

## BLAST®

## Basic Local Alignment Search Tool

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channel\_110\_read\_9\_template channel\_110\_read\_9

**RID** [TGE39ZBV01R](#) (Expires on 06-12 19:07 pm)

**Query ID** Id|209235

**Description** channel\_110\_read\_9\_template  
channel\_110\_read\_9

**Molecule type** nucleic acid

**Query Length** 8476

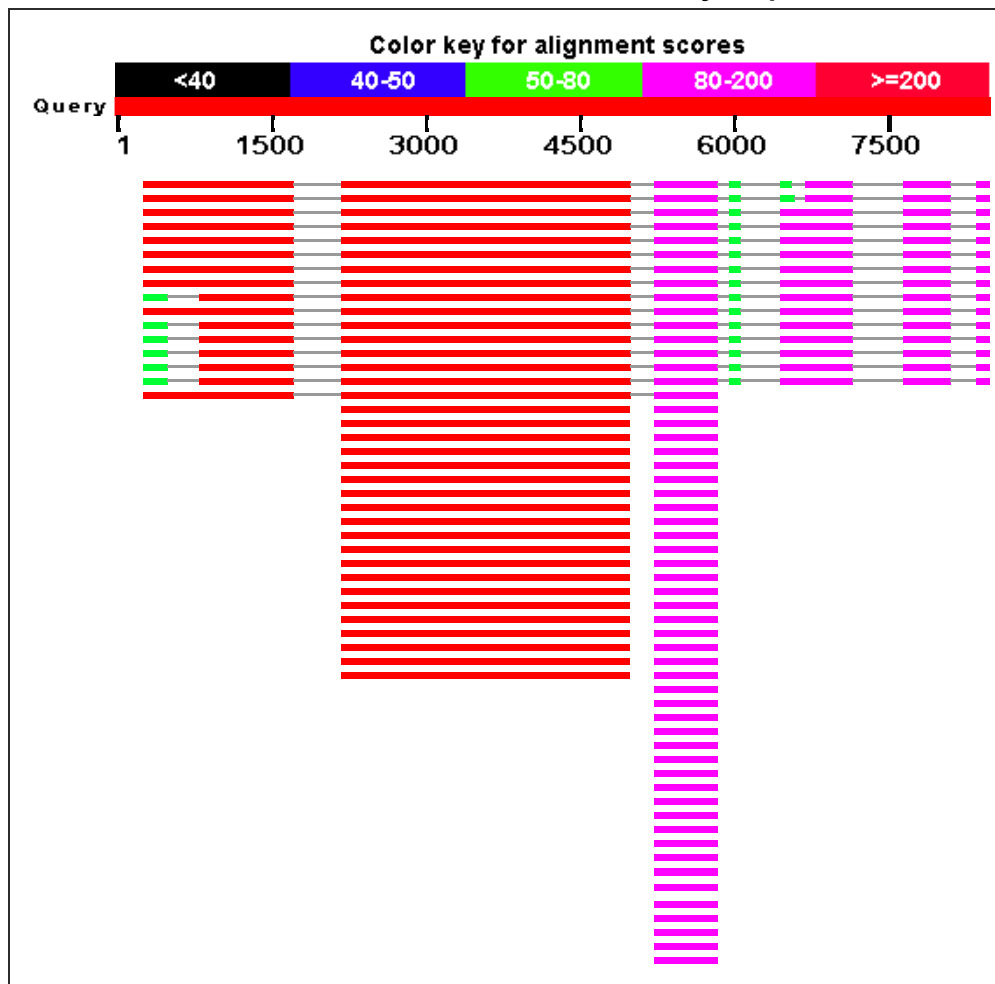
**Database Name** refseq\_genomic

**Description** NCBI Genomic Reference Sequences

**Program** BLASTN 2.2.29+

## Graphic Summary

Distribution of 200 Blast Hits on the Query Sequence



## Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pseudomonas aeruginosa BL05 genomic scaffold adgfv-supercont1.1, whole genome shotgun sequence	544	1368	71%	5e-149	68%	<a href="#">NZ_KI518928.1</a>
Pseudomonas aeruginosa M8A.4 genomic scaffold adgfJ-supercont1.1, whole genome shotgun sequence	542	1375	72%	2e-148	68%	<a href="#">NZ_KI518732.1</a>
Pseudomonas aeruginosa LESB65	540	1314	73%	7e-148	68%	<a href="#">NZ_CP006983.1</a>
Pseudomonas aeruginosa LESlike7	540	1314	73%	7e-148	68%	<a href="#">NZ_CP006981.1</a>
Pseudomonas aeruginosa LES400	540	1314	73%	7e-148	68%	<a href="#">NZ_CP006982.1</a>
Pseudomonas aeruginosa LESlike4	540	1314	73%	7e-148	68%	<a href="#">NZ_CP006985.1</a>
Pseudomonas aeruginosa LES431, complete genome	540	1314	73%	7e-148	68%	<a href="#">NC_023066.1</a>
Pseudomonas aeruginosa 62 genomic scaffold adgfr-supercont1.2, whole genome shotgun sequence	540	1314	73%	7e-148	68%	<a href="#">NZ_KI519316.1</a>
Pseudomonas aeruginosa CF127 genomic scaffold adgeA-supercont1.1, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI519287.1</a>
Pseudomonas aeruginosa UDL genomic scaffold adgeV-supercont1.1, whole genome shotgun sequence	540	1314	73%	7e-148	68%	<a href="#">NZ_KI519264.1</a>
Pseudomonas aeruginosa S35004 genomic scaffold adgfr-supercont1.2, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI519208.1</a>
Pseudomonas aeruginosa BWHPA002 genomic scaffold adgeG-supercont1.1, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI519173.1</a>
Pseudomonas aeruginosa BWHPA003 genomic scaffold adggi-supercont1.1, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI519160.1</a>
Pseudomonas aeruginosa BWHPA017 genomic scaffold adgeW-supercont1.2, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI519064.1</a>
Pseudomonas aeruginosa BL24 genomic scaffold adgeY-supercont1.2, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI518758.1</a>
Pseudomonas aeruginosa M8A.1 genomic scaffold adgfk-supercont1.2, whole genome shotgun sequence	540	1314	73%	7e-148	68%	<a href="#">NZ_KI518748.1</a>
Pseudomonas aeruginosa C40 genomic scaffold adgfo-supercont1.1, whole genome shotgun sequence	540	1309	73%	7e-148	68%	<a href="#">NZ_KI518712.1</a>
Pseudomonas aeruginosa C51 genomic scaffold adgeS-supercont1.3, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI518696.1</a>
Pseudomonas aeruginosa C52 genomic scaffold adgfp-supercont1.2, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI518678.1</a>
Pseudomonas aeruginosa CF77 genomic scaffold adgeU-supercont1.1, whole genome shotgun sequence	540	1379	69%	7e-148	68%	<a href="#">NZ_KI518663.1</a>
Pseudomonas aeruginosa LESB58	540	1314	73%	7e-148	68%	<a href="#">NC_011770.1</a>

chromosome, complete genome

Pseudomonas aeruginosa M18 chromosome, complete genome	538	1312	73%	2e-147	68%	<a href="#">NC_017548.1</a>
Pseudomonas aeruginosa LESlike5	535	1309	73%	3e-146	68%	<a href="#">NZ_CP006980.1</a>
Pseudomonas aeruginosa CF5 genomic scaffold adgfB-supercont1.1, whole genome shotgun sequence	535	1332	71%	3e-146	68%	<a href="#">NZ_KI519271.1</a>
Pseudomonas aeruginosa BWHPA018 genomic scaffold adgft-supercont1.2, whole genome shotgun sequence	535	1309	73%	3e-146	67%	<a href="#">NZ_KI519055.1</a>
Pseudomonas aeruginosa BL07 genomic scaffold adgfo-supercont1.1, whole genome shotgun sequence	531	1300	73%	3e-145	67%	<a href="#">NZ_KI518906.1</a>
Pseudomonas aeruginosa M8A.2 genomic scaffold adgfd-supercont1.1, whole genome shotgun sequence	531	1328	71%	3e-145	67%	<a href="#">NZ_KI518741.1</a>
Pseudomonas aeruginosa M8A.3 genomic scaffold adger-supercont1.2, whole genome shotgun sequence	531	1328	71%	3e-145	67%	<a href="#">NZ_KI518738.1</a>
Pseudomonas aeruginosa C48 genomic scaffold adgeZ-supercont1.1, whole genome shotgun sequence	531	1323	71%	3e-145	67%	<a href="#">NZ_KI518703.1</a>
Pseudomonas aeruginosa PAK genomic scaffold acUKM-supercont-complete, whole genome shotgun sequence	531	1289	73%	3e-145	67%	<a href="#">NZ_KE137323.1</a>
Pseudomonas aeruginosa BWHPA001 genomic scaffold adges-supercont1.1, whole genome shotgun sequence	526	1294	73%	1e-143	67%	<a href="#">NZ_KI519184.1</a>
Pseudomonas aeruginosa BWHPA009 genomic scaffold adggc-supercont1.1, whole genome shotgun sequence	526	1294	73%	1e-143	67%	<a href="#">NZ_KI519116.1</a>
Pseudomonas aeruginosa BWHPA015 genomic scaffold adggh-supercont1.1, whole genome shotgun sequence	522	1291	73%	2e-142	67%	<a href="#">NZ_KI519071.1</a>
Pseudomonas aeruginosa BWHPA025 genomic scaffold adggk-supercont1.1, whole genome shotgun sequence	522	1280	71%	2e-142	67%	<a href="#">NZ_KI518992.1</a>
Pseudomonas aeruginosa PA1, complete genome	517	1271	73%	8e-141	67%	<a href="#">NC_022808.1</a>
Pseudomonas aeruginosa PA1R, complete genome	517	1271	73%	8e-141	67%	<a href="#">NC_022806.1</a>
Pseudomonas aeruginosa BL01 genomic scaffold adgeu-supercont1.1, whole genome shotgun sequence	165	518	23%	6e-35	69%	<a href="#">NZ_KI518955.1</a>
Pseudomonas aeruginosa RP73, complete genome	165	534	23%	6e-35	69%	<a href="#">NC_021577.1</a>
Pseudomonas aeruginosa BL02 genomic scaffold adggf-supercont1.3, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI518951.1</a>
Pseudomonas aeruginosa BWHPA005 genomic scaffold adgjf-supercont1.1, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI519153.1</a>
Pseudomonas aeruginosa BWHPA013 genomic scaffold adgnn-supercont1.1, whole genome shotgun sequence	161	604	27%	7e-34	69%	<a href="#">NZ_KI519078.1</a>
Pseudomonas aeruginosa BWHPA019 genomic scaffold adgfe-supercont1.2, whole genome shotgun sequence	161	527	23%	7e-34	69%	<a href="#">NZ_KI519052.1</a>
Pseudomonas aeruginosa BWHPA023 genomic scaffold adgeL-supercont1.2, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI519009.1</a>
Pseudomonas aeruginosa BWHPA024						

genomic scaffold adgfW-supercont1.1, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI518996.1</a>
Pseudomonas aeruginosa BL10 genomic scaffold adgez-supercont1.1, whole genome shotgun sequence	161	527	23%	7e-34	69%	<a href="#">NZ_KI518883.1</a>
Pseudomonas aeruginosa M9A.1 genomic scaffold adget-supercont1.1, whole genome shotgun sequence	161	527	23%	7e-34	69%	<a href="#">NZ_KI518722.1</a>
Pseudomonas aeruginosa C20 genomic scaffold adgfy-supercont1.1, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI518719.1</a>
Pseudomonas aeruginosa C23 genomic scaffold adggj-supercont1.1, whole genome shotgun sequence	161	522	23%	7e-34	69%	<a href="#">NZ_KI518716.1</a>
Pseudomonas aeruginosa c7447m	158	523	23%	8e-33	69%	<a href="#">NZ_CP006728.1</a>
Pseudomonas aeruginosa E2 genomic scaffold adgft-supercont1.1, whole genome shotgun sequence	158	523	23%	8e-33	69%	<a href="#">NZ_KI519305.1</a>
Pseudomonas aeruginosa BWHPA011 genomic scaffold adfgg-supercont1.1, whole genome shotgun sequence	158	523	23%	8e-33	69%	<a href="#">NZ_KI519084.1</a>
Pseudomonas aeruginosa BWHPA022 genomic scaffold adgeq-supercont1.1, whole genome shotgun sequence	158	523	23%	8e-33	69%	<a href="#">NZ_KI519017.1</a>
Pseudomonas aeruginosa BWHPA007 genomic scaffold adgeP-supercont1.2, whole genome shotgun sequence	156	593	27%	3e-32	69%	<a href="#">NZ_KI519140.1</a>
Pseudomonas aeruginosa BL06 genomic scaffold adgfq-supercont1.1, whole genome shotgun sequence	156	593	27%	3e-32	69%	<a href="#">NZ_KI518915.1</a>
Pseudomonas aeruginosa BL11 genomic scaffold adgfl-supercont1.1, whole genome shotgun sequence	156	593	27%	3e-32	69%	<a href="#">NZ_KI518875.1</a>
Pseudomonas aeruginosa CF614 genomic scaffold adggb-supercont1.1, whole genome shotgun sequence	156	593	27%	3e-32	69%	<a href="#">NZ_KI518656.1</a>
Pseudomonas aeruginosa PAO581	154	520	23%	1e-31	69%	<a href="#">NZ_CP006705.1</a>
Pseudomonas aeruginosa PAO1-VE2	154	520	23%	1e-31	69%	<a href="#">NZ_CP006831.1</a>
Pseudomonas aeruginosa PAO1-VE13	154	520	23%	1e-31	69%	<a href="#">NZ_CP006832.1</a>
Pseudomonas aeruginosa SCV20265, complete genome	154	592	27%	1e-31	69%	<a href="#">NC_023149.1</a>
Pseudomonas aeruginosa MSH3 genomic scaffold adgeF-supercont1.1, whole genome shotgun sequence	154	629	26%	1e-31	69%	<a href="#">NZ_KI519298.1</a>
Pseudomonas aeruginosa BWHPA008 genomic scaffold adgga-supercont1.2, whole genome shotgun sequence	154	592	27%	1e-31	69%	<a href="#">NZ_KI519135.1</a>
Pseudomonas aeruginosa BWHPA028 genomic scaffold adgfi-supercont1.1, whole genome shotgun sequence	154	514	23%	1e-31	69%	<a href="#">NZ_KI518959.1</a>
Pseudomonas aeruginosa C41 genomic scaffold adgfh-supercont1.1, whole genome shotgun sequence	154	514	23%	1e-31	69%	<a href="#">NZ_KI518709.1</a>
Pseudomonas aeruginosa 2192 supercont1.1 genomic scaffold, whole genome shotgun sequence	154	511	23%	1e-31	69%	<a href="#">NZ_CH482384.1</a>
Pseudomonas aeruginosa BWHPA020 genomic scaffold adgeC-supercont1.7, whole genome shotgun sequence	150	509	20%	1e-30	68%	<a href="#">NZ_KI519048.1</a>
Pseudomonas aeruginosa BL23 genomic scaffold adgfb-supercont1.7,	150	581	27%	1e-30	68%	<a href="#">NZ_KI518778.1</a>

## whole genome shotgun sequence

Pseudomonas aeruginosa CF18 genomic scaffold adgd-supercont1.1, whole genome shotgun sequence	150	487	23%	1e-30	68%	<a href="#">NZ_KI519281.1</a>
Pseudomonas aeruginosa X24509 genomic scaffold adgeH-supercont1.1, whole genome shotgun sequence	150	509	20%	1e-30	68%	<a href="#">NZ_KI519266.1</a>
Pseudomonas aeruginosa BWHPA016 genomic scaffold adgn-supercont1.1, whole genome shotgun sequence	150	550	27%	1e-30	68%	<a href="#">NZ_KI519068.1</a>
Pseudomonas aeruginosa BWHPA027 genomic scaffold adgz-supercont1.1, whole genome shotgun sequence	150	581	27%	1e-30	68%	<a href="#">NZ_KI518973.1</a>
Pseudomonas aeruginosa BL12 genomic scaffold adgc-supercont1.1, whole genome shotgun sequence	150	573	27%	1e-30	68%	<a href="#">NZ_KI518856.1</a>
Pseudomonas aeruginosa BL19 genomic scaffold adgeJ-supercont1.1, whole genome shotgun sequence	150	581	27%	1e-30	68%	<a href="#">NZ_KI518814.1</a>
Pseudomonas aeruginosa str. Stone 130 genomic scaffold aczk-supercont1.1, whole genome shotgun sequence	150	581	27%	1e-30	68%	<a href="#">NZ_KI517348.1</a>
Pseudomonas aeruginosa NCMG1179 DNA, contig: scaffold00001, whole genome shotgun sequence	150	573	27%	1e-30	68%	<a href="#">NZ_DF126593.1</a>
Pseudomonas aeruginosa BWHPA004 genomic scaffold adgz-supercont1.1, whole genome shotgun sequence	147	516	23%	1e-29	68%	<a href="#">NZ_KI519157.1</a>
Pseudomonas aeruginosa BWHPA012 genomic scaffold adgc-supercont1.1, whole genome shotgun sequence	147	516	23%	1e-29	68%	<a href="#">NZ_KI519080.1</a>
Pseudomonas aeruginosa BWHPA014 genomic scaffold adgeT-supercont1.1, whole genome shotgun sequence	147	516	23%	1e-29	68%	<a href="#">NZ_KI519076.1</a>
Pseudomonas aeruginosa BWHPA021 genomic scaffold adgeQ-supercont1.1, whole genome shotgun sequence	147	516	23%	1e-29	68%	<a href="#">NZ_KI519023.1</a>
Pseudomonas aeruginosa MTB-1, complete genome	141	541	27%	6e-28	68%	<a href="#">NC_023019.1</a>
Pseudomonas aeruginosa JJ692 genomic scaffold adgf-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI519251.1</a>
Pseudomonas aeruginosa U2504 genomic scaffold adgfx-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI519240.1</a>
Pseudomonas aeruginosa 6077 genomic scaffold adgeN-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI519216.1</a>
Pseudomonas aeruginosa BWHPA006 genomic scaffold adhwj-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI519145.1</a>
Pseudomonas aeruginosa BL03 genomic scaffold adgeM-supercont1.1, whole genome shotgun sequence	141	614	27%	6e-28	68%	<a href="#">NZ_KI518942.1</a>
Pseudomonas aeruginosa BL04 genomic scaffold adgfk-supercont1.1, whole genome shotgun sequence	141	548	26%	6e-28	68%	<a href="#">NZ_KI518931.1</a>
Pseudomonas aeruginosa BL08 genomic scaffold adgeD-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI518897.1</a>
Pseudomonas aeruginosa BL13 genomic scaffold adgfQ-supercont1.1, whole genome shotgun sequence	141	475	23%	6e-28	68%	<a href="#">NZ_KI518852.1</a>

Pseudomonas aeruginosa BL14 genomic scaffold adggl-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI518844.1</a>
Pseudomonas aeruginosa BL17 genomic scaffold adggm-supercont1.1, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_KI518822.1</a>
Pseudomonas aeruginosa BL25 genomic scaffold adgfY-supercont1.1, whole genome shotgun sequence	141	536	27%	6e-28	68%	<a href="#">NZ_KI518750.1</a>
Pseudomonas aeruginosa NCGM2.S1 chromosome 1, complete genome	141	469	23%	6e-28	68%	<a href="#">NC_017549.1</a>
Pseudomonas aeruginosa 39016 chromosome, whole genome shotgun sequence	141	469	23%	6e-28	68%	<a href="#">NZ_CM001020.1</a>
Pseudomonas aeruginosa S54485 genomic scaffold adgfS-supercont1.4, whole genome shotgun sequence	138	428	22%	8e-27	68%	<a href="#">NZ_KI519259.1</a>
Pseudomonas aeruginosa 19660 genomic scaffold adgew-supercont1.1, whole genome shotgun sequence	138	552	25%	8e-27	68%	<a href="#">NZ_KI519229.1</a>
Pseudomonas aeruginosa X13273 genomic scaffold adgeE-supercont1.1, whole genome shotgun sequence	138	480	23%	8e-27	68%	<a href="#">NZ_KI519192.1</a>
Pseudomonas aeruginosa BWHPA026 genomic scaffold adgfp-supercont1.1, whole genome shotgun sequence	138	598	20%	8e-27	68%	<a href="#">NZ_KI518981.1</a>
Pseudomonas aeruginosa BL15 genomic scaffold adgeO-supercont1.1, whole genome shotgun sequence	138	554	27%	8e-27	68%	<a href="#">NZ_KI518835.1</a>
Pseudomonas aeruginosa BL21 genomic scaffold adgep-supercont1.1, whole genome shotgun sequence	138	480	23%	8e-27	68%	<a href="#">NZ_KI518793.1</a>
Pseudomonas sp. 2_1_26 genomic scaffold supercont1.1, whole genome shotgun sequence	138	482	23%	8e-27	68%	<a href="#">NZ_JH376461.1</a>

## Alignments

Pseudomonas aeruginosa BL05 genomic scaffold adgfv-supercont1.1, whole genome shotgun sequence  
 Sequence ID: [ref|NZ\\_KI518928.1|](#) Length: 5663406 Number of Matches: 8  
 Range 1: 1243506 to 1246502

Score	Expect	Identities	Gaps	Strand	Frame
544 bits(602)	5e-149()	2129/3151(68%)	496/3151(15%)	Plus/Plus	
Features: <b>glycosyl transferase family 1hypothetical protein</b>					
Query	2184	GGATGCAACCCAGGCTGATGTTACGGGCCTTAACGTGCGGTTAGTCGTG-TTATGCTGCT			2242
Sbjct	1243506	GGATGCAATCCAGGCTGATGTTACGGGCCTGCTCGTGCCGGTG--CGTGATTCTGCTGCT			1243563
Query	2243	CTGGCGGATGCCATTCA-CGTCTGCTT-AGTCGCG-GA-TTGC GCAAGGAGCAATGGGGA			2298
Sbjct	1243564	CTGGCGGATGCCATTCAAGCGTCTTATCGAGTCGCCAGAGTTGCCAAGAAG--ATGGG-A			1243620
Query	2299	GATGCTGA---AGCGTTGGCAGGTCGT----TTGCAATCCATATATCGTCCAACA--AC			2349
Sbjct	1243621	GCTGCTGGGCGAGCGTTGGCAGAGCGTGATTTTGGCATCGAAAGTATCGTCCAACAGCAC			1243680
Query	2350	CA---ACTTCT-GGGCA-TAGGGAGCG---CTTGACGCAA---ATGTAATTGATACAG			2396
Sbjct	1243681	CTGGATATTTATCGGGCACTAGGGAGCGGAGCTTGACGCGACATAATGTATTGGTAACGG			1243740
Query	2397	----AAACGGATTCCATGAGTATCACGCTGGTTATTAATAGTCTCTGTTCTTCCGGGCA			2452
Sbjct	1243741	GGGCAACCGGATTC-ATCGGGGCCGCGCTGGTCA----ATAGTCTCTGTTCTTCCGGGCA			1243795
Query	2453	ATGATAAAGATTGACATTAGGGCGC--AA----TGGGGCCTGGCA-CGACCAAGAATCC			2505
Sbjct	1243796	GT-ACAAGTTTGGGCCGGGTGCCGCCAAGAGGTGGGGCCTGGCCTCGAGGGGTTACTC			1243854

Query 2506 CCTTGCTTCCTGATG-----GCAGTTCGTGTGTCTGGGATCCCGTA----CAACCGATA 2555  
Sbjct 1243855 CCTTGCTTCTGGGTGAAC TGGGCAGTTCGTGTGTCTGGGATGCGGAGTCGGCCATCGATA 1243914

Query 2556 CGGTGATGTGTGTGTCGTGTGCATTGCCGCCTTACAGTGTGCATCGAATAACGACAGCG-- 2613  
Sbjct 1243915 CGGTGGTTCATTG-----CGCTGCCCGCGTGCA-TGTCAT-GAGCGA-GACGGCCTC 1243963

Query 2614 CGATGCTTAGGTAAGGACCGTCGAGGTCCCAAAGC--ACGTTCCGGGAGAG-CTTGA--- 2667  
Sbjct 1243964 CGATCC-----GCTCGTCGAGTTCGCAAGGCCAACGTTCAAGGGACACTTGATCT 1244014

Query 2668 -GTCTAGGAGG-----TCCCGGGGAAGAGGGGGCGCGCTTCCCTGTCT-TAA--TAGAT 2718  
Sbjct 1244015 GGCCCGGGAGGCCGTATCCCGGGGA-----GTGCGCGCT-TTCATCTTTATCAGCTCGAT 1244068

Query 2719 A--GGTCATCTG-GAGGGAGTGA---CGGATTCGGGCCT---CTGC--ACCGTCTAGCC 2767  
Sbjct 1244069 AAAGGTCAATGGCGAGGGAAGT GAGCCCGG--TCGCCCTATACTGCGGACAGTCCG--C 1244124

Query 2768 CCAATCATGTGCGTACCTAAC-CGTTCC--ATCGGAAAGCGGAGCAGGC--TATTGGATT 2822  
Sbjct 1244125 CCAATCCTGTCGATCCCTATGGCGTTTCCAAACGGGAAGCGGAGCAAGCGCTATTGGATC 1244184

Query 2823 AAGAAGAACA-----ACTGGAAGTTGAATGAACATTCGGC-----TTTATGGTCC 2867  
Sbjct 1244185 TGGCGGAAGAGACCGGACTGGAGGTTG--TGATCATCCGACCGGTCTGGTTTATGGTCC 1244242

Query 2868 CCCATTATAGGCCAACGTACAA--CATC-TGCGCTGGCTGAAGGGCGAGGGGGCGGACGC 2924  
Sbjct 1244243 AGGGGTCAAGGCCAACGTACAGACCATGATGCGCTGGCTGAAGCGG-----GCGTGCC 1244297

Query 2925 GTGCTAAACACTACAGAC----CTAAATCAG--TAGTCTGGTGTCACTGGGACTATCTTC 2978  
Sbjct 1244298 CTCC----CTCTAGGGGCTATTCATAATCGGCGTAGTCTGGTGTGCTGG-ATAATCTTG 1244352

Query 2979 TTGTCACTCATCA--ACCTGCATCGAGCATCCATCAATCGGTCCGGCAAATTTTCTATAG 3036  
Sbjct 1244353 TCGAC-CTCATCATCACCTGCATCGAGCATCCGGTG-CGGTCCGGCAAAGTTTTC-TCG 1244409

Query 3037 TTAGCAAAGTGGAA----TTTCG-----CGAGTGTGCTGCGGAGATCGGATAGGGCCTT 3087  
Sbjct 1244410 TAAGCGACGGTGAGGATCTTTCACCACCGAGT--TGCTGCGGAGAATGGGACGCGCCTT 1244467

Query 3088 AGGGCACAATAGGCGCGGCCAATGCTGC-TGTTCC-GCCAGTACTTAGTTAAGGGCGGG 3145  
Sbjct 1244468 -GGGCGCTCCCG-CTCGCC---TGCTGCTGTTCCCGCCAGTTGGATCGGTGCAG-CGGC 1244521

Query 3146 GTAGAGCAGCGTTGGACTAGGCAGGCATTTAGC---CCGCTGTAGACCTAATTGCAAG 3202  
Sbjct 1244522 GAA---AGTTCTGAAC-AGGCAGGCATTT-GCTCGCCGCTGTGCGGC-TCATTGCAAG 1244574

Query 3203 TCAAA--CCTGAAAACC-GCCA-GTACTTGGCTGGACCGC-CCGGTAGGGTA----CAGG 3253  
Sbjct 1244575 TCGATATCATGAAAACCCGCCAAGTGTCTGGCTGGACTCCGCCGTTAGGGTGGACCAGG 1244634

Query 3254 CAT----GCAAACCGC----TCTTTCCTGGATCTCGA-TGATGAATCTATGGTTGTTGT 3304  
Sbjct 1244635 CATTGGAGAAAACCGCCCGCTCTTTCTCGATCGCAATGATGAATCTATGTTGTTGT 1244694

Query 3305 -CAAGCA-TTGGAGTAATTTTCGCTGCTGTCTCCTAAGCGTCTTCCCTTCAACGAAA 3362  
Sbjct 1244695 GCCGGCGGTTGCCGCTC--TTTCCCTGCTGTTGACCGC-CGGCTTGCGCCGTTA-CGCGA 1244750

Query 3363 TTTGCCGAGCTTGATCGAT---CACAATGCCCATGT---CTCTAGGTGCC--CTCCG- 3413  
Sbjct 1244751 TTGCCCGAGCTTGATCGATGTACCCAATGCTCGAAGTTCTACCAGGTGCCGACGCCTA 1244810

Query 3414 GAGCATGTGGGACTTTAACGT-----CCTTAAT-CTGGCAGTGTGCTTGCGGCAATAT 3467  
Sbjct 1244811 GGGGGGGCGGTGTCGCTATCGTGCTCTCCTTCTGCTGGCAGTGTGCTTGCGGCGATAT 1244870

Query 3468 TGGGCTAAGTGGAT--GGATC---CCACTG--ATCACTGGGGCGGACTGTGGGATCGCAT 3520  
Sbjct 1244871 TGGGCGCGGTGAAACCGGATCTGGCCACTGGTATCCTGGGGCGGGTATTGGGATCGCAT 1244930

Query 3521 CTTGCTGGGCTTCCACTA--ATC-TGGCCATATCCCTGCCCGTTGGCGTTTGTCTCGGCGG 3577  
Sbjct 1244931 --TGCTGGGCTTCTCGACGATCATGGCCATATCGCTGCCCGTTGGCGTTTGTCT--CGG 1244985

Query 3578 CCATTTTAGCGCTGCTTCCCT-GATGTGGTA----CGTGGAGGGTTGCCTGCATTGGCCTT 3632  
Sbjct 1244986 CCATTTGCGCGGTGCTTGTGCTGCTGCTACTGGCTTGGAGGTTGCTGCAATTGGCCTT 1245045

Query 3633 T---CGCCTTGTGGTCG---TGGGGTAG--TG---CCATAGCTGC-CCGTTCTATCTG-- 3678  
Sbjct 1245046 TTTCCGGCCTTGTGGTCGATCTGGGGTGGGTTGGACACATAGCTGCGGCGTTCTATCTGGT 1245105

Query 3679 --GGATCGTAAATCTCT--AATTCAT-----CTATCAATGGGATTGCCACCGTTGAGGC 3728  
Sbjct 1245106 ATGGATGCTCAATCTCTACAATTTATGGACGGTATCGATGGGATTGCCAGCGTTGAGGC 1245165

Query 3729 -----TGTGCGTTGG-----CCTGCGTGGGTTGGTCATATCCTTAAGGTCCGATGA 3774  
Sbjct 1245166 TGTGTGTGTGTGCGTTGGCGCTGCCCTGCTTGTGCTGGTCAGTGGTGTAGGTTCCGATGA 1245225

Query 3775 GGCATCCGA-GGCGTTTCTTGGCCTCGGCGCGCT--TAGGA-TAGAAGTGACGGGATTC 3830  
Sbjct 1245226 GGCATCCAGGGCGT--TTGG--TTGGCGGCGCTGCTGGCAGCCGCGGTGACGGGATTC 1245280

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Query 3831 C-TTCTGGAATATTTCT-ATGC-TAGATCTTCAT-GGGGAT--TAGTA--AGTT--TTG 3880
Sbjct 1245281 CTTTTCTGGAATTTCCCTCCTGCGCGGATCTTCATGGGGATGCTGGTAGCGGTTTCTTG 1245340
Query 3881 GG----AT--GTAATGCCCTTTCCCTGCG-AGCCG-ATGGCATTATCGCCGCAACTTTCCG 3932
Sbjct 1245341 GGGGTATCATTGGTGGCTTTCCCTGCAAGCCGATGG--GTCTCGCCGCAACT---CT 1245395
Query 3933 TCTGGGGTCTACT-ATCCTGCT-CCGATATTCGACTTTGATGCCTACATGGCTCTTGTTG 3990
Sbjct 1245396 TCTGGGGTTGGCTCATCTGCTGGGGTATTTCATTGTTGATGCCACCCTGAC-CTTGTTG 1245454
Query 3991 CCC---TTGCTGCGGCTCGGAAAGGGTATGAGGCATCATCGAGTCACCCA-ACGA- 4045
Sbjct 1245455 CGCCGGTTGCTGCGG--GGAGACAAGGTTTATGAGGC-GCATCGCAGTCACGCATACCAG 1245511
Query 4046 TCTGCTTCTCGTCATTACGGGCG---TCGTCCTGTACCTATCGATCCGGAGGCATCAAC 4102
Sbjct 1245512 TATGCTTCTCGTCATTACGGGCGTCATCTTCTGTACCCTGGCAGTGGGAGGCATCAAC 1245571
Query 4103 ATCTTCTGGTTGTT-----AAACCATATTTAA---AGGAA-ATCGACGGGATCGAT 4149
Sbjct 1245572 ATCTTCTGGTTGTTGCCACTGGCACTGCTTGTGCGAGCGGGGAAGATCGACGGCAT-GCT 1245630
Query 4150 TGATTTTGTATTGGCTACTTAACTCTGGCGTTCCCT-GAAAACCG-TTTAAG--CCGAGT 4205
Sbjct 1245631 TGCTTTGTTGATTGGCTACCTGCCTCTGGCGTTCCCTGGCGCTCCGTTTTAAGCCGGAGT 1245690
Query 4206 TATGGAATC-GGAGCACATGCAATGTCCCGG-TCCCTGAAGCACAAAGCGGATTTTC-- 4261
Sbjct 1245691 CCTGGAATCACGCGCTGCTTGAATGTCCCGGTTGGCTGGAG-GCGCGGACGATTTTCCG 1245749
Query 4262 GGAACCTA-GCTCTGAAAGGAATGTGCGA-CGATGATCAGTAATGGTAGTAACTA-TGCC 4318
Sbjct 1245750 GGACGATAAATATGAAAGGAATGTGCAAGCGATGATCA-----GTAGTACTACTGCC 1245803
Query 4319 GGACGCGTGATTGATTT-----AGAGTACTTGCC--ATCA--GGAATGGACTTGCCAGA 4369
Sbjct 1245804 GATAGCGTGATTTGGGTTCCGGAATGTTATTTGCCAGACCAAGGAAATGGACTGCCCGGA 1245863
Query 4370 -TTGTTTCGGGTGGATGCAGGTG-AGTGAA--GAACTTACTGATGGGATGTTGG-TAAGGT 4424
Sbjct 1245864 CTTGTTTCGGGTGGATGCAGGTGAGTGAAGGGGGCTGATTAATAGGATGTTGGATAA--- 1245920
Query 4425 ATTGCGT-GACGCTACCTGGAGGGGGATTGCCG---CGCCCCAA--GCATTTTGTGCGA 4478
Sbjct 1245921 CTTGCGTGGACGCCTCCT-----GGGATTGCCGCGCCGAGGAGCGCATTCCT--CAGG 1245973
Query 4479 TTGCTTAGACGGGATATCAACCTGGTG-----CGTTCTGCCTGGCTTTTAAACCGTCTC 4531
Sbjct 1245974 TTGC---GAC-GGACATCGGCCTGGTGTGGCTTTTCATTGTGGCTGGCTT-----TC 1246020
Query 4532 CTCGAG---CAAGACACCGAAGACATGATCGATCCCGTTCGG---AAACCCCTG---ATT 4582
Sbjct 1246021 CTGGTGCCTCTCGGCACCGAAGACATGATCGAT-CCGTTTCGGGGATCACGCCTGGCTGTT 1246079
Query 4583 TCTAGCACCGCCTATAAACCGCCATCC--GACTTCATCC-ATTCGGCATGTACCGGGCGG 4639
Sbjct 1246080 CATAGCGGCGCCTCT-AACCGCCATCCCGCTCTTCATCCGCTTCGGCATGTACCGGGCGG 1246138
Query 4640 TGAATGCTACCACCTAGCGAAGACCGTGTGACGGCCAGATCGCCA--GCGGTCA-CAT 4696
Sbjct 1246139 TG-ATGC-GCTACCTGGGCAACGA-CGCCCTTATCGC--GATCGCCAAGGCCGTCACCAT 1246193
Query 4697 TTCTAAGACT--TGCT-TCG-TGCTG---TACTGGTACCCATCCC--TAATAAGTGAT-C 4746
Sbjct 1246194 TTCCGCG-CTGGTCTGTCTGTTGCTGGTCTACTGGTACCCTCCCGCGGCGGTTGGTGC 1246252
Query 4747 CCCGTT-CCTGGTGTTCATC-ACTGGTG--TTACCATGCATGCCTGATC----CATTGCG 4798
Sbjct 1246253 CCCGTTCCCTGGTGTTCAACTACTGGTGGTTGAGCATGC-TG-CTGATCGGCGGCTTGCG 1246310
Query 4799 --TGGCACATGCGCC--TAATTCAT-CGAGACTGGTA--CTGCTGTGCAGTTCGGTAGAG 4851
Sbjct 1246311 TCTGGC-CATGCGCCAGTATTTTCATGGGCGACTGTTACTCTGCTGTGCAG-TCGGTA--- 1246365
Query 4852 AATGATGGGTTTCTTTACCATCACGCGCGGATGG-ATGCCAGGGTGAATA-CTAT---- 4905
Sbjct 1246366 -----CCATTTCT---CAAT--CGCCAGGATGGCTGCCAGGGTGGCCATCTATGGCG 1246414
Query 4906 -GAGGAGGACGGGCAACCAGTTGGTGCCGGCATTGCATTCTCATTC--GCGATGCGTCTA 4962
Sbjct 1246415 CGGGGGCGGCGGCAACCAGTTGGTGGCGGCATTGC-ATGCTCGGTCGGGCGATGCGTCCG 1246473
Query 4963 GT-CCGTTTCATACCATCCACGGCAAGCTGAT 4992
Sbjct 1246474 GTGGCGTTCAT-CGAT-GACGACAAGCAGAT 1246502

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Range 2: 1241449 to 1243044

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	2e-60()	1120/1652(68%)	262/1652(15%)	Plus/Plus	

Features: glycosyl transferaseglycosyl transferase family 1

Query 280 AGCTAATGCTCAAGGCGGTTGGTGAAGACTCAA--TGCGGACTTAGGAAGAGTTCCCAT 337



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Sbjct 1241449 AGCTAATGCTCAAG-CGGTTGATCGAGACTCAAAATGGCGGCAGT-----GAATTCGAAC 1241502
Query 338 ACTTCTAATTATTCATGTCT-TCTGGTGTATTGGTGAGTTTGGGCAAGATCTGATTG--- 393
Sbjct 1241503 A-TTCGATTATTTCA---CTGTCTGATCT--TGGTGAGTTTGGGCAGGGTCTGATTGAGG 1241556
Query 394 CTAGTA---CTGTTGGT-TGCTGTGGCGGTATAATGATGAGGGAAATGC---GGCATTAA 446
Sbjct 1241557 CTGGTATATCTGTTGATGTCT-TGGCATGACCTCGATGAGGGATATGCCTCGGGTGCTC 1241615
Query 447 CGTCGT-TGATCTGGATATTTCTTTA--GGAGGC--GGTCAA----AAACATGGATGTA- 496
Sbjct 1241616 CTTCTGCTGATAGGGATATTTCTGTAAAGGAGGCCCGATATAGTCCAAACATGGATGTAT 1241675
Query 497 -ATTCCGATCTTCTTGATC-ATTAG-TGCGATCA-----ATTGGCAGGGT-----GG 540
Sbjct 1241676 CATTCCGATCTTCTTGGTGGATTGGCTGCCAGAATGGCCGGTATTGGCGGGATTATATGG 1241735
Query 541 GGAGTCGCCCTGAACGTGGGTGAGGCGAGGGCAGCA-GAATACGACT-TTCTCTGACGGA 598
Sbjct 1241736 GGAGTCCGCACGACCGACCTCAAG--AGGGCGCAAGAGTACGACTGTTCTGGTACGGA 1241793
Query 599 AAATGTTA--CTGGCTATCC--ATTCTTC---AGATATATTGTCCC-CAGGCTAGGGCT 650
Sbjct 1241794 AGGTGTGTGCCGTGGCTATCCGGATTCCTGCCAAAAATATATTGTTGCGCCCGCAGGCC 1241853
Query 651 ACCGGCGCGA-----TGCTGTCTAGGCTCG--GCAAGCAGGATCCTCCTGGTCTG--C 699
Sbjct 1241854 CAAGGCGCTCACACATTGCTGTT--GGCTACAACGCAAGCAGGATGCT---GGTCATTCC 1241908
Query 700 CAACTCCGTTTGA-CATTATAGCCCTGC-GGC-ATGGAGCGCATCGCGGTCA---ATGAG 753
Sbjct 1241909 CAACG--GTTTCGATCTCACTCGCCTGCAGGCGACCGA-CGAACAGCGGTCCGCTATCAG 1241965
Query 754 GAATGGAGCTGGCAGAGACG--AGC-ATCAGTTGAGTCCAGTCCGACGAGATTCTAGCA 810
Sbjct 1241966 GAGTGGAGCTGGCATAGAGGCCAGCGATATCGTGATTGGCAGTCTAGGCAGATTCCACCC 1242025
Query 811 GAGGTCGGGATC-TGCTTCCTTC----CAGCTTA-GGTCTGCTGGAAC-TGTTATGC-C 862
Sbjct 1242026 G-GTAAAGGATCATGCTTCTTTGTGCGAGCTGCCGGTCTGCTGGCTCCACGTTATTCGC 1242084
Query 863 ACTTGAAGTTTTCTTTTGTATCTCCAACGGAGCTGCTGTCTC--ATGCTGAAGTTGCATA 920
Sbjct 1242085 GCTTGAAGTTT-CTTTTGGTGGG-ACGGGAGCTGCTGTCTTCCAATGCTGAA-TTGCAGC 1242141
Query 921 G----AT-GAGGC-ACCTCATATTAGGGGGAGCGCTTTAATCACTGCTTGGCAGA-CAGC 973
Sbjct 1242142 GCCTCATCGAAGCTACCGGTAT--GCGGAGCGCTTCA-TC-CTGCTTGG-AGAGCGGC 1242195
Query 974 AAGATCTA--TTGGTTGCTTGGCAGCCATGGATATCTTCTGTCTGCGGTCTCGCAC-CA 1030
Sbjct 1242196 AAGATGTAGCTTCGTGTCT--GAAAGCCATGGATATCTTCTGTCTGCATTCTCGCACGGA 1242253
Query 1031 GGGATTCCCAATG-TCTTAG---AGCCATG--AATGGGATTGCCTTGAT--GCACTGG 1082
Sbjct 1242254 GGGATTCCCAATGTTCTTGGTGAAGCCATGGCCATGGGATTGCCTTGATATTACCACTGA 1242313
Query 1083 T---TAGGATGC--ATTATTTGGCTCGGT-----TGGTCTGCTCGTTCCGGCGCGCTTTA 1130
Sbjct 1242314 TGTGGGGGATGCGGCTTATTT-GCTAGGTAACGACGGCGTCTGCTGTTCCGGC---CTT-- 1242367
Query 1131 GGGTCC-AATGC-CT---CCAAGGTATGTAGAAGTACCATTCCGTTGGAT----TGGGTCT 1181
Sbjct 1242368 GGATCCGAATGCGCTCGGCAAAGGTATCGAGGA-TCTCATTGCGTTGGATGTCGAGGGTC 1242426
Query 1182 GTCGGGCACTTGTGGTAAGG-TCC--GAC--AGGATTTATAACGCAACTGC-CCAT-CCT 1234
Sbjct 1242427 GTCGGGCACT--TGGTGAAGCTGCAAGACAGAGGATTTA-CTCG-AACTTCACGATGGCC 1242482
Query 1235 AGTG---CTCAGCG-TTCATGAGTC----TCAGGTC-TGTGTGT--AAGAAAAGCTT-A 1281
Sbjct 1242483 AGTGCCCTCTCAGCGTTTCTATGAGTCTGTATCGCGACATTCTTGTAAAAAGAAAAGCTTGA 1242542
Query 1282 CG---CTGCAGGTTATGTT--TAGCCTCCATC--GGAATTCGC-TGAAGCC-GTATTGTT 1332
Sbjct 1242543 CGAGCTTGAAGGTTATGTTTGTAAAACGCATCGAGGAGTTTGCATGAAGCCGGTATTGTT 1242602
Query 1333 GATGATA-----ACTC--CGTTCTTCATGTCTCACCGTTTACCGGTC-CTGTCCGGAG- 1381
Sbjct 1242603 GATGATAGTGAACGACCCGGCTTTCTTTCATGTCTCACCGTTTACCGGTCGCTGTCCGGAGC 1242662
Query 1382 CCAGCAACGTG-----CA-----ATAAAAACTAAAGTACT-----CTAAGTG-AAAAGAT 1425
Sbjct 1242663 CCAGCAGGCTGGTTTCCAGGTACATATCGCCACACGCCCTGGTGACGCGGTGAAAAAGAT 1242722
Query 1426 CGTCTCCTCCAGGTTTTCTGCA-CCTGATCTGATTCCACTGTTCCCGCAGCCGAAAAA-- 1482
Sbjct 1242723 CGTCTCC-CAAGGTTTTCTGCATCATGAATTG---CCACTG-TCCAGAAGCGGAAAAAAT 1242777
Query 1483 TCATTTCAAGTGGCGTAT-----GCGTATGTC--CCACCTTT--TGGAGATTGC--AAT 1530
Sbjct 1242778 CCTTTTTTCAAGCTGTATCTGCTGACTTATGTCTGGCGCCTTTTGTGGAGATTGCGGCC 1242837
Query 1531 AGTG-TTTACACCTGGTTA--AGTAAGCCGGTA--GTAGTGTGGAGTACCCTAAG-GTG 1584
Sbjct 1242838 GATGTTTTTACACCTGGTTACCATCAAGCCGGTAATCTATGGCGGTATCGCCGCACGCTTG 1242897
Query 1585 GCGCCGGTGAAGAGAATCGTGGCGGCCGTTT-CAGACGTGG-TTCG--TTCATGAGGGC 1640

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Sbjct 1242898 GCGCCGGTG-AAGGGGGTCGTGGCGGCCGTTTCCGGACTTGGTTTCGTTTTTCAT--GGCC 1242954  
 Query 1641 GAGGGTCTGAAG--CTGCG---TTCGGTTTACTGTGTGCGCTGGCTTTATCGGCGACCGT 1695  
 Sbjct 1242955 AAGGGTCTGAAGGCCTGCGCGTTTCG--TGCCTGTGTGCGCTGGCTTTATCGGCGGGCTT 1243012  
 Query 1696 TGG--AAAGAAAAGTTGCGTGTGCATCTTTCAA 1725  
 Sbjct 1243013 TGGGCAAGAAAAAGTTGCGTGTGCATCTTTCAA 1243044

Range 3: 1246779 to 1247392

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	4e-30()	453/660(69%)	95/660(14%)	Plus/Plus	

Features: membrane protein

Query 5215 GCTGCTGAAATAGTCCATCCCATTCCAGGTGGTA--GGTGATGGGGCGGT---TCCTGG 5269  
 Sbjct 1246779 GCTGCTGGAACGGTGCATCCGCGGTCCAGGTGGTGTGATGGTGACCGGGGCGGGCGGTTCAT 1246838  
 Query 5270 CTTTGTGCGGAATACTGTCTGAA-ATCATGAGGCAGTTGTTCCGGACTAGCGTGCTTA--CT 5326  
 Sbjct 1246839 CCGT-TCGGAACCTGTGCGCAGATCATGAG----TTGTTTCG-CTAGCGTGTGATCCT 1246892  
 Query 5327 GTTCCGCGCCCCCGCAAT-CAGATACGCC--CATCCATC-GGAA-TGGCACGTGCGGT-A 5380  
 Sbjct 1246893 GTTC-GAGCACAGCAATAACAACCTCTACAGCATCCATCAGGAACTGGAGCGTCGGATCA 1246951  
 Query 5381 AGC---AATCCCTTTCCGGTGAACCTGTTGTTGAGTCCCTCAGTTTTAGTCCCAATCCCAG 5437  
 Sbjct 1246952 AGCGCGAGTTCGCTTTCCGGTGAACCTGTTGCCGA-TCCCTCGGTTCCGGTGCGAATCCCAG 1247010  
 Query 5438 ---CTGG-CTCTGTGATGCGTACCTGGAAAGGTCAATACGGTC-GCCATGCAGCGgcgcg 5492  
 Sbjct 1247011 CGCCTGGTGGACGTGATGCGTACCTGG-AAGGTCAATACCGTCTACCATGCGGCG----- 1247064  
 Query 5493 cgcgcgCCTAAAAGGCCAGGCATGT-TAGATCGTC-AGCACAAATCAAGCGCCCGCAA 5550  
 Sbjct 1247065 -----GCCTA-----CAAGCATGTGCCGATCGTCGAGCACAAACATC-----GCCGAGG 1247107  
 Query 5551 GGGTTCGCCTCAACGTG--ACGGAGCTTCCAT-TAGTCCAAGC--AGTTGAAAATC--CG 5603  
 Sbjct 1247108 GCGTTCTCAACAACGTGATAGGCACCTTGCATGCGGTGCAGGCCGCGGTGCAGGTCGGCG 1247167  
 Query 5604 TGC-GAACTTCGTGCTGATTTTCAGGCCGACAAGGCCGAGGTCCGGCGCATAACAATGT-AT 5661  
 Sbjct 1247168 TGCAGAACTTCGTGCTGATTTTC-CACCGACAAGGC---GGTGCGGC-CGACCAATGTGAT 1247222  
 Query 5662 GGGCAGCACC-AGCACATGGCGGAGATG---CTTCAAGCGACTAGCCAACGGGAGAATCC 5717  
 Sbjct 1247223 GGGCAGCACC AAGCGCCTGCGGAGATGGTCTTCCAGCGC-CTCAGCAAC----GAATCG 1247277  
 Query 5718 AAACAAGTCCGTTCGGCAATC--CAGGACGTGCAAC-CGTCAAGA----CCGTTCTCC 5770  
 Sbjct 1247278 GCGCCGGTGTGTTTCGGCGACCGGAAGGACGTGCATCACGTCAACAAGACCCGTTTACC 1247337  
 Query 5771 ATGGTCTTACTTCACCGATATACTTCCCTCAGTTTCGTCCGTTGC-----TTCGGCTGTTCC 5825  
 Sbjct 1247338 ATGGTC-CGTTTCGGC----AACGTCTCGGTTTCGTCCGGTTCGGTTCATTCGGCTGTTCC 1247392

Range 4: 1248329 to 1248826

Score	Expect	Identities	Gaps	Strand	Frame
113 bits(124)	3e-19()	359/522(69%)	90/522(17%)	Plus/Plus	

Features: hypothetical protein aspartate aminotransferase

Query 6678 GCCCATCGTCAGTTTCGAC--GGTGGATGA--TGCTGGAAGTGAAAGGAC--GGCTGGGC 6731  
 Sbjct 1248329 GCCCATGGTCCGTT-CGTCTCGGTGGATCAACTGTGGAAGTGAAAGGGTAGGCCCGGC 1248387  
 Query 6732 GTTGTCTGGAGAGAAACCGGGCGCGGATCGTTAG---GTGGGGCAATGAATCCACTGGAT 6788  
 Sbjct 1248388 GTTGTCT-GGAGAAGAACCGGGCGCGGATCGTCATCGAGTGAGG---TG---CGACTG--- 1248437  
 Query 6789 GAAGAGGCGGGGCATCTTTTCGTCGCCATGATGGATGGAAAAGCCGCGGCTTG--CCCAGG 6846  
 Sbjct 1248438 -AAGGGGCG---AACTTTTCGTCGCCATAACGAA---AAAGCCCCGGCATGTGCCGAGG 1248489  
 Query 6847 GCTTTGCAGTTCTCATCACAATAACA-TCGAACC CGGAGAATACAATGAT---CCCTGC 6902  
 Sbjct 1248490 GCTTTGAATTTGGCTCCGCGACCTGGACTCGAACCAGGG--ACCAATGATTAACAGTCA 1248547  
 Query 6903 TTTACTCAACT--CTGACCTA-----GAACA-CGAGGCG-ATGTTACTGATTA----GGG 6949  
 Sbjct 1248548 TTTGCTCTACCGACTGAGCTATCGCGGAACAGCGAGGCGTATGTTACTGATTA AAAAGGG 1248607  
 Query 6950 GAA-TCAATAATACC---ATC-CTTCCCATT--CGCTACAATAT---ACATGGGCCTT 6998

Sbjct 1248608 GAAGTCAAGCCTCTCCCGATGACTTCCCATTTTCCCTACAGGACCTGGACGATGGCCTT 1248667  
 Query 6999 ----ATGGTCTCA--GTTGAATTTGTTTAGC-CGCCG--GCAGCAAACGACCG-TGCTGG 7048  
 Sbjct 1248668 GGTGATGGTCTCCAGGTTTCGATTTGTTTCAGCGCGGCACGCAG-ATACGGCCGGTGTCTG- 1248725  
 Query 7049 AC--CGTAGATACCGAAC-CGGTC---AGGCGCTCGACCTGGTTCGGGCGGTTCAGGCTGGG 7102  
 Sbjct 1248726 ACGGCGTAGATACCGAACTCGGTCTTCAGGCGCTCGACCTGGTC--GGCGGTTCAGGCCGGA 1248784  
 Query 7103 A-AGGTG-----CGTTGGCGA-CGACGAAGCTGAAAGTC 7133  
 Sbjct 1248785 ATAGGAGAACATGCCACGTTGGCGACCGACGAAGCTGAAAGTC 1248826

Range 5: 1249344 to 1249846

Score	Expect	Identities	Gaps	Strand	Frame
109 bits(120)	4e-18()	352/517(68%)	76/517(14%)	Plus/Plus	

Features:  
aspartate aminotransferase

Query 7626 TCGAGCAGGCCAGCCAAGTTC--GCCATTGCTGGCGGCGTTCGGCAGAGAGCC--TTCGGG 7681  
 Sbjct 1249344 TCCAGCAGGCCGGCGCGGTTTCACGCCATTGCTGGCGGCGTTCGTAATAGCGGTAGTTCTGC 1249403  
 Query 7682 A----GTAG--GGCGGCTTCGAAAGGGCAGTCCAAGTCAGTTTTTCCAGCTCGGTAC-CT 7734  
 Sbjct 1249404 ACCGGAAGCCGGCGGCTTCGAA----CAGTGC CGGTGTTTTTCCAGCTCGGGTCGCT 1249459  
 Query 7735 GAT--CAAAAGTGGCGTCGGGCAAGCTCGGAGGGG-TGCAGGAAGTCGCCCC-AGCTT- 7789  
 Sbjct 1249460 GATGGCCACGGTGGCGTTCGGCA----GCAGGCGCTTGAGGAAGTCGGCGCCGAGCTTG 1249514  
 Query 7790 AGGGCACACGGTGCCACGACGGGCTGAGTC---ACTTGACGACCGCGGACA----- 7840  
 Sbjct 1249515 AGCGCGC-CGGTGCCGCCGACGG-CCTGGGTCGTGACCACACGGCCGGCGCCAGCAGCT 1249572  
 Query 7841 CGAACATCGTCCCC-ATGAGCAGTTTCT-TAAATTCTG-----ACGCAATG--CCTTTAG 7891  
 Sbjct 1249573 CGGAC-TCGTTACCGAACAGCAGTTTCTGTACGCCCTGGTTCGTAGGCGGCGATCCCTTCG 1249631  
 Query 7892 ATCC-CAGG----CCCACAGCGGTCGAGC---GATGCCCGGGCCTTC-CGGCAGCCTGCT 7942  
 Sbjct 1249632 ATCGGCAGGTAGCCGCGCGCGGCGTGGGCTCGATGC--GGGCTTCTCGGCAGCCTGCA 1249689  
 Query 7943 AG-CACCGATAAGCACGATGCGCC--TCCTCGT-GTAGTACACACC-----AGGT-GA 7990  
 Sbjct 1249690 CGGCACGCAACAGCGGAATGCGCCCCCTCTCGTTGTAGTACACGCCACGCCAGGTTGA 1249749  
 Query 7991 TCTTGCCCT-ATGGGTATCGGCGTTGAAGGCTTCTGTTCTACCTAAGGATGGGAT-ACTAA 8048  
 Sbjct 1249750 TCTTGCCCGGACGGGTATCGGCGTTGAAGGCTTCTGTTTCAGGCCAAGGATGGGATCACGG 1249809  
 Query 8049 GTTACATTTTCGGC-----AAATAGAACCATTTTGCG 8080  
 Sbjct 1249810 GTGCCATTTTCGACGGCAGAAAACAGACTCATTTTGCG 1249846

Range 6: 1250145 to 1250266

Score	Expect	Identities	Gaps	Strand	Frame
82.4 bits(90)	5e-10()	100/128(78%)	19/128(14%)	Plus/Plus	

Features:  
excinuclease ABC subunit B

Query 8337 ACGGGCTCTGGCA-GACTTTCA-CATCA--AACGTGATTGCT-AGGTG----GCCCGACC 8387  
 Sbjct 1250145 ACGGGCTCTGGCAAGACTTTCAGCATCGCCAACGTGATTGCCAGGTGCAGCGCCCGACC 1250204  
 Query 8388 CTGGTCTTGGCGCCGAGAATGGGCGGACCTGGCGGCC--CATAACGGGGGAATTC--G 8443  
 Sbjct 1250205 CTGGTCTTGGCGCCGAACA-----AGACCCTGGCGGCCAGCTCTAC-GGGGAGTTCAAG 1250258  
 Query 8444 ACGTTCTT 8451  
 Sbjct 1250259 ACGTTCTT 1250266

Range 7: 1248074 to 1248164

Score	Expect	Identities	Gaps	Strand	Frame
62.6 bits(68)	5e-04()	74/95(78%)	4/95(4%)	Plus/Plus	

Features:  
hypothetical protein

Query 6445 ATTCATCTACCGGGGAGATGCACCCATGCTACAGATCAAATCCGCTCTTATGTCTCATCC 6504

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Sbjct 1248074  ATTCATCTCTGAAGGAG-TGCACCCATGCACCTAATCAAATCCGCTCTGCT-TCTCATCC 1248131
Query 6505      TGTTCTCATGTATTTGCGTTCAACGGCTTCCGCCG 6539
Sbjct 1248132  TGTTTCGCCTGT-CTTCCGTT-TTCGGCTTCCGCCG 1248164

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Range 8: 1247549 to 1247667

Score	Expect	Identities	Gaps	Strand	Frame
57.2 bits(62)	0.021()	90/122(74%)	13/122(10%)	Plus/Plus	

Features:  
membrane protein

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Query 5946      AGATCCTGAAGCCC-CCGAAGAGATGATCC--CTGT---GCCTG--CGTGCGTTCAAGCA 5997
Sbjct 1247549  AGATCCTGGAGCTCGCCGAGAAGATGATCCACCTGTCCGGCCTGAGCGTGCCTTCCG--A 1247606
Query 5998      GCGTTCGCCCCATGATGACACTCTAAACGGATTCAATCTCACTGCGTGTGGC--GAAGC 6055
Sbjct 1247607  GCGTTCGCCCCATGGTGCATCGCCATCGAGTTTCAGTGGC-CTGCGTCTTGGCGAGAAGC 1247665
Query 6056      TC 6057
Sbjct 1247666  TC 1247667

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Pseudomonas aeruginosa M8A.4 genomic scaffold adgfJ-supercont1.1, whole genome shotgun sequence  
Sequence ID: **ref|NZ\_KI518732.1|** Length: 4897873 Number of Matches: 8  
Range 1: 2934221 to 2937217

Score	Expect	Identities	Gaps	Strand	Frame
542 bits(600)	2e-148()	2130/3154(68%)	502/3154(15%)	Plus/Minus	

Features:  
membrane proteinglycosyl transferase

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Query 2184      GGATGCAACCCAGGCTGATGTTACGGGCCTTAACGTGCGGTTAGTCTGTG-TTATGCTGCT 2242
Sbjct 2937217  GGATGCAATCCAGGCTGATGTTACGGGCCTGCTCGTGCCGGTG--CGTGATTCTGCTGCT 2937160
Query 2243      CTGGCGGATGCCATTCA-CGTCTGCTT-AGTCGCG-GA-TTGGCGAAGGAGCAATGGGGA 2298
Sbjct 2937159  CTGGCGGATGCCATTGAGCTCTTATTGAGTCGCCAGAGTTGCGCAAGAAG--ATGGG-A 2937103
Query 2299      GATGCTGA---AGCGTTGGCAGGTCGT---TTGCAATCCATATATCGTCCAACA--AC 2349
Sbjct 2937102  GCTGCTGGGCGAGCGTTGGCAGAGCGTGATTTTGGCATCGAAAGTATCGTCCAACAGCAC 2937043
Query 2350      CA---ACTTCT-GGGCA-TAGGGAGCG---CTTGACGCAA---ATGTAATTGATACAG 2396
Sbjct 2937042  CTGGATATTTATCGGGCACTAGGGAGCGGAGCTTGACGCGACATAATGTATTGGTAACGG 2936983
Query 2397      ---AAACGGATTCCATGAGTATCACGCTGGTTATTAATAGTCTCTGTTCTTCCGGGCA 2452
Sbjct 2936982  GGGCAACCGGATTC-ATCGGGCCGCGCTGGTCA---ATAGTCTCTGTTCTTCCGGGCA 2936928
Query 2453      ATGATAAAGATTGACATTAGGGCGC--AA---TGGGGCCTGGCACGACCAAGA---A 2502
Sbjct 2936927  GT-ACAAGGTTTGGGCCGGGTGCCGCCAAGAGGTGGGGCCTGGCCT--CAAGGGGTTA 2936872
Query 2503      TCCCTTGCTTCTGATG-----GCAGTCTGTTGTCTGGGATCCCGTA---CAACCG 2552
Sbjct 2936871  CTCCCTTGCTTCTGGGTGAACTGGGCAGTTCTGTTGTCTGGGATGCGGAGTCGGCCATCG 2936812
Query 2553      ATACGGTGATGTGTTGTCGTGTGTCATTGCCGCCTTACAGTGTTCATCGAATAACGACAGC 2612
Sbjct 2936811  ATACGGTGGTTCATTG-----CGCTGCCCGCTGCA-TGTCAT-GAGCGA-GACGGC 2936763
Query 2613      G--CGATGCTTAGGTAAGGACCGTCGAGGTCCCAAAGC--ACGTTCCGGGAGAG-CTTGA 2667
Sbjct 2936762  CTCGATCC-----GCTCGTCGAGTTCGCAAGGCCAACGTTTCAGGGGACACTTGA 2936712
Query 2668      ---GTCTAGGAGG-----TCCCGGGGAAGAGGGGGCGCGCTCCTGTCT-TAA--TA 2715
Sbjct 2936711  TCTGGCCCGGAGGCGGTATCCCGGGGA-----GTGCGGCGT-TTCATCTTTATCAGCTC 2936658
Query 2716      GATA--GGTCATCTG-GAGGGAGTGGA---CGGATTCGGGCCT---CTGC--ACCGTCTA 2764
Sbjct 2936657  GATAAAGGTCAATGGCGAGGGAAGTGCAGCCCG--TCGGCCCTATACTGCGGACAGTCCG 2936600
Query 2765      GCCCCAATCATGTGCGTACCTAAC-CGTTCC--ATCGGAAAGCGGAGCAGGC--TATTGG 2819
Sbjct 2936599  --CCCAATCTGTCGATCCCTATGGCGTTTCCAACGGGAAGCGGAGCAAGCGCTATTGG 2936542
Query 2820      ATTAAGAAGAACA-----ACTGGAAGTTGAATGAACATTCCGGC-----TTTATGG 2864
Sbjct 2936541  ATCTGGCGGAAGAGACCGGACTGGAGTTG--TGATCATTCGACCGGCTCTGGTTTATGG 2936484

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Query 2865 TCCCCATTATAGGCCAACGTACAA--CATC-TGCGCTGGCTGAAGGGCGAGGGGCGGA 2921  
Sbjct 2936483 TCCAGGGGTCAAGGCCAACGTACAGACCATGATGCGCTGGCTGAAGCGCG-----GCGTG 2936429

Query 2922 CGCGTGCTAAACACTACAGAC----CTAAATCAG--TAGTCTGGTGTCACTGGGACTATC 2975  
Sbjct 2936428 CCCCTCC----CTCTAGGGGCTATTTCATAATCGGCGTAGTCTGGTGTGCTGG-ATAATC 2936374

Query 2976 TTCTTGTCACATCA--ACCTGCATCGAGCATCCATCAATCGGTGGGCAAAATTTTCTA 3033  
Sbjct 2936373 TTGTCGAC-CTCATCATCACTGCATCGAGCATCCGGCTG-CGGTCGGGCAAGTTTTC- 2936317

Query 3034 TAGTTAGCAAAGTGGAA----TTTCG-----CGAGTGCTGCTGCGGAGATCGGATAGGGC 3084  
Sbjct 2936316 TCGTAAGCGACGGTGAGGATCTTTCCACCACCAGT--TGCTGCGGAGAATGGGACGCGC 2936259

Query 3085 CTTAGGGCACAAATAGGCGCGGCAATGTGC-TGTTCC-GCCAGTTACTTAGTTAAGGGC 3142  
Sbjct 2936258 CTT-GGGCGTCCCG-CTCGCC---TGCTGCTGTTCCCGCCAGTTGGATCGGTGCAG-C 2936205

Query 3143 GGGGTAGAGCAGCGTTGGACTAGGCAGGCATTTAGC---CCGCCTGTTAGACCTAATTGC 3199  
Sbjct 2936204 GGCAGAA----AGTTCTGAAC-AGGCAGGCATTT-GCTCGCCGCTGTGCGGC-TCATTGC 2936152

Query 3200 AAGTCAA--CCTGAAAACC-GCCA-GTACTTGGCTGGACCGC-CCGGTAGGGTA----C 3250  
Sbjct 2936151 AAGTCGATATCATGAAAACCCGCCAAGTGTCTGGCTGGACTCCGCCGTTAGGGGTGGACC 2936092

Query 3251 AGGCAT----GCAAACCGC----TCTTTCCTGGATCTCGA-TGATGAATCTATGGTTGTT 3301  
Sbjct 2936091 AGGCATTGGAGAAAACCGCCCGCTCTTTCCTGGATCGCCAATGATGAATCTATGGTTGTT 2936032

Query 3302 TGT-CAAGCA-TTGGGAGTAATTTTCGCTGCTGTCTCCTAAGCGTCTTCCCCTTCAACG 3359  
Sbjct 2936031 GTTGCCGGCGGTTGCCGCTC--TTTCCCTGCTGTTGACCGC-CGGCTTGCGCCGTTA-CG 2935976

Query 3360 AAATTTGCCGACGCTTGATCGAT---CACAAATGCCCATGT---CTCTAGGTGCC--CTC 3411  
Sbjct 2935975 CGATTGCCCGACGCTTGATCGATGTACCAATGCTCGAAGTTCTCACCAGGTGCCGACGC 2935916

Query 3412 CG-GAGCATGTGGCGACTTTAACGT-----CCTTAAT-CTGGCAGTGTGCTTGGCGCAA 3464  
Sbjct 2935915 CTAGGGGGGGCGGTGTGCTATCGTGTCTCTTCTGCTGGCAGTGTGCTTGGCGCGA 2935856

Query 3465 TATTGGGCTAAGTGGAT--GGATC---CCACTG--ATCACTGGGGCGGACTGTGGGATCG 3517  
Sbjct 2935855 TATTGGGCGCGGTGAAACCGATCTGGCCACTGGTATCCTGGGGCGGGTATTGGGATCG 2935796

Query 3518 CATCTTGCTGGGCTTCCACTA--ATC-TGGCCATATCCCTGCCCGTTGGCGTTTGGCTCGG 3574  
Sbjct 2935795 CAT--TGCTGGGCTTCCCTGACGATCATGGCCATATCGCTGCCCGTTGGCGTTTGGCT--- 2935741

Query 3575 CGGCCATTTTAGCGCTGCTTCCT-GATGTGGTA----CGTGGAGGGTTGCCCTGCATTGGC 3629  
Sbjct 2935740 CGGCCATTTGCGCGGTGCTTGCTGGCTGCTGTACTGGCTTGGAGGTTTGCCTGCATTGGC 2935681

Query 3630 CTTT---CGCCTTGTTGGTCG--TGGGGTAG--TG---CCATAGCTGC-CCGTTCTATCT 3677  
Sbjct 2935680 CTTTTCGCGCTTGTTGGTCGATCTGGGTGGGTTGGACACATAGCTGCGGCGTTCTATCT 2935621

Query 3678 G----GGATCGTAAATCTCT---AATTCAT-----CTATCAATGGGATTGCCACCGTTGA 3725  
Sbjct 2935620 GGTATGGATGCTCAATCTCTACAATTTTCATGGACGGTATCGATGGGATTGCCACCGTTGA 2935561

Query 3726 GGC-----TGTGCGTTGG-----CCTGCGTGGGTTGGTCATATCCTTAAGGTCCGA 3771  
Sbjct 2935560 GGTGTTGTTGTTGTTGCGTTGGCGCTGCCCTGCTTGTGCTGGTCACTGGTGTAGGTTCCGA 2935501

Query 3772 TGAGGCATCCGA-GGCGTTTCTTGGCCTCGGCGGCGCT--TAGGA-TAGAAGTGACGGGA 3827  
Sbjct 2935500 TGAGGCATCCAGGGCGT---TTGG--TTGGCGGCGCTGCTGGCAGCCGCGGTGACGGGG 2935446

Query 3828 TTCC-TTTCTGGAATATTTCT-ATGC-TAGATCTTCAT-GGGGAT--TAGTA--AGTT-- 3877  
Sbjct 2935445 TTCTTTTCTGGAATTTCCCTCTGCGCGGATCTTCATGGGGATGCTGGTAGCGGTTTC 2935386

Query 3878 TTGGG---AT--GTAATGCCCTTTCCTGC-AGCCG-ATGGCATTATCGCCGCAACTTT 3929  
Sbjct 2935385 TTGGGGTTATCATTTGGTGCCTTTCCTGCAAGCCGATGG--GTCTCGCCGCAACT-- 2935330

Query 3930 CCGTCTGGGGTCTACT-ATCTGCT-CCGATATTCGACTTTGATGCCTACATGGCTCTTG 3987  
Sbjct 2935329 -CTTCTGGGGTTGGCTCATCTGCTGGGGTATTCATTTGATGCCACCTGAC-CTTG 2935272

Query 3988 TTGCC---TTGCTGCGGTCGGGAAAGGGGTTATGAGGCATCATCGCAGTACCCA-AC 4043  
Sbjct 2935271 TTGCGCCGGTTGCTGCGG--GGAGACAAGGTTTATGAGGC-GCATCGCAGTACGCATAC 2935215

Query 4044 GA-TCTGCTTCTCGTCATTACGGGCG---TCGTCTGTTACCTATCGATCCGGAGGCATC 4099  
Sbjct 2935214 CAGTATGCTTCTCGTCATTACGGGCGTCATCTTCTGTTACCTGGCAGTGGGAGGCATC 2935155

Query 4100 AACATCTTCTGGTTGTT-----AAACCATATTTAAA---AGGAA-ATCGACGGGATC 4146  
Sbjct 2935154 AACATCTTCTGGTTGTTGCCACTGGCACTGCTTGTGCGAGCGGGAAGATCGACGGCAT- 2935096

Query 4147 GATTGATTTTGTATTGGCTACTTAACCTGCGGTTCTTCT-GAAAACCG-TTTAAG--CCG 4202  
Sbjct 2935095 GCTTGCTTTGTTGATTGGCTACCTGCTTCTGCGGTTCTTGGCGTCCGTTTAAAGCCGG 2935036

Query 4203 AGTTATGGAATC-GGAGCACATGCAATGTCCCG-TCCCTGAAGCACAAAGGCGGATTTT 4260

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Sbjct 2935035 AGTCCTGGAATCACGCGCTGCTTGAATGTCCCAGTTGGCTGGAG-GCGCGGGACGATTTT 2934977
Query 4261 C--GGAACTTA-GCTCTGAAAGGAATGTGCGA-CGATGATCAGTAATGGTAGTAACTA-T 4315
Sbjct 2934976 CCGGGAACGTATAATATGAAAGGAATGTGCAAGCGATGATCA-----GTAGTACTACT 2934923
Query 4316 GCCGGACGCGTGATTGATTT-----AGAGTACTTGCC--ATCA--GGAATGGACTTGCC 4366
Sbjct 2934922 GCCGATAGCGTGATTGGGTTCCGGAATGGTATTTGCCAGACCAGGAAATGGACTGCC 2934863
Query 4367 AGA-TTGTTCGGGTGGATGCAGGTG-AGTGAA--GAACTTACTGATGGGATGTTGG-TAA 4421
Sbjct 2934862 GGACTTGTTCGGGTGGATGCGGGTGCAGTGAAGGGGGCTGATTAATAGGATGTTGGATAA 2934803
Query 4422 GGTATTGCGT-GACGCTACCTGGAGGGGGATTGCCG---CGCCCGAA--GCATTCTTTGT 4475
Sbjct 2934802 ---CTTGCGTGGACGCCTCCT-----GGGATTGCCGCGCCGCGCAGAAAGCGCATTCTT--C 2934753
Query 4476 CGATTGCTTAGACGGGATATCAACCTGGTG-----CGTTCGCTGGCTTTTAAACCGT 4528
Sbjct 2934752 AGGTTGC---GAC-GGACATCGGCCTGTTGTGGCTTTCATTGTGGCTGGCTT----- 2934705
Query 4529 CTCCTCGAG---CAAGACACCGAAGACATGATCGATCCCCTTCGG---AAACCCCTG--- 4579
Sbjct 2934704 -TCCTGGTGCCTCTCGGCACCGAAGACATGATCGAT-CCGTTGCGGGATCACGCCTGGCT 2934647
Query 4580 ATTTCTAGCACCGCCTATAAACCGCCATCC--GACTTCATCC-ATTCGGCATGTACCGGG 4636
Sbjct 2934646 GTTCATAGCGGCGCCTCT-AACCGCCATCCCGCTTTCATCCGCTTCGGCATGTACCGGG 2934588
Query 4637 CGGTGAATGCTACCACCTAGCGAACGACCGTGATGACGGCCAGATCGCCA--GCGGTCA- 4693
Sbjct 2934587 CGGTG-ATGC-GCTACCTGGGCAACGA-CGCCCTTATCGC--GATCGCCAAGGCCGCTCAC 2934533
Query 4694 CATTTCTAAGACT--TGCT-TCG-TGCTG---TACTGGTACCCATCCC--TAATAAGTGA 4744
Sbjct 2934532 CATTTCCGCG-CTGGTCTGTGCTTGTGGTCTACTGGTACCGCTCCC CGCCGGCGGTGG 2934474
Query 4745 T-CCCCGTT-CCTGGTGTTCATC-ACTGGTG--TTACCATGCATGCCTGATC----CATT 4795
Sbjct 2934473 TGCCGCGTTCCTTGGTGTTCAACTACTGGTGGTTGAGCATGC-TG-CTGATCGCGGCTT 2934416
Query 4796 GCG--TGGCACATGCGCC--TAATTCAT-CGAGACTGGTA--CTGCTGTGCAGTTCGGTA 4848
Sbjct 2934415 GCGTCTGGC-CATGCGCCAGTATTTTCATGGGCGACTGGTACTCTGCTGTGCAG-TCGGTA 2934358
Query 4849 GAGAATGATGGGTTTCTTTACCATCACGCGCGGATGG-ATGCCCAGGGTGAATA-CTAT- 4905
Sbjct 2934357 -----CCATTTCT---CAAT--CGCCAGGATGGCCTGCCAGGGTGGCCATCTATG 2934312
Query 4906 ----GAGGAGGACGGGCAACCAGTTGGTGCCGGCATTGCATTCTCATTC--GCGATGCGT 4959
Sbjct 2934311 GCGCGGGGGCGGCCGCAACCAGTTGGTTGCGGCATTGC-GTCTCGGTGCGGCGATGCGT 2934253
Query 4960 CTAGT-CCGTTACATACCATCCACGGCAAGCTGAT 4992
Sbjct 2934252 CCGGTGGCGTTCAT-CGAT-GACGACAGCAGAT 2934221
    
```

Range 2: 2937679 to 2939274

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	2e-60()	1120/1652(68%)	262/1652(15%)	Plus/Minus	

Features:  
**glycosyl transferase family 1glycosyl transferase**

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Query 280 AGCTAATGCTCAAGGCGGTGGTGAAGACTCAA--TGGCGGACTTAGGAAGAGTTCCCAT 337
Sbjct 2939274 AGCTAATGCTCAAG-CGGTTGATCGAGACTCAAATGGCGGCAGT-----GAATTCGAAC 2939221
Query 338 ACTTCTAATTATTCATGTCT-TCTGGTGTATTGGTGAAGTTGGGCAAGATCTGATTG--- 393
Sbjct 2939220 A-TTCGATTATTTCA---CTGTCTGATCT--TGGTGAAGTTGGGCAAGGTTCTGATTGAGG 2939167
Query 394 CTAGTA---CTGTTGGT-TGCTGTGGCGGTATAATGATGAGGGAATGC---GGCATTAA 446
Sbjct 2939166 CTGGTATATCTGTTGATGTCT-TGGCATGACCTCGATGAGGGATATGCCTCGGGTGCTC 2939108
Query 447 CGTCGT-TGATCTGGATATTTCTTTA--GGAGGC--GGTCAA----AAACATGGATGTA- 496
Sbjct 2939107 CTTCGTCTGATAGGGATATTTCTGTAAGGAGGCCGATATAGTCCAAACATGGATGTAT 2939048
Query 497 -ATTCCGATCTTCTTGATC-ATTAG-TGCGATCA-----ATTGGCAGGGT-----GG 540
Sbjct 2939047 CATTCGATCTTCTTGGTGGATTGGCTGCCAGAATGGCCGATTTGGCGGGATTATATGG 2938988
Query 541 GGAGTCGCCCTGAACGTGGGTGAGGCGAGGGCAGCA-GAATACGACT-TTCTCTGACGGA 598
Sbjct 2938987 GGAGTCCGCACGACCGACCTTCAAG--AGGGCGGCAAGAGTACGACTGTTCTGGTACGGA 2938930
Query 599 AAATGTTA--CTGGCTATCC--ATTCTTC---AGATATATTGTCCC-CAGGCTAGGGCT 650
Sbjct 2938929 AGGTGTGTGCTGGCTATCCGGATTTCTGCAAAATATATTGTTTGGCGCCGCGAGGCC 2938870
Query 651 ACCGGCGCGA-----TGCTGTCTAGGCTCG---GCAAGCAGGATCCTCTGGTTCGT--C 699
    
```

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Sbjct 2938869 CAAGGCGCTCACACATTGCTGTT--GGCTACAACGCAAGCAGGATGCT---GGTCATTCC 2938815
Query 700 CAACTCCGTTTGCA-CTTATAGCCCTGC-GGC-ATGGAGCGCATCGCGGTCA---ATGAG 753
Sbjct 2938814 CAACG--GTTTCGATCTCACTCGCCTGCAGGCGACCGA-CGAACAGCGGTCCGCTATCAG 2938758
Query 754 GAATGGAGCTGGCAGAGACG--AGC-ATCAGTTGAGTCCCAGTCCGACGAGATTCTAGCA 810
Sbjct 2938757 GAGTGGAGCTGGCATAGAGGCCAGCGATATCGTGATTGGCAGTCTAGGCAGATTCCACCC 2938698
Query 811 GAGTCCGGGATC-TGCTTCCTTC----CAGCTTA-GGCTGCTGGAAC-TGTTATGC-C 862
Sbjct 2938697 G-GTAAAGGATCATGCTTCCTTTGTGCGAGCTGCCGGTCTGCTGGCTCCACGTTATTTCGC 2938639
Query 863 ACTTGAAGTTTTCTTTTGATCTCCAACGGAGCTGCTGTCATC--ATGCTGAAGTTGCATA 920
Sbjct 2938638 GCTTGAAGTTT-CTTTTGGTGGG-ACGGGAGCTGCTGTCTTCCAATGCTGAA-TTGCAGC 2938582
Query 921 G----AT-GAGGC-ACCTCATATTAGGGGGAGCGCTTTAATCACTGCTTGGCAGA-CAGC 973
Sbjct 2938581 GCCTCATCGAAGCTACCGGTAT---GCGGAGCGTTCA-TC-CTGCTTGG-AGAGCGGC 2938528
Query 974 AAGATCTA--TTGGTTGCTTGGCAGCCCATGGATATCTTCTGTCTGCGGTCTCGCAC-CA 1030
Sbjct 2938527 AAGATGTAGCTTCGTGTCT--GAAAGCCATGGATATCTTCTGTCTGCATTCTCGCACGGA 2938470
Query 1031 GGGATTCCCCAATG-TCTTAG---AGCCATG--AATGGGATTGCCTTGTAT--GCACTGG 1082
Sbjct 2938469 GGGATTCCCCAATGTTCTTGGTGAAGCCATGGCCATGGGATTGCCTTGTATTACCCTGA 2938410
Query 1083 T---TAGGATGC--ATTATTTGGCTCGGT-----TGGTCTGCTTCCGGGCGCGCTTTA 1130
Sbjct 2938409 TGTGGGGGATGCGGCTTATTT-GCTAGGTAACGACGGTGTCTGCTCGTTCCGGC---CTT-- 2938356
Query 1131 GGGTCC-AATGC-CT---CCAAGGTATGTAGAAGTACCATTCCGTTGGAT----TGGGTC 1181
Sbjct 2938355 GGATCCGAATGCGCTCGGCAAAGGTATCGAGGA-TCTCATTGCGTTGGATGTCGAGGGTC 2938297
Query 1182 GTCGGGCACTTGTGGTAAGG-TCC--GAC--AGGATTTATAACGCAACTGC-CCAT-CCT 1234
Sbjct 2938296 GTCGGGCACT--TGGTGAAGCTGCAAGACAGGATTTA-CTCG-AACTTCACGATGGCC 2938241
Query 1235 AGTG---CTCAGCG-TTCATGAGTC----TCAGGTC-TGTGTGT---AAGAAAAGCTT-A 1281
Sbjct 2938240 AGTGCTCTCAGCGTTTCATGAGTCTGTATCGCGACATTCTTGTAAAAGAAAAGCTTGA 2938181
Query 1282 CG---CTGCAGGTTATGTT--TAGCCTCCATC--GGAATTCGC-TGAAGCC-GTATTGTT 1332
Sbjct 2938180 CGAGCTTGAAGTTATGTTTGTAAAACGCATCGAGGAGTTTGCATGAAGCCGGTATTGTT 2938121
Query 1333 GATGATA-----ACTC--CGTTCTTCATGTCTCACCGTTTACCGGTC-CTGTCCGAG- 1381
Sbjct 2938120 GATGATAGTGAACGACCCGGCTTTCTTCATGTCTCACCGTTTACCGGTCGCTGTCGGAGC 2938061
Query 1382 CCAGCAACGTG-----CA-----ATAAAAATAAAGTACT-----CTAAGTG-AAAAGAT 1425
Sbjct 2938060 CCAGCAGGCTGGTTTCCAGGTACATATCGCCACACGCCCTGGTGACCGGTGAAAAAGAT 2938001
Query 1426 CGTCTCCTCCAGGTTTTCTGCA-CCTGATCTGATTCCACTGTTCCCGCAGCCGAAAAA-- 1482
Sbjct 2938000 CGTCTCC-CAAGGTTTTCTGCATCATGAATTG---CCACTG-TCCAGAAGCGGAAAAAAT 2937946
Query 1483 TCATTTCAAGTGGCGTAT-----GCGTATGTC--CCACCTTT--TGGAGATTGC--AAT 1530
Sbjct 2937945 CCTTTTTCAGAGCTGTATCTGCTGACTTATGTCTGGCGCCTTTTGTGGAGATTGCGGCC 2937886
Query 1531 AGTG-TTTACACCTGGTTA--AGTAAGCCGGTA--GTAGTGTGGAGTACCCTAAG-GTG 1584
Sbjct 2937885 GATGTTTTTACACCTGGTTACCATCAAGCCGGTAATCTATGGCGGTATCGCCGCACGCTTG 2937826
Query 1585 GCGCCGGTGAAGAGAATCGTGGCGGCCGTTT-CAGACGTGG-TTCG--TTCATGAGGCG 1640
Sbjct 2937825 GCGCCGGTG-AAGGGGGTCTGCGCGGCCGTTTCCGGAATTGGTTTCGTTTTTCAT--GGCC 2937769
Query 1641 GAGGGTCTGAAG--CTGCG---TTCGGTTTACTGTGTCGCCTGGCTTTATCGGCGACCGT 1695
Sbjct 2937768 AAGGGTCTGAAGGCTGCGCGTTTCG--TGCCTGTGTCGCCTGGCTTTATCGGCGGGCTT 2937711
Query 1696 TGG--AAAGAAAAGTTGCGTGTTCATCTTTCAA 1725
Sbjct 2937710 TGGGCAAGAAAAGTTGCGTGTTCATCTTTCAA 2937679

```

Range 3: 2933331 to 2933944

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(174)	8e-33()	455/660(69%)	95/660(14%)	Plus/Minus	

Features:  
**membrane protein**

```

Query 5215 GCTGCTGAAATAGTCCATCCCATTCCAGGTGGTA--GGTGATGGGGGCGGT---TCCTGG 5269
Sbjct 2933944 GCTGCTGGAACGGTGCATCCGCGGTGAGGTGGTGGTGGTACCGGGGCGGGCGGTTCTAT 2933885

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Query 5270      CTTTGTTCGGAATACTGTCTGAA-ATCATGAGGCAGTTGTTTCGGACTAGCGTGCTTA--CT 5326
Sbjct 2933884    CGGT-TCGGAACCTGTTCGGCAGATCATGAG----TTGTTTCGC-CTAGCGTGCTGATCCT 2933831
Query 5327      GTTCCGCGCCCCCGGAAT-CAGATACGCC--CATCCATC-GGAA-TGGCACGTTCGCGT-A 5380
Sbjct 2933830    GTTC-GAGCACAGCGAATAACAACCTCTACAGCATCCATCAGGAACTGGAGCGTCGGATCA 2933772
Query 5381      AGC---AATCCCTTTTCGGTGAACCTGTTGTTGAGTCCCTCAGTTTTAGTCCCAATCCCAG 5437
Sbjct 2933771    AGCGCGAGTTCGCTTTTCGGTGAACCTGTTGCCGA-TCCTCGGTTTCGGTGCGAATCCCAG 2933713
Query 5438      C---TGGCTCT-GTGATGCGTACCTGGAAAGGTCAATACGGTTCG-CCATGCAGCGgcgcg 5492
Sbjct 2933712    CGCCTGGTGGACGTGATGCGTACCTGGAA-GGTCAATACCGTCTACCATGCGGCGGC--- 2933657
Query 5493      cgcgcgcgCTAAAAGGCCAGGCATGTTA-GATCGTC-AGCACAAATCAAGCGCCCGCAA 5550
Sbjct 2933656    -----CTACAA-----GCATGTGCCGATCGTCGAGCACAAACATCG-----CCGAGG 2933616
Query 5551      GGGTTCGCCTCAACGTGACGG--AGCTTCCATTAG-TCCAAGCAGT--TGAAAATC--CG 5603
Sbjct 2933615    GCGTTCTCAACAACGTGATAGGCACCTTGCATGCGGTCAGGCCCGGGTGCAGGTCGGCG 2933556
Query 5604      TGC-GAACTTTCGTGCTGATTTTCAGGCCGACAAGCCGGAGGTCGGCGCATAACAATGT-AT 5661
Sbjct 2933555    TGCAGAACTTTCGTGCTGATTTTC-CACCGACAAGGC---GGTGCGGC-CGACCAATGTGAT 2933501
Query 5662      GGGCAGCACC-AGCACATGGCGGAGATG---CTTCAAGCGACTAGCCAACGGGAGAATCC 5717
Sbjct 2933500    GGGCAGCACC AAGCGCCTGGCGGAGATGGTCTTCAGGCG-CTCAGCAAC----GAATCG 2933446
Query 5718      AAACAAGTCCGTTCGGCAATC--CAGGACGTGCAAC-CGTCAAGA----CCGTTCTTCC 5770
Sbjct 2933445    GCACCGGTGCTGTTTCGGCGATCGGAAGGACGTGCATCACGTCAACAAGACCCGTTTACC 2933386
Query 5771      ATGGTCTTACTTCACCGATATACTTCCCTCAGTTCGTCCGTTGC-----TTCCGCTGTTCC 5825
Sbjct 2933385    ATGGTC-CGCTTCGGC----AACGTCTCGGTTTCGTTCCGGTTCGGTCATTCCGCTGTTCC 2933331
    
```

Range 4: 2931897 to 2932394

Score	Expect	Identities	Gaps	Strand	Frame
116 bits(128)	3e-20()	360/522(69%)	90/522(17%)	Plus/Minus	

Features:  
**aspartate aminotransferasehypothetical protein**

```

Query 6678      GCCCATCGTCAGTTTCGAC--GGTGGATGA--TGCTGGAAGTGAAAGGAC--GGCTGGGC 6731
Sbjct 2932394    GCCCATGGTCCGTT-CGTCTCGGTGGATCAACTGCTGGAAGTGAAAGGGGTAGGCCCGGC 2932336
Query 6732      GTTGTCTGGAGAGAAACCGGGCGCGGATCGTTAG---GTGGGGCAATGAATCCACTGGAT 6788
Sbjct 2932335    GTTGTCT-GGAGAAGAACCGGGCGCGGATCGTCATCGAGTGAGG---TG---CGACTG--- 2932286
Query 6789      GAAGAGGCGGGGCATCTTTTCGTCCTCCATGATGGATGGAAAAGCCGCGGCTTG--CCCAGG 6846
Sbjct 2932285    -AAGGGGCG---AACTTTTCGTCCTCCGATAATGAA---AAAGCCCCCGGCATGTGCCGAGG 2932234
Query 6847      GCTTTGCAGTTCTCATCACAATAACA-TCGAACCCTGGAGAATACAATGAT---CCCTGC 6902
Sbjct 2932233    GCTTTGAATTTGGCTCCGCGACCTGGACTCGAACCAGGG--ACCAATGATTAACAGTCA 2932176
Query 6903      TTTACTCAACT--CTGACCTA-----GAACA-CGAGGCG-ATGTTACTGATTA----GGG 6949
Sbjct 2932175    TTTGCTCTACCGACTGAGCTATCGCGGAACAGCGAGGCGTATGTTACTGATTA AAAAGGG 2932116
Query 6950      GAA-TCAATAATACC---ATC-CTTCCCATT--CGCTACAATAT---ACATGGGCCTT 6998
Sbjct 2932115    GAAGTCAAGCCTCTCCCGATGACTTCCCATTTCCTTACAGGACCTGGACGATGGCCTT 2932056
Query 6999      ----ATGGTCTCA--GTTGAATTTGTTTAGC-CGCCG--GCAGCAAACGACCG-TGCTGG 7048
Sbjct 2932055    GGTGATGGTCTCCAGGTTTCGATTTGTTTCAGCGCGGCGACGCAG-ATACGGCCGGTGTG- 2931998
Query 7049      AC--CGTAGATACCGAAC-CGGTC---AGGCGCTCGACCTGGTTCGGGCGGTCAGGCTGGG 7102
Sbjct 2931997    ACGGCGTAGATACCGAACTCGGTCCTCAGGCGCTCGACCTGGTC-GGCGGTCAGGCCGGA 2931939
Query 7103      A-AGGTG-----CGTTGGCGA-CGACGAAGCTGAAGTC 7133
Sbjct 2931938    ATAGGAGAACATGCCACGTTGGCGACCGACGAAGCTGAAGTC 2931897
    
```

Range 5: 2930877 to 2931379

Score	Expect	Identities	Gaps	Strand	Frame
109 bits(120)	4e-18()	351/516(68%)	74/516(14%)	Plus/Minus	

Features:  
**aspartate aminotransferase**



```

Query 7626      TCGAGCAGGCCAGCCAAGTTC--GCCATTGCTGGCGGCGTTCGGCAGAGAGCC--TTCGGG      7681
Sbjct 2931379    TCCAGCAGGCCGGCGCGGTTACGCCATTGCTGGCGGCGTCTGTAATAGCGGTAGTTCTGC      2931320
Query 7682      A----GTAG--GGCGGCTTCGAAAGGGCAGTCCAAGTCAGTTTTCCAGCTCGGTAC-CT      7734
Sbjct 2931319    ACCGGGAAGCCGGCGGCTTCGAA----CAGTGCGCAGTGGTTTTCCAGCTCGGGTCGCT      2931264
Query 7735      GAT--CAAAAGTGGCGTGGGCAAGCTCGGAGGGG-TGCAGGAAGTCGCCCC-AGCTT-      7789
Sbjct 2931263    GATGGCCACGCTGGCGTGGGCA----GCAGGCGCTTGGAGGAAGTCGGCGCCGAGCTTG      2931209
Query 7790      AGGGCACACGGTGGCCACGACGGGCTGAGTC---ACTTGACGACGGCGGACACGAACA      7846
Sbjct 2931208    AGCGCGC-CGGTGC CGCCGACGG-CCTGGGTCGTGACCACACGGCCGGCGCCAGCAACT      2931151
Query 7847      -----TCGTCCC-ATGAGCAGTTTCT-TAAATTCTG-----ACGCAATG--CCTTTAGA      7892
Sbjct 2931150    CGGACTCGTTACCGAACAGCAGTTTCTGTACGCCCTGGTCGTAGGCGCGATCCCTTCGA      2931091
Query 7893      TCC-CAGG----CCACAGCGGTCGAGC---GATGCCCGGGCTTC-CGGCAGCCTGCTA      7943
Sbjct 2931090    TCGGCAGGTAGCCGCGCGCGTGGGCTCGATGC--GGGCTTCTCGGCAGCCTGCAC      2931033
Query 7944      G-CACCGATAAGCACGATGCGCC--TCCTCGT-GTAGTACACACC-----AGGT-GAT      7991
Sbjct 2931032    GGCACGCAACAGCGGAATGCGCCCTCTCGTTGTAGTACACGCCACGCCAGGTTGAT      2930973
Query 7992      CTTGCCCT-ATGGGTATCGGCGTTGAAGGCTTCGTTCTACCTAAGGATGGGAT-ACTAAG      8049
Sbjct 2930972    CTTGCCCGGACGGGTATCGGCGTTGAAGGCTTCGTTTCAGGCCAAGGATGGGATCACGCGG      2930913
Query 8050      TTACATTTTCGGCG-----AAATAGAACCATTTTGGC      8080
Sbjct 2930912    TGCCATTTTCGACGGCAGAAACAGACTCATTTTGGC      2930877
    
```

Range 6: 2930457 to 2930578

Score	Expect	Identities	Gaps	Strand	Frame
82.4 bits(90)	5e-10()	100/128(78%)	19/128(14%)	Plus/Minus	

Features:  
**excinuclease ABC subunit B**

```

Query 8337      ACGGGCTCTGGCA-GACTTTCA-CATCA--AACGTGATTGCT-AGGTG----GCCCGACC      8387
Sbjct 2930578    ACGGGCTCTGGCAAGACTTTCAGCATCGCCAACGTGATTGCCAGGTGCAGCGCCCGACC      2930519
Query 8388      CTGGTCTTGGCGCCGAGAAATGGGCGGACCTGGCGGCC--CATAACGGGGGAATTC--G      8443
Sbjct 2930518    CTGGTCTTGGCGCCGAACA-----AGACCCTGGCGGCCAGCTCTAC-GGGGAGTTCAAG      2930465
Query 8444      ACGTTCTT      8451
Sbjct 2930464    ACGTTCTT      2930457
    
```

Range 7: 2932513 to 2932649

Score	Expect	Identities	Gaps	Strand	Frame
59.0 bits(64)	0.006()	104/141(74%)	12/141(8%)	Plus/Minus	

Features:  
**hypothetical protein**

```

Query 6445      ATTTCATCTACCGGGGAGATGCACCCATGCTACAGATCAAATCCGCTCTTATGTCTCATCC      6504
Sbjct 2932649    ATTTCATCTCTGAAGGAG-TGTACCCATGCACCTAATCAAATCCGCTCTGCT-TCTCATCC      2932592
Query 6505      TGTTCATCATGTATTTGCGTTCAACGGCTTCCGCCG--GCATTTCGCCGT--CTAGGAATC-      6559
Sbjct 2932591    TGTTCGCTGT-CTTCCGTT-TTCGGCTTCCGCCGCACCGGTCGCCGTGCGCAAGAATCC      2932534
Query 6560      -CTAACC-CAACGACA-CTGC      6577
Sbjct 2932533    GCTGGCCGCAACGACACCTGC      2932513
    
```

Range 8: 2933056 to 2933174

Score	Expect	Identities	Gaps	Strand	Frame
57.2 bits(62)	0.021()	90/122(74%)	13/122(10%)	Plus/Minus	

Features:  
**membrane protein**

```

Query 5946      AGATCCTGAAGCCC-CCGAAGAGATGATCC--CTGT---GCCTG--CGTGCCTTCAAGCA      5997
Sbjct 2933174    AGATCCTGGAGCTCGCCGAGAAGATGATCCACCTGTCCGGCTGAGCGTGCCTTCG--A      2933117
    
```

```
Query 5998      GCGTTCGCCCCATGATGACACTCTAAACGGATTCAATCTCACTGCGTGCTGGC--GAAGC 6055
                |||
Sbjct 2933116    GCGTTCGCCCCATGGTGACATCGCCATCGAGTTCAGTGGC-CTGCGTCCTGGCGAGAAGC 2933058
                |||
Query 6056      TC 6057
                |
Sbjct 2933057  TC 2933056
```