## Sequences producing significant alignments

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select all 10 sequences selected	<u>GenBank</u>	Graphics		Distance tree of result			New MSA Viewer	
Description	Scientific Name	Max Score		Query Cover	E value	Per. Ident	Acc. Len	Accession
Leptospira interrogans serovar Canicola strain 611 chromosome 1, complete sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4255595	CP044513.1
Leptospira interrogans serovar Canicola strain LJ178 chromosome 1, complete sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4259066	<u>CP044509.1</u>
Leptospira interrogans serovar Canicola strain 114 chromosome I sequence	Leptospira interrogans serovar C	510	510	100%	2e-143	100.00%	4218946	CP022883.1
Leptospira interrogans serovar Linhai str. 56609 chromosome 1, complete sequence	Leptospira interrogans serovar Li	510	510	100%	2e-143	100.00%	4331770	CP006723.1
Leptospira interrogans serovar Gem strain Simon secY gene, partial sequence	Leptospira interrogans serovar G	510	510	100%	2e-143	100.00%	1408	EU358039.1
Leptospira interrogans serovar Pomona strain LT 1026 SecY (secY) gene, partial cds	Leptospira interrogans serovar P	510	510	100%	2e-143	100.00%	1375	EU358017.1
Leptospira interrogans serovar Monjakov SecY (secY) gene, partial cds	Leptospira interrogans serovar M	510	510	100%	2e-143	100.00%	1386	EU358014.1
Leptospira interrogans serovar Pomona SecY (secY) gene, partial cds	Leptospira interrogans serovar P	510	510	100%	2e-143	100.00%	1382	EU358013.1
Leptospira interrogans serovar Medanensis strain Hond HC SecY (secY) gene, partial cds	Leptospira interrogans serovar M	510	510	100%	2e-143	100.00%	1386	EU357984.1
Leptospira interrogans serovar Bratislava strain Jez Bratislava SecY (secY) gene, partial cds	Leptospira interrogans serovar Br	510	510	100%	2e-143	100.00%	1386	EU357939.1

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Leptospira interrogans serovar Gem strain Simon secY gene, partial sequence Sequence ID: EU358039.1 Length: 1408 Number of Matches: 1

Range 1: 163 to 438 GenBank Graphics Vext Match A P										
Score 510 bit	s(276)	Expect 2e-143	Identities 276/276(100%)	Gaps 0/276(0%)	Strand Plus/Plus	_				
Query	1	CTTGTTCCTGCCCT	TCaaaaacttcaaaaaga	aggagaagaaggaa	gaaaaaaaa <b>TTGGT</b> 	60				
Sbjct	163	CTTGTTCCTGCCCT	TCAAAAACTTCAAAAAG	AGGAGAAGAAGGAA	GAAAAAAAATTGGT	222				
Query	61	СААТАТАСТААСТА	TGGAACCGTAATTCTTTG	TGCGATTCAATCTT	TAGCAGTGATCCAA	120				
Sbjct	223	CAATATACTAAGTA	TGGAACCGTAATTCTTTC	JIIIIIIIIIIIIII GTGCGATTCAATCTT	TAGCAGTGATCCAA	282				
Query	121	CTCGCAAAGGGCTG	GTCTACCGGCACGGAACI	TGAGCCTGCGCGTT.	ACCCGGGCTTAATC	180				
Sbjct	283	CTCGCAAAGGGCTG	GTCTACCGGCACGGAACI	TGAGCCTGCGCGTT	ACCCGGGCTTAATC	342				
Query	181	AATTCTTCTGTTGT	TCCTTATTTTTATTTAA	CGGAATCTTATCCA	TTACTACCGGAACC	240				
Sbjct	343	AATTCTTCTGTTGT	 TCCTTATTTTTATTTAAT	CGGAATCTTATCCA	TTACTACCGGAACC	402				
Query	241	GTTCTTCTCATTTG	GTTAGGAGAACAGATCAC	CGAA 276						
Sbjct	403	GTTCTTCTCATTTG		 CGAA 438						

Figure S4. Sequencing and BLAST analysis of PCR reaction products from clinical urine samples (Sample 001).