

Query_name	Length	Single-copy	Function
brucella- chr1_1290	393	○	transposase
brucella- chr1_1291	369	○	transposase
brucella- chr1_1340	129	○	hypothetical protein, partial
brucella- chr1_1847	777	●	3-mercaptopyruvate sulfurtransferase
brucella- chr1_1918	369	○	transposase
brucella- chr1_1919	609	○	queuine trna-ribosyltransferas
brucella- chr1_1972	369	○	transposase
brucella- chr1_239	2232	●	gtp pyrophosphokinase rsh
brucella- chr1_277	1140	●	cytochrome c-type biogenesis protein
brucella- chr1_347	417	○	transposase orfb
brucella- chr1_705	393	○	transposase
brucella- chr1_706	369	○	transposase
brucella- chr1_995	4782	●	outer membrane autotransporter barrel domain-containing protein
brucella- chr2_1	255	○	protein
brucella- chr2_2	882	○	is3 family transposase orfb
brucella- chr2_256	393	○	protein
brucella- chr2_257	369	○	transposase
brucella- chr2_47	909	○	is3 family transposase orfb
brucella- chr2_524	363	○	transposase orfa

Query= brucella-chr1\_239 # 247920 # 250151 # -1 #  
ID=1\_239;partial=00;start\_type=ATG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-  
10bp;gc\_cont=0.577  
(2232 letters)

		Score	E
		(bits)	Value
Sequences producing significant alignments:			
<del>gb</del>  CP006961.1		3157	0.0
> <del>gb</del>  CP006961.1			
Length = 2107842			
Score = 3157 bits (2209), Expect = 0.0			
Identities = 2232/2253 (99%), Gaps = 21/2253 (0%)			
Strand = Plus / Plus			
Query: 1	atgatgcgccaatatgagcttgtggagcgtgtgcagcgataacaagcctgatgtgaacgag 60		
Sbjct: 642046	atgatgcgccaatatgagcttgtggagcgtgtgcagcgataacaagcctgatgtgaacgag 642105		
Query: 61	gcgcttcttaacaaggcatatgtttatgccatgcagaaacacggcgagtc----- 109		
Sbjct: 642106	gcgcttcttaacaaggcatatgtttatgccatgcagaaacacggcgagtcagaagcgggct 642165		
Query: 110	-----cctatttctcccatccgctggaagtggcggctatttctcacagatatgcat 159		
Sbjct: 642166	tccggcgatccctatttctcccatccgctggaagtggcggctatttctcacagatatgcat 642225		
Query: 160	ttggacgaggcgacaatcgccatcgcgcttctgcacgacacgatcgaggataccacggcc 219		
Sbjct: 642226	ttggacgaggcgacaatcgccatcgcgcttctgcacgacacgatcgaggataccacggcc 642285		
Query: 220	acccggcaggaaaatcgaccagcttttcgggccggaaaatcggaagcttgatcgaggggctg 279		
Sbjct: 642286	acccggcaggaaaatcgaccagcttttcgggccggaaaatcggaagcttgatcgaggggctg 642345		
Query: 280	accaagctcaagaaactcgatctcgtttccaagaaggctgtccaggcggaaaacctgcgt 339		
Sbjct: 642346	accaagctcaagaaactcgatctcgtttccaagaaggctgtccaggcggaaaacctgcgt 642405		

The latter part of this record is omitted

Query= brucella-chr1\_239  
 (2232 letters)  
 Database: BSS2\_I0634.fa  
 1 sequences; 749 total letters

		Score	E
		(bits)	Value
Sequences producing significant alignments:			
BSS2_I0634		1461	0.0
>BSS2_I0634			
	Length = 749		
Score = 1461 bits (3781), Expect = 0.0			
Identities = 742/749 (99%), Positives = 742/749 (99%), Gaps = 7/749 (0%)			
Frame = +1			
Query: 1	MMRQYELVERVQRYKPDVNEALLNKAYVYAMQKHGS-----PYFSHPLEVAAILTDMH	159	
	MMRQYELVERVQRYKPDVNEALLNKAYVYAMQKHGS PYFSHPLEVAAILTDMH		
Sbjct: 1	MMRQYELVERVQRYKPDVNEALLNKAYVYAMQKHGSQKRASGDPYFSHPLEVAAILTDMH	60	
Query: 160	LDEATIAIALHDTIEDTTATRQEIDQLFGPEIGKLVEGLTKLKKLDLVSKKAVQAENLR	339	
	LDEATIAIALHDTIEDTTATRQEIDQLFGPEIGKLVEGLTKLKKLDLVSKKAVQAENLR		
Sbjct: 61	LDEATIAIALHDTIEDTTATRQEIDQLFGPEIGKLVEGLTKLKKLDLVSKKAVQAENLR	120	
Query: 340	KLLLAISEDVRVLLVKLADRLHNMRTLGVMCEDKRLRIAEETMDIYAPLAGRMGMQDMRE	519	
	KLLLAISEDVRVLLVKLADRLHNMRTLGVMCEDKRLRIAEETMDIYAPLAGRMGMQDMRE		
Sbjct: 121	KLLLAISEDVRVLLVKLADRLHNMRTLGVMCEDKRLRIAEETMDIYAPLAGRMGMQDMRE	180	
Query: 520	ELEELAFRYINPDRAWRAVTDRLAELLEKNRGLLQKIETDLSEIFEKNGIKASVKSQKKP	699	
	ELEELAFRYINPDRAWRAVTDRLAELLEKNRGLLQKIETDLSEIFEKNGIKASVKSQKKP		
Sbjct: 181	ELEELAFRYINPDRAWRAVTDRLAELLEKNRGLLQKIETDLSEIFEKNGIKASVKSQKKP	240	
Query: 700	WSVFRKMETKGLSFEQLSDIFGFRVMVDTVQDCYRALGLIHTTWSMVPGRFKDYISTPKQ	879	
	WSVFRKMETKGLSFEQLSDIFGFRVMVDTVQDCYRALGLIHTTWSMVPGRFKDYISTPKQ		
Sbjct: 241	WSVFRKMETKGLSFEQLSDIFGFRVMVDTVQDCYRALGLIHTTWSMVPGRFKDYISTPKQ	300	
Query: 880	NDYRSIHNTTIIGPSRQRIELQIRTREMDEIAEFGVAAHSIYKDRGSANNPHKISTETNAY	1059	
	NDYRSIHNTTIIGPSRQRIELQIRTREMDEIAEFGVAAHSIYKDRGSANNPHKISTETNAY		
Sbjct: 301	NDYRSIHNTTIIGPSRQRIELQIRTREMDEIAEFGVAAHSIYKDRGSANNPHKISTETNAY	360	
Query: 1060	AWLRQTIEQLSEGDNPPEEFLEHTKLELFQDQVFCFTPKGRILALPRGATPIDFAYAVHTD	1239	
	AWLRQTIEQLSEGDNPPEEFLEHTKLELFQDQVFCFTPKGRILALPRGATPIDFAYAVHTD		
Sbjct: 361	AWLRQTIEQLSEGDNPPEEFLEHTKLELFQDQVFCFTPKGRILALPRGATPIDFAYAVHTD	420	
Query: 1240	IGDSCVGAKVNGRIMPLMTELKNGDEVVDIIRSKAQVPPAAWESLVATGKARAAIRRATRS	1419	
	IGDSCVGAKVNGRIMPLMTELKNGDEVVDIIRSKAQVPPAAWESLVATGKARAAIRRATRS		
Sbjct: 421	IGDSCVGAKVNGRIMPLMTELKNGDEVVDIIRSKAQVPPAAWESLVATGKARAAIRRATRS	480	

The latter part of this record is omitted

Query= brucella-chr1\_1847 # 1965361 # 1966137 # -1 #  
 ID=1\_1847;partial=00;start\_type=ATG;rbs\_motif=GGAGG;rbs\_spacer=5-  
 10bp;gc\_cont=0.574  
 (777 letters)

	Score	E
	(bits)	Value
Sequences producing significant alignments:		
gb CP006961.1	1100	0.0
gb CP006962.1	31	1.0
>gb CP006961.1		
Length = 2107842		
Score = 1100 bits (769), Expect = 0.0		
Identities = 775/779 (99%), Gaps = 2/779 (0%)		
Strand = Plus / Plus		

The first part of this record is omitted

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Query: 481      atgcgcaagatcggttgatgaaaaacgctcgagattgccgatgcgcgtggcgcgggccgt 540
                |||
Sbjct: 1024952 atgcgcaagatcggttgatgaaaaacgctcgagattgccgatgcgcgtggcgcgggccgt 1025011

Query: 541      ttacggggcgcgacgcggaacctcgcgcggaatgcgctcgggccatatgccgggtgcg 600
                |||
Sbjct: 1025012 ttacggggcgcgacgcggaacctcgcgcggaatgcgctcgggccatatgccgggtgcg 1025071

Query: 601      cgcaatgttcctgttacaaccctttccgaaaacggtgaattgaaagacctcgaaagcctg 660
                |||
Sbjct: 1025072 cgcaatgttcctgttacaaccctttccgaaaacggtgaattgaaagacctcgaaagcctg 1025131

Query: 661      cgcaggatttttgacgaggcggtatcgacctgtcggggcccgtggtcaccagttgcggt 720
                |||
Sbjct: 1025132 cgcaggatttttgacgaggcggtatcgacctgtcggggcccgtggtcaccagttgcggt 1025191

Query: 721      ttcggtgttacgcgtgccgtgattacgctcgcgcttacctcg--ggggcaaaaggataa 777
                | |||
Sbjct: 1025192 ttcggtgttacgcgtgccgtgattacgctcgcgcttacctcgctggggcacaaggataa 1025250
  
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Query= brucella-chr1\_277 # 295318 # 296457 # -1 #  
ID=1\_277;partial=00;start\_type=ATG;rbs\_motif=None;rbs\_spacer=None;gc\_content=0.619  
(1140 letters)

Sequences producing significant alignments:	Score (bits)	E Value
gb CP006961.1	1625	0.0
gb CP006962.1	35	0.079

>gb|CP006961.1|  
Length = 2107842

Score = 1625 bits (1136), Expect = 0.0  
Identities = 1138/1140 (99%)  
Strand = Plus / Plus

The first part of this record is omitted

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Query: 781      ccttggcgcgccagcttgagaaaaccattgccatccttcgtgatcccgcgagcgccaaa 840
                |||
Sbjct: 596520   ccttggcgcgccagcttgagaaaaccattgccatccttcgtgatcccgcgagcgccaaa 596579

Query: 841      caggcgagggcgaaaagggtccgagcgccgaagatgtcgaagcggcttcacgctcagcgcc 900
                |||
Sbjct: 596580   caggcgagggcgaaaagggtccgagcgccgaagatgtcgaagcggcttcacgctcagcgcc 596639

Query: 901      agagatcggcgaggcgatggtggaaggcatggttcaacgcctcgatgaaacacttcgccag 960
                |||
Sbjct: 596640   agagatcggcgaggcgatggtggaaggcatggttcaacgcctcgatgaaacacttcgccag 596699

Query: 961      aatggcggggatatcgatggctggaagcggctgggccgctcttatatgatcctcaaccgc 1020
                |||
Sbjct: 596700   aatggcggggatatcgatggctggaagcggctgggccgctcttatatgatcctcaaccgc 596759

Query: 1021     cgcaacgatgcgcaggatgcgctggctcgcgccatgaaggctcttcagggtgaaaaccgg 1080
                |||
Sbjct: 596760   cgcaacgatgcgcaggatgcgctggctcgcgccatgaaggctcttcagggtgaaaaccgg 596819

Query: 1081     accgaacttcaaagcttcgccaccacacttggactggacgtggggactgcacaagaatga 1140
                |||
Sbjct: 596820   accgaacttcaaagcttcgccaccacacttggactggacgtggggactgcacaagaatga 596879

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Query= brucella-chr1\_995 # 1054415 # 1059196 # -1 #  
ID=1\_995;partial=00;start\_type=ATG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-  
10bp;gc\_cont=0.522  
(4782 letters)

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Sequences producing significant alignments:

Score      E
(bits) Value

gb|CP006961.1|      6823    0.0
gb|CP006962.1|      242    2e-63

>gb|CP006961.1|
    Length = 2107842

Score = 6823 bits (4776), Expect = 0.0
Identities = 4780/4782 (99%), Gaps = 2/4782 (0%)
Strand = Plus / Plus

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The first part of this record is omitted

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Query: 3001      aaagctgatcttcattgattttaacacgtcagtcgggggggggggggcttattggggcaggt 3060
                |||
Sbjct: 1938311 aaagctgatcttcattgattttaacacgtcagtc--gggggggggggcttattggggcaggt 1938368

Query: 3061      gatgtaacgctcggcagcggaacattgactgtcaatcaaggcttcgacagtattttttcc 3120
                |||
Sbjct: 1938369 gatgtaacgctcggcagcggaacattgactgtcaatcaaggcttcgacagtattttttcc 1938428

Query: 3121      ggcgtcatatctggagacggggggctgaacaaaagcggcgcggggcagttaactctttca 3180
                |||
Sbjct: 1938429 ggcgtcatatctggagacggggggctgaacaaaagcggcgcggggcagttaactctttca 1938488

Query: 3181      ggcgccaataacttatggcgcgccacgaccattgatggaggggtgctccttcaagggtgag 3240
                |||
Sbjct: 1938489 ggcgccaataacttatggcgcgccacgaccattgatggaggggtgctccttcaagggtgag 1938548

Query: 3241      agcggagctttcagcagtagttccgcctatcgaaccggcgcaagcggaaccgtggattta 3300
                |||
Sbjct: 1938549 agcggagctttcagcagtagttccgcctatcgaaccggcgcaagcggaaccgtggattta 1938608

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The latter part of this record is omitted