTCCACGGTAAATGGCGCGCGGGCGTCCGGAAATCGTCAACAACCTTAGGTTGT	4288243
Query	481	GCCGATTGCCATAACACCGCTCTCCAGAGTTCGCCAAAGGCAAACGGAGTTAACCTT	540
Sbjct	4288244	GCCGATTGCCATAACACCGCTCTCCAGAGTTCGCCAAAGGCAAACGGAGTTAACCTT	4288303
Query	541	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGGAGAAAGCCGGA	600
Sbjct	4288304	TCCCGTCCGATGCGGCTCGCGCGATGGAAGCCATTGGTAAACCTTTTGGAGAAAGCCGGA	4288363
Query	601	CGTTTCGACCAGCAATCGATGGTTTGCAGTGCATGTGGAGTATTACTTCGACGGC	660
Sbjct	4288364	CGTTTCGACCAGCAATCGATGGTTTGCAGTGCATGTGGAGTATTACTTCGACGGC	4288423
Query	661	AAAAACAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG	720
Sbjct	4288424	AAAAACAAGCGGTTAAATCCCGTGGGATGACGGCATGAAAGTCGAAAATATGGAGCAG	4288483
Query	721	TATTACGACAAAATGGCTTCTCTGACTGGACTAACTCCCTGTGCAAAAACGCCAATGCTG	780
Sbjct	4288484	TATTACGACAAAATGGCTTCTCTGACTGGACTAACTCCCTGTGCAAAAACGCCAATGCTG	4288543
Query	781	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGTAAAAACAACGTG	840
Sbjct	4288544	AAAGCGCAGCACCCGGAATATGAAACCTGGACAGCGGGCATTACGGTAAAAACAACGTG	4288603
Query	841	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCAAGGCAAACCTTACACCGAC	900
Sbjct	4288604	ACCTGTATCGACTGCCATATGCCAAAAGTGCAGAACGCCAAGGCAAACCTTACACCGAC	4288663
Query	901	CATAAAAATGGTAAATCCGTTTGATAACTTCGCCAGACTTGTGCGAACTGCCATACCCAG	960
Sbjct	4288664	CATAAAAATGGTAAATCCGTTTGATAACTTCGCCAGACTTGTGCGAACTGCCATACCCAG	4288723

Query	961	GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGCAGTCGATTAACGACCTGAAA	1020
Sbjct	4288724	GACAAAGCTGCCTTGCAAAAAGTGGTCGCGGAACGTAAGCAGTCGATTAACGACCTGAAA	4288783
Query	1021	ATCAAGGTTGAAGATCAACTGGTTCACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA	1080
Sbjct	4288784	ATCAAGGTTGAAGATCAACTGGTTCACGCTCACTTCGAAGCGAAAGCAGCGCTGGATGCA	4288843
Query	1081	GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATATCCGTCATGCCCAGTGGCGC	1140
Sbjct	4288844	GGCGCGACGGAAGCTGAAATGAAGCCAATTCAGGACGATATCCGTCATGCCCAGTGGCGC	4288903
Query	1141	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGAAGAAGGTTTACGG	1200
Sbjct	4288904	TGGGATCTGGCGATCGCTTCCACGGCATTATATGCACGCACCGGAAGAAGGTTTACGG	4288963
Query	1201	ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAACCTGGCGCGCCTGCTG	1260
Sbjct	4288964	ATGCTCGGTACGGCGATGGATAAAGCGGCGGATGCACGCACCAAACCTGGCGCGCCTGCTG	4289023
Query	1261	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAGCC	1320
Sbjct	4289024	GCGACCAAAGGCATCACCCATGAAATCCAGATCCCGGATATCTCAACCAAAGAGAAAGCC	4289083
Query	1321	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA	1380
Sbjct	4289084	CAGCAGGCCATTGGCCTGAACATGGAACAAATCAAGGCCGAGAAGCAGGACTTCATCAA	4289143
Query	1381	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA	1437
Sbjct	4289144	ACGGTGATCCCGCAGTGGGAAGAACAGGCACGTAAAAACGGTCTGTTAAGCCAATAA	4289200

## Basic Local Alignment Search Tool

NCBI/ [BLAST/ blastn suite/](#) Formatting Results - 3Z5C6EA201R

▶ [Formatting options](#)

▶ [Download](#)

[Blast report description](#)

Nucleotide Sequence (1281 letters)

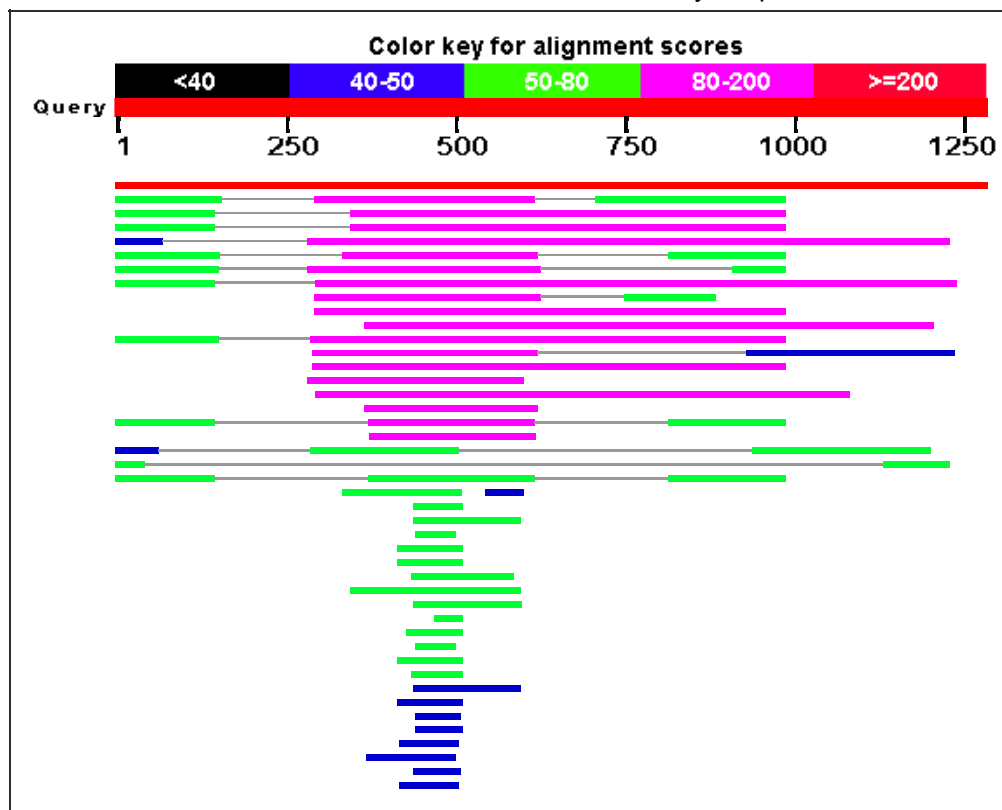
RID [3Z5C6EA201R](#) (Expires on 10-17 17:53 pm)

Query ID |cl|74083  
Description |None  
Molecule type |nucleic acid  
Query Length |1281

Database Name |chromosome  
Description |NCBI Chromosome Sequences  
Program |BLASTN 2.2.30+

### Graphic Summary

Distribution of 67 Blast Hits on the Query Sequence



## ☰ Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Synechococcus sp. PCC 7002 plasmid pAQ7, complete sequence	2311	2311	100%	0.0	100%	<a href="#">NC_010474.1</a>
Acaryochloris marina MBIC11017 chromosome, complete genome	183	324	59%	2e-41	73%	<a href="#">NC_009925.1</a>
Cyanothece sp. ATCC 51472 Cy51472_Contig181.1_C, whole genome shotgun sequence	181	253	61%	7e-41	67%	<a href="#">NZ_AGJC02000001.1</a>
Cyanothece sp. ATCC 51142 chromosome circular, complete sequence	181	253	61%	7e-41	67%	<a href="#">NC_010546.1</a>
Pleurocapsa sp. PCC 7327 chromosome, complete genome	163	209	78%	2e-35	64%	<a href="#">NC_019689.1</a>
Pseudanabaena sp. PCC 6802 Pse6802_scaffold_5, whole genome shotgun sequence	158	286	47%	8e-34	72%	<a href="#">NZ_KB235914.1</a>
Calothrix sp. PCC 7103 Cal7103DRAFT_CPM.1, whole genome shotgun sequence	152	276	44%	4e-32	70%	<a href="#">NZ_KB217483.1</a>
Filamentous cyanobacterium ESFC-1 A3MYDRAFT_scaffold1.1, whole genome shotgun sequence	150	226	84%	1e-31	64%	<a href="#">NZ_KB904821.1</a>
Nodosilinea nodulosa PCC 7104 Lepto7104DRAFT_LPD.2, whole genome shotgun sequence	150	353	36%	1e-31	72%	<a href="#">NZ_JH976537.1</a>
Cyanothece sp. PCC 7425 chromosome, complete genome	150	150	54%	1e-31	66%	<a href="#">NC_011884.1</a>
Cyanothece sp. PCC 7424 chromosome, complete genome	145	145	65%	5e-30	64%	<a href="#">NC_011729.1</a>
Nostoc sp. PCC 7524 chromosome, complete genome	129	193	66%	4e-25	65%	<a href="#">NC_019684.1</a>
Dactylococcopsis salina PCC 8305 chromosome, complete genome	123	172	49%	2e-23	68%	<a href="#">NC_019780.1</a>
Thermosynechococcus sp. NK55 genome	118	118	54%	7e-22	64%	<a href="#">NC_023033.1</a>
Leptolyngbya sp. PCC 7375 genomic scaffold Lepto7375DRAFT_LPA.5, whole genome shotgun sequence	114	204	24%	9e-21	68%	<a href="#">NZ_JH993797.1</a>
Geitlerinema sp. PCC 7105 Gei7105DRAFT_GPC.5, whole genome shotgun sequence	105	105	61%	5e-18	63%	<a href="#">NZ_KB235958.1</a>
Halothece sp. PCC 7418 chromosome, complete genome	98.7	98.7	19%	7e-16	69%	<a href="#">NC_019779.1</a>
Anabaena variabilis ATCC 29413 chromosome, complete genome	95.1	243	43%	8e-15	69%	<a href="#">NC_007413.1</a>
Thermosynechococcus elongatus BP-1 chromosome, complete genome	86.0	86.0	19%	4e-12	68%	<a href="#">NC_004113.1</a>
Leptolyngbya sp. PCC 6406 LEP6406DRAFT_scaffold1.1,						

whole genome shotgun sequence	78.8	176	42%	6e-10	68%	<a href="#">NZ_KI913949.1</a>
<i>Microcoleus</i> sp. PCC 7113 chromosome, complete genome	78.8	132	11%	6e-10	78%	<a href="#">NC_019738.1</a>
<i>Nostoc</i> sp. PCC 7120 chromosome, complete genome	78.8	222	43%	6e-10	70%	<a href="#">NC_003272.1</a>
<i>Marinimicrobium</i> sp. LS-A18 contig6, whole genome shotgun sequence	71.6	71.6	13%	1e-07	69%	<a href="#">NZ_AWEP01000006.1</a>
<i>Rhodobacter sphaeroides</i> KD131 chromosome 2, complete sequence	60.8	60.8	5%	2e-04	79%	<a href="#">NC_011958.1</a>
<i>Hahella chejuensis</i> KCTC 2396 chromosome, complete genome	60.8	60.8	12%	2e-04	69%	<a href="#">NC_007645.1</a>
<i>Rhodovibrio salinarum</i> DSM 9154 RHOSADRAFT_scaffold1.1, whole genome shotgun sequence	57.2	57.2	4%	0.002	81%	<a href="#">NZ_KI911559.1</a>
<i>Hydrogenobaculum</i> sp. SN, complete genome	57.2	57.2	7%	0.002	73%	<a href="#">NC_020814.1</a>
<i>Hydrogenobaculum</i> sp. HO, complete genome	57.2	57.2	7%	0.002	73%	<a href="#">NC_020411.1</a>
<i>Phenylobacterium zucineum</i> HLK1 chromosome, complete genome	55.4	55.4	11%	0.007	68%	<a href="#">NC_011144.1</a>
<i>Bradyrhizobium</i> sp. BTAi1 chromosome, complete genome	55.4	55.4	19%	0.007	65%	<a href="#">NC_009485.1</a>
<i>Rhodobacter sphaeroides</i> 2.4.1 chromosome 2, complete sequence	53.6	53.6	12%	0.026	68%	<a href="#">NC_007494.2</a>
<i>Leptospirillum ferriphilum</i> ML-04 chromosome, complete genome	53.6	53.6	3%	0.026	90%	<a href="#">NC_018649.1</a>
<i>Methylophaga</i> sp. JAM1 chromosome, complete genome	53.6	53.6	6%	0.026	74%	<a href="#">NC_017857.1</a>
<i>Dechlorosoma suillum</i> PS chromosome, complete genome	53.6	53.6	4%	0.026	80%	<a href="#">NC_016616.1</a>
<i>Hydrogenobaculum</i> sp. Y04AAS1 chromosome, complete genome	53.6	53.6	7%	0.026	72%	<a href="#">NC_011126.1</a>
<i>Rhodoferax ferrireducens</i> T118 chromosome, complete genome	51.8	51.8	5%	0.090	75%	<a href="#">NC_007908.1</a>
<i>Maritalea myrionectae</i> DSM 19524 G549DRAFT_scaffold00002.2_C, whole genome shotgun sequence	50.0	50.0	4%	0.32	79%	<a href="#">NZ_AUHV01000003.1</a>
<i>Rhodobacter sphaeroides</i> ATCC 17029 chromosome 2, complete sequence	50.0	50.0	12%	0.32	68%	<a href="#">NC_009050.1</a>
<i>Thiomicrospira halophila</i> DSM 15072 A377DRAFT_scaffold1.1, whole genome shotgun sequence	48.2	48.2	7%	1.1	71%	<a href="#">NZ_KB913033.1</a>
<i>Sphingobium</i> sp. SYK-6 chromosome, complete genome	48.2	48.2	5%	1.1	76%	<a href="#">NC_015976.1</a>
<i>Methyloferula stellata</i> AR4 strain AR4T A3OQDRAFT_chromosome1.1_C, whole genome shotgun sequence	46.4	46.4	5%	3.8	75%	<a href="#">NZ_ARWA01000001.1</a>
<i>Synechocystis</i> sp. PCC 6803 plasmid pSYSM_M, complete sequence	46.4	46.4	6%	3.8	72%	<a href="#">NC_020296.1</a>
<i>Kangiella koreensis</i> DSM 16069 chromosome, complete genome	46.4	46.4	10%	3.8	68%	<a href="#">NC_013166.1</a>

Caulobacter sp. K31 chromosome, complete genome	46.4	46.4	5%	3.8	75%	<a href="#">NC_010338.1</a>
Synechocystis sp. PCC 6803 plasmid pSYSM, complete sequence	46.4	46.4	6%	3.8	72%	<a href="#">NC_005229.1</a>

## Alignments

Synechococcus sp. PCC 7002 plasmid pAQ7, complete sequence  
Sequence ID: ref|NC\_010474.1| Length: 186459 Number of Matches: 1  
Range 1: 85060 to 86340

Score	Expect	Identities	Gaps	Strand	Frame
2311 bits(2562)	0.0()	1281/1281(100%)	0/1281(0%)	Plus/Plus	

Features:

Query	1	ATGGCTCATATTGTTGTAATCGGTGCTGGTATTGGTGGTCTGCCGACGGCCATGAACTG	60
Sbjct	85060	ATGGCTCATATTGTTGTAATCGGTGCTGGTATTGGTGGTCTGCCGACGGCCATGAACTG	85119
Query	61	AGGCACCTGTTGACTACCGACCACACTGTTACCCCTATTGCTGATACACCCACTTTACG	120
Sbjct	85120	AGGCACCTGTTGACTACCGACCACACTGTTACCCCTATTGCTGATACACCCACTTTACG	85179
Query	121	TTTATCCCTTCTTTGCCCTGGGTGGCCCTTGGTCTGAAAAGATTGGATCAGGTGCAATTA	180
Sbjct	85180	TTTATCCCTTCTTTGCCCTGGGTGGCCCTTGGTCTGAAAAGATTGGATCAGGTGCAATTA	85239
Query	181	CCCTTGCCAACGTTGGCCCGTCGCCATGGTCTGCATTGGGTACAGGGGGCTGTGCAGCAG	240
Sbjct	85240	CCCTTGCCAACGTTGGCCCGTCGCCATGGTCTGCATTGGGTACAGGGGGCTGTGCAGCAG	85299
Query	241	ATTAATCCCAGGAAAGGCATGTTTTGGTGGGTGAGACGCAAAACGAATTGACTATGAC	300
Sbjct	85300	ATTAATCCCAGGAAAGGCATGTTTTGGTGGGTGAGACGCAAAACGAATTGACTATGAC	85359
Query	301	TATGTGGTGATCGCACCGGGCGCAGCTTTAAATCTCGATGCTTTACCGGGTCTCGGTCCA	360
Sbjct	85360	TATGTGGTGATCGCACCGGGCGCAGCTTTAAATCTCGATGCTTTACCGGGTCTCGGTCCA	85419
Query	361	GAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCACCATGCACTGCTTGCCCATGAAGCT	420
Sbjct	85420	GAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCACCATGCACTGCTTGCCCATGAAGCT	85479
Query	421	TGGGAAAAATTTATCCAGAATCCAGGCCCGTTGGTCTGGGGGGCGGCACCGGGGGCGAGT	480
Sbjct	85480	TGGGAAAAATTTATCCAGAATCCAGGCCCGTTGGTCTGGGGGGCGGCACCGGGGGCGAGT	85539
Query	481	TGTTTTGGCCCGGCTATGAGTTTGCCTTGTGGCAGATTGGCAACTGCCGACGGTTGGGT	540
Sbjct	85540	TGTTTTGGCCCGGCTATGAGTTTGCCTTGTGGCAGATTGGCAACTGCCGACGGTTGGGT	85599
Query	541	TTGCGGGAGCAGGTACCGATCACATTGGTCACCCAGAACCCATTTGGGTCAATTTGGGG	600
Sbjct	85600	TTGCGGGAGCAGGTACCGATCACATTGGTCACCCAGAACCCATTTGGGTCAATTTGGGG	85659
Query	601	ATTGGGGGATGGCCCACTCGCAGGAATGGTTGAGCAGGTTCTCCAGCAACAGGATATT	660
Sbjct	85660	ATTGGGGGATGGCCCACTCGCAGGAATGGTTGAGCAGGTTCTCCAGCAACAGGATATT	85719
Query	661	GCGACCCGTGCCAATGCTGAGATTACCGCCATTAACCGGATATGATTGGTTTGGCGGAT	720
Sbjct	85720	GCGACCCGTGCCAATGCTGAGATTACCGCCATTAACCGGATATGATTGGTTTGGCGGAT	85779
Query	721	GGGGAACAGCTACCCCTTGCCACAGTATGGTTTTGCCGTCGTTCCAGGGGCTGCTTTT	780
Sbjct	85780	GGGGAACAGCTACCCCTTGCCACAGTATGGTTTTGCCGTCGTTCCAGGGGCTGCTTTT	85839
Query	781	TTGCGTGACTGTCCGGCGATCTCCAATCCCAGGGGTTATTCCCGTCTTGCCACCTAT	840
Sbjct	85840	TTGCGTGACTGTCCGGCGATCTCCAATCCCAGGGGTTATTCCCGTCTTGCCACCTAT	85899
Query	841	CAACATCCAGCGTTTCGATTCCGTGTATGCGGGCGGGGTGATTGTTGAACAAACGCCCAT	900
Sbjct	85900	CAACATCCAGCGTTTCGATTCCGTGTATGCGGGCGGGGTGATTGTTGAACAAACGCCCAT	85959
Query	901	GAAGCCACACCAATCCCCACGGGTCTACCGAAAACAGGACAAATGACGGAGGCGATGGGG	960
Sbjct	85960	GAAGCCACACCAATCCCCACGGGTCTACCGAAAACAGGACAAATGACGGAGGCGATGGGG	86019
Query	961	ATGGCCGCCGCCACAATATTGCCCGACAGCTTAACTCCAATCTGGGTGCTCCGGTCACG	1020
Sbjct	86020	ATGGCCGCCGCCACAATATTGCCCGACAGCTTAACTCCAATCTGGGTGCTCCGGTCACG	86079
Query	1021	GCGACCCCTCGCCGCAATTTGTATGAGTGATTTGGCGATCGCGGCAATATCTTCATCGCC	1080
Sbjct	86080	GCGACCCCTCGCCGCAATTTGTATGAGTGATTTGGCGATCGCGGCAATATCTTCATCGCC	86139



Query 1081 GATCCGGTACAGCGGGAGCCAGGCATGGTCAAACGTCGCCGCTGTGTCGCCCTCGAAGGA 1140  
 Sbjct 86140 GATCCGGTACAGCGGGAGCCAGGCATGGTCAAACGTCGCCGCTGTGTCGCCCTCGAAGGA 86199  
 Query 1141 CGGTGGGTGAGTTGGAGCAAAAACCTTTTTGAACTGTTTTCTGACGAAAATGCGTTGG 1200  
 Sbjct 86200 CGGTGGGTGAGTTGGAGCAAAAACCTTTTTGAACTGTTTTCTGACGAAAATGCGTTGG 86259  
 Query 1201 GGTCTAACGATACCTTGGTTTGGAGAACTGGGCTTAAAGACATTGGGATTGCAGCTTGTG 1260  
 Sbjct 86260 GGTCTAACGATACCTTGGTTTGGAGAACTGGGCTTAAAGACATTGGGATTGCAGCTTGTG 86319  
 Query 1261 CGTCCCTTCTCCAGACTAA 1281  
 Sbjct 86320 CGTCCCTTCTCCAGACTAA 86340

Acaryochloris marina MBIC11017 chromosome, complete genome  
 Sequence ID: ref|NC\_009925.1| Length: 6503724 Number of Matches: 3  
 Range 1: 432354 to 432674

Score	Expect	Identities	Gaps	Strand	Frame
183 bits(202)	2e-41()	233/321(73%)	0/321(0%)	Plus/Plus	

Features:  
 sulfide quinone reductase

Query 294 CTATGACTATGTGGTGATCGCACCGGGCGCAGCTTTAAATCTCGATGCTTTACCGGGTCT 353  
 Sbjct 432354 CTATGACTACGTCGTCATTGCCACCGGAGCCGAGTTAGCCTTGGATACGGTATCCGGCCT 432413  
 Query 354 CCGTCCAGAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCACCATGCACTGCTTGCCCA 413  
 Sbjct 432414 GGGACCAGAGCAGGGCTTTACCCAGTCGATTGCAATCCTCACCATGCTTTAATGGCCAA 432473  
 Query 414 TGAAGCTTGGGAAAAATTTATCCAGAATCCAGGCCCGTTGGTCGTGGGGGCGCACCGGG 473  
 Sbjct 432474 CAGTGCTTGGCAAAAATTTTTACAGAATCCGGGTCTTTAGTGGTGGGGGCGAGTGCCCGG 432533  
 Query 474 GGCAGATTGTTTTGGCCCGGCCTATGAGTTTGCCTTGTGGCAGATTGGCAACTGCGACG 533  
 Sbjct 432534 GGCAGACTGTTTTGGCCCTGCCTATGAGTTTGCCTTATTAGCCGATTACACTCTTCGCCA 432593  
 Query 534 GTTGGGTTTGGGGAGCAGGTACCGATCACATTTGGTACCCCCAGAACCCTATTTGGGTCA 593  
 Sbjct 432594 GCAAGGGTTGCGGGATCAAGTTCCCTTACATTTGTGACACCGGAACCCTATGCGGGGCA 432653  
 Query 594 TTTGGGGATTGGGGGCATGGC 614  
 Sbjct 432654 TTTGGGGATTGGCGGCATGGC 432674

Range 2: 432067 to 432223

Score	Expect	Identities	Gaps	Strand	Frame
71.6 bits(78)	1e-07()	112/158(71%)	2/158(1%)	Plus/Plus	

Features:  
 sulfide quinone reductase

Query 1 ATGGCTCATATTGTTGTAATCGGTGCTGGTATTGG-TGGTCTGCCGACGGCCTATGAACT 59  
 Sbjct 432067 ATGGCTCATATTGTTGTCATTGGAGCAGG-ATTGGCAGGATTGCCGACTGCCTATGAGTT 432125  
 Query 60 GAGGCACCTGTTGACTACCGACCACACTGTTACCCCTATTGCTGATACACCCACTTTAC 119  
 Sbjct 432126 GAGGTACCTGTTACCTAGTCAGCATCAAATTACCCGATCTCCAATACCTCTAAATTAC 432185  
 Query 120 GTTTATCCCTTCTTTGCCCTGGGTGGCCCTTGGTCTGA 157  
 Sbjct 432186 ATTTATTCCATCCCTTCTTTGGGTGCGCTAGGGCTGA 432223

Range 3: 432765 to 433045

Score	Expect	Identities	Gaps	Strand	Frame
69.8 bits(76)	3e-07()	184/281(65%)	0/281(0%)	Plus/Plus	

Features:  
 sulfide quinone reductase

Query 705 GATTGGTTTTGGCGGATGGGGAACAGCTACCCCTTGCCTACAGTATGGTTTTGCCGTCGTT 764  
 Sbjct 432765 GATTATTTTGGCCAAATGGCGACGCGGTGCCCTTCCAGTACGCTATGTTGCTGCCGACGTT 432824  
 Query 765 CCAGGGGCGCTGCTTTTTTGGCTGACTGTCCGGCGATCTCCAATCCCAAGGGGTTTATTC 824

Sbjct 432825 TCGAGGGCCTGGCTTTGTTCGTGAGACAGCGGGTTAGGGGATACCAAGGGTTTCTGCC 432884  
 Query 825 CGTCTTGCCACCTATCAACATCCAGCGTTCGATTCGGTGTATGCGGCGGGGGTGATTGT 884  
 Sbjct 432885 CATATTGCCACCTATCAGCATCCTGTTTTCCCTCAGTGTAGTGACAGGTGTGTGCAC 432944  
 Query 885 TGAACTAACGCCCATGAAGCCACACCAATCCCACGGGTCTACCGAAAACAGGACAAAT 944  
 Sbjct 432945 TCAATTAGCACCACAGAGGTAACCTCGATAGCAATCGGGGTGCCAAAAACTGGACAAAT 433004  
 Query 945 GACGGAGGCGATGGGGATGGCCGCCGCCACAATATTGCC 985  
 Sbjct 433005 GGTGAAAGCAATGGGGATGGCAGTGGCTCACAATATTGCC 433045

Cyanothece sp. ATCC 51472 Cy51472\_Contig181.1\_C, whole genome shotgun sequence  
 Sequence ID: ref|NZ\_AGJC0200001.1| Length: 4932779 Number of Matches: 2  
 Range 1: 4639890 to 4640527

Score	Expect	Identities	Gaps	Strand	Frame
181 bits(200)	7e-41()	436/648(67%)	20/648(3%)	Plus/Plus	

Features:  
 sulfide-quinone reductase

Query 346 CCGGGTCTCGGTCCAGAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCACCATGCACTG 405  
 Sbjct 4639890 CCTGGACTTGGACCTGAGATGGGATATACTCAATCTGTGTAAATCCTCACCATGCAACG 4639949  
 Query 406 CTTGCCCATGAAGCTTGGGAAAAATTTATCCAGAATCCAGGCCCGTTGGTCGTGGGGGCG 465  
 Sbjct 4639950 CAAGCGGGTGAAGCTTGGTCTGAATTTTAGCTGATCCTGGCCCGTTAATTGTGGGGGCA 4640009  
 Query 466 GCACCGGGGCGAGTTGTTTTGGCCCGCCTATGAGTTTGCCTTGTGGCAGATTGGCAA 525  
 Sbjct 4640010 GTTCCAGGGGCAAGTTGTTTTGGACCAGCCTATGAATTTGCGATGTTAGCAAAT--GCAA 4640067  
 Query 526 C--TGCAGCGGTGGGTTTGGGGAGCAGGTACCGATCACATTGGTCACCCAGAACCCCT 583  
 Sbjct 4640068 CCTCAGACAGTCTCAACCGTGAAACAAGTTCCTATTACCTTTGTACCCAGAACCCCT 4640127  
 Query 584 ATTTGGGTCAATTTGGGGATTGGGGGCATGGCCCACTCGCAGGAATTGGTTGAGCAGGTTT 643  
 Sbjct 4640128 ATGTGGGACATTTAGGGATAGGTAGCATGGCTAACTCTCAGGCATTAGTT-AG--GGAAC 4640184  
 Query 644 TC-CAGCAA--CAGGATATTGCGACCCGTGCCAATGCTGAGATTACCGCCATTAACCCGG 700  
 Sbjct 4640185 TCATGGCAAAGCATAACATTAATATTCTAGAAAATGCTGCTATTTGTCATATTCACCTG 4640244  
 Query 701 ATATGATTGGTTTGGCGGATGGGGAACAGCTACCCTTTGCCTACAGTATGGTTTTGCCGT 760  
 Sbjct 4640245 ATACGATTTACTTATCCAACGGTGAAAGGTTGCCCTTTAAGTATGCCATGGTGTACCTC 4640304  
 Query 761 CGTTCAGGGGCTGCTTTTTTGCCTGACTGTCCGGCGATCTCCAATCCCAGGGGTTTA 820  
 Sbjct 4640305 CCTTTCGAGGACCTAGTTTCTTGCAGAAATCCCTGGCTTAACCGATGAACAAGGATTTT 4640364  
 Query 821 TTCCCGTCTTGCCACCTATCAACATCCAG-CGTTGATTCGGTGTATGCGGCGGGGGTG 879  
 Sbjct 4640365 TACCGGTTTTGCCACTGGGCAACATCCTGACTATCCAT---CTCTTACGGTATCGGTG 4640421  
 Query 880 ATTGTTG----AACTAACGCCCATGAAGCCACACCAATCCCACGGGTCTACCGAAAAC 935  
 Sbjct 4640422 -TTGTTGTCAAATTAACCCCCA-GAAGTCACATCTATCCCATCGGGGTCCCAAAAC 4640479  
 Query 936 AGGACAAATGACGGAGGCGATGGGGATGGCCGCCGCCACAATATTGC 983  
 Sbjct 4640480 TGGACAAATGACAGAAGCAATGGGAATGGCAGCAGCCATAATATTGC 4640527

Range 2: 4639551 to 4639696

Score	Expect	Identities	Gaps	Strand	Frame
71.6 bits(78)	1e-07()	106/149(71%)	6/149(4%)	Plus/Plus	

Features:  
 sulfide-quinone reductase

Query 1 ATGGCTCATATTGTTGTAAATCGGTGCTGGTATTGGTGGTCTGCCGACGGCCTATGAACTG 60  
 Sbjct 4639551 ATGGCTCATATTGTTGTATTGCGGGAGGAATAGGAGGATTACCAACAGCCTATGAATTG 4639610  
 Query 61 AGGCA---CCTGTTGACTACCGACCACACTGTTACCCCTCATGCTGATACACCCACTTT 117  
 Sbjct 4639611 CGCCATTTACTCTGTCTTCCCATCAAAA---TTACCTTGTCTTAATCAACCAAACCTT 4639667  
 Query 118 ACGTTTATCCCTTCTTTGCCCTGGGTGGC 146  
 Sbjct 4639668 ACTTTTATTCCGTCCTTACCTTGGGTAGC 4639696

Cyanothece sp. ATCC 51142 chromosome circular, complete sequence  
 Sequence ID: ref|NC\_010546.1| Length: 4934271 Number of Matches: 2  
 Range 1: 3505984 to 3506621

Score	Expect	Identities	Gaps	Strand	Frame
181 bits(200)	7e-41()	436/648(67%)	20/648(3%)	Plus/Plus	
Features: sulfide-quinone reductase					
Query 346		CCGGTCTCGGTCCAGAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCACCATGCACTG			405
Sbjct 3505984		CCTGGACTTGGACCTGAGATGGGATATACTCAATCTGTGTAAATCCTCACCATGCAACG			3506043
Query 406		CTTGCCCATGAAGCTTGGGAAAAATTTATCCAGAATCCAGGCCCGTTGGTCGTGGGGGCG			465
Sbjct 3506044		CAAGCGGTGAAGCTTGGTCTGAATTTTAGTCTGATCCTGGCCCGTTAATTGTGGGGGCA			3506103
Query 466		GCACCGGGGGCGAGTTGTTTTGGCCCGGCTATGAGTTTGCCTTGTGGCAGATTGGCAA			525
Sbjct 3506104		GTTCACGGGGCAAGTTGTTTTGGACCAGCCTATGAATTTGCGATGTTAGCAAAT--GCAA			3506161
Query 526		C--TGCACGGTTGGGTTTGGGGAGCAGGTACCGATCACATTTGGTCAACCCAGAACCTT			583
Sbjct 3506162		CCCTCAGACAGTCTCAACCGTGGAAACAAGTTCTATTACCTTTGTCAACCCAGAACCTT			3506221
Query 584		ATTTGGGTCAATTTGGGGATTGGGGGATGGCCCACTCGCAGGAATTGGTTGAGCAGGTTT			643
Sbjct 3506222		ATGTGGGACATTTAGGGATAGGTAGCATGGCTAACTCTCAGGCATTAGTT-AG--GGAAC			3506278
Query 644		TC-CAGCAA--CAGGATATTGCACCCGTGCCAATGCTGAGATTACCGCCATTAAACCGG			700
Sbjct 3506279		TCATGGCAAAGCATAACATTAATATTCTAGAAAAATGCTGCTATTTGTCATATTTACCTG			3506338
Query 701		ATATGATTTGGTTTGGCGGATGGGGAACAGCTACCCTTTGCCTACAGTATGGTTTGGCGT			760
Sbjct 3506339		ATACGATTTACTTATCCAACGGTGAAAGGTTGCCCTTAAAGTATGCCATGGTGTACCTC			3506398
Query 761		CGTTCCAGGGGCTGCTTTTTTGCCTGACTGTCCGGCGATCTCCAATCCCAGGGGTTTA			820
Sbjct 3506399		CCTTTCGAGGACCTAGTTTCTTTCGAGAAATCCCTGGCTTAACCGATGAACAAGGATTTT			3506458
Query 821		TTCCCGTCTTGGCCACCTATCAACATCCAG-CGTTTCGATTCCGTGTATGCGGCGGGGGTG			879
Sbjct 3506459		TACCGGTTTGGCCACTGGGCAACATCCTGACTATCCAT---CTCTTACGGTATCGGTG			3506515
Query 880		ATTGTTG----AACTAACGCCCCATGAAGCCACACCAATCCCACGGGTCTACCGAAAC			935
Sbjct 3506516		-TTGTTGTCAAATTAACCCCCCA-GAAGTACATCTATCCCATCGGGGTTCACAAAAAC			3506573
Query 936		AGGACAAATGACGGAGGCGATGGGGATGGCCGCCGCCACAATATTGC			983
Sbjct 3506574		TGGACAAATGACAGAAGCAATGGGAATGGCAGCAGCCATAAATATTGC			3506621

Range 2: 3505645 to 3505790

Score	Expect	Identities	Gaps	Strand	Frame
71.6 bits(78)	1e-07()	106/149(71%)	6/149(4%)	Plus/Plus	
Features: sulfide-quinone reductase					
Query 1		ATGGCTCATATTGTTGTAATCGGTGCTGGTATTGGTGGTCTGCCGACGGCCTATGAACCTG			60
Sbjct 3505645		ATGGCTCATATTGTTGTTATTGGCGGAGGAATAGGAGGATTACCAACAGCCTATGAATTG			3505704
Query 61		AGGCA---CCTGTTGACTACCGACCACACTGTTACCCTCATTTGCTGATACACCCACTTTT			117
Sbjct 3505705		CGCCATTTACTCTTGTCTTCCCATCAAA--TTACCCTTGTCTTAATCAACCAAACCTTT			3505761
Query 118		ACGTTTATCCCTTCTTTGCCCTGGGTGGC			146
Sbjct 3505762		ACTTTTATCCGTCTTTACCTTGGGTAGC			3505790

Pleurocapsa sp. PCC 7327 chromosome, complete genome  
 Sequence ID: ref|NC\_019689.1| Length: 4986817 Number of Matches: 2  
 Range 1: 3099133 to 3100074

Score	Expect	Identities	Gaps	Strand	Frame
163 bits(180)	2e-35()	606/945(64%)	5/945(0%)	Plus/Plus	
Features: NADH dehydrogenase, FAD-containing subunit					

```

Query 282      AAAACGAATTGACTATGACTATGTGGTGATCGCACCGGGCGCAGCTTTAAATCTCGATGC 341
Sbjct 3099133  AAAAC-AATTGATTACGATTATGCCGTTATTGCTACGGGAGCCTCCCTCAAACCTCGATGC 3099191
Query 342      TTTACCGGGTCTCGGTCCAGAGACAGGCTTTACCCAGTCAGTTTGTAAATCCCCACCATGC 401
Sbjct 3099192  CATCCCTGGTTTGGGACCCGAAGGCGGTTATACCCACTCAGTCTGCAATCCTCATCATGC 3099251
Query 402      ACTGCTTGCCCATGAAGCTTGGGAAAAATTTATCCAGAAATCCAGGCCGTTGGTCGTGGG 461
Sbjct 3099252  CCTGCTAGCGCGAGAAGCCTGGAAAGAAATCGAGCAAAATCCAGGGGCTTGTAGTCGTGGG 3099311
Query 462      GGCGGCACCGGGGGCGAGTTGTTTTGGCCCGGCTATGAGTTTGCCTTGTGGCAGATTG 521
Sbjct 3099312  AGCCGTGCCGTTGGGCTAGCTGTATGGGACCCGCTACGAGTTTGTCTCCTAGCAGATTA 3099371
Query 522      GCAACTGCGACGGTTGGGTTTGCGGGAGCAGGTACCGATCACATTGGTCACCCAGAAC 581
Sbjct 3099372  CGTACTGCGTCAAAAAAGATTGCGCAATCGCGTTTCCATTACCTTGTACCCCGAAC 3099431
Query 582      CTATTTGGGTCATTTGGGGATTGGGGGCATGGCCACTCGCAGGAATTGGTTGAGCAGGT 641
Sbjct 3099432  CTATGCGGGTCACTTGGGCATTGGAGGGATGGCAAATCAGGGAAACTGGTGACACAATT 3099491
Query 642      TCTCCAGCAACAGGATATTGCGACCCGTGCCAATGCTGAGATTACCGCCATTAACCGGA 701
Sbjct 3099492  AATGCAAGAACGGAACGTAGAATTGATTGAAAATGCTGCCATTATTAAGATTGATGCTGA 3099551
Query 702      TATGATTGGTTTGGCGGATGGGGAACAGTACCCTTTGCTACAGTATGGTTTGGCGTC 761
Sbjct 3099552  GAGAATCTGCCTAGCAGACAGTCGCCAGTTACCGTTCAAATACGCCATGCTCCTGCCACC 3099611
Query 762      GTTCCAGGGGCTGCTTTTTGCGTACTGTCCGGCGATCTCAAATCCCAGGGTTTTAT 821
Sbjct 3099612  TTTCTGCGGAGCCAAGTTCTTGCGGGAGTACCAGGATTGACTGATGCTAAAGGCTTTTT 3099671
Query 822      TCCCGTCTTGCCACCATCAACATCCAGCGTTCGATTCCGTGTATGCGGCGGGGTGAT 881
Sbjct 3099672  ACCAGTCTACCGACCTATCAACATCCCGATTTCCCTTCTATTTATAGTTTGGGGTGAC 3099731
Query 882      TGTGAACTAACGCCCATGAAGCCACACCAATCCCACGGGTCTACCGAAAACAGGACA 941
Sbjct 3099732  CGTGGAACCTGCCCTCCCGAACCAACTCCAATTCGAGCGGCGTTCGAAAACGGGTCA 3099791
Query 942      AATGACGGAGGCGATGGGGATGGCCGCGCCACAATATTGCCCGACAGCTTAACCCAA 1001
Sbjct 3099792  GATGACCGAATCGATGGGCATGCGAGTCGCCACAATCTTGCAGAGAG-TTAGGGGAAA 3099850
Query 1002     TCTG--GGTGCTCCGGTACGGCGACCCTCGCCGCAATTTGTATGAGTGATTTGGCGAT 1059
Sbjct 3099851  T-TGAAGCAGCGCCCGTAACTCTACCCTAGGAGCCATTTGCATGGCGGACTTTGGCGAT 3099909
Query 1060     CGCGGCATTATCTTCATCGCCGATCCGGTACAGCGGGAGCCAGGCATGGTCAAACGTCCG 1119
Sbjct 3099910  ACCGGGATCTCTTTGTTGCCAATCCCGTTTTGCCGATCCGGTGACGGGAAAGCGGCGC 3099969
Query 1120     CGCTGTGTGCGCCTCGAAGGACGGTGGGTGAGTTGGAGCAAAACCCTTTTTGAAGTGT 1179
Sbjct 3099970  AGAGCTTTTGCAGTGCGGGGCTGGTGGGTGAGTTGGATTAAGACGGCTTTTGAAGAAAT 3100029
Query 1180     TTCTGACGAAAATGCGTTGGGGTCTAACGATACCTGGTTGAG 1224
Sbjct 3100030  TTCTTAGCCAAGATGCGTTTAGGAATGTCTATCCCTTGGTTCGAG 3100074

```

Range 2: 3098857 to 3098924

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	3.8()	51/68(75%)	0/68(0%)	Plus/Plus	

Features:  
NADH dehydrogenase, FAD-containing subunit

```

Query 1      ATGGCTCATAATTGTTGTAATCGGTGCTGGTATTGGTGGTCTGCCGACGGCCTATGAACTG 60
Sbjct 3098857  ATGGCTCACATTATCGTAATCGGTGCGGGACTAGGAGGATTGCCAACAGCTTACGAACTG 3098916
Query 61      AGGCACCT 68
Sbjct 3098917  CGACATCT 3098924

```