BLAST ® » blastn suite » RID-9JT540KY014

BLAST Results

Questions/comments

Job title: ref|NW_003385628.1| (7613 letters)

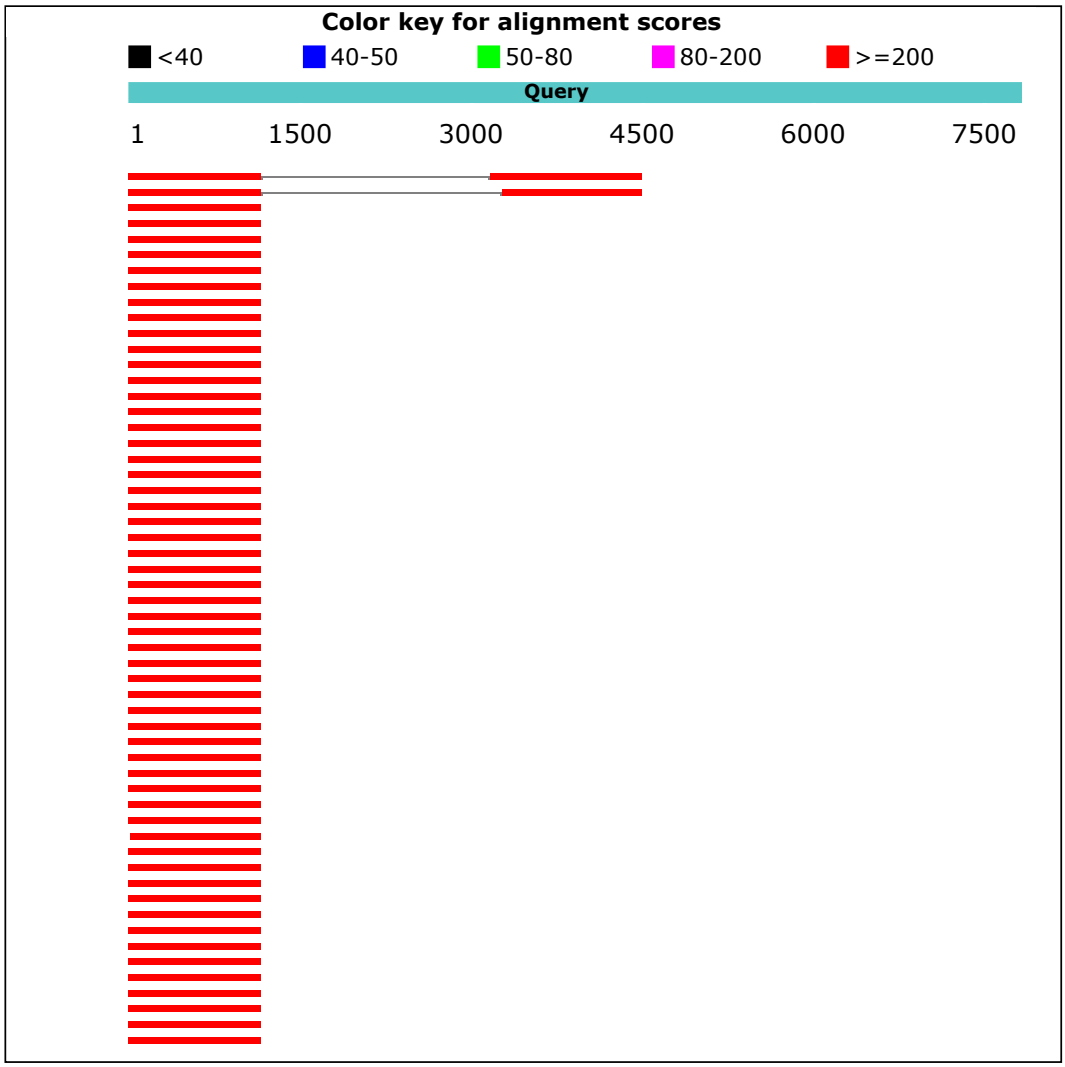
RID 9JT540KY014 (Expires on 03-03 21:50 pm)

Query ID NW_003385628.1
Description Acyrthosiphon pisum strain LSR1 unplaced genomic scaffold, Acyr_2.0 Scaffold2139
Molecule type dna
Query Length 7613

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.8.0+

Graphic Summary

Distribution of the top 102 Blast Hits on 106 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pantoea rwandensis strain ND04, complete genome	1855	3702	31%	0.0	92%	CP009454.1
Pantoea vagans strain ND02, complete genome	1471	2569	30%	0.0	90%	CP011427.1
Plautia stali symbiont DNA, complete genome	1203	1203	14%	0.0	86%	AP012551.1
Pantoea sp. At-9b, complete genome	1149	1149	14%	0.0	85%	CP002433.1
Pantoea sp. PSNIH1, complete genome	1077	1077	14%	0.0	84%	CP009880.2
Pantoea ananatis LMG 20103, complete genome	1050	1050	14%	0.0	84%	CP001875.2
Pantoea ananatis AJ13355 DNA, complete genome	1038	1038	14%	0.0	83%	AP012032.2
Pantoea ananatis strain R100, complete genome	1038	1038	14%	0.0	83%	CP014207.1
Pantoea ananatis LMG 5342 main chromosome complete genome	1038	1038	14%	0.0	83%	HE617160.1
Pantoea ananatis strain 97-1 genome	1027	1027	14%	0.0	83%	CP020943.1
Pantoea ananatis strain YJ76, complete genome	1022	1022	14%	0.0	83%	CP022427.1
Pantoea ananatis PA13, complete genome	1022	1022	14%	0.0	83%	CP003085.1
Pantoea stewartii subsp. stewartii DC283, complete genome	998	998	14%	0.0	83%	CP017581.1
Erwinia sp. EM595 genome assembly EM595, chromosome : 1	905	905	14%	0.0	81%	LN907827.1
Erwinia billingiae strain Eb661 complete chromosome	828	828	14%	0.0	80%	FP236843.1
Serratia marcescens strain SOLR4 chromosome	754	754	14%	0.0	79%	CP025698.1
Serratia sp. FS14, complete genome	750	750	14%	0.0	79%	CP005927.1
Serratia marcescens strain UMH2, complete genome	749	749	14%	0.0	79%	CP018924.1
Serratia marcescens strain UMH7, complete genome	749	749	14%	0.0	79%	CP018919.1
Serratia marcescens strain RSC-14, complete genome	749	749	14%	0.0	79%	CP012639.1
Gibbsiella quercinecans strain FRB97, complete genome	745	745	14%	0.0	79%	CP014136.1
Serratia marcescens strain S2I7 genome	745	745	14%	0.0	79%	CP021984.1
Serratia marcescens WW4, complete genome	745	745	14%	0.0	79%	CP003959.1
Serratia sp. JKS000199 genome assembly, chromosome: I	743	743	14%	0.0	79%	LT907843.1
Cronobacter turicensis z3032 complete genome	739	739	14%	0.0	79%	FN543093.2
Serratia marcescens strain UMH3, complete genome	737	737	14%	0.0	79%	CP018925.1
Serratia proteamaculans 568, complete genome	734	734	14%	0.0	79%	CP000826.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter cloacae subsp. cloacae ATCC 13047, complete genome	728	728	14%	0.0	79%	CP001918.1
Serratia liquefaciens ATCC 27592, complete genome	723	723	14%	0.0	79%	CP006252.1
Serratia liquefaciens strain FDAARGOS_125 chromosome, complete genome	717	717	14%	0.0	78%	CP014017.2
Escherichia coli strain AR_0019 chromosome, complete genome	717	717	14%	0.0	78%	CP024889.1
Escherichia coli isolate Co6114 genome	717	717	14%	0.0	78%	CP016034.1
Serratia liquefaciens strain HUMV-21, complete genome	717	717	14%	0.0	78%	CP011303.1
Enterobacter hormaechei subsp. hormaechei strain 34983, complete genome	713	713	14%	0.0	78%	CP010377.1
Enterobacter cloacae strain M12X01451 chromosome complete genome	712	712	14%	0.0	78%	CP017475.1
Kluyvera georgiana strain YDC799, complete genome	708	708	14%	0.0	78%	CP022114.1
Enterobacter cloacae subsp. dissolvens SDM, complete genome	704	704	14%	0.0	78%	CP003678.1
Enterobacter cloacae isolate SBP-8 genome	701	701	14%	0.0	78%	CP016906.1
Enterobacter cloacae strain GGT036, complete genome	701	701	14%	0.0	78%	CP009756.1
Serratia rubidaea strain 1122, complete genome	695	695	14%	0.0	78%	CP014474.1
Enterobacter sp. DKU_NT_01 chromosome	693	693	14%	0.0	78%	CP021137.1
Enterobacter cloacae strain DG6 genome assembly, chromosome: I	693	693	14%	0.0	78%	LT840187.1
Enterobacter cloacae strain FRM, complete genome	689	689	14%	0.0	78%	CP019889.1
Enterobacter cloacae strain AR_0072, complete genome	688	688	14%	0.0	78%	CP026850.1
Enterobacter hormaechei subsp. oharae strain DSM 16687, complete genome	688	688	14%	0.0	78%	CP017180.1
Lelliottia sp. PFL01, complete genome	684	684	14%	0.0	78%	CP018628.1
Enterobacter cloacae strain AR_0163, complete genome	684	684	14%	0.0	78%	CP021749.1
Klebsiella quasipneumoniae strain HKUOPL4, complete genome	678	678	14%	0.0	78%	CP014156.1
Klebsiella quasipneumoniae strain HKUOPJ4, complete genome	678	678	14%	0.0	78%	CP014155.1
Klebsiella quasipneumoniae strain HKUOPA4, complete genome	678	678	14%	0.0	78%	CP014154.1
Klebsiella pneumoniae subsp. pneumoniae strain HKUOPLC, complete genome	678	678	14%	0.0	78%	CP012300.1
Klebsiella variicola strain HKUOPLA, complete genome	678	678	14%	0.0	78%	CP012252.1
Citrobacter werkmanii strain BF-6, complete genome	673	673	14%	0.0	78%	CP019986.1
Enterobacter cloacae subsp. cloacae DNA, nearly complete genome, strain: 2016_smu953	669	669	14%	0.0	78%	AP018340.1
Klebsiella quasivariicola strain KPN1705 chromosome, complete genome	667	667	14%	0.0	78%	CP022823.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Enterobacter cloacae strain MS7884A, complete genome	665	665	14%	0.0	78%	CP022532.1
Enterobacter hormaechei subsp. steigerwaltii strain DSM 16691, complete genome	662	662	14%	0.0	77%	CP017179.1
Citrobacter freundii CFNIH1, complete genome	662	662	14%	0.0	78%	CP007557.1
Enterobacter cloacae strain AR_0060 chromosome, complete genome	660	660	14%	0.0	77%	CP026719.1
Raoultella ornithinolytica strain S12, complete genome	660	660	14%	0.0	78%	CP010557.1
Klebsiella quasipneumoniae strain ATCC 700603 chromosome, complete genome	656	656	14%	0.0	78%	CP014071.1
Klebsiella quasipneumoniae strain ATCC 700603, complete genome	656	656	14%	0.0	78%	CP014696.2
Klebsiella pneumoniae strain KSB1_10J chromosome, complete genome	651	651	14%	0.0	78%	CP024515.1
Klebsiella pneumoniae strain KSB2_1B chromosome, complete genome	651	651	14%	0.0	78%	CP024504.1
Klebsiella pneumoniae strain KSB1_4E chromosome, complete genome	651	651	14%	0.0	78%	CP024499.1
Klebsiella pneumoniae strain KSB1_7E chromosome, complete genome	651	651	14%	0.0	78%	CP024496.1
Enterobacter cloacae strain AR_0136, complete genome	651	651	14%	0.0	77%	CP021902.1
Enterobacter cloacae strain AR_0053, complete genome	651	651	14%	0.0	77%	CP021776.1
Enterobacter cloacae strain AR_0002, complete genome	651	651	14%	0.0	77%	CP018814.1
Enterobacter hormaechei subsp. oharae strain 34978, complete genome	651	651	14%	0.0	77%	CP012165.1
Leclercia sp. LSNIH3 chromosome, complete genome	645	645	14%	6e-180	77%	CP026387.1
Dickeya paradisiaca Ech703 chromosome, complete genome	645	645	14%	6e-180	77%	CP001654.1
Lelliottia amnigena strain FDAARGOS_395 chromosome, complete genome	640	640	14%	3e-178	77%	CP023529.1
Enterobacter xiangfangensis strain LMG27195, complete genome	640	640	14%	3e-178	77%	CP017183.1
Leclercia adecarboxylata strain USDA-ARS-USMARC-60222, complete genome	640	640	14%	3e-178	77%	CP013990.1
Pectobacterium carotovorum strain SCC1 chromosome	623	623	14%	3e-173	77%	CP021894.1
Kosakonia sacchari strain BO-1, complete genome	614	614	14%	2e-170	77%	CP016337.1
Pectobacterium polaris strain NIBIO1392 chromosome, complete genome	606	606	14%	3e-168	77%	CP017482.1
Enterobacteriaceae bacterium strain FGI 57, complete genome	603	603	14%	4e-167	77%	CP003938.1
Lelliottia amnigena strain ZB04, complete genome	601	601	14%	1e-166	76%	CP015774.2
Pectobacterium polaris strain NIBIO1006 chromosome, complete genome	584	584	14%	1e-161	76%	CP017481.1
Klebsiella oxytoca strain CAV1015, complete genome	584	584	14%	1e-161	77%	CP017928.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Klebsiella oxytoca strain CAV1335, complete genome	584	584	14%	1e-161	77%	CP011618.1
Klebsiella oxytoca strain CAV1099, complete genome	584	584	14%	1e-161	77%	CP011597.1
Pectobacterium carotovorum subsp. odoriferum strain BC S7, complete genome	569	569	14%	4e-157	76%	CP009678.1
Enterobacter cancerogenus strain CR-Eb1 chromosome, complete genome	560	560	14%	2e-154	76%	CP025225.1
Pectobacterium atrosepticum strain 36A chromosome, complete genome	518	518	14%	1e-141	75%	CP024956.1
Pectobacterium atrosepticum strain 21A, complete genome	518	518	14%	1e-141	75%	CP009125.1
Pectobacterium atrosepticum strain JG10-08, complete genome	518	518	14%	1e-141	75%	CP007744.1
Rouxiella sp. ERMR1:05 chromosome, complete genome	492	492	8%	8e-134	80%	CP019062.1
Rahnella aquatilis CIP 78.65 = ATCC 33071, complete genome	459	459	8%	8e-124	79%	CP003244.1
Enterobacteriaceae bacterium bta3-1, complete genome	442	442	14%	8e-119	74%	CP004083.1
Rahnella aquatilis HX2, complete genome	420	420	8%	4e-112	78%	CP003403.1
Edwardsiella hoshinae strain ATCC 35051, complete genome	379	379	14%	6e-100	73%	CP016043.1
Vibrio fluvialis strain 12605 chromosome 1, complete sequence	351	351	8%	1e-91	77%	CP019118.1
Tolumonas auensis DSM 9187, complete genome	342	342	6%	9e-89	80%	CP001616.1
Vibrio coralliilyticus strain 58 chromosome I, complete sequence	302	302	8%	1e-76	75%	CP016556.1
Aeromonas veronii strain CB51, complete genome	298	298	7%	2e-75	76%	CP015448.1
Vibrio coralliilyticus strain RE98 chromosome 1, complete sequence	291	291	8%	3e-73	75%	CP009617.1
Vibrio coralliilyticus strain OCN014 chromosome 1, complete sequence	279	279	8%	7e-70	75%	CP009264.2
Vibrio vulnificus strain CECT 4999 chromosome I, complete sequence	276	276	8%	9e-69	75%	CP014636.1
Vibrio vulnificus strain FORC_037 chromosome I, complete sequence	270	270	8%	4e-67	75%	CP016321.1
Klebsiella quasipneumoniae subsp. similipneumoniae DNA, lipopolysaccharide biosynthesis gene cluster, complete sequence, serotype: O12:K80, strain: 708	267	267	5%	5e-66	78%	AB795942.1
Vibrio vulnificus strain FORC_054 chromosome 1, complete sequence	265	265	8%	2e-65	74%	CP019121.1
Vibrio vulnificus NBRC 15645 = ATCC 27562 chromosome 1, complete sequence	265	265	8%	2e-65	74%	CP012881.1
Klebsiella pneumoniae DNA, lipopolysaccharide biosynthesis gene cluster, serotype: O8, complete sequence, strain: 889	244	244	5%	2e-59	78%	AB819963.1

Alignments

Pantoea rwandensis strain ND04, complete genome

Sequence ID: **CP009454.1** Length: 4327607 Number of Matches: 2
Range 1: 2084962 to 2086262

Score	Expect	Identities	Gaps	Strand	Frame
1855 bits(1004)	0.0()	1203/1302(92%)	2/1302(0%)	Plus/Minus	

Features:

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Query  3087     CAGAAGAAGTACTTCGCCACCGACATCTCGATCCAGCAGTAATCAATGTAGAGGCGGTCT  3146
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Sbjct  2086262  CAGAAGAAGTACTTCGCCACTGACATCTCGATCCAGCATTAATCAATGCAGGGGCGGTCT  2086203

Query  3147     CAAGGCCGCCCTATTCGCGCCGCTAACATGAGCGAGCGCAAATTTAGCGGCTTCATTTCC  3206
                  ||||||||||  ||||||| ||||||||||||||||||||||||||||||||||  ||
Sbjct  2086202  TCAGGCCGCCCTGTTCGCGCTGCTAACATGAGCGAGCGCAAATTTAGCGGCTTCATCCCC  2086143

Query  3207     GCTCATTCTCACAGCAGCACTATAATTCCAATCAATAAAATTAATCAGGCACGACGTTCA  3266
                ||||||| ||||||||||||||||||||| |||||||||||| |||||||||||||||||
Sbjct  2086142  GCTCATTTTCACAGCAGCACTATAATTCCAGTCAATAAAATTAATCAGGCACGACGTTCA  2086083

Query  3267     ACGTGCCGTAGATACAGGACATCGACCTCGTCATGCAACAACAACATCATCCTC-TGCTA  3325
                  ||||||||||| ||||||||||||  || ||||||||||||||||||| || |||||
Sbjct  2086082  GTGTGCCGTAGATATAGGACATCGACCGCGCCATGCAACAACAACATCATC-TCTTGCTA  2086024

Query  3326     AGTGCTTCCCTCGGTACACAGCGCGAAATCGTCAGCTTCCATTTCGGTACCGATTCCCAG  3385
                ||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Sbjct  2086023  AGTGCTTCCCTCGGTACACAGCGCGAAATCGTCAGCTTTCATTTCGGTACCGATTCCCAG  2085964

Query  3386     CAGCGCGTCTACATTCAGGCGGCACTGCACGGTGATGAACTGCCGGGTATGGCGGTGGCG  3445
                || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2085963  CAACGCGTCTACATTCAGGCGGCACTGCACGGTGATGAACTGCCGGGTATGGCGGTGGCG  2085904

Query  3446     TGGTATCTGAAACACAAGCTGCTGGCGCTGGAATCGGCCGGGCAGCTCAAATCCAAAATT  3505
                ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Sbjct  2085903  TGGTATCTGAAACACAAGCTGCTGGCGCTGGAATCTGCCGGGCAGCTCAAATCCAAAATT  2085844

Query  3506     ACGCTGGTGCCGGTGGCAAATCCGCTGGCGATGGGGCAACACTGGCACGGCAGCCATTTG  3565
                ||||||||||||||||| ||||||||||||||||| ||||||||||||||||| ||||||
Sbjct  2085843  ACGCTGGTGCCGGTGGCCAATCCGCTGGCGATGGGTCAACACTGGCACGGCAGTCATTTG  2085784

Query  3566     GGTCGATTCCATACGCTTTCAGGTCAGGATTTCAATCGCCGTTTCCCGGCATTAGGCGAT  3625
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2085783  GGTCGATTCCATACGCTTTCAGGTCAGGATTTCAATCGCCGTTTCCCGGCGTTAGGCGAT  2085724

Query  3626     ACCCTGGCTGAAGAGTTGGCCGGTTCGTTGACACAGAGTGAATATGAGAACAAACGGTTG  3685
                ||||||||||||||||||||||||||||||||||  || ||  ||||||||||||||||||
Sbjct  2085723  ACCCTGGCTGAAGAGTTGGCCGGTTCGTTGACGCAAAGCGAATATGAGAACAAACGGCTG  2085664

Query  3686     ATCCGTGATGCCATTGATCGCCACTATCGAGACCGCGTTGCTCGTACCGAACTGGATGCG  3745
                ||||||||||||||||||||||||||||||||||  ||| ||||||||||||||||||||
Sbjct  2085663  ATCCGTGATGCCATTGATCGCCACTATCGCGATCGCATTGCTCGTACCGAACTGGATGCG  2085604

Query  3746     CAGCGCTTCACGCTAATGCGTATGGCCAGCCAGGCAGATTTGATGATTGATCTGCACTGC  3805
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Sbjct  2085603  CAGCGCTTCACGCTAATGCGTATGGCCAGCCAGGCAGATTTGATGATTGATCTGCACTGC  2085544

Query  3806     GACTGGGACGCATTGCCGCATCTCTACACGACCCCGCATGCGTGGCAGGATATCGAGCCT  3865
                ||||||||||||||||||||||||||  ||  ||  |||||  ||  |||||||||||||
Sbjct  2085543  GACTGGGACGCATTGCCGCATCTGTATACCACGCCGCACGCATGGCAGGATATCGAACCA  2085484

Query  3866     TTAGCGCGTTGGTTAGGTAGCGAAGTACAGCTTCTGGCCCAAATCTCTGGTGGCGAGCCG  3925
                ||||||||||||||||| ||  |||||  ||  ||  |||||  |||||  || |||||||
Sbjct  2085483  TTAGCGCGTTGGTTAGGCAGTGAAGTGCAACTGCTGGCGCAAATATCCGGTGGCGAACCC  2085424

Query  3926     TTTGATGAAGCCTGCTGCGAGCCGTGGTTAACGTTGGCCGAGCGGTTTGGTGGTGAGTAT  3985
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Sbjct  2085423  TTTGATGAGGCCTGCTGTGAACCGTGGCTGACACTGGCTGAGCGATTTGGTGGTGAGTAT  2085364

Query  3986     CCGATGCCACGGGGTTTGTTACCGGTGACGCTCGAATTACGTGGTGTGGCGGATGTGTCG  4045
                |||||||| || |||||||| || |||||||| || |||||||| || ||||||||||||
Sbjct  2085363  CCGATGCCTCGTGGTTTGTTGCCAGTGACGCTGGAGTTACGTGGGGTTGCGGATGTGTCG  2085304

Query  4046     CCTGGACAAGCTGAGAAGGATGCGGATGCGATTATTAACGCGCTGATTGAAGGTGGCTAC  4105
                ||   ||| || ||||||||||||||||||||||||| |||||||| |||||||| ||||
Sbjct  2085303  CCGCAACAGGCGGAGAAGGATGCGGATGCGATTATTAACGCGTTGATTGAAGGCGGCTAT  2085244

Query  4106     ATTGCGGGTGACGTGGGTGAGTCCCCTGCTCTGATCAATCCTGCGACACCGCTGGCAGGT  4165
                ||  ||||||||     ||||||||||||||| ||||||||||||||||||||||||||
Sbjct  2085243  ATCGCGGGTGAAACAGGTGAGTCCCCTGCCCTGATCAATCCCGCGACACCGCTGGCAGGT  2085184

Query  4166     TGTGAGTATATCCATGCACCGCATTCTGGAATGCTGTTGAATCGCCGTGAGTTGGGTGAG  4225
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2085183  TGTGAGTATATCCATGCACCGCATTCTGGATTGCTGTTGAATCGCCGTGAGTTGGGTGAG  2085124

Query  4226     TGGATCAAGCCGGGTGAAGTGGTAGCGGAGATTGTGGACCCGATTACCGACCAGGTGACG  4285
                ||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||
Sbjct  2085123  TGGATCAAGCCGGGTGAAGTGGTGGCGGAGATTGTGGATCCGATTACCGACCAGGTGACA  2085064

Query  4286     CCGCTGGTGGCAGAGTTTGGTGGGGTGCTGTATGCAAGGAACCTGATGAAGTTTGCTACG  4345
                ||||||||||||||||||||||||||||||||||    | ||| |  ||||||||||||
Sbjct  2085063  CCGCTGGTGGCAGAGTTTGGTGGGGTGCTGTATGCGCGAAATCTCATGAAGTTTGCTACG  2085004

Query  4346     GCTGGGATGCTGGTGGTGCGGTTGGCGGGTGAAAATGCGGGC  4387
                || || |||||||||  || |||||  |||||||||||||
Sbjct  2085003  GCGGGAATGCTGGTGGTAAGGCTTGCGGGGGAAAATGCGGGC  2084962
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Range 2: 2087356 to 2088478

Score	Expect	Identities	Gaps	Strand	Frame
1847 bits(1000)	0.0()	1082/1123(96%)	0/1123(0%)	Plus/Minus	

Features:

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Query  1        TCGTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  60
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Sbjct  2088478  TCGTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  2088419
Query  61       TCACCGCCTCTTCCGATGGCCGTGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAG  120
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Sbjct  2088418  TCACCGCCTCTTCCGATGGCCGCGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAG  2088359
Query  121      TGATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCA  180
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Sbjct  2088358  TGATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCA  2088299
Query  181      TTCTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGACCCTACGC  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  2088298  TTCTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGACCCGACGC  2088239
Query  241      TGATCACGCGTCTGGCAGATCGCTTTGGTGTGCAGTGTATCGTGGTGGGTATTGATACCT  300
                ||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  2088238  TGATCACGCGTCTGGCGGATCGCTTTGGTGTGCAGTGCATCGTGGTGGGTATTGATACCT  2088179
Query  301      GGTTCGATGAAGCCACCGGCAAGTATCACGTCAATCAATATACCGGCGATGAATCACGTA  360
                ||||| ||||||||||||| ||||||||||||||||| || ||||||||||||||| |||||
Sbjct  2088178  GGTTTGATGAAGCCACAGGCAAGTATCACGTCAACCAGTATACCGGCGATGAGTCACGTA  2088119
Query  361      CCCGTGTCACCACCTGGGAAACCCTGGATTGGGTACAGGAAGTGCAGAAGCTAGGCGCGG  420
                |||||||||||||||||||||||||||||||||| |||||||||||||||| || |||||
Sbjct  2088118  CCCGTGTCACCACCTGGGAAACCCTGGATTGGGTGCAGGAAGTGCAGAAGCTGGGTGCGG  2088059
Query  421      GCGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGTGC  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2088058  GCGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGTGC  2087999
Query  481      AGCTGAAGAAAGTGCGTGAGGTATGTAAAGTGCCCCTCATCGCTTCTGGCGGCGCGGGCA  540
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Sbjct  2087998  AGCTGAAGAAAGTCCGAGACGTGTGTAAAGTGCCCCTCATCGCTTCTGGCGGAGCAGGCA  2087939
Query  541      CCATGCCACACTTTCTCGAAGCCTTTGAACAGGCAAACGTTGATGGCGCACTGGCCGCTT  600
                ||||||| || || ||||||||||||||||||||||| |||||| || ||||||||||||
Sbjct  2087938  CCATGCCGCATTTCCTCGAAGCCTTTGAACAGGCAAACGTCGATGGTGCGCTGGCCGCTT  2087879
Query  601      CGGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAACG  660
                | |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||
Sbjct  2087878  CAGTGTTTCACAAACAAATTATTAATATCGGCGAGTTGAAAAACTTCCTGATCGACAACG  2087819
Query  661      GTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAAC  720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2087818  GTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAAC  2087759
Query  721      CGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCACGG  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2087758  CGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCACGG  2087699
Query  781      TTATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAATGTCACTTTCTTCTC  840
                ||||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Sbjct  2087698  TTATATGAATGAGGAAGCACTGCAAAAGACGCTGGCGGAAGGCAACGTCACTTTCTTCTC  2087639
Query  841      TCGCACCAAAAACCGCTTGTGGACCAAGGGGGAAACCTCCGGTCACTTTTTGAAGGTCGC  900
                |||||||||||||||||||||||||| |||||||||||||||||||||   || ||||||||
Sbjct  2087638  TCGCACCAAAAACCGCTTGTGGACCAAAGGGGAAACCTCCGGTCACTTCCTGCAGGTCGC  2087579
Query  901      GAGCATCACGCCGGATTGTGATAACGACACCCTGCTAGTGCTGGCAAACCCGATTGGGCC  960
                |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Sbjct  2087578  GAGCATCACGCCGGATTGTGATAACGACACCCTGCTGGTGCTGGCAAACCCGATTGGGCC  2087519
Query  961      AACCTGCCACCTTGGCACCTCAAGCTGCTTCTCACCGGCTGCGCCAGATTGGGCGTTCCT  1020
                ||||||||||||  || ||| |||||||||||||  ||||||||||||||||||||||||
Sbjct  2087518  AACCTGCCACCTCGGAACATCAAGCTGCTTCTCTCCAGCTGCGCCAGATTGGGCGTTCCT  2087459
Query  1021     GTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGCGCCGATCCTGAGAGTTCTTACAC  1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2087458  GTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGCGCCGATCCTGAGAGTTCTTACAC  2087399
Query  1081     CGCGAAACTCTATGCCAGCGGCACAAAGCGTATCGCGCAGAAA  1123
                |||||||| |||||||||||||| |||||||||||||||||||
Sbjct  2087398  CGCGAAACTGTATGCCAGCGGCACCAAGCGTATCGCGCAGAAA  2087356
```

Pantoea vagans strain ND02, complete genome

Sequence ID: **CP011427.1** Length: 4313264 Number of Matches: 2

Range 1: 1341479 to 1342601

Score	Expect	Identities	Gaps	Strand	Frame
1471 bits(796)	0.0()	1014/1123(90%)	0/1123(0%)	Plus/Minus	

Features:

```
Query  1        TCGTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  60
Sbjct  1342601  TCGTGCCGCTGGCGCAGCGTTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  1342542
Query  61       TCACCGCCTCTTCCGATGGCCGTGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAG  120
Sbjct  1342541  TCACCGCCTCTTCAGATGGCCGTGTCGTCGATAAAAGCTGGGTGTCACGCGTTGCGGAAG  1342482
Query  121      TGATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCA  180
Sbjct  1342481  TGATCGATATTCCTTTCTGCGTGGCCGGTGGCATTAAAACCCCGGAAGACGCAGCGCGCA  1342422
Query  181      TTCTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGACCCTACGC  240
Sbjct  1342421  TTCTGCAGTTCGGTGCGGACAAGATCTCCATCAACTCCCCCGCACTGGCAGACCCGACGC  1342362
Query  241      TGATCACGCGTCTGGCAGATCGCTTTGGTGTGCAGTGTATCGTGGTGGGTATTGATACCT  300
Sbjct  1342361  TGATTACCCGTCTGGCCGATCGCTTTGGCGTGCAGTGTATCGTGGTAGGCATTGATACCT  1342302
Query  301      GGTTCGATGAAGCCACCGGCAAGTATCACGTCAATCAATATACCGGCGATGAATCACGTA  360
Sbjct  1342301  GGTTCGATGAAGCAACCGGCAAGTATCACGTTAACCAGTACACCGGTGACGAATCACGTA  1342242
Query  361      CCCGTGTCACCACCTGGGAAACCCTGGATTGGGTACAGGAAGTGCAGAAGCTAGGCGCGG  420
Sbjct  1342241  CCCGTGTCACCACCTGGGAAACCCTCGACTGGGTGCAGGAAGTGCAGAAGTTGGGCGCGG  1342182
Query  421      GCGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGTGC  480
Sbjct  1342181  GCGAAATCGTACTGAATATGATGAACCAGGATGGCGTGCGCAACGGCTATGATCTGATAC  1342122
Query  481      AGCTGAAGAAAGTGCGTGAGGTATGTAAAGTGCCCCTCATCGCTTCTGGCGGCGCGGGCA  540
Sbjct  1342121  AGCTGAAGAAAGTGCGTGACGTGTGTAGAGTGCCACTGATCGCCTCTGGCGGCGCGGGCA  1342062
Query  541      CCATGCCACACTTTCTCGAAGCCTTTGAACAGGCAAACGTTGATGGCGCACTGGCCGCTT  600
Sbjct  1342061  CCATGCCGCACTTCCTCGAAGCCTTCGAGCAAGCGAACGTGGATGGCGCTCTGGCTGCTT  1342002
Query  601      CGGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAACG  660
Sbjct  1342001  CCGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTCCTGATCGACAACG  1341942
Query  661      GTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAAC  720
Sbjct  1341941  GTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAAC  1341882
Query  721      CGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCACGG  780
Sbjct  1341881  CGCGGGCATGATGCCTGTTATCGTCCAGCACAATGTCTCTGGCGAAGTGCTGATGCACGG  1341822
Query  781      TTATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAATGTCACTTTCTTCTC  840
Sbjct  1341821  TTATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAACGTCACCTTCTTCTC  1341762
Query  841      TCGCACCAAAAACCGCTTGTGGACCAAGGGGGAAACCTCCGGTCACTTTTTGAAGGTCGC  900
Sbjct  1341761  GCGCACCAAAAACCGCTTGTGGACCAAAGGTGAAACCTCAGGTCACTTCCTGCAGGTGGC  1341702
Query  901      GAGCATCACGCCGGATTGTGATAACGACACCCTGCTAGTGCTGGCAAACCCGATTGGGCC  960
Sbjct  1341701  GAGCATCACACCTGATTGCGATAACGATACGCTGTTGGTGCTGGCGAATCCGATTGGGCC  1341642
Query  961      AACCTGCCACCTTGGCACCTCAAGCTGCTTCTCACCGGCTGCGCCAGATTGGGCGTTCCT  1020
Sbjct  1341641  GACCTGCCACTTGGGCACATCAAGCTGCTTCTCGCCTGCCGCACCTGATTGGGCGTTCCT  1341582
Query  1021     GTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGCGCCGATCCTGAGAGTTCTTACAC  1080
Sbjct  1341581  GTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGTGCCGATCCGGAAAGCTCTTACAC  1341522
Query  1081     CGCGAAACTCTATGCCAGCGGCACAAAGCGTATCGCGCAGAAA  1123
Sbjct  1341521  CGCAAAACTGTACGCCAGCGGCACAAAGCGCATCGCGCAGAAA  1341479
```

Range 2: 1336957 to 1338137

Score	Expect	Identities	Gaps	Strand	Frame
1098 bits(594)	0.0()	990/1186(83%)	7/1186(0%)	Plus/Minus	

Features:

```
Query  3203     TTCCGCTCATTCTCACAGCAGCACTATAATTCCAATCAATAAAATTAATCAGGCACG-AC  3261
Sbjct  1338137  TTCCGCTCATTTTCACAGCAGCACTATAATTCCAATCAATAAA-TT--TTAGGCACGAAT  1338081
Query  3262     GTTCAACGTGCCGTAGATACAGGACATCGACCTCGTCATGCAACAACAACATCATCCTCT  3321
Sbjct  1338080  CTT-TAGGTGCCGTAGAGACAGGACATCGACAACCTCATGCAACAGCAACATCATCCTCT  1338022
Query  3322     GCTAAGTGCTTCCCTCGGTACACAGCGCGAAATCGTCAGCTTCCATTTCGGTACCGATTC  3381
Sbjct  1338021  GTTGAGTGCTTCCCTTGGAACACAGCGCGAAATCGTTAGCTTCCACTTCGGTACCGATTC  1337962
```

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Query  3382     CCAGCAGCGCGTCTACATTCAGGCGGCACTGCACGGTGATGAACTGCCGGGTATGGCGGT  3441
Sbjct  1337961  CCAGCAGCGCGTCTATATTCAGGCCGCCTTACACGGTGATGAGCTGCCCGGTATGGCGGT  1337902

Query  3442     GGCGTGGTATCTGAAACACAAGCTGCTGGCGCTGGAATCGGCCGGGCAGCTCAAATCCAA  3501
Sbjct  1337901  AGCGTGGTATTTAAAACACAAACTGCTGGCACTGGAATCCGCCGGACAGCTTAAGTCAAA  1337842

Query  3502     AATTACGCTGGTGCCGGTGGCAAATCCGCTGGCGATGGGGCAACACTGGCACGGCAGCCA  3561
Sbjct  1337841  GATCACCCTGGTGCCGGTCGCCAACCCCTTAGCGATGGGCCAGCACTGGCACGGCAGCCA  1337782

Query  3562     TTTGGGTCGATTCCATACGCTT-TCAGGTCAGGATTTCAATCGCCGTTTCCCGGCATTAG  3620
Sbjct  1337781  TCTGGGACGCTTCCATAC-CTTATCAGGTCAGGATTTCAACCGTCGCTTCCCGGCATTGG  1337723

Query  3621     GCGATACCCTGGCTGAAGAGTTGGCCGGTTCGTTGACACAGAGTGAATATGAGAACAAAC  3680
Sbjct  1337722  GTGAAACCCTGGCCGCCGAACTTGCGGATTCACTGACGCAAAGTGAGTACGAAAACAAAC  1337663

Query  3681     GGTTGATCCGTGATGCCATTGATCGCCACTATCGAGACCGCGTTGCTCGTACCGAACTGG  3740
Sbjct  1337662  GTCTGATTCGCGAAGCGATTGACCGTCATTATCGCGACCGTATTGCCAAGACTGAGCTGG  1337603

Query  3741     ATGCGCAGCGCTTCACGCTAATGCGTATGGCCAGCCAGGCAGATTTGATGATTGATCTGC  3800
Sbjct  1337602  ATTCGCAGCGCTTTACCCTGATGCGCATGGCCAGCCAGGCGGATCTCATGATCGATCTGC  1337543

Query  3801     ACTGCGACTGGGACGCATTGCCGCATCTCTACACGACCCCGCATGCGTGGCAGGATATCG  3860
Sbjct  1337542  ACTGCGACTGGGATGCACTGCCACACCTCTACACCACTCCGCATGCCTGGCAGGACATCG  1337483

Query  3861     AGCCTTTAGCGCGTTGGTTAGGTAGCGAAGTACAGCTTCTGGCCCAAATCTCTGGTGGCG  3920
Sbjct  1337482  AACCGCTGGCGCGCTGGCTAGGCAGTGAAGTGCAGCTGCTGGCGCAGATTTCAGGTGGAG  1337423

Query  3921     AGCCGTTTGATGAAGCCTGCTGCGAGCCGTGGTTAACGTTGGCCGAGCGGTTTGGTGGTG  3980
Sbjct  1337422  AGCCATTTGATGAAGCCTGCTGCGAGCCGTGGTTAACACTGGCAGAGCGCTTTGGTGATA  1337363

Query  3981     AGTATCCGATGCCACGGGGTTTGTTACCGGTGACGCTCGAATTACGTGGTGTGGCGGATG  4040
Sbjct  1337362  AGTACCCCATGCCGCGTGGATTGTTGCCAGTGACGCTGGAGTTACGCGGCGTGGCAGATG  1337303

Query  4041     TGTCGCCTGGACAAGCTGAGAAGGATGCGGATGCGATTATTAACGCGCTGATTGAAGGTG  4100
Sbjct  1337302  TTGAGCCTGAACAGGCAGAAAAAGATGCCGATGCAATTATCAATGCGCTGATTGAAGGTG  1337243

Query  4101     GCTACATTGCGGGTGACGTGGGTGAGTCCCCTGCTCTGATCAATCCTGCGACACCGCTGG  4160
Sbjct  1337242  GCTACATTGCGGGTGAGTTGGGTGAGTCCCCTGCCCTGATTAACCCAGCCACGCCGTTAG  1337183

Query  4161     CAGGTTGTGAGTATATCCATGCACCGCATTCTGGAATGCTGTTGAATCGCCGTGAGTTGG  4220
Sbjct  1337182  CAGGCTGTGAGTATATTCATGCGCCGCACTCTGGGCTGCTATTGAACCGCCGCAAGTTGG  1337123

Query  4221     GTGAGTGGATCAAGCCGGGTGAAGTGGTAGCGGAGATTGTGGACCCGATTACCGACCAGG  4280
Sbjct  1337122  GTGAGTGGATTAAGCCTGGTGAAGTGGTGGCTGAGATTGTTGACCCGATTACCGACCAGG  1337063

Query  4281     TGACGCCGCTGGTGGCAGAGTTTGGTGGGGTGCTGTATGCAAGGAACCTGATGAAGTTTG  4340
Sbjct  1337062  TGACGCCGCTGTTTGCTGAGTTTGGTGGCGTGCTGTATGCGAGGAATTTGATGAAGTTTG  1337003

Query  4341     CTACGGCTGGGATGCTGGTGGTGCGGTTGGCGGGTGAAAATGCGGG  4386
Sbjct  1337002  CGACGGCGGGGATGCTGGTGGTGAGGCTGGCTGGAGAGAATGCGGG  1336957
```

Plautia stali symbiont DNA, complete genome

Sequence ID: **AP012551.1** Length: 4035456 Number of Matches: 1
Range 1: 3902663 to 3903784

Score	Expect	Identities	Gaps	Strand	Frame
1203 bits(651)	0.0()	965/1122(86%)	0/1122(0%)	Plus/Plus	

Features:

```
Query  1        TCGTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  60
Sbjct  3902663  TCGTACCGCTGGCGCAGCGCTATGCCCAGGAAGGCGCTGACGAACTGGTGTTTTACGATA  3902722

Query  61       TCACCGCCTCTTCCGATGGCCGTGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAG  120
Sbjct  3902723  TCACCGCCTCTTCCGACGGCCGCGTGGTGGATAAAAGCTGGGTATCGCGCGTGGCGGAAG  3902782

Query  121      TGATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCA  180
Sbjct  3902783  TGATCGACATTCCGTTCTGCGTCGCCGGGGGCATCAAAACCCCGGAAGATGCGGCGCGCA  3902842

Query  181      TTCTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGACCCTACGC  240
Sbjct  3902843  TTCTGCAGTTTGGCGCAGATAAGATCTCCATCAACTCACCCGCGCTGGCCGATCCGACGC  3902902

Query  241      TGATCACGCGTCTGGCAGATCGCTTTGGTGTGCAGTGTATCGTGGTGGGTATTGATACCT  300
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                 |||| || || |||||| |||||||| || |||||||| |||||||| || |||||||||||
Sbjct  3902903   TGATTACCCGGCTGGCGGATCGCTTCGGCGTGCAGTGCATCGTGGTCGGCATTGATACCT  3902962

Query  301       GGTTCGATGAAGCCACCGGCAAGTATCACGTCAATCAATATACCGGCGATGAATCACGTA  360
                 |||| ||||||||||| ||||||||||||||||||||| || |||||||| ||| | || |
Sbjct  3902963   GGTTTGATGAAGCCAGCGGCAAGTATCACGTCAATCAGTACACCGGCGACGAAGCGCGCA  3903022

Query  361       CCCGTGTCACCACCTGGGAAACCCTGGATTGGGTACAGGAAGTGCAGAAGCTAGGCGCGG  420
                 |||| || |||     |||||||| || || |||||| ||||||||||||||||| |||||| |
Sbjct  3903023   CCCGCGTTACCCAGTGGGAAACACTCGACTGGGTAGAGGAAGTGCAGAAGCTGGGCGCTG  3903082

Query  421       GCGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGTGC  480
                 ||||||||||| ||||| |||||||||||| || ||||| |||||| |||||||| |||||||
Sbjct  3903083   GCGAAATCGTACTGAATATGATGAACCAAGACGGCGTGCGTAACGGCTACGACCTGGTGC  3903142

Query  481       AGCTGAAGAAAGTGCGTGAGGTATGTAAAGTGCCCCTCATCGCTTCTGGCGGCGCGGGCA  540
                 ||||||||||| ||| |||| |||||||||| || |||||| || |||||| || | |||
Sbjct  3903143   AGCTGAAGAAGGTGTGTGACCTGTGTAAGGTGCCGCTGATCGCCTCCGGTGGCGCAGGGA  3903202

Query  541       CCATGCCACACTTTCTCGAAGCCTTTGAACAGGCAAACGTTGATGGCGCACTGGCCGCTT  600
                 ||||| | |||||| ||||||||||||| ||||||||||| || ||||| ||||| ||||
Sbjct  3903203   CCATGGCGCACTTCCTCGAAGCCTTTGAGCAGGCAAACGTCGACGGCGCGCTGGCGGCTT  3903262

Query  601       CGGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAACG  660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3903263   CGGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAACG  3903322

Query  661       GTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAAC  720
                 ||||||||||||||||||||||||||||||||||||| ||| |||||| ||||||||||||
Sbjct  3903323   GTGTGGAGATTCGCGCGTGTTAACTGCAGAGCAACTGTCCAGACTGGACTGGGCCAAAAC  3903382

Query  721       CGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCACGG  780
                 ||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Sbjct  3903383   CGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTCTCCGGCGAAGTGCTGATGCACGG  3903442

Query  781       TTATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAATGTCACTTTCTTCTC  840
                 |||  |||||  ||||| |||||||| ||||||||||| || ||||||||||| ||||||||
Sbjct  3903443   TTACATGAACGAGGACGCGCTGCACAAGACGCTGGCCGACGGCAATGTCACCTTCTTCTC  3903502

Query  841       TCGCACCAAAAACCGCTTGTGGACCAAGGGGGAAACCTCCGGTCACTTTTTGAAGGTCGC  900
                  ||||||||||||||| ||||||||| || |||||| ||  | |||||| || |||  |||
Sbjct  3903503   CCGCACCAAAAACCGTTTATGGACCAAAGGCGAAACTTCGGACCACTTCCTCAAAGTGGT  3903562

Query  901       GAGCATCACGCCGGATTGTGATAACGACACCCTGCTAGTGCTGGCAAACCCGATTGGGCC  960
                  |||||  ||||| |||||| |||||||||||  |||||  |||||||| ||| |||||||
Sbjct  3903563   TAGCATTACGCCAGATTGCGATAACGACACGCTGCTGGTGCTGGCCAATCCGATTGGCCC  3903622

Query  961       AACCTGCCACCTTGGCACCTCAAGCTGCTTCTCACCGGCTGCGCCAGATTGGGCGTTCCT  1020
                  |||||||  ||  |||||| |||||||||| |||||  ||||||||  || |||| ||||
Sbjct  3903623   CACCTGCCATCTCGGTACCTCGAGCTGCTTTTCGCCTGCCGCACCCGACTGGACGTTCCT  3903682

Query  1021      GTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGCGCCGATCCTGAGAGTTCTTACAC  1080
                 |||||||||||||||| |||||||  ||  |||||| ||  |||||||| |  ||| ||| |||
Sbjct  3903683   GTATCAGCTGGAGCAGTTGCTGGCCTCGCGTAAAAGTGCCGATCCCGCCAGCTCCTATAC  3903742

Query  1081      CGCGAAACTCTATGCCAGCGGCACAAAGCGTATCGCGCAGAA  1122
                  |||||  |||  |||||||||||| |||||| |||| ||||||
Sbjct  3903743   GGCGAAGCTGTACGCCAGCGGCACCAAGCGCATCGCACAGAA  3903784
```

Pantoea sp. At-9b, complete genome

Sequence ID: **CP002433.1** Length: 4368708 Number of Matches: 1
Range 1: 2804260 to 2805382

Score	Expect	Identities	Gaps	Strand	Frame
1149 bits(622)	0.0()	958/1125(85%)	4/1125(0%)	Plus/Plus	

Features:

```
Query  1         TCGTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATA  60
                 |||||||||||||||| || |||||||||||||| || || || |||||||||||||||||
Sbjct  2804260   TCGTGCCACTGGCGCAACGTTATGCGCAGGAAGGGGCGGATGAACTGGTGTTTTATGATA  2804319

Query  61        TCACCGCCTCTTCCGATGGCCGTGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAG  120
                 |||||||||| ||||||||||| |||||||||||||||| || || || || || |||||
Sbjct  2804320   TCACCGCCTCGTCTGATGGCCGTGTCGTGGATAAAAGCTGGGTCTCGCGTGTGGCGGAAG  2804379

Query  121       TGATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCA  180
                 |||||||||||| |||||| || || || || |||||||| || | |||||||||||||||
Sbjct  2804380   TGATTGATATTCCTTTCTGTGTAGCAGGGGGAATCAAGAGCGAAGCGGATGCCGCGCGCA  2804439

Query  181       TTCTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGA-CCCTACG  239
                 ||||| | || ||||||||||||||||||||||||||| || |||||||||||| |||| ||
Sbjct  2804440   TTCTGGAATTTGGTGCGGATAAGATCTCCATCAACTCACCCGCGCTGGCTGATCCCT-CG  2804498

Query  240       CTGATCACGCGTCTGGCAGATCGCTTTGGTGTGCAGTGTATCGTGGTGGGTATTGATACC  299
                 ||||| || |||||||| |||||||| |||| |||||||| |||||||| || ||||||||
Sbjct  2804499   CTGATTACCCGTCTGGCCGATCGCTTTGGCGTGCAATGTATTGTGGTGGGGATCGATACC  2804558

Query  300       TGGTTCGATGAAGCCACCGGCAAGTATCACGTCAATCAATATACCGGCGATGAATCACGT  359
                 ||||| || || || |||||||| |||||| |||||||| |||||||| ||||||||| ||
Sbjct  2804559   TGGTTTGACGACGCGACCGGCAAATATCACGTTAATCAGTATACCGGTGATGAATCCCGC  2804618

Query  360       ACCCGTGTCAC-CACCTGGGAAACCCTGGATTGGGTACAGGAAGTGCAGAAGCTAGGCGC  418
                 ||||||| || ||  |||||||||||||||||||| ||||||||||||||| ||||||
```

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Sbjct  2804619  ACCCGTGTGACGCA-ATGGGAAACCCTGGATTGGGTGCAGGAAGTGCAGAAGCTGGGCGC  2804677
Query  419      GGGCGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGT  478
                ||||||||||||  || ||| ||||||||||||| |||||  || ||  ||  || |||||
Sbjct  2804678  GGGCGAAATCGTTCTCAATATGATGAACCAGGACGGCGTGCGCAACGGTTATGACCTGGT  2804737
Query  479      GCAGCTGAAGAAAGTGCGTGAGGTATGTAAAGTGCCCCTCATCGCTTCTGGCGGCGCGGG  538
                 ||||||||||||||  || |  ||  |||||  | ||   |  |||||| ||  |||||  ||
Sbjct  2804738  ACAGCTGAAGAAAGTCCGCGATGTCTGTAAGGTACCGTTGATTGCTTCCGGTGGCGCTGG  2804797
Query  539      CACCATGCCACACTTTCTCGAAGCCTTTGAACAGGCAAACGTTGATGGCGCACTGGCCGC  598
                ||||||| ||||||| |||||||| |||||||| || |||||| ||||||||  ||||| ||
Sbjct  2804798  CACCATGGCACACTTCCTCGAAGCGTTTGAACAAGCTAACGTCGATGGCGCGCTGGCGGC  2804857
Query  599      TTCGGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAA  658
                 |||||||||||||||||||| |||| ||||||||||| |||||| ||| |||| |||||
Sbjct  2804858  ATCGGTGTTTCACAAACAGATTATTAATATCGGCGAGCTGAAAAGCTTCCTGATTGACAA  2804917
Query  659      CGGTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAA  718
                ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||| ||||
Sbjct  2804918  CGGTGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGACCCGTCTGGATTGGGTCAAA  2804977
Query  719      ACCGCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCAC  778
                ||||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||
Sbjct  2804978  ACCGCGGGCATGATGCCCGTTATCGTCCAGCACAACGTCTCTGGCGAAGTGCTGATGCAC  2805037
Query  779      GGTTATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAATGTCACTTTCTTC  838
                ||||||||||| ||||||||| |||| || || || |||||| ||||||||||| ||||||
Sbjct  2805038  GGTTATATGAACGAGGAAGCGTTGCAGAAAACCCTCGCGGAGGGCAATGTCACCTTCTTC  2805097
Query  839      TCTCGCACCAAAAACCGCTTGTGGACCAAGGGGGAAACCTCCGGTCACTTTTTGAAGGTC  898
                || |||||||||| ||| |||||||||| || |||||| || ||||||  |||| ||||
Sbjct  2805098  TCGCGCACCAAAAATCGCCTGTGGACCAAAGGTGAAACCTCAGGCCACTTCCTGAAAGTG  2805157
Query  899      GCGAGCATCACGCCGGATTGTGATAACGACACCCTGCTAGTGCTGGCAAACCCGATTGGG  958
                | ||||||  || ||  |||||||| |||||  || |||||  |||||||| ||||||||||
Sbjct  2805158  GTGAGCATTACTCCCGATTGTGACAACGATACGCTGCTGGTGCTGGCGAACCCGATTGGC  2805217
Query  959      CCAACCTGCCACCTTGGCACCTCAAGCTGCTTCTCACCGGCTGCGCCAGATTGGGCGTTC  1018
                || |||||||| ||  ||  || ||  ||  ||  ||||| |||||  || ||  ||| | ||||
Sbjct  2805218  CCCACCTGCCATCTCGGTACTTCCAGTTGTTTCTCTCCGGCAGCACCGGACTGGACTTTC  2805277
Query  1019     CTGTATCAGCTGGAGCAGCTGCTGGCTTCACGTAAGAGCGCCGATCCTGAGAGTTCTTAC  1078
                || |||||| |||| ||  ||||||||     ||||| || || ||  ||  |  ||| ||| |||
Sbjct  2805278  CTCTATCAGTTGGAACAACTGCTGGCGGAGCGTAAAAGTGCTGACCCCGCCAGCTCCTAC  2805337
Query  1079     ACCGCGAAACTCTATGCCAGCGGCACAAAGCGTATCGCGCAGAAA  1123
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Sbjct  2805338  ACCGCGAAGTTGTATGCCAGCGGCACCAAGCGTATCGCACAGAAA  2805382
```

Pantoea sp. PSNIH1, complete genome

Sequence ID: **CP009880.2** Length: 3488376 Number of Matches: 1
Range 1: 3324633 to 3325752

Score	Expect	Identities	Gaps	Strand	Frame
1077 bits(583)	0.0()	943/1122(84%)	4/1122(0%)	Plus/Plus	

Features:

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Query  3        GTGCCACTGGCGCAGCGCTATGCGCAGGAAGGCGCTGACGAGCTGGTGTTCTATGATATC  62
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Sbjct  3324633  GTGCCGCTGGCGCAGCGCTACGCGCAGGAAGGGGCCGACGAGCTGGTGTTTTATGACATC  3324692
Query  63       ACCGCCTCTTCCGATGGCCGTGTGGTGGATAAAAGCTGGGTGTCACGCGTCGCAGAAGTG  122
                ||||||| || |||||||| ||||| || ||||||||||||| |||||  || ||||||
Sbjct  3324693  ACCGCCTCATCGGATGGCCGCGTGGTCGACAAAAGCTGGGTCTCCCGCGTAGCGGAAGTG  3324752
Query  123      ATTGATATTCCGTTCTGCGTGGCGGGCGGTATCAAGAGTGAGGAGGATGCCGCGCGCATT  182
                || ||  |||||||||||||| |||||||| |||   || ||||||||||||||||||||
Sbjct  3324753  ATCGACATTCCGTTCTGCGTCGCGGGCGGCATCAGAAGCGAGGAGGATGCCGCGCGCATT  3324812
Query  183      CTGCAGTTCGGTGCGGATAAGATCTCCATCAACTCCCCGGCGCTGGCTGACCCTACGCTG  242
                ||||||||  || ||  || ||  ||  |||||||||||||||||| ||  || ||||||
Sbjct  3324813  CTGCAGTTTGGCGCTGACAAAATATCTGTCAACTCCCCGGCGCTGGCCGATCCGACGCTG  3324872
Query  243      ATCACGCGTCTGGCAGATCGCTTTGGTGTGCAGTGTATCGTGGTGGGTATTGATACCTGG  302
                ||||| |||||  || ||  |||||| |||||||| ||  ||  |||||||  |||| ||||
Sbjct  3324873  ATCACCCGTCTCGCCGACCGTTTTGGCGTGCAGTGCATAGTAGTGGGTATCGATACTTGG  3324932
Query  303      TTCGATGAAGCCACCGGCAAGTATCACGTCAATCAATATACCGGCGATGAATCACGTACC  362
                || |||||| ||  |||| ||||||||||  ||  ||||||||||||||  |  ||||||
Sbjct  3324933  TTTGATGAGGCGAGCGGTAAATATCACGTTAACCAGTATACCGGTGATGAAGCGCGTACC  3324992
Query  363      CGTGTCAC-CACCTGGGAAACCCTGGATTGGGTACAGGAAGTGCAGAAGCTAGGCGCGGG  421
                || ||  ||  ||  |||||||||||  || |||||| |||||||||||||||  ||||||||
Sbjct  3324993  CGGGTAACGCA-GTGGGAAACCCTTGACTGGGTGCGGGAAGTGCAGAAGCTCGGCGCGGG  3325051
Query  422      CGAAATCGTGCTGAACATGATGAACCAGGATGGCGTACGTAATGGCTACGATCTGGTGCA  481
                ||| |||||||||||  |||||||| ||||||||||||||| |||||||||||||  |||
Sbjct  3325052  CGAGATCGTGCTGAATATGATGAATCAGGATGGCGTACGTAACGGCTACGATCTGGTTCA  3325111
Query  482      GCTGAAGAAAGTGCGTGAGGTATGTAAAGTGCCCCTCATCGCTTCTGGCGGCGCGGGCAC  541
                ||||| |||||  || ||  ||  ||  |||||  || |||||  ||  |||||  ||||||
Sbjct  3325112  GCTGCAGAAGGTCCGCGAAGTGTGCAGCGTGCCGCTAATCGCGTCCGGCGGTGCCGGCAC  3325171
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Query  542      CATGCCACACTTTCTCGAAGCCTTTGAACAGGCAAACGTTGATGGCGCACTGGCCGCTTC  601
Sbjct  3325172  CATGCCGCACTTCCTTGACGCCTTTACGCAGGCAAACGTTGATGGTGCCCTGGCGGCGTC  3325231
Query  602      GGTGTTTCACAAACAAATTATCAATATCGGCGAGTTGAAAAACTTTCTGATCGACAACGG  661
Sbjct  3325232  GGTGTTCCATAAGCAGATTATTAATATCAGTGAGCTGAAAAACTTTCTGATCGACAACGG  3325291
Query  662      TGTGGAGATTCGCGCGTGTTAACTGCAGAACAACTGGCCAAACTGGATTGGGCCAAAACC  721
Sbjct  3325292  TGTGGAGATTCGCGCGTGTTAACAGCAGACCAACTGGCCCGCCTGGACTGGGTCAAAACC  3325351
Query  722      GCGGGCATGATGCCCGTCATCGTCCAGCACAACGTTTCTGGCGAAGTGCTGATGCACGGT  781
Sbjct  3325352  GCGGGCATGATGCCCGTTATCGTGCAGCACAACGTCTCCGGCGAAGTGCTGATGCACGGT  3325411
Query  782      TATATGAATGAGGAAGCGCTGCAAAAGACGCTGGCGGAAGGCAATGTCACTTTCTTCTCT  841
Sbjct  3325412  TATATGAATGAGGCGGCGCTGGAAAAAACGCTGGCGGAAGGCAACGTCACCTTTTTCTCG  3325471
Query  842      CGCACCAAAAACCGCTTGTGGACCAAGGGGGAAACCTCCGGTCACTTTTTGAAGGTCGCG  901
Sbjct  3325472  CGCACCAAAGAGCGGCTCTGGACCAAAGGCGAATCCTCCGGCCACTTTCTGCAAGTGGTG  3325531
Query  902      AGCATCACGCCGGATTGTGATAACGACACCCTGCTAGTGCTGGCAAACCCGATTGGGCCA  961
Sbjct  3325532  AGCATTACGCCAGACTGTGATAACGATACGCTGCTGGTGCTGGCGAACCCCATCGGACCG  3325591
Query  962      ACCTGCCACCTTGGCACCTCAAGCTGCTTCTCACCGGCTGCGCCAGATTGGGCGTTCCTG  1021
Sbjct  3325592  ACGTGCCATCTTGGCACCTCCAGCTGCTTCTCGCCTGCCGCCCCGGAGTGGACGTTCCTC  3325651
Query  1022     TATCAGCTGGAGCAGCTGCTGGCTTCACGTAA-GAGCGCCGATCCTGAGAGTTCTTACAC  1080
Sbjct  3325652  TATCAACTGGAGCAGCTGCTGGCGTCGCGGAAAGAT-GCCGATCCCGCCAGCTCCTATAC  3325710
Query  1081     CGCGAAACTCTATGCCAGCGGCACAAAGCGTATCGCGCAGAA  1122
Sbjct  3325711  CGCCAGCCTCTACGCCAGCGGCACCAAGCGTATTGCGCAGAA  3325752
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