

Supplementary data S2. BLAST search of the *KU_R21_2271* gene (NCBI accession: JX522460) yielded no significant similarity for the alignment with the genome of *L. interrogans* serovar Pomona (taxid:44276). Blast search of the *KU_R21_2271* sequence similarities were 75.58% to 78.19% identity with 75 genes from other *L. interrogans* strains.

Your search is limited to records that include: Leptospira interrogans (taxid:173), Leptospira interrogans serovar Pomona (taxid:44276), Leptospira interrogans serovar Pomona str. UT364 (taxid:1049925), Leptospira interrogans serovar Pomona str. Kennewicki LC82-25 (taxid:1049924), Leptospira interrogans serovar Pomona str. CSL4002 (taxid:1240691), Leptospira interrogans serovar Pomona str. Pomona (taxid:1001587), Leptospira interrogans serovar Pomona str. Fox 32256 (taxid:1218574), Leptospira interrogans serovar Pomona str. CSL10083 (taxid:1240692), Leptospira kirschneri serovar Pomona (taxid:561005), Leptospira borgpetersenii serovar Pomona (taxid:1192865), Leptospira borgpetersenii serovar Pomona str. 200901868 (taxid:1192866)

RID: DRCNYJJB01R
 Job Title:JN627495:Leptospira borgpetersenii serovar...
 Program: BLASTN
 Query: Leptospira borgpetersenii serovar Sejroe leucine-rich repeat protein (LRR) gene, partial cds ID: JX522460.1(nucleic acid) Length: 612
 Database: nt Nucleotide collection (nt)

Sequences producing significant alignments:

					Scientific	Common	Max				
Total Query	E	Per.	Acc.		Name	Name	Taxid	Score			
Description	Score	cover	Value	Ident	Len	Accession					
Leptospira interrogans strain UI29382 chromosome 1, complete...	95%	7e-135	78.19	4311919		CP072853.1	Leptospira i...	NA	173	482	482
Leptospira interrogans serovar Canicola strain 611 chromosome ...	95%	3e-133	78.02	4255595		CP044513.1	Leptospira i...	NA	211880	478	478
Leptospira interrogans serovar Canicola strain LJ178 chromosom...	95%	3e-133	78.02	4259066		CP044509.1	Leptospira i...	NA	211880	478	478
Leptospira interrogans serovar Canicola strain 114 chromosome ...	95%	3e-133	78.02	4218946		CP022883.1	Leptospira i...	NA	211880	478	478
Leptospira interrogans strain FMAS_PN3 chromosome 1, complete...	95%	3e-133	78.02	4263490		CP092663.1	Leptospira i...	NA	173	478	478
Leptospira interrogans strain FMAS_AP1 chromosome 1, complete...	95%	3e-133	78.02	4281936		CP092681.1	Leptospira i...	NA	173	478	478
Leptospira interrogans strain FMAS_AP7 chromosome 1, complete...	95%	3e-133	78.02	4298104		CP092152.1	Leptospira i...	NA	173	478	478
Leptospira interrogans serovar Bataviae strain D64 chromosome ...	95%	3e-133	78.02	4355742		CP077942.1	Leptospira i...	NA	312175	478	478
Leptospira interrogans serovar Bataviae strain 1548 chromosome...	95%	3e-133	78.02	4354848		CP043880.1	Leptospira i...	NA	312175	478	478

Leptospira interrogans serovar Canicola strain RUFN chromosome I	Leptospira i...	NA	211880	474	474
95% 4e-132 78.02 4208129 CP022885.1					
Leptospira interrogans strain FMAS_KW2 chromosome I, complete...	Leptospira i...	NA	173	473	473
95% 4e-132 77.85 4293951 CP039256.1					
Leptospira interrogans serovar Manilae strain UP-MMC-NIID HP...	Leptospira i...	NA	214675	473	473
95% 4e-132 77.85 4238922 CP011934.1					
Leptospira interrogans serovar Manilae strain UP-MMC-NIID LP...	Leptospira i...	NA	214675	473	473
95% 4e-132 77.85 4238972 CP011931.1					
Leptospira interrogans strain FMAS_RT2 chromosome 1, complete...	Leptospira i...	NA	173	473	473
95% 4e-132 77.85 4342805 CP092166.1					
Leptospira interrogans strain FMAS_PN2 chromosome 1, complete...	Leptospira i...	NA	173	473	473
95% 4e-132 77.85 4302184 CP092151.1					
Leptospira interrogans serovar Canicola strain 782 chromosome ...	Leptospira i...	NA	211880	473	473
95% 4e-132 77.85 4556406 CP043884.1					
Leptospira interrogans serovar Copenhageni strain SK1 chromoso...	Leptospira i...	NA	44275	469	469
95% 2e-130 77.68 4279936 CP048830.1					
Leptospira interrogans strain R12 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4223477 CP047508.1					
Leptospira interrogans strain R19 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4213431 CP047514.1					
Leptospira interrogans strain R7 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4212939 CP047512.1					
Leptospira interrogans strain R11 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4214328 CP047510.1					
Leptospira interrogans strain R13-L chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4233607 CP047518.1					
Leptospira interrogans strain R17 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4213733 CP047500.1					
Leptospira interrogans strain R13 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4214175 CP047506.1					
Leptospira interrogans strain R22 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4206042 CP047496.1					
Leptospira interrogans strain R21 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4214555 CP047498.1					
Leptospira interrogans strain R16 chromosome 1	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4213648 CP047502.1					
Leptospira interrogans serovar Hardjo strain L53 chromosome 1,...	Leptospira i...	NA	176	469	469
95% 2e-130 77.68 4355568 CP043041.1					
Leptospira interrogans strain FMAS_KW1 chromosome I, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4306144 CP039258.1					
Leptospira interrogans strain FMAS_AW1 chromosome I, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4497709 CP039283.1					
Leptospira interrogans serovar Copenhageni strain FDAARGOS_203...	Leptospira i...	NA	44275	469	469
95% 2e-130 77.68 4280582 CP020414.2					
Leptospira interrogans strain RCA chromosome I	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4241665 CP022538.1					

Leptospira interrogans serovar Hardjo-prajitno strain...	Leptospira i...	NA	38347	469	469
95% 2e-130 77.68 4339653 CP013147.1					
Leptospira interrogans serovar Hardjo str. Norma chromosome I,...	Leptospira i...	NA	1279460	469	469
95% 2e-130 77.68 4406718 CP012603.1					
Leptospira interrogans serovar Bratislava strain PigK151...	Leptospira i...	NA	338215	469	469
95% 2e-130 77.68 4370471 CP011410.1					
Leptospira interrogans serovar Linhai str. 56609 chromosome 1,...	Leptospira i...	NA	1395589	469	469
95% 2e-130 77.68 4331770 CP006723.1					
Leptospira interrogans strain KR40 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4315670 CP096129.2					
Leptospira interrogans strain N 116 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4312952 CP097315.1					
Leptospira interrogans strain NEG7 chromosome I	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4297584 CP093938.1					
Leptospira interrogans strain FMAS_KG2 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4721761 CP092985.1					
Leptospira interrogans strain FMAS_PD1 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4503505 CP092743.1					
Leptospira interrogans strain FMAS_AW2 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4634565 CP092739.1					
Leptospira interrogans strain FMAS_AW3 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4526110 CP092676.1					
Leptospira interrogans strain FMAS_KG1 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4458643 CP092672.1					
Leptospira interrogans strain FMAS_AP6 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4525852 CP092156.1					
Leptospira interrogans strain FMAS_AP5 chromosome 1, complete...	Leptospira i...	NA	173	469	469
95% 2e-130 77.68 4478874 CP092161.1					
Leptospira interrogans serovar Bataviae strain 1489 chromosome...	Leptospira i...	NA	312175	469	469
95% 2e-130 77.68 4431091 CP043893.1					
Leptospira interrogans serovar Icterohaemorrhagiae strain 898...	Leptospira i...	NA	90062	469	469
95% 2e-130 77.68 4280412 CP043891.1					
Leptospira interrogans serovar Icterohaemorrhagiae strain...	Leptospira i...	NA	90062	469	469
95% 2e-130 77.68 4367462 CP043876.1					
Leptospira interrogans serovar Lai str. IPAV chromosome 1,...	Leptospira i...	NA	573825	469	469
95% 2e-130 77.68 4349158 CP001221.1					
Leptospira interrogans serovar Lai str. 56601 chromosome I,...	Leptospira i...	NA	189518	469	469
95% 2e-130 77.68 4338762 AE010300.2					
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130...	Leptospira i...	NA	267671	469	469
95% 2e-130 77.68 4277185 AE016823.1					
Leptospira interrogans serovar Copenhageni/Icterohaemorrhagiae...	Leptospira i...	NA	766041	465	465
95% 2e-129 77.68 4221879 CP018146.1					
Leptospira interrogans serovar Canicola leucine-rich repeat...	Leptospira i...	NA	211880	325	325
66% 1e-87 77.78 410 JX426070.1					
Leptospira interrogans serovar Autumnalis leucine-rich repeat...	Leptospira i...	NA	174157	321	321
66% 5e-86 77.53 411 JX426069.1					

Leptospira interrogans serovar Hebdomadis leucine-rich repeat...	Leptospira i... NA	211881	259	259
47% 1e-67 79.86 303 JX426072.1				
Leptospira interrogans serovar Pyrogenes leucine-rich repeat...	Leptospira i... NA	280500	214	214
49% 5e-54 75.58 312 JX426071.1				

Alignments:

>Leptospira interrogans strain UI29382 chromosome 1, complete sequence
Sequence ID: CP072853.1 Length: 4311919
Range 1: 1377193 to 1377779

Score:482 bits(534), Expect:7e-135,
Identities:459/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	1377193	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAGAGAAAATCGGAATCGA	1377252
Query	86	TTCAAACCTTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	1377253	TTCAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1377312
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1377313	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1377372
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1377373	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	1377432
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1377433	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1377492
Query	326	CGATTCTACCCTCCGAACCTTTTGTTCCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1377493	CTTTTCTACCTTCGGAACCTTTTGTTCCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	1377552
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1377553	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1377612
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1377613	AATTGGATCTTAATTTGAACCTCTGGAATTAAGTGCTTCCTTCTAACTATAATAAATTGA	1377672
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1377673	AAAATCTGACTCATTTAAAAAGATTGAATATTA AAAAATTCATTAAAGGGGAAGATG	1377732
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	1377733	CTGATAAATTACAAGCAGTTCTCCCAAATACAAAATAGACTATTGA	1377779

>Leptospira interrogans serovar Canicola strain 611 chromosome 1, complete sequence
Sequence ID: CP044513.1 Length: 4255595
Range 1: 1351973 to 1352559

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	1351973	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1352032

Query	26	TCGACTGTAAAAAAGAAATGCGGAAGAGATTTTGGGAGAGGCCAAAAGGCCAAAACCGGAATTGG	85
Sbjct	1357390	TCGATTGTAAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1357449
Query	86	TTCAAACCTTTGGATTTTGGAAATGCAGAAGTTGTCCACGGTTCGGAAGAAGTTTGC GGTT	145
Sbjct	1357450	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCCTCTT	1357509
Query	146	TTCCGAATTTAAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1357510	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTCGGTTGGA	1357569
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1357570	TTGGAGCTTGTAAAAATCTGGAACAAATTAACCTTTTCGGAATGATCTAAATACGGTTTC	1357629
Query	266	CGTCTACGTTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325

Sbjct	1357630	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1357689
Query	326	CGATTCTACCCCTCCGAACTTTGTTCCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1357690	CTTTTCTACCTTCGGAACTTTGTTCCTGCCTTTGATTAAAACCTGTACTTGGATCAAA	1357749
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCCTTGGAGG	445
Sbjct	1357750	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	1357809
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	1357810	AATTGGATCTTAATTTGAACTCTGGAATTAAAGTGCTTCTTCTAACTATAATAAATTGA	1357869
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1357870	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGAGAAGATG	1357929
Query	566	CAGATAAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	1357930	CTGATAAAATTACAAGCAGTTCTCCCAAAATACAAGAATAGACTATTGA	1357976

[illegible]

Sbjct	3467444	AATTGGATCTTAATTTGAACTCTGGAATTAAGTGCTTCCTTCTAACTATAATAAATTGA	3467503
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	3467504	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAAACTTCATTAAAGGGAGAAGATG	3467563
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	3467564	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	3467610

>Leptospira interrogans strain FMAS_PN3 chromosome 1, complete sequence
Sequence ID: CP092663.1 Length: 4263490
Range 1: 2862050 to 2862636

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCCAAACCGGAATTGG	85
Sbjct	2862636	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2862577
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2862576	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2862517
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2862516	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2862457
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2862456	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTTC	2862397
Query	266	CGTCTACGTTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2862396	CATCTTCTTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2862337
Query	326	CGATTCTACCCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2862336	CTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	2862277
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2862276	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	2862217
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2862216	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAATTATAATAAATTGA	2862157
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2862156	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAAACTTCATTAAAGGGGAGGATG	2862097
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2862096	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2862050

>Leptospira interrogans strain FMAS_AP1 chromosome 1, complete sequence

Sequence ID: CP092681.1 Length: 4281936

Range 1: 2877199 to 2877785

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	2877785	TCGATTGTAAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2877726
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	2877725	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2877666
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2877665	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTCGTTTGA	2877606
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2877605	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2877546
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2877545	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2877486
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2877485	CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	2877426
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGGAGG	445
Sbjct	2877425	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCAGTTTGAAG	2877366
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2877365	AATTGGATCTTAATTTGAACCTCTGGAATCAAGTGCTTCCTTCTAATTATAATAAATTGA	2877306
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2877305	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2877246
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2877245	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2877199

>Leptospira interrogans strain FMAS_AP7 chromosome 1, complete sequence

Sequence ID: CP092152.1 Length: 4298104

Range 1: 4193201 to 4193787

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	4193787	TCGATTGTAAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	4193728
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145

Sbjct	4193727	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	4193668
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGAATTTA	205
Sbjct	4193667	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	4193608
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	4193607	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	4193548
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	4193547	CATCTTCTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	4193488
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	4193487	CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	4193428
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTCTCCTTGGAGG	445
Sbjct	4193427	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTCCAGTTTGGAAG	4193368
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	4193367	AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCTCTTAATTATAATAAATTGA	4193308
Query	506	TAAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	4193307	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	4193248
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	4193247	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	4193201

>Leptospira interrogans serovar Bataviae strain D64 chromosome I, complete sequence
Sequence ID: CP077942.1 Length: 4355742
Range 1: 1430617 to 1431203

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	1430617	TCGATTGTAAAAAAACGCGGTAGAGATTTAGAGAAGCAAAAAGAAAATCGGAATCGA	1430676
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	1430677	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1430736
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGAATTTA	205
Sbjct	1430737	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1430796
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	1430797	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	1430856
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1430857	CATCTTCTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1430916

Query	326	CGATTCTACCCTCCGAAC TTTTGT TTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1430917	CTTTTCTACCCTCGGAAC TTTTGT TTTCTGCCTTTGATTA AAACCTGTACTTGGATCAAA	1430976
Query	386	ATAAATTAAC TCTAACGGAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1430977	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	1431036
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1431037	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1431096
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1431097	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1431156
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	1431157	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1431203

>Leptospira interrogans serovar Bataviae strain 1548 chromosome, complete genome
Sequence ID: CP043880.1 Length: 4354848
Range 1: 1430028 to 1430614

Score:478 bits(529), Expect:3e-133,
Identities:458/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAG AATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAACCGGAATTGG	85
Sbjct	1430028	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1430087
Query	86	TTCAAAC TTTGGATTTTGG AATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	1430088	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1430147
Query	146	TTCCGAATTTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1430148	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1430207
Query	206	TCGGAGAATGTAAACGCCTTGAACAAC TTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1430208	TTGGAGCTTGTA AAAATCTGGAACAAATTAAC TTTTCGGAAATGATCTAAATACGGTTC	1430267
Query	266	CGTCTACGTTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1430268	CATCTTCTTTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1430327
Query	326	CGATTCTACCCTCCGAAC TTTTGT TTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1430328	CTTTTCTACCCTCGGAAC TTTTGT TTTCTGCCTTTGATTA AAACCTGTACTTGGATCAAA	1430387
Query	386	ATAAATTAAC TCTAACGGAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1430388	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	1430447
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1430448	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1430507

Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGGAGAGGATG	565
Sbjct	1430508	AAAATCTGACTCATTATAAAAAAGATTGAATATTAAAAAAAACTTCATTAAAGGGGGAGGATG	1430567
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	1430568	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1430614

Score:474 bits(525), Expect:4e-132,
Identities:458/587(78%), Gaps:1/587(0%), Strand: Plus/Plus

>Leptospira interrogans strain FMAS_KW2 chromosome I, complete sequence
Sequence ID: CP039256.1 Length: 4293951

Query	146	TTCCGAATTTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2850819	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCCTGGTTGGA	2850760
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2850759	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACTGTTC	2850700
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2850699	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2850640
Query	326	CGATTCTACCCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2850639	CTTTTCTACCCTCGGAACCTTTTGTTTCTGCCTTTGCTTAAACCCTGTACTTGGATCAAA	2850580
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2850579	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTTCAGTTTGGAAG	2850520
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2850519	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2850460
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2850459	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2850400
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2850399	CTGATAAATTACAAGCAGTTCTCCCAAATACAAAATAGACTATTGA	2850353

>Leptospira interrogans serovar Manilae strain UP-MMC-NIID LP chromosome 1, complete sequence

Sequence ID: CP011931.1 Length: 4238972

Range 1: 2850352 to 2850938

Score:473 bits(524), Expect:4e-132,
Identities:457/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	2850938	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2850879
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2850878	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2850819
Query	146	TTCCGAATTTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2850818	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCCTGGTTGGA	2850759
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2850758	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACTGTTC	2850699
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2850698	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2850639

Query	326	CGATTCTACCCTCCGAAC TTTTGTTCCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2850638	CTTTTCTACCCTCGGAAC TTTTGTTCCTGCCTTTGCTTAAACCCCTGTACTTGGATCAAA	2850579
Query	386	ATAAATTAAC TCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2850578	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTTCAGTTTGAAG	2850519
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2850518	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2850459
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2850458	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2850399
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2850398	CTGATAAATTACAAGCAGTTCTCCCAAATACAAAATAGACTATTGA	2850352

>Leptospira interrogans strain FMAS_RT2 chromosome 1, complete sequence
Sequence ID: CP092166.1 Length: 4342805
Range 1: 2179558 to 2180144

Score:473 bits(524), Expect:4e-132,
Identities:457/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAACCGGAATTGG	85
Sbjct	2180144	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2180085
Query	86	TTCAAAC TTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	2180084	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2180025
Query	146	TTCCGAATTTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2180024	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2179965
Query	206	TCGGAGAATGTAAACGCCTTGAACAAC TTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2179964	TTGGAGCTTGTA AAAATCTGGAACAAATTAAC TTTTCGGAAATGATCTAAATACGGTTC	2179905
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2179904	CATCTTCTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2179845
Query	326	CGATTCTACCCTCCGAAC TTTTGTTCCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2179844	CTTTTCTACCTTCGGAAC TTTTGTTCCTGCCTTTGATTA AAACCCCTGTACTTGGATCAAA	2179785
Query	386	ATAAATTAAC TCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2179784	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	2179725
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2179724	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAATTATAATAAATTGA	2179665

Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGGAGAGGATG	565
Sbjct	2179664	AAAATCTGACTCATT'TAAAAAGATTGAATATTAAAAAAAACTTCATTAAAGGGGGAGGACG	2179605
Query	566	CAGATAAATTGCAGGCCGATTCTTCCAAATACC AAAATCGACTACTGA	612
Sbjct	2179604	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2179558

Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2909862	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCCTGTTTGA	2909803
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2909802	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2909743
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2909742	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2909683
Query	326	CGATTCTACCCTCCGAAC TTTTGTTTCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2909682	CTTTTCTACCTTCGGAAC TTTTGTTTCTGCCTTTGCTTAAACCTGTATTTGGATCAAA	2909623
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2909622	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	2909563
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2909562	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2909503
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2909502	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2909443
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2909442	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2909396

>Leptospira interrogans strain R12 chromosome 1
Sequence ID: CP047508.1 Length: 4223477
Range 1: 2872427 to 2873013

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAAACCGGAATTGG	85
Sbjct	2873013	TCGATTGTAAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2872954
Query	86	TTCAAAC TTTGGATTTTGGAAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2872953	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2872894
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2872893	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCCTGTTTGA	2872834
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2872833	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2872774
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2872773	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2872714
Query	326	CGATTCTACCCTCCGAAC TTTTGTTTCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385

Sbjct	2872713	CTTTTCTACCTTCGGAACCTTTTGTCTGCCTTTGCTTAAACCCCTGTATTTGGATCAAA	2872654
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2872653	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	2872594
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2872593	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2872534
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2872533	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2872474
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2872473	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2872427

>Leptospira interrogans strain R19 chromosome 1
Sequence ID: CP047514.1 Length: 4213431
Range 1: 2873903 to 2874489

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAACCGGAATTGG	85
Sbjct	2874489	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2874430
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2874429	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2874370
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2874369	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2874310
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2874309	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2874250
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2874249	CATCTTCTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2874190
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2874189	CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCCCTGTATTTGGATCAAA	2874130
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2874129	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	2874070
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2874069	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2874010
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565

Sbjct	2874009	AAAAATCTGACTCATTTTAAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2873950
Query	566	CAGATAAAATTGCAGGCGATTCTTCCAAAATACCAAAATCGACTACTGA	612
Sbjct	2873949	CTGATAAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2873903

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

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>Leptospira interrogans strain R11 chromosome 1
Sequence ID: CP047510.1 Length: 4214328
Range 1: 2865468 to 2866054
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Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCCAAAACCGGAATTGG 	85
Sbjct	2866054	TCGATTGTAAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2865995
Query	86	TTCAAACTTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT 	145
Sbjct	2865994	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2865935
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA 	205
Sbjct	2865934	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCCTGGTTGGA	2865875
Query	206	TCGGAGAATGTAAACGCCTTGAACAACTTAATCTTTTCGGGAACGACCTTACAACATTTTC 	265
Sbjct	2865874	TTGGAGCTTGTAAAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2865815
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA 	325
Sbjct	2865814	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2865755
Query	326	CGATTCTACCCTCCGAACTTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA 	385
Sbjct	2865754	CTTTTCTACCTTCGGAACTTTTGTTTCTGCCTTTGCTTAAAACCCTGTATTTGGATCAAA	2865695
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCCTCGCTTCTCTTTCCTCCTTGGAGG 	445
Sbjct	2865694	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCCTAGCTTCTCTTTCAGTTTGAAG	2865635
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAAGGCGCTCCCTTTTAATTACGAAAAACTTG 	505
Sbjct	2865634	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGC'TTCC'TTCTAACTATAATAAATTGA	2865575
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG 	565
Sbjct	2865574	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2865515
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA 612 	
Sbjct	2865514	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA 2865468	

>Leptospira interrogans strain R13-L chromosome 1
Sequence ID: CP047518.1 Length: 4233607
Range 1: 2882682 to 2883268

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCCAAAACCGGAATTGG	85
Sbjct	2883268	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2883209
Query	86	TTCAAACCTTTGGATTTTGGAAATGCAGAAGTTGTCCACGGTTCGGAAGAAGTTTGC GGTT	145
Sbjct	2883208	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2883149
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTCCGGAATTTA	205

Query	386	ATAAAATAACTCTAACGGAAACGGATGTGGAAATTCTCGTTCTCTTTCTCCTTGGAGG	445
Sbjct	2875060	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	2875001
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	2875000	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTTCTAACTATAATAAATTGA	2874941
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2874940	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2874881
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2874880	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2874834

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

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Query   566      CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA   612
          ||||| ||| || ||| ||||| ||| ||| ||||| |||
Sbjct   2865339  CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA   2865293

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>Leptospira interrogans strain R22 chromosome 1
Sequence ID: CP047496.1 Length: 4206042
Range 1: 2873918 to 2874504

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

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Query   26      TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAACCGGAATTGG   85
          |||| | ||||| || |||| | ||||| ||| ||| ||||| |||
Sbjct   2874504  TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA   2874445

Query   86      TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT   145
          ||||| || ||||| ||||| ||||| ||| ||| ||||| ||||| |||
Sbjct   2874444  TTCAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT   2874385

Query   146     TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA   205
          ||||| ||| || ||||| || ||||| ||||| ||| ||||| |||
Sbjct   2874384  TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA   2874325

Query   206     TCGGAGAATGTAAACGCCTTGAACAACCTAATCTTTTCGGGAACGACCTTACAACATTTT   265
          || |||| | ||||| || ||||| ||| ||||| ||| ||| |||
Sbjct   2874324  TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC   2874265

Query   266     CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA   325
          || ||| | ||||| ||||| ||| ||||| ||||| ||| ||||| |||||
Sbjct   2874264  CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA   2874205

Query   326     CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA   385
          | ||||| || ||||| ||||| || ||| ||||| ||| ||| |||||
Sbjct   2874204  CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCCTGTATTTGGATCAAA   2874145

Query   386     ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG   445
          || | || | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   2874144  ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG   2874085

Query   446     AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG   505
          ||||| ||||| || |||| | ||| ||| ||| ||||| ||| ||| |||
Sbjct   2874084  AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCTTCTAACTATAATAAATTGA   2874025

Query   506     TAAATCTCATTAACTCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGGAGGATG   565
          ||||| || | || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   2874024  AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG   2873965

Query   566      CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA   612
          ||||| ||| || ||| ||||| ||| ||| ||||| |||
Sbjct   2873964  CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA   2873918

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>Leptospira interrogans strain R21 chromosome 1
Sequence ID: CP047498.1 Length: 4214555
Range 1: 2874543 to 2875129

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	2875129	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2875070
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2875069	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2875010
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2875009	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTTGA	2874950
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGAACGACCTTACAACATTTTC	265
Sbjct	2874949	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAATGATCTAAATACGGTTC	2874890
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2874889	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2874830
Query	326	CGATTCTACCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2874829	CTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGCTTAAACCTGTATTTGGATCAAA	2874770
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2874769	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	2874710
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2874709	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2874650
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2874649	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2874590
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2874589	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2874543

>Leptospira interrogans strain R16 chromosome 1
Sequence ID: CP047502.1 Length: 4213648
Range 1: 2865029 to 2865615

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	2865615	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2865556
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2865555	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2865496
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2865495	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTTGA	2865436

Query	206	TCGAGAGATGTAAACGCCTTGAACAACTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2865435	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAATGATCTAAATACGGTTC	2865376
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2865375	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAAGTATTACTCTTGGGTAATAACGATTTTA	2865316
Query	326	CGATTCTACCCTCCGAAC TTTGTTTCTTCCGTTGATCAAAAT TCTATACGTAGATCGGA	385
Sbjct	2865315	CTTTTCTACCTTCGGAAC TTTGTTTCTGCCTTTGCTTAA AACCTGTATTTGGATCAAA	2865256
Query	386	ATAAATTAAC TCTAACGGAACGGATGTGGAAAT TCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2865255	ACAAGCTTACGTTGACTGAAACGGATGTGAAAT TCTAGCTTCTCTTTCCAGTTTGAAG	2865196
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	2865195	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTTCTAACTATAATAAATTGA	2865136
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2865135	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2865076
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2865075	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2865029

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Sbjct	1437769	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1437828
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1437829	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1437888
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1437889	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1437948
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	1437949	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1437995

>Leptospira interrogans strain FMAS_KW1 chromosome I, complete sequence
Sequence ID: CP039258.1 Length: 4306144
Range 1: 1377410 to 1377996

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAAACCGGAATTGG	85
Sbjct	1377410	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1377469
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	1377470	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1377529
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1377530	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1377589
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1377590	TTGGGGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	1377649
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1377650	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1377709
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1377710	CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	1377769
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGGAGG	445
Sbjct	1377770	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1377829
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1377830	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAATTATAATAAATTGA	1377889
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1377890	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGACG	1377949
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612

Sbjct 1377950 CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA 1377996

>Leptospira interrogans strain FMAS_AW1 chromosome I, complete sequence
Sequence ID: CP039283.1 Length: 4497709
Range 1: 2831793 to 2832379

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCCAAACCGGAATTGG	85
Sbjct	2832379	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2832320
Query	86	TTCAAACCTTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	2832319	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2832260
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2832259	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTG GTTGA	2832200
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2832199	TTGGAGCTTGTAAAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2832140
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2832139	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2832080
Query	326	CGATTCTACCCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2832079	CTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGCTTAAACCCTGTATTTGGATCAAA	2832020
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGGAGG	445
Sbjct	2832019	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCAGTTTGAAG	2831960
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2831959	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTTCTTAATAATAAATTGA	2831900
Query	506	TAAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGGAGAGGATG	565
Sbjct	2831899	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2831840
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2831839	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2831793

>Leptospira interrogans serovar Copenhageni strain FDAARGOS_203 chromosome, complete genome
Sequence ID: CP020414.2 Length: 4280582
Range 1: 918642 to 919228

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	919228	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	919169
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	919168	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	919109
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	919108	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	919049
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	919048	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	918989
Query	266	CGTCTACGTTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	918988	CATCTTCTTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	918929
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	918928	CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCTGTATTTGGATCAAA	918869
Query	386	ATAAATTAACCTCTAACGGAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGAGG	445
Sbjct	918868	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCAGTTTGGAAG	918809
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	918808	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	918749
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	918748	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	918689
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	918688	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	918642

>Leptospira interrogans strain RCA chromosome I

Sequence ID: CP022538.1 Length: 4241665

Range 1: 3328085 to 3328671

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	3328671	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	3328612
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	3328611	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	3328552
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	3328551	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	3328492
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265

Sbjct	3328491	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAATGATCTAAATACGGTTC	3328432
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	3328431	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	3328372
Query	326	CGATTCTACCCTCCGAAC TTTTGTTCCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	3328371	CTTTTCTACCTTCGGAAC TTTTGTTCCTGCCTTTGCTTAAACCTGTATTTGGATCAAA	3328312
Query	386	ATAAATTAAC TCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	3328311	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	3328252
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	3328251	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	3328192
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	3328191	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	3328132
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	3328131	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	3328085

>Leptospira interrogans serovar Hardjo-prajitno strain Hardjoprajitno chromosome 1 sequence

Sequence ID: CP013147.1 Length: 4339653

Range 1: 1431712 to 1432298

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAAACCGGAATTGG	85
Sbjct	1431712	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1431771
Query	86	TTCAAAC TTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	1431772	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1431831
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1431832	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTCCTGGTTGGA	1431891
Query	206	TCGGAGAATGTAAACGCCTTGAACAAC TTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1431892	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAATGATCTAAATATGGTTC	1431951
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1431952	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	1432011
Query	326	CGATTCTACCCTCCGAAC TTTTGTTCCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1432012	CTTTTCTACCTTCGGAAC TTTTGTTCCTGCCTTTGATTAAACCTGTACTTGGATCAAA	1432071
Query	386	ATAAATTAAC TCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445

Sbjct	1432072	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1432131
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1432132	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1432191
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1432192	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1432251
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	1432252	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1432298

>Leptospira interrogans serovar Hardjo str. Norma chromosome I, complete sequence
Sequence ID: CP012603.1 Length: 4406718
Range 1: 1409557 to 1410143

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAAACCGGAATTGG	85
Sbjct	1409557	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	1409616
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	1409617	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1409676
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1409677	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1409736
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	1409737	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATATGGTTC	1409796
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1409797	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGCGTAATAACGATTTTA	1409856
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1409857	CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGATTAAACCCTGTACTTGGATCAAA	1409916
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGGAGG	445
Sbjct	1409917	ACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1409976
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1409977	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1410036
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1410037	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1410096
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612

[illegible]

>Leptospira interrogans strain FMAS_KG2 chromosome 1, complete sequence
Sequence ID: CP092985.1 Length: 4721761
Range 1: 3364108 to 3364694

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	3364694	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	3364635
Query	86	TTCAAACCTTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	3364634	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	3364575
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	3364574	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	3364515
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	3364514	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	3364455
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	3364454	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	3364395
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	3364394	CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGCTTAAACCCTGTACTTGGATCAAA	3364335
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	3364334	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	3364275
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	3364274	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTTCTAATAATAAATTGA	3364215
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	3364214	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	3364155
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	3364154	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	3364108

>Leptospira interrogans strain FMAS_PD1 chromosome 1, complete sequence
Sequence ID: CP092743.1 Length: 4503505
Range 1: 2921059 to 2921645

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	2921645	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2921586

Query	86	TTCAAACCTTTGGATTTTGGGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC	145
Sbjct	2921585	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2921526
Query	146	TTCCGAATTTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGAATTTA	205
Sbjct	2921525	TTCCGAATTTGACTCAGCTGGATTACGTTTGAACAGTTTGAATTCTCTTCTGGTTGGA	2921466
Query	206	TCGGAGAATGTAAACGCCTTGAACAACTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2921465	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2921406
Query	266	CGTCTACGTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2921405	CATCTTCTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGGTAATAACGATTTTA	2921346
Query	326	CGATTCTACCCCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAAATCTATACGTAGATCGGA	385
Sbjct	2921345	CTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGCTTAAACCCTGTACTTGGAATCAA	2921286
Query	386	ATAAATTAACCTCTAACGGAACGGATGTGGAAATTCCTCGCTTCTCTTTCCTCCTTGAGG	445
Sbjct	2921285	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCAGCTTCTCTTTCAGTTTGAAG	2921226
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	2921225	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2921166
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2921165	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2921106
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2921105	CTGATAAATTACAAGCAGTTCTCCCAAAATACAAGAATAGACTATTGA	2921059

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	266	CGTCTACGTTTTCTAAATTAATAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1387840	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	1387899
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1387900	CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCCTGTATTTGGATCAAA	1387959
Query	386	ATAAATTAACCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1387960	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	1388019
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1388020	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1388079
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1388080	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1388139
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	1388140	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1388186

>Leptospira interrogans strain FMAS_AW3 chromosome 1, complete sequence
Sequence ID: CP092676.1 Length: 4526110
Range 1: 1241524 to 1242110

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAACCGGAATTGG	85
Sbjct	1241524	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAGAAAATCGGAATCGA	1241583
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGC GGTT	145
Sbjct	1241584	TTCAAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	1241643
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1241644	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1241703
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	1241704	TTGGAGCTTGTAATAATCTGGAACAAATTAACCTTTTTCGGAAATGATCTAAATACGGTTC	1241763
Query	266	CGTCTACGTTTTCTAAATTAATAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1241764	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	1241823
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1241824	CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCCTGTATTTGGATCAAA	1241883
Query	386	ATAAATTAACCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1241884	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGAAG	1241943
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505

Sbjct	1241944	 AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	1242003
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1242004	 AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAAACTTCATTAAAGGGGGAGGATG	1242063
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	1242064	 CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1242110

>Leptospira interrogans strain FMAS_KG1 chromosome 1, complete sequence
Sequence ID: CP092672.1 Length: 4458643
Range 1: 3022201 to 3022787

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCCAAACCGGAATTGG	85
Sbjct	3022787	 TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	3022728
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	3022727	 TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	3022668
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGAATTTA	205
Sbjct	3022667	 TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	3022608
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	3022607	 TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	3022548
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	3022547	 CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	3022488
Query	326	CGATTCTACCCTCCGAACCTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	3022487	 CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGCTTAAACCCTGTATTTGGATCAAA	3022428
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTTGAGG	445
Sbjct	3022427	 ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTCCAGTTTGGAAG	3022368
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	3022367	 AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	3022308
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	3022307	 AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAAACTTCATTAAAGGGGGAGGATG	3022248
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	3022247	 CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	3022201

>Leptospira interrogans strain FMAS_AP6 chromosome 1, complete sequence
Sequence ID: CP092156.1 Length: 4525852
Range 1: 2149342 to 2149928

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	2149928	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2149869
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2149868	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2149809
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2149808	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2149749
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2149748	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2149689
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2149688	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2149629
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2149628	CTTTTCTACCTTCGGAACCTTTTGTCTTGCCTTTGCTTAAACCCTGTATTTGGATCAAA	2149569
Query	386	ATAAATTAACCTTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	2149568	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	2149509
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2149508	AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2149449
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2149448	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2149389
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2149388	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2149342

>Leptospira interrogans strain FMAS_AP5 chromosome 1, complete sequence
Sequence ID: CP092161.1 Length: 4478874
Range 1: 2832820 to 2833406

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG	85
Sbjct	2832820	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2832879
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145

Sbjct	2832880		2832939
		TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2832940	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2832999
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2833000	TTGGAGCTTGTAAAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2833059
Query	266	CGTCTACGTTTTCTAAATTAATAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2833060	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	2833119
Query	326	CGATTCTACCCTCCGAACCTTTTGTCTTCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2833120	CTTTTCTACCTTCGGAACCTTTTGTCTTCTGCCTTTGCTTAAACCTGTATTTGGATCAAA	2833179
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTCTCCTTGGAGG	445
Sbjct	2833180	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTCCAGTTTGGAAG	2833239
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	2833240	AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCTTCTAACTATAATAAATTGA	2833299
Query	506	TAAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2833300	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2833359
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	2833360	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2833406

>Leptospira interrogans serovar Bataviae strain 1489 chromosome 1, complete sequence
Sequence ID: CP043893.1 Length: 4431091
Range 1: 3000720 to 3001306

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTGGGAGAGGCCAAAGGCAAAACCGGAATTGG	85
Sbjct	3001306	TCGATTGTAAAAAAACGCGGTAGAGATTTAGAGAAGCAAAGAGAAAATCGGAATCGA	3001247
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	3001246	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	3001187
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	3001186	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	3001127
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	3001126	TTGGAGCTTGTAAAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	3001067
Query	266	CGTCTACGTTTTCTAAATTAATAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325

Sbjct	3001066	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAAGTATTACTCTTGGGTAATAACGATTTTA	3001007
Query	326	CGATTCTACCCCTCCGAACTTTGTTCCTTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	3001006	CTTTTCTACCTTCGGAACTTTGTTCCTGCCTTTGCTTAAACCCCTGTATTTGGATCAAA	3000947
Query	386	ATAAATTAACCTCTAACCGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCCTCCTTGGAGG	445
Sbjct	3000946	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTTTAGCTTCTCTTTCCAGTTTGGAAG	3000887
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	3000886	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTCTTAATAATAAATTGA	3000827
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	3000826	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	3000767
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	3000766	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	3000720

[illegible]

[illegible]

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

>Leptospira interrogans serovar Lai str. IPAV chromosome 1, complete sequence
Sequence ID: CP001221.1 Length: 4349158
Range 1: 1315702 to 1316288

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

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Query 26      TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG 85
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1315702 TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA 1315761

Query 86      TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT 145
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1315762 TTCAATCTTAGATTTAGGAATGCAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT 1315821

Query 146     TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA 205
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1315822 TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA 1315881

Query 206     TCGGAGAATGTAAACGCCTTGAACAACCTTAATCTTTTCGGGAACGACCTTACAACATTTT 265
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1315882 TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC 1315941

Query 266     CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA 325
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1315942 CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA 1316001

Query 326     CGATTCTACCCTCCGAACCTTTGTTTCTTCCGTTGATCAAAATTCTATACGTAGATCGGA 385
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316002 CTTTTCTACCTTCGGAACCTTTGTTTCTGCCTTTGCTTAAACCCTGTATTTGGATCAAA 1316061

Query 386     ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCTCCTGGAGG 445
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316062 ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCAGTTTGGAAG 1316121

Query 446     AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG 505
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316122 AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA 1316181

Query 506     TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG 565
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316182 AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG 1316241

Query 566     CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA 612
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316242 CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA 1316288
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>Leptospira interrogans serovar Lai str. 56601 chromosome I, complete sequence
Sequence ID: AE010300.2 Length: 4338762
Range 1: 1316631 to 1317217

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Plus

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Query 26      TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAGGCAAAACCGGAATTGG 85
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1316631 TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA 1316690

Query 86      TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT 145
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Sbjct	1316691		1316750
		TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	1316751	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	1316810
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	1316811	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	1316870
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	1316871	CATCTTCTTTTTCTAAATTAAGAATTTGAAAGTATTACTCTTGGGTAATAACGATTTTA	1316930
Query	326	CGATTCTACCCTCCGAACCTTTTGTTCCTTCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	1316931	CTTTTCTACCTTCGGAACCTTTTGTTCCTGCCTTTGCTTAAACCTGTATTTGGATCAAA	1316990
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCTCCTTGGAGG	445
Sbjct	1316991	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	1317050
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAATTACGAAAACTTG	505
Sbjct	1317051	AATTGGATCTTAATTTGAACCTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAATTGA	1317110
Query	506	TAAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	1317111	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	1317170
Query	566	CAGATAAATTGCAGGCGATTCTTCCAAATACCAAATCGACTACTGA	612
Sbjct	1317171	CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	1317217

>Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130, chromosome I, complete sequence
Sequence ID: AE016823.1 Length: 4277185
Range 1: 2909058 to 2909644

Score:469 bits(519), Expect:2e-130,
Identities:456/587(78%), Gaps:0/587(0%), Strand: Plus/Minus

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCCAAAGGCAAACCGGAATTGG	85
Sbjct	2909644	TCGATTGTAAAAAAACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2909585
Query	86	TTCAAACCTTTGGATTTTGAATGCAGAAGTTGTCCACGGTTCCGGAAGAAGTTTGCGGTT	145
Sbjct	2909584	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCTCGATTCCAGAAGGAGTTTGCTCTT	2909525
Query	146	TTCCGAATTTAACCAAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGGAATTTA	205
Sbjct	2909524	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTGTTGGA	2909465
Query	206	TCGGAGAATGTAAACGCCTTGAACAACCTAATCTTTTCGGGAACGACCTTACAACATTTT	265
Sbjct	2909464	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTC	2909405
Query	266	CGTCTACGTTTTCTAAATTA AAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325

Sbjct	2909404	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAAATAACGATTTTA	2909345
Query	326	CGATTCTACCCCTCCGAACTTTGTCTTCTCCGTTGATCAAAATTCTATACGTAGATCGGA	385
Sbjct	2909344	CTTTTCTACCTTCGGAACTTTGTCTGCCTTTGCTTAAACCCCTGTATTTGGATCAAA	2909285
Query	386	ATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCTTTCCCTCCTTGGAGG	445
Sbjct	2909284	ACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCTTTCCAGTTTGGAAG	2909225
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAAGGCGCTCCCTTTTAATTACGAAAAACTTG	505
Sbjct	2909224	AATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCTTCTAACTATAATAAATTGA	2909165
Query	506	TAAATCTCATTAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565
Sbjct	2909164	AAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATTAAAGGGGGAGGATG	2909105
Query	566	CAGATAAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612
Sbjct	2909104	CTGATAAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2909058

Query	26	TCGACTGTAAAAAGAATGCGGAAGAGATTTTGGGAGAGGCAAAAGGCCAAAACCGGAATTGG	85
Sbjct	2867691	TCGATTGTAAAAA-AACGCGGTAGAGATTTTAGAAGAAGCAAAAAGAAAATCGGAATCGA	2867633
Query	86	TTCAAAC TTTGGATTTT GGAATGCAGAAGTTGTCCACGGTTC CGGAAGAAGTTTGC GGTT	145
Sbjct	2867632	TTCAAATCTTAGATTTAGGAATGCAAAAGTTAACCCTCGATTCCAGAAGGAGTTTGCCTCTT	2867573
Query	146	TTCCGAATTTAACC AAGTTGGATCTTCGTTTAAACAGTTTGACTTTTCTTCCGAATTTA	205
Sbjct	2867572	TTCCGAATTTGACTCAGCTGGATTTACGTTTGAACAGTTTGAATTCTCTTCTCTGGTTGGA	2867513
Query	206	TCGGAGAATGTAAACGCCTTGAACAAC TTAATCTTTTCGGGAACGACCTTACAACATTTTC	265
Sbjct	2867512	TTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGATCTAAATACGGTTTC	2867453
Query	266	CGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGGAAATAACGATTTTA	325
Sbjct	2867452	CATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGGTAAATAACGATTTTA	2867393
Query	326	CGATTCTACCCCTCCGAAC TTTTGT TTTCTTCCGTTGATCAAAAATCTATACGTAGATCGGA	385
Sbjct	2867392	CTTTTCTACCTTCGGAACTTTTGT TTTCTGCCTTTGCTTAA AACCTGTATTTGGATCAAA	2867333
Query	386	ATAAATTAAC TCTAACGGAACGGATGTGGAAAT TCTCGCTTCTCTTTCTCTCTTGGAGG	445
Sbjct	2867332	ACAAGCTTACGTTGACTGAAACGGATGTTGAAAT TCTAGCTTCTCTTTCCAGTTTGAAG	2867273
Query	446	AATTGGATCTGAGTCTGAATTCGGGGATTAAAGGCGCTCCCTTTTAAATTACGAAAAA CTTG	505

Sbjct	2867272		AATTGGATCTTAATTTGA	ACTCTGGAATCAAAGTGCTTCCTTCTAACTATAATAAATTGA	2867213
Query	506		TAAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaaCTTCATTAAAGGGAGAGGATG	565	
Sbjct	2867212		AAAATCTGACTCATT	TAAAAAGATTGAATATTAAAAAAACTTCATTAAAGGGGGAGGATG	2867153
Query	566		CAGATAAATTGCAGGCGATTCTTCCAAATACCAAAATCGACTACTGA	612	
Sbjct	2867152		CTGATAAATTACAAGCAGTTCTCCCAAATACAAGAATAGACTATTGA	2867106	

>Leptospira interrogans serovar Canicola leucine-rich repeat protein gene, partial cds
Sequence ID: JX426070.1 Length: 410
Range 1: 3 to 407

Score:325 bits(360), Expect:1e-87,
Identities:315/405(78%), Gaps:0/405(0%), Strand: Plus/Plus

Query	192	TCTTCCGGAATTTATCGGAGAATGTAAACGCCTTGAACAACTTAATCTTTTCGGGAACGA	251	
Sbjct	3	TCTTCCTGGTTGGATTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGA	62	
Query	252	CCTTACAACATTTCCGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGG	311	
Sbjct	63	TCTAAATACGGTTCATCTTCTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGG	122	
Query	312	AAATAACGATTTTACGATTCTACCCTCCGAACCTTTTGTTTCTTCCGTTGATCAAAATTCT	371	
Sbjct	123	TAATAACGATTTTACTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGATTAAACCCT	182	
Query	372	ATACGTAGATCGGAATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCT	431	
Sbjct	183	GTA CT TGGATCAAAACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCT	242	
Query	432	TTCCTCCTTGGAGGAATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAA	491	
Sbjct	243	TTCCAGTTTGAAGAATTGGATCTTAATTTGAACCTCTGGAATTAAGTGCTTCCTTCTAA	302	
Query	492	TTACGAAAACTTGTAATCTCATTAAATCTAAAAAGATTGAATATTaaaaaaaCTTCATT	551	
Sbjct	303	CTATAATAAATTGAAAAATCTGACTCATT	TAAAAAGATTGAATATTAAAAAAACTTCATT	362
Query	552	AAAGGGAGAGGATGCAGATAAATTGCAGGCGATTCTTCCAAATAC	596	
Sbjct	363	AAAGGGAGAAGATGCTGATAAATTACAAGCAGTTCTCCCAAATAC	407	

>Leptospira interrogans serovar Autumnalis leucine-rich repeat protein gene, partial cds
Sequence ID: JX426069.1 Length: 411
Range 1: 3 to 407

Score:321 bits(355), Expect:5e-86,
Identities:314/405(78%), Gaps:0/405(0%), Strand: Plus/Plus

Query	192	TCTTCCGGAATTTATCGGAGAATGTAAACGCCTTGAACAACTTAATCTTTTCGGGAACGA	251
Sbjct	3	TCTTCCTGGTTGGATTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGA	62

Query	252	CCTTACAACATTTCCGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGG	311
Sbjct	63	TCTAAATACGTTCCATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTGCTCTTGGG	122
Query	312	AAATAACGATTTTACGATTCTACCCTCCGAACCTTTTGTTCCTCCGTTGATCAAAATTCT	371
Sbjct	123	TAATAACGATTTTACTTTTCTACCTTCGGAACCTTTTGTTCCTGCCTTTGATTAAACCT	182
Query	372	ATACGTAGATCGGAATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCT	431
Sbjct	183	GTAATTGGATCAAAACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTCTCT	242
Query	432	TTCCTCCTTGAGGAATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAA	491
Sbjct	243	TTCCAGTTTGGAAGAATTGGATCTTAATTTGAACTCTGGAATTAAAGTGCTTCCTTCTAA	302
Query	492	TTACGAAAACTTGTAATCTCATTAACTCTAAAAAGATTGAATATTaaaaaaaCTTCATT	551
Sbjct	303	CTATAATAAATTGAAAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTCATT	362
Query	552	AAAGGGAGAGGATGCAGATAAATTGCAGGCGATTCTTCCAAATAC	596
Sbjct	363	AAAGGGGGAAGATGCTGATAAATTACAAGCAGTTCTCCCAAATAC	407

>Leptospira interrogans serovar Hebdomadis leucine-rich repeat protein gene, partial cds
Sequence ID: JX426072.1 Length: 303
Range 1: 12 to 299

Score:259 bits(286), Expect:1e-67,
Identities:230/288(80%), Gaps:0/288(0%), Strand: Plus/Plus

Query	309	GGGAAATAACGATTTTACGATTCTACCCTCCGAACCTTTTGTTCCTTCGTTGATCAAAAT	368
Sbjct	12	GGGTAATAACGATTTTACTTTTCTACCTTCGGAACCTTTTGTTCCTGCCTTTGATTAAAC	71
Query	369	TCTATACGTAGATCGGAATAAATTAACCTCTAACGGAAACGGATGTGGAAATTCTCGCTTC	428
Sbjct	72	CCTGTACTTGATCAAAACAAGCTTACGTTGACCGAAACGGATGTTGAAATTCTAGCTTC	131
Query	429	TCTTTCCTCCTTGAGGAATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTT	488
Sbjct	132	TCTTTCAGTTTGGAAGAATTGGATCTTAATTTGAACTCTGGAATTAAAGTGCTTCCTTC	191
Query	489	TAATTACGAAAACTTGTAATCTCATTAACTCTAAAAAGATTGAATATTaaaaaaaCTTC	548
Sbjct	192	TAACTATAATAAATTGAAAAATCTGACTCATTTAAAAAGATTGAATATTAAAAAACTTC	251
Query	549	ATTAAAGGGAGAGGATGCAGATAAATTGCAGGCGATTCTTCCAAATAC	596
Sbjct	252	ATTAAAGGGAGAAGATGCTGATAAATTACAAGCAGTTCTCCCAAATAC	299

>Leptospira interrogans serovar Pyrogenes leucine-rich repeat protein gene, partial cds
Sequence ID: JX426071.1 Length: 312
Range 1: 3 to 305

Score:214 bits(236), Expect:5e-54,
Identities:229/303(76%), Gaps:0/303(0%), Strand: Plus/Plus

Query	192	TCTTCCGGAATTTATCGGAGAATGTAAACGCCCTGAACAACCTTAATCTTTTCGGGAACGA	251
Sbjct	3	TCTTCCTGGTTGGATTGGAGCTTGTA AAAATCTGGAACAAATTAACCTTTTCGGAAATGA	62
Query	252	CCTTACAACATTTCCGTCTACGTTTTCTAAATTAAAAAATCTGAAAGTGTTACTGGCGGG	311
Sbjct	63	TCTAAATACGTTCCATCTTCTTTTTCTAAATTAAAGAATTTGAAAGTATTACTCTTGGG	122
Query	312	AAATAACGATTTTACGATTCTACCTCCGAACTTTTGTTTCTTCCGTTGATCAAAATTCT	371
Sbjct	123	TAATAACGATTTTACTTTTCTACCTTCGGAACCTTTTGTTTCTGCCTTTGCTTAAACCT	182
Query	372	ATACGTAGATCGGAATAAATTAACCTAACGGAAACGGATGTGGAAATTCTCGCTTCTCT	431
Sbjct	183	GTATTTGGATCAAAACAAGCTTACGTTGACTGAAACGGATGTTGAAATTCTAGCTTCTCT	242
Query	432	TTCTCTCTTGAGGAATTGGATCTGAGTCTGAATTCGGGGATTAAGGCGCTCCCTTTTAA	491
Sbjct	243	TTCCAGTTTGGAAGAATTGGATCTTAATTTGAACTCTGGAATCAAAGTGCTTCCTTCTAA	302
Query	492	TTA	494
Sbjct	303	CTA	305