

Supplementary data

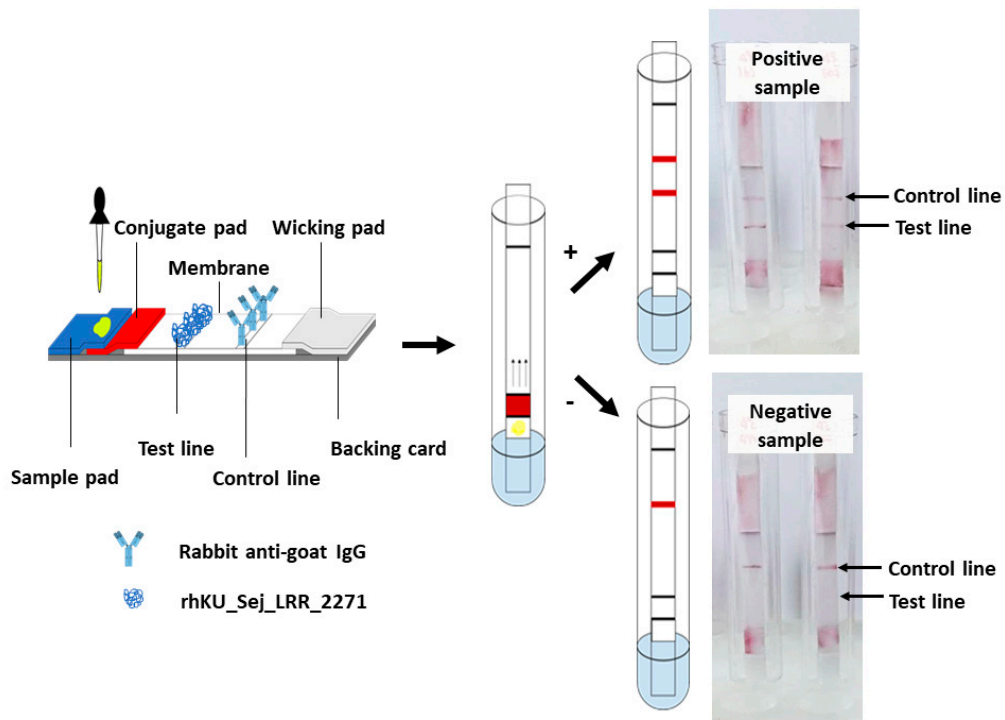
Evaluation of a Leucine-rich-repeat protein-based lateral flow assay for detection of anti-leptospiral IgG in Thai canine

Sineenat Sripattanakul ^{1,2,†}, Kanpapat Boonchuay ^{3,4,†}, Teerasak Prapong ², Worawidh Wajjwalku ^{3,4}, Gerd Katzenmeier ^{3,4}, Dietmar Haltrich ⁵, Ratchanee Hongprayoon ¹ and Siriwan Prapong ^{1,2,*}

Supplementary Table S1: The reference serovars and strains of *Leptospira* spp. utilized in real-time PCR and MAT.

Genospecies	Serovars ^a	Strain ^a
<i>L. interrogans</i>	Autumnalis	Akiyami
	Bataviae	A Swart
	Bratislava	Jez Bratislava
	Canicola	Houd UtrechtIV
	Djasiman	Djasiman
	Hebdomadis	Hebdomadis
	Icterohaemorrhagiae	RGA
	Pomona	Pomona
	Pyrogenes	Salinem
<i>L. noguchii</i>	Louisiana	LSU 1945
	Panama	CZ 214 K
<i>L. borgpetersenii</i>	Ballum	MUS 127
	Javanica	Veldrat Batavia 46
	Mini	Sari
	Sejroe	M 84
	Tarassovi	Perepelitsin
<i>L. santarosai</i>	Shermani	1342 K
<i>L. weilii</i>	Celledoni	Celledoni
	Manhao	L 105
	Sarmin	Sarmin
<i>L. kirschneri</i>	Cynopteri	3522 C
	Grippotyphosa	Moskva V
<i>L. meyeri</i>	Ranarum	ICF
<i>L. biflexa</i>	Patoc	Patoc 1

^a The serovars and strains of *Leptospira* were kindly provided by the National Institute of Animal Health, department of Livestock Department, Thailand.



Supplementary Figure S1: Schematic representation of the different parts of the rhKU_Sej_LRR_2271 lateral flow strip and representation of the results after testing with positive and negative dog plasma samples. The test line contained 800 $\mu\text{g/ml}$ of rhKU_Sej_LRR_2271 and the control line 100 $\mu\text{g/ml}$ of rabbit anti-goat IgG. The conjugate pad contained of gold nanoparticle conjugated goat anti-dog IgG. The running buffer was 0.2 M SBB with 1 % Tween20 and 0.02 % NaN_3 .

Supplementary data S1: Amino sequence alignment of rhKU_Sej_LRR_2271

BLASTP 2.13.0+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: PN3VPV8W013

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

512,909,985 sequences; 200,317,139,153 total letters

Query= AFV46188.1 leucine-rich repeat protein, partial [*Leptospira borgpetersenii* serovar Sejroe]

Length=203

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
leucine-rich repeat protein [Leptospira borgpetersenii serovar Ballum]	358	358	100%	6.00E-124	100.00%	AFV46186.1
leucine rich repeat protein [Leptospira borgpetersenii serovar Ballum]	359	359	100%	8.00E-124	100.00%	ALO26640.1
leucine-rich repeat domain-containing protein [Leptospira]	358	358	100%	1.00E-123	100.00%	WP_002731979.1
leucine-rich repeat protein [Leptospira borgpetersenii serovar Javanica]	354	354	100%	3.00E-122	99.01%	AFV46185.1
leucine rich repeat protein [Leptospira borgpetersenii serovar Pomona str. 200901868]	354	354	100%	7.00E-122	99.01%	EMO62774.1
leucine-rich repeat domain-containing protein [Leptospira borgpetersenii]	352	352	100%	4.00E-121	98.52%	WP_011669694.1
hypothetical protein [Leptospira mayottensis]	331	331	100%	8.00E-113	91.63%	WP_002745429.1
hypothetical protein [Leptospira weilii]	330	330	100%	1.00E-112	90.15%	WP_235596156.1
leucine rich repeat protein [Leptospira sp. P2653]	328	328	100%	1.00E-111	91.13%	EMJ66028.1
leucine-rich repeat domain-containing protein [Leptospira]	328	328	100%	1.00E-111	91.13%	WP_004496751.1
leucine-rich repeat domain-containing protein [Leptospira weilii]	326	326	100%	8.00E-111	90.64%	WP_061219130.1
leucine rich repeat protein [Leptospira weilii str. UI 13098]	325	325	100%	1.00E-110	90.64%	EMN91031.1
leucine-rich repeat domain-containing protein [Leptospira weilii]	325	325	100%	2.00E-110	90.64%	WP_026054684.1
leucine-rich repeat domain-containing protein [Leptospira weilii]	322	322	99%	2.00E-109	90.59%	WP_061217745.1
leucine rich repeat protein [Leptospira alexanderi serovar Manhao 3 str. L 60]	312	312	100%	2.00E-105	86.70%	EQA64549.1
hypothetical protein [Leptospira alexanderi]	311	311	100%	3.00E-105	86.70%	WP_039940928.1
hypothetical protein [Leptospira alexanderi]	309	309	100%	4.00E-104	86.21%	WP_078124592.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	307	307	100%	2.00E-103	86.34%	WP_004466481.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	306	306	100%	4.00E-103	85.85%	WP_046692451.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein LSS_15741 [Leptospira santarosai serovar Shermani str. LT 821]	305	305	100%	1.00E-102	85.85%	EKT85788.2
leucine-rich repeat domain-containing protein [Leptospira]	305	305	100%	2.00E-102	85.85%	WP_004471631.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	305	305	100%	2.00E-102	85.85%	WP_061216203.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	304	304	100%	3.00E-102	85.85%	WP_004492778.1
leucine rich repeat protein [Leptospira santarosai str. CBC1416]	305	305	100%	3.00E-102	85.37%	EMO58507.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	304	304	100%	4.00E-102	85.37%	WP_004468285.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	303	303	100%	6.00E-102	84.88%	WP_004486481.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	303	303	100%	8.00E-102	85.37%	WP_004473752.1
leucine-rich repeat domain-containing protein [Leptospira santarosai]	302	302	100%	2.00E-101	84.88%	WP_004476114.1
leucine rich repeat protein [Leptospira weilii serovar Topaz str. LT2116]	294	294	91%	1.00E-98	90.27%	EMF79993.1
leucine rich repeat protein [Leptospira weilii str. Ecochallenge]	290	290	91%	4.00E-97	90.27%	EMY13797.1
leucine-rich repeat domain-containing protein [Leptospira barantonii]	289	289	96%	4.00E-96	84.62%	WP_100761136.1
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	280	280	96%	1.00E-92	82.05%	WP_123179347.1
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	280	280	96%	1.00E-92	82.56%	WP_100755326.1
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	279	279	96%	3.00E-92	82.05%	WP_135607718.1
leucine-rich repeat domain-containing protein [Leptospira alstonii]	278	278	96%	6.00E-92	83.59%	WP_020775386.1
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	278	278	96%	6.00E-92	82.05%	WP_010574016.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	278	278	96%	7.00E-92	81.54%	WP_135653950.1
leucine-rich repeat domain-containing protein [Leptospira kmetyi]	278	278	96%	7.00E-92	81.54%	WP_100738364.1
hypothetical protein [Leptospira yasudae]	277	277	95%	1.00E-91	81.87%	MBW0432169.1
hypothetical protein EHR10_00815 [Leptospira yasudae]	277	277	95%	2.00E-91	81.87%	TGN02502.1
hypothetical protein [Leptospira yasudae]	276	276	95%	2.00E-91	82.38%	WP_118964127.1
leucine-rich repeat domain-containing protein [Leptospira alstonii]	276	276	96%	3.00E-91	83.08%	WP_061249228.1
leucine rich repeat protein [Leptospira weilii serovar Ranarum str. ICFT]	277	277	100%	4.00E-91	78.05%	EMY77189.1
hypothetical protein [Leptospira sanjuanensis]	276	276	95%	4.00E-91	81.87%	WP_238730679.1
hypothetical protein [Leptospira sanjuanensis]	276	276	95%	6.00E-91	81.87%	WP_238747060.1
hypothetical protein [Leptospira yasudae]	275	275	99%	9.00E-91	79.70%	WP_135574399.1
hypothetical protein [Leptospira yasudae]	273	273	95%	7.00E-90	81.35%	WP_135581985.1
hypothetical protein [Leptospira yasudae]	271	271	95%	2.00E-89	80.83%	WP_118956310.1
hypothetical protein [Leptospira kirschneri]	270	270	95%	2.00E-88	81.44%	WP_004767299.1
hypothetical protein [Leptospira kirschneri]	270	270	95%	2.00E-88	81.44%	WP_004759233.1
hypothetical protein [Leptospira]	269	269	95%	3.00E-88	80.93%	WP_004750770.1
hypothetical protein [Leptospira kirschneri]	269	269	95%	3.00E-88	80.93%	WP_004779378.1
hypothetical protein [Leptospira kirschneri]	268	268	95%	4.00E-88	80.93%	WP_016752856.1
hypothetical protein [Leptospira kirschneri]	268	268	95%	7.00E-88	80.93%	WP_020778543.1
hypothetical protein [Leptospira kirschneri]	268	268	95%	1.00E-87	80.41%	WP_082292870.1
hypothetical protein [Leptospira kirschneri]	267	267	95%	2.00E-87	80.41%	WP_004768364.1
hypothetical protein [Leptospira kirschneri]	266	266	95%	2.00E-87	80.93%	WP_004760926.1
hypothetical protein [Leptospira tipperaryensis]	261	261	95%	4.00E-85	78.24%	WP_069608131.1
hypothetical protein [Leptospira ainlahdjerensis]	261	261	95%	4.00E-85	77.72%	WP_205279762.1
hypothetical protein [Leptospira ainazelensis]	258	258	95%	5.00E-84	77.20%	WP_232371773.1
hypothetical protein [Leptospira ainazelensis]	258	258	95%	6.00E-84	77.20%	MBM9502464.1
hypothetical protein [Leptospira noguchii]	255	255	99%	7.00E-83	78.22%	WP_004443975.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein [Leptospira noguchii]	254	254	95%	1.00E-82	80.93%	WP_004449517.1
hypothetical protein [Leptospira noguchii]	254	254	95%	2.00E-82	80.93%	WP_004422093.1
hypothetical protein [Leptospira noguchii]	254	254	95%	2.00E-82	80.93%	WP_004455400.1
hypothetical protein [Leptospira noguchii]	254	254	95%	3.00E-82	80.41%	WP_243817925.1
hypothetical protein [Leptospira noguchii]	254	254	95%	3.00E-82	80.41%	WP_053522720.1
hypothetical protein [Leptospira noguchii]	253	253	99%	4.00E-82	77.72%	WP_004452014.1
hypothetical protein [Leptospira noguchii]	253	253	99%	5.00E-82	77.72%	WP_243827912.1
hypothetical protein [Leptospira noguchii]	253	253	99%	8.00E-82	77.72%	WP_061233070.1
hypothetical protein [Leptospira interrogans]	252	252	95%	1.00E-81	80.93%	WP_017852233.1
hypothetical protein [Leptospira interrogans]	251	251	95%	3.00E-81	80.93%	WP_061241709.1
hypothetical protein [Leptospira interrogans]	251	251	95%	3.00E-81	80.93%	WP_001010180.1
hypothetical protein [Leptospira]	251	251	95%	3.00E-81	80.93%	WP_001011126.1
hypothetical protein [Leptospira stimsonii]	251	251	96%	4.00E-81	74.36%	WP_118981207.1
hypothetical protein [Leptospira noguchii]	251	251	95%	4.00E-81	79.38%	WP_004427427.1
hypothetical protein [Leptospira noguchii]	251	251	99%	5.00E-81	77.23%	WP_004438578.1
leucine rich repeat protein [Leptospira interrogans str. L1207]	250	250	95%	6.00E-81	80.41%	EMN50877.1
hypothetical protein [Leptospira]	250	250	95%	7.00E-81	80.41%	WP_001010181.1
hypothetical protein [Leptospira interrogans]	250	250	95%	8.00E-81	80.41%	WP_001010177.1
hypothetical protein [Leptospira noguchii]	250	250	95%	1.00E-80	79.90%	WP_002177142.1
hypothetical protein [Leptospira adleri]	249	249	95%	1.00E-80	74.61%	WP_100785841.1
hypothetical protein [Leptospira adleri]	249	249	95%	2.00E-80	74.61%	WP_135691680.1
hypothetical protein CH379_21015 [Leptospira ellisii]	248	248	98%	4.00E-80	71.50%	PJZ91020.1
hypothetical protein [Leptospira interrogans]	248	248	95%	5.00E-80	79.90%	WP_002188945.1
hypothetical protein [Leptospira stimsonii]	248	248	95%	6.00E-80	75.13%	WP_118970865.1
hypothetical protein [Leptospira ellisii]	246	246	95%	2.00E-79	73.20%	WP_243399589.1
leucine-rich repeat domain-containing protein [Leptospira gomenensis]	244	244	95%	2.00E-78	70.47%	WP_135589926.1
hypothetical protein [Leptospira interrogans]	232	232	95%	1.00E-73	80.41%	WP_250180949.1
hypothetical protein [Leptospira interrogans]	231	231	95%	2.00E-73	80.41%	WP_061272825.1

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
hypothetical protein [Leptospira interrogans]	231	231	95%	2.00E-73	80.41%	WP_002127204.1
hypothetical protein [Leptospira interrogans]	231	231	95%	2.00E-73	79.38%	WP_061286495.1
hypothetical protein [Leptospira interrogans]	231	231	95%	3.00E-73	79.90%	WP_001010185.1
hypothetical protein [Leptospira]	231	231	95%	3.00E-73	79.90%	WP_001010184.1
hypothetical protein [Leptospira interrogans]	231	231	95%	3.00E-73	79.38%	WP_001010182.1
hypothetical protein [Leptospira interrogans]	231	231	95%	3.00E-73	79.90%	WP_001010178.1
hypothetical protein [Leptospira interrogans]	231	231	95%	4.00E-73	79.90%	WP_001010183.1
hypothetical protein [Leptospira interrogans]	229	229	95%	1.00E-72	79.38%	WP_192505591.1
leucine rich repeat protein [Leptospira interrogans serovar Zanoni str. LT2156]	218	218	92%	1.00E-68	78.61%	EMM97254.1
hypothetical protein [Leptospira interrogans]	216	216	91%	5.00E-68	79.03%	MBW9228790.1

ALIGNMENTS

>AFV46186.1 leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Ballum]

AFV46187.1 leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Mini]

AFV46188.1 leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Sejroe]

Length=203

Score = 358 bits (920), Expect = 6e-124, Method: Compositional matrix adjust.
Identities = 203/203 (100%), Positives = 203/203 (100%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTKLDLRLN	60
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Sbjct	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTKLDLRLN	60
Query	61	SLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
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Sbjct	61	SLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
Query	121	IKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	
Sbjct	121	IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	180
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	181	KTSLKGEDADKLQAILPNTKIDY	203

>AL026640.1 leucine rich repeat protein [Leptospira borgpetersenii serovar Ballum]
 ANH01207.1 leucine rich repeat protein [Leptospira borgpetersenii str. 4E]
 EMN15214.1 leucine rich repeat protein [Leptospira borgpetersenii str. Brem 307]
 EMN18108.1 leucine rich repeat protein [Leptospira borgpetersenii str. Brem 328]
 PTM44326.1 leucine rich repeat (LRR) protein [Leptospira borgpetersenii serovar Javanica]
 GIM19917.1 hypothetical protein KHM09_23680 [Leptospira borgpetersenii]
 Length=222

Score = 359 bits (921), Expect = 8e-124, Method: Compositional matrix adjust.
 Identities = 203/203 (100%), Positives = 203/203 (100%), Gaps = 0/203 (0%)

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		GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN	
Sbjct	20	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN	79
Query	61	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	
Sbjct	80	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	139
Query	121	IKILYVDRNKLTLTETDVeilaslsleeeldslslnsGIKALPFNYEKL VNLINLKRNLNIK	180
		IKILYVDRNKLTLTETDVEILASLSLEEELDSLNSGIKALPFNYEKL VNLINLKRNLNIK	
Sbjct	140	IKILYVDRNKLTLTETDVEILASLSLEEELDSLNSGIKALPFNYEKL VNLINLKRNLNIK	199
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	200	KTSLKGEDADKLQAILPNTKIDY	222

>WP_002731979.1 MULTISPECIES: leucine-rich repeat domain-containing protein [Leptospira]
 EMG00720.1 leucine rich repeat protein [Leptospira borgpetersenii str. 200701203]
 EM009583.1 leucine rich repeat protein [Leptospira borgpetersenii str. Noumea 25]
 AXX17321.1 hypothetical protein C4Q31_14790 [Leptospira borgpetersenii serovar Ceylonica]
 EKP15606.1 leucine rich repeat protein [Leptospira borgpetersenii str. 200801926]
 EKQ91706.1 leucine rich repeat protein [Leptospira borgpetersenii str. UI 09149]
 Length=215

Score = 358 bits (920), Expect = 1e-123, Method: Compositional matrix adjust.
 Identities = 203/203 (100%), Positives = 203/203 (100%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN	60
		GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN	
Sbjct	13	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN	72
Query	61	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
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Sbjct	73	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	132

Query	121	IKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	
Sbjct	133	IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	192
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	193	KTSLKGEDADKLQAILPNTKIDY	215

>AFV46185.1 leucine-rich repeat protein, partial [*Leptospira borgpetersenii* serovar Javanica]
Length=203
Score = 354 bits (909), Expect = 3e-122, Method: Compositional matrix adjust.
Identities = 201/203 (99%), Positives = 202/203 (99%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKLDLRLN	60
		GF+CFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKLDLRLN	
Sbjct	1	GFLCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKLDLRLN	60
Query	61	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	
Sbjct	61	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
Query	121	IKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	
Sbjct	121	IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	180
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAIL NTKIDY	
Sbjct	181	KTSLKGEDADKLQAILRNTKIDY	203

>EM062774.1 leucine rich repeat protein [*Leptospira borgpetersenii* serovar Pomona str. 200901868]
Length=215
Score = 354 bits (908), Expect = 7e-122, Method: Compositional matrix adjust.
Identities = 201/203 (99%), Positives = 202/203 (99%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKLDLRLN	60
		GFVCFTASF+CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPE VCGFPNLTKLDLRLN	
Sbjct	13	GFVCFTASFNCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEGVC GFPNLTKLDLRLN	72
Query	61	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	
Sbjct	73	SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	132
Query	121	IKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	
Sbjct	133	IKILYVDRNKLTLTETDVEILASLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIK	192
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	193	KTSLKGEDADKLQAILPNTKIDY	215

>WP_011669694.1 leucine-rich repeat domain-containing protein [Leptospira borgpetersenii]
 ABJ76745.1 Leucine-rich-repeat protein [Leptospira borgpetersenii serovar Hardjo-bovis str. JB197]
 ABJ78391.1 Leucine-rich-repeat protein [Leptospira borgpetersenii serovar Hardjo-bovis str. L550]
 AMX57620.1 hypothetical protein LBK6_04345 [Leptospira borgpetersenii serovar Hardjo]
 AWW71582.1 hypothetical protein B9T54_04730 [Leptospira borgpetersenii serovar Hardjo-bovis]
 EMJ80931.1 leucine rich repeat protein [Leptospira borgpetersenii serovar Hardjo-bovis str. Sponselee]
 Length=215

Score = 352 bits (903), Expect = 4e-121, Method: Compositional matrix adjust.
 Identities = 200/203 (99%), Positives = 201/203 (99%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFNPNTKLDLRLN	60
		GFVCFTASF+CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPE VCGFPNTKLDLRLN	
Sbjct	13	GFVCFTASFNCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEGVCGFPNTKLDLRLN	72
Query	61	SLTFLPEFIGECKRLEQLNLFNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLTFLPEFIGECKRLEQLNLFNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	
Sbjct	73	SLTFLPEFIGECKRLEQLNLFNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	132
Query	121	IKILYVDRNKLTLTETDVeilaslsleeeldslslnsGIKALPFNYEKLVLNLNLRNLK	180
		IKILYVDRNKL LTETDVEILASLSLEEELDLSLNSGIKALPFNYEKLVLNLNLRNLK	
Sbjct	133	IKILYVDRNKLTLTETDVEILASLSLEEELDLSLNSGIKALPFNYEKLVLNLNLRNLK	192
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	193	KTSLKGEDADKLQAILPNTKIDY	215

>WP_002745429.1 hypothetical protein [Leptospira mayottensis]
 AXR62112.1 hypothetical protein DQM68_17050 [Leptospira mayottensis]
 AXR62988.1 hypothetical protein DQM28_00680 [Leptospira mayottensis]
 AXR66734.1 hypothetical protein DPV73_00510 [Leptospira mayottensis]
 AZQ01438.1 hypothetical protein LEP1GSC190_04660 [Leptospira mayottensis 200901116]
 EKS00741.1 leucine rich repeat protein [Leptospira mayottensis 200901122]
 Length=219

Score = 331 bits (849), Expect = 8e-113, Method: Compositional matrix adjust.
 Identities = 186/203 (92%), Positives = 191/203 (94%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFNPNTKLDLRLN	60
		GF+CFTASFDCKKNAEEILGEAKAKPELVQ LDFGMQKLSTVPE VCGFPNTKLDLRLN	
Sbjct	17	GFICFTASFDCKKNAEEILGEAKAKPELVQILDFGMQKLSTVPEAVCGFPNTKLDLRLN	76
Query	61	SLTFLPEFIGECKRLEQLNLFNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLTFLPE IGEC+RLEQLNLFNDLT PSTFSKLKNLKVLLAG NDFITLPSELLFLPL	
Sbjct	77	SLTFLPESIGECRRLEQLNLFNDLTALPSTFSKLKNLKVLLAGGNDFTILPSELLFLPL	136
Query	121	IKILYVDRNKLTLTETDVeilaslsleeeldslslnsGIKALPFNYEKLVLNLNLRNLK	180
		I+ LY D+NKLTLTETDVEILASLSLEEELDL+LN GIK LPFNYEKL NL NLKRLNIK	
Sbjct	137	IRTLYFDQNKLTLTETDVEILASLSLEEELDLNLNLGIKTLPFNYEKLRLNLNLRNLK	196

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
 KTSKKGEDADKLQAILPNTKIDY
 Sbjct 197 KTSKKGEDADKLQAILPNTKIDY 219

>WP_235596156.1 hypothetical protein [Leptospira weilii]
 Length=205

Score = 330 bits (846), Expect = 1e-112, Method: Compositional matrix adjust.
 Identities = 183/203 (90%), Positives = 194/203 (96%), Gaps = 0/203 (0%)

Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KLDLRLN 60
 GF+CF ASFDCKKNAEEILGEAKAKP+ +QTLDFGMQKLST+PE VCGFPNLT KLDLRLN
 Sbjct 3 GFICFAASFDCKKNAEEILGEAKAKPKSIQTLDFGMQKLSTIPEGVC GFPNLT KLDLRLN 62

Query 61 SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL 120
 SL LPEFIGEC+RLEQLNLF GNDL TFPSTFSKLKNLKVLLAG+NDF+ILPSELLFLPL
 Sbjct 63 SLISLPEFIGECRRLEQLNLF GNDLATFPSTFSKLKNLKVLLAGSNDFSILPSELLFLPL 122

Query 121 IKILYVDRNKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKL VNLINLKRLNIK 180
 IKILYVD+NKLTLTETDVEILASLS+LEELD+LN GIK+LPFNYEKL NL NLKRLNIK
 Sbjct 123 IKILYVDQNKLTLTETDVEILASLSNLEELDNLNLGIKSLPFNYEKLGNLTNLKRLNIK 182

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
 KTSKKGEDADKLQAILPNTKIDY
 Sbjct 183 KTSKKGEDADKLQAILPNTKIDY 205

>EMJ66028.1 leucine rich repeat protein [Leptospira sp. P2653]
 Length=222

Score = 328 bits (842), Expect = 1e-111, Method: Compositional matrix adjust.
 Identities = 185/203 (91%), Positives = 193/203 (95%), Gaps = 0/203 (0%)

Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KLDLRLN 60
 GF+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNLT KLDLRLN
 Sbjct 20 GFICFTASFDCKKNAEEILGEAKAKSESIRTLD FGMQKLSTVPEGVC GFPNLT KLDLRLN 79

Query 61 SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL 120
 SLT LPEFIG+CK LEQLNLF GNDL TFP TFSKLKNLKVLLAG+NDF+ILPSELLFLPL
 Sbjct 80 SLTSLPEFIGDCKNLEQLNLF GNDLATFPPTFSKLKNLKVLLAGSNDF+ILPSELLFLPL 139

Query 121 IKILYVDRNKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKL VNLINLKRLNIK 180
 IKILYVDRNKLTLTETDVEILASLS+LEELD+LN GIK+LPFNYEKL NL NLKRLNIK
 Sbjct 140 IKILYVDRNKLTLTETDVEILASLSNLEELDNLNLGIKSLPFNYEKLGNLTNLKRLNIK 199

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
 KTSKKGEDADKLQAILPNTKIDY
 Sbjct 200 KTSKKGEDADKLQAILPNTKIDY 222

>WP_004496751.1 MULTISPECIES: leucine-rich repeat domain-containing protein [Leptospira]
 EMM72486.1 leucine rich repeat protein [Leptospira weilii str. 2006001855]
 EKR63142.1 leucine rich repeat protein [Leptospira weilii str. 2006001853]
 EMN43504.1 leucine rich repeat protein [Leptospira weilii str. LNT 1234]
 MCL8266298.1 leucine-rich repeat domain-containing protein [Leptospira weilii]
 OMI17312.1 hypothetical protein BUQ74_11030 [Leptospira weilii serovar Heyan]
 Length=215

Score = 328 bits (840), Expect = 1e-111, Method: Compositional matrix adjust.
 Identities = 185/203 (91%), Positives = 193/203 (95%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFNPNTKLDLRLN	60
		GF+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNTKLDLRLN	
Sbjct	13	GFICFTASFDCKKNAEEILGEAKAKSESIRTLDFGMQKLSTVPEGVCGFPNTKLDLRLN	72
Query	61	SLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLT LPEFIG+CK LEQLNLFGNL TFP TFSKLKNLKVLLAG+NDFTILPSELLFLPL	
Sbjct	73	SLTSLPEFIGDCKNLEQLNLFGNLDTFPPTFSKLKNLKVLLAGSNDFITLPSSELLFLPL	132
Query	121	IKILYVDRNKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVDRNKLTLTETDVEILASLS+LEELD+LN GIK+LPFNYEKL NL NLKRLNIK	
Sbjct	133	IKILYVDRNKLTLTETDVEILASLSNLEELDNLNLGIKSLPFNYEKLGNLTNLKRLNIK	192
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	193	KTSLKGEDADKLQAILPNTKIDY	215

>WP_061219130.1 leucine-rich repeat domain-containing protein [Leptospira weilii]
 Length=215

Score = 326 bits (835), Expect = 8e-111, Method: Compositional matrix adjust.
 Identities = 184/203 (91%), Positives = 193/203 (95%), Gaps = 0/203 (0%)

Query	1	GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFNPNTKLDLRLN	60
		GF+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNTKLDLRLN	
Sbjct	13	GFICFTASFDCKKNAEEILGEAKAKSESIRTLDFGMQKLSTVPEGVCGFPNTKLDLRLN	72
Query	61	SLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL	120
		SLT LPEFIG+CK LEQLNLFGNL TFP TFSKLKNLKVLLAG+NDFTILPSELLFLPL	
Sbjct	73	SLTSLPEFIGDCKNLEQLNLFGNLDTFPPTFSKLKNLKVLLAGSNDFITLPSSELLFLPL	132
Query	121	IKILYVDRNKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRLNIK	180
		IKILYVD+NKLTLTETDVEILASLS+LEELD+LN GIK+LPFNYEKL NL NLKRLNIK	
Sbjct	133	IKILYVDQNKLTLTETDVEILASLSNLEELDNLNLGIKSLPFNYEKLGNLTNLKRLNIK	192
Query	181	KTSLKGEDADKLQAILPNTKIDY	203
		KTSLKGEDADKLQAILPNTKIDY	
Sbjct	193	KTSLKGEDADKLQAILPNTKIDY	215

>EMN91031.1 leucine rich repeat protein [Leptospira weilii str. UI 13098]
Length=222

Score = 325 bits (834), Expect = 1e-110, Method: Compositional matrix adjust.
Identities = 184/203 (91%), Positives = 192/203 (95%), Gaps = 0/203 (0%)

```
Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLN 60
        GF+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNLTCLDLRLN
Sbjct 20 GFICFTASFDCKKNAEEILGEAKAKSESIRTLDFGMQKLSTVPEGVCGFNLTCLDLRLN 79

Query 61 SLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL 120
        SLT LPEFIG+CK LEQLNLFGNDL TFP TFSKLKNLKVLLAG+NDFTILPSELLFLPL
Sbjct 80 SLTSLPEFIGDCKNLEQLNLFGNDLATFPPTFSKLKNLKVLLAGSNDFILPSELLFLPL 139

Query 121 IKILYVDRNKLTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNLNLKRLNIK 180
        IKILYVDRNKLTLTETDVEILASLS+LEELDL+LN IK+LPFNYEKL NL NLKRLNIK
Sbjct 140 IKILYVDRNKLTLTETDVEILASLSNLEELDLNLNLEIKSLPFNYEKLGNLTNLKRLNIK 199

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
        KTSKKGEDADKLQAILPNTKIDY
Sbjct 200 KTSKKGEDADKLQAILPNTKIDY 222
```

>WP_026054684.1 leucine-rich repeat domain-containing protein [Leptospira weilii]
Length=215

Score = 325 bits (832), Expect = 2e-110, Method: Compositional matrix adjust.
Identities = 184/203 (91%), Positives = 192/203 (95%), Gaps = 0/203 (0%)

```
Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLN 60
        GF+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNLTCLDLRLN
Sbjct 13 GFICFTASFDCKKNAEEILGEAKAKSESIRTLDFGMQKLSTVPEGVCGFNLTCLDLRLN 72

Query 61 SLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL 120
        SLT LPEFIG+CK LEQLNLFGNDL TFP TFSKLKNLKVLLAG+NDFTILPSELLFLPL
Sbjct 73 SLTSLPEFIGDCKNLEQLNLFGNDLATFPPTFSKLKNLKVLLAGSNDFILPSELLFLPL 132

Query 121 IKILYVDRNKLTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNLNLKRLNIK 180
        IKILYVDRNKLTLTETDVEILASLS+LEELDL+LN IK+LPFNYEKL NL NLKRLNIK
Sbjct 133 IKILYVDRNKLTLTETDVEILASLSNLEELDLNLNLEIKSLPFNYEKLGNLTNLKRLNIK 192

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
        KTSKKGEDADKLQAILPNTKIDY
Sbjct 193 KTSKKGEDADKLQAILPNTKIDY 215
```

>WP_061217745.1 leucine-rich repeat domain-containing protein [Leptospira weilii]
Length=215

Score = 322 bits (826), Expect = 2e-109, Method: Compositional matrix adjust.
Identities = 183/202 (91%), Positives = 191/202 (95%), Gaps = 0/202 (0%)

```
Query 2 FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNS 61
      F+CFTASFDCKKNAEEILGEAKAK E ++TLDFGMQKLSTVPE VCGFPNLTKDLRLNS
Sbjct 14 FICFTASFDCKKNAEEILGEAKAKSESIRTLDFGMQKLSTVPEGVC GFPNLTKDLRLNS 73

Query 62 LTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLI 121
      LT LPEFIG+CK LEQLNLFGNDL TFP TFSKLKNLKVLLAG+NDFTILPSELLFLPLI
Sbjct 74 LTSLPEFIGDCKNLEQLNLFGNDLATFPPTFSKLKNLKVLLAGSNDFTILPSELLFLPLI 133

Query 122 KILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKK 181
      KILYVDRNKLTLTETDVEILASLS+LEELD+LN IK+LPFNYEKL NL NLKRLNIKK
Sbjct 134 KILYVDRNKLTLTETDVEILASLSNLEELDNLNLLEIKSLPFNYEKLGNLTNLKRLNIKK 193

Query 182 TSLKGEDADKLQAILPNTKIDY 203
      TSLKGEDADKLQAILPNTKIDY
Sbjct 194 TSLKGEDADKLQAILPNTKIDY 215
```

>EQA64549.1 leucine rich repeat protein [Leptospira alexanderi serovar Manhao
3 str. L 60]
Length=222

Score = 312 bits (800), Expect = 2e-105, Method: Compositional matrix adjust.
Identities = 176/203 (87%), Positives = 187/203 (92%), Gaps = 0/203 (0%)

```
Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLN 60
      GF+CFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPE VCGFPNLTKDLRLN
Sbjct 20 GFICFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEGVC GFPNLTKDLRLN 79

Query 61 SLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPL 120
      SL+ LP+ IG+CK LEQLNLFGNDLTTFP+ SKLK L++LLAGNND LPSELLFLP
Sbjct 80 SLSSLPDEIGDCKNLEQLNLFGNDLTTFPAALSKLKKLRILLAGNNDLKFLPSELLFLPE 139

Query 121 IKILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIK 180
      IK +Y+D+NKLTLTETDVEILASLSLEELD+LN GIK LPFNYEKL NL NLKRLNIK
Sbjct 140 IKTIYMDQNKLTLTETDVEILASLSLEELDNLNLGIKTLPFNYEKLGNLTNLKRLNIK 199

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
      KTSKKGEDADKLQAILPNTKIDY
Sbjct 200 KTSKKGEDADKLQAILPNTKIDY 222
```


>WP_039940928.1 hypothetical protein [Leptospira alexanderi]
Length=215

Score = 311 bits (798), Expect = 3e-105, Method: Compositional matrix adjust.
Identities = 176/203 (87%), Positives = 187/203 (92%), Gaps = 0/203 (0%)

```
Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KDLRLN 60
        GF+CFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPE VCGFPNLT KDLRLN
Sbjct 13 GFICFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEGVC GFPNLT KDLRLN 72

Query 61 SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTF SKLKNLKVLLAGNNDFTILPSELLFLPL 120
        SL+ LP+ IG+CK LEQLNLF GNDLTTFP+ SKLK L++LLAGNND LPSELLFLP
Sbjct 73 SLSSLPDEIGDCKNLEQLNLF GNDLTTFPAALSKLKKLRILLAGNNDLKFLPSELLFLPE 132

Query 121 IKILYVDRNKLTLTETDVeilaslssleeldslnsGIKALPFNYEKL VNLINLKRLNIK 180
        IK +Y+D+NKLTLTETDVEILASLSSLEELD+LN GIK LPFNYEKL NL NLKRLNIK
Sbjct 133 IKTIYMDQNKLTLTETDVEILASLSSLEELDNLNLGIKTLPFNYEKLGNLTNLKRLNIK 192

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
        KTSKKGEDADKLQAILPNTKIDY
Sbjct 193 KTSKKGEDADKLQAILPNTKIDY 215
```

>WP_078124592.1 hypothetical protein [Leptospira alexanderi]
Length=215

Score = 309 bits (791), Expect = 4e-104, Method: Compositional matrix adjust.
Identities = 175/203 (86%), Positives = 186/203 (92%), Gaps = 0/203 (0%)

```
Query 1 GFVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KDLRLN 60
        GF+CFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPE VCGFPNLT KDLRLN
Sbjct 13 GFICFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEGVC GFPNLT KDLRLN 72

Query 61 SLTFLPEFIGECKRLEQLNLF GNDLTTFPSTF SKLKNLKVLLAGNNDFTILPSELLFLPL 120
        SL+ LP+ IG+CK LEQLNLF GNDLTTFP+ SKLK L++LLAGNND LPSELLFLP
Sbjct 73 SLSSLPDEIGDCKNLEQLNLF GNDLTTFPAALSKLKKLRILLAGNNDLKFLPSELLFLPE 132

Query 121 IKILYVDRNKLTLTETDVeilaslssleeldslnsGIKALPFNYEKL VNLINLKRLNIK 180
        IK +Y+D+NKLTLTETDVEILASLSSLEELD+LN GIK LPFNYEKL NL NLKRLNIK
Sbjct 133 IKTIYMDQNKLTLTETDVEILASLSSLEELDNLNLGIKTLPFNYEKLGNLTNLKRLNIK 192

Query 181 KTSKKGEDADKLQAILPNTKIDY 203
        KTSKKG DADKLQAILPNTKIDY
Sbjct 193 KTSKGGDADKLQAILPNTKIDY 215
```

>WP_004466481.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
EMM76134.1 leucine rich repeat protein [Leptospira santarosai str. 2000030832]
Length=217

Score = 307 bits (787), Expect = 2e-103, Method: Compositional matrix adjust.
Identities = 177/205 (86%), Positives = 184/205 (90%), Gaps = 2/205 (1%)

```
Query 1 GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLR 58
        GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNLTKDLR
Sbjct 13 GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLTKDLR 72

Query 59 LNSLTFLPEFIGECKRLEQLNLFNDLTTFSTFSKLKLNKVLLAGNNDFTILPSELLFL 118
        LNSLT LPEFIGECK LEQLNLFNDLTTFSTFSKLKLNKVLLAG+NDFT+LPSELLFL
Sbjct 73 LNSLTSLPEFIGECKSLEQLNLFNDLTTFSTFSKLKLNKVLLAGSNDFTVLPSELLFL 132

Query 119 PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN 178
        P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN
Sbjct 133 PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTGLKRLN 192

Query 179 IKKTSLKGEDADKLQAILPNTKIDY 203
        IKKTSLKGEDA KLQAILPN KIDY
Sbjct 193 IKKTSLKGEDAGKLQAILPNAKIDY 217
```

>WP_046692451.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
AVQ11281.1 Leucine rich repeat protein [Leptospira santarosai]
Length=217

Score = 306 bits (785), Expect = 4e-103, Method: Compositional matrix adjust.
Identities = 176/205 (86%), Positives = 184/205 (90%), Gaps = 2/205 (1%)

```
Query 1 GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLR 58
        GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KDLR
Sbjct 13 GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLIKDLR 72

Query 59 LNSLTFLPEFIGECKRLEQLNLFNDLTTFSTFSKLKLNKVLLAGNNDFTILPSELLFL 118
        LNSLT LPEFIGECKRLEQLNLFNDLTTFSTFSKLKLNKVLL G+NDFT+LPSELLFL
Sbjct 73 LNSLTSLPEFIGECKRLEQLNLFNDLTTFSTFSKLKLNKVLLVGSNDFTVLPSELLFL 132

Query 119 PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN 178
        P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI+ LPFNYEKL NL LKRLN
Sbjct 133 PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIETLPFNYEKLRLNLTGLKRLN 192

Query 179 IKKTSLKGEDADKLQAILPNTKIDY 203
        IKKTSLKGEDA KLQAILPN KIDY
Sbjct 193 IKKTSLKGEDAGKLQAILPNAKIDY 217
```

>EKT85788.2 hypothetical protein LSS_15741 [Leptospira santarosai serovar
Shermani str. LT 821]
Length=224

Score = 305 bits (782), Expect = 1e-102, Method: Compositional matrix adjust.
Identities = 176/205 (86%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLR	58
		GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KDLR	
Sbjct	20	GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLIKDLR	79
Query	59	LNSLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLFGNLTT PSTFSKLKNLKVLLAG+NDFT+LPSELLFL	
Sbjct	80	LNSLTSLPEFIGECKSLEQLNLFGNLTTLPSTFSKLKNLKVLLAGSNDFTVLPSELLFL	139
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeIdlslnsGIKALPFNYEKLVLNLINLKRLN	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN	
Sbjct	140	PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTGLKRLN	199
Query	179	IKKTSLKGEDADKLQAILPNTKIDY	203
		IKKTSLKGEDA KLQAILPN KIDY	
Sbjct	200	IKKTSLKGEDAGKLQAILPNAKIDY	224

>WP_004471631.1 MULTISPECIES: leucine-rich repeat domain-containing protein [Leptospira]

ASV13101.1 hypothetical protein B2G51_00410 [Leptospira santarosai]
EK079664.1 leucine rich repeat protein [Leptospira sp. Fiocruz LV3954]
EKS08892.1 leucine rich repeat protein [Leptospira santarosai str. JET]
EMI62768.1 leucine rich repeat protein [Leptospira sp. Fiocruz LV4135]
EMN21750.1 leucine rich repeat protein [Leptospira santarosai serovar Arenal str. MAVJ 401]
Length=217

Score = 305 bits (781), Expect = 2e-102, Method: Compositional matrix adjust.
Identities = 176/205 (86%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLR	58
		GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLFGNLTT PSTFSKLKNLKVLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLFGNLTTLPSTFSKLKNLKVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldslnsGIKALPFNYEKLVLNLINLKRNL	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRNL	
Sbjct	133	PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTKLRNL	192
Query	179	IKKTSLKGEDADKLQAILPNTKIDY	203
		IKKTSLKGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSLKGEDAGKLQAILPNAKIDY	217

>WP_061216203.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
Length=217

Score = 305 bits (781), Expect = 2e-102, Method: Compositional matrix adjust.
Identities = 176/205 (86%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLR	58
		GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLFGNLTT PSTFSKLKNLKVLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLFGNLTTLPSTFSKLKNLKVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldslnsGIKALPFNYEKLVLNLINLKRNL	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRNL	
Sbjct	133	PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTKLRNL	192
Query	179	IKKTSLKGEDADKLQAILPNTKIDY	203
		IKKTSLKGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSLKGEDAGKLQAILPNVKIDY	217

>WP_004492778.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
EMF91397.1 leucine rich repeat protein [Leptospira santarosai str. ST188]
Length=217

Score = 304 bits (779), Expect = 3e-102, Method: Compositional matrix adjust.
Identities = 176/205 (86%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

```
Query 1 GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLR 58
        GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KDLR
Sbjct 13 GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSEVPEGVCGFPNLIKDLR 72

Query 59 LNSLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFL 118
        LNSLT LPEFIGECK LEQLNLFGNDLTTFSTFSKLKLNKVLLAG+NDFT+LPSELLFL
Sbjct 73 LNSLTSLPEFIGECKSLEQLNLFGNDLTTLPTFSKLKLNKVLLAGSNDFTVLPSELLFL 132

Query 119 PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN 178
        P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN
Sbjct 133 PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNTGLKRLN 192

Query 179 IKKTSLKGEDADKLQAILPNTKIDY 203
        IKKTSLKGEDA KLQAILPN KIDY
Sbjct 193 IKKTSLKGEDAGKLQAILPNAKIDY 217
```

>EM058507.1 leucine rich repeat protein [Leptospira santarosai str. CBC1416]
Length=224

Score = 305 bits (780), Expect = 3e-102, Method: Compositional matrix adjust.
Identities = 175/205 (85%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

```
Query 1 GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLR 58
        GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KDLR
Sbjct 20 GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLIKDLR 79

Query 59 LNSLTFLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFL 118
        LNSLT LPEFIGECK LEQLNLFGNDLTTFSTFSKLKLN+VLLAG+NDFT+LPSELLFL
Sbjct 80 LNSLTSLPEFIGECKSLEQLNLFGNDLTTLPTFSKLKLNQVLLAGSNDFTVLPSELLFL 139

Query 119 PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN 178
        P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN
Sbjct 140 PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNTGLKRLN 199

Query 179 IKKTSLKGEDADKLQAILPNTKIDY 203
        IKKTSLKGEDA KLQAILPN KIDY
Sbjct 200 IKKTSLKGEDAGKLQAILPNAKIDY 224
```

>WP_004468285.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
EK033314.1 leucine rich repeat protein [Leptospira santarosai str. MOR084]
EMM87883.1 leucine rich repeat protein [Leptospira santarosai str. 2000027870]
EM012096.1 leucine rich repeat protein [Leptospira santarosai str. CBC523]
EM021776.1 leucine rich repeat protein [Leptospira santarosai str. HAI134]
Length=217

Score = 304 bits (779), Expect = 4e-102, Method: Compositional matrix adjust.
Identities = 175/205 (85%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKLDLR	58
		GF+CFTAS DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTASLEIDCKKNTEEILEEAKARPESVQTLDFGMRLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLFGNLTT PSTFSKLKNL+VLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLFGNLTTLPSTFSKLKNLQVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN	
Sbjct	133	PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTKLRLN	192
Query	179	IKKTSKKGEDADKLQAILPNTKIDY	203
		IKKTSKKGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSKKGEDAGKLQAILPNAKIDY	217

>WP_004486481.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
EMJ51727.1 leucine rich repeat protein [Leptospira santarosai str. HAI1349]
EM043962.1 leucine rich repeat protein [Leptospira santarosai str. ZUN179]
EMP80142.1 leucine rich repeat protein [Leptospira santarosai str. CBC1531]
Length=217

Score = 303 bits (777), Expect = 6e-102, Method: Compositional matrix adjust.
Identities = 174/205 (85%), Positives = 183/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKLDLR	58
		GF+CFTAS DCKKN EEIL EAKA+PE +QTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTASLEIDCKKNTEEILEEAKARPESIQTLDFGMRLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLFGNLTTFPSTFSKLKNLVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLFGNLTT PSTFSKLKNL+VLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLFGNLTTLPSTFSKLKNLQVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINKRLN	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN	
Sbjct	133	PSIKTLYVDRNRLTLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTKLRLN	192
Query	179	IKKTSKKGEDADKLQAILPNTKIDY	203
		IKKTSKKGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSKKGEDAGKLQAILPNAKIDY	217

>WP_004473752.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
 AVV50234.1 Leucine rich repeat protein [Leptospira santarosai]
 AVV80614.1 Leucine rich repeat protein [Leptospira santarosai]
 EM070761.1 leucine rich repeat protein [Leptospira santarosai str. 200403458]
 EM099203.1 leucine rich repeat protein [Leptospira santarosai str. 200702252]
 KXZ30505.1 hypothetical protein AYB33_17160 [Leptospira santarosai]
 Length=217

Score = 303 bits (776), Expect = 8e-102, Method: Compositional matrix adjust.
 Identities = 175/205 (85%), Positives = 182/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLR	58
		GF+CFTA DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTAGLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLF GNDLTTFSTFSKLKLNKVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLF GNDLTTFSTFSKLKLNKVLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLF GNDLTTLPTFSKLKLNKVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKRLN	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN	
Sbjct	133	PSIKTLYVDRNRLLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTGLKRLN	192
Query	179	IKKTSKLGEDADKLQAILPNTKIDY	203
		IKKTSKLGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSKLGEDAGKLQAILPNAKIDY	217

>WP_004476114.1 leucine-rich repeat domain-containing protein [Leptospira santarosai]
 EKR92365.1 leucine rich repeat protein [Leptospira santarosai str. CBC379]
 EM032349.1 leucine rich repeat protein [Leptospira santarosai str. HAI821]
 EMP02889.1 leucine rich repeat protein [Leptospira santarosai str. HAI1380]
 Length=217

Score = 302 bits (774), Expect = 2e-101, Method: Compositional matrix adjust.
 Identities = 174/205 (85%), Positives = 182/205 (89%), Gaps = 2/205 (1%)

Query	1	GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLR	58
		GF+CFTA DCKKN EEIL EAKA+PE VQTLDFGM+KLS VPE VCGFPNL KLDLR	
Sbjct	13	GFICFTAGLEIDCKKNTEEILEEAKARPESVQTLDFGMRKLSAVPEGVCGFPNLIKLDLR	72
Query	59	LNSLTFLPEFIGECKRLEQLNLF GNDLTTFSTFSKLKLNKVLLAGNNDFTILPSELLFL	118
		LNSLT LPEFIGECK LEQLNLF GNDLTTFSTFSKLKLN+VLLAG+NDFT+LPSELLFL	
Sbjct	73	LNSLTSLPEFIGECKSLEQLNLF GNDLTTLPTFSKLKLNQVLLAGSNDFTVLPSELLFL	132
Query	119	PLIKILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKRLN	178
		P IK LYVDRN+LTLTETDVEILASLSSLEELD+ NSGI LPFNYEKL NL LKRLN	
Sbjct	133	PSIKTLYVDRNRLLTETDVEILASLSSLEELDNLQNSGIGTLPFNYEKLRLNLTGLKRLN	192
Query	179	IKKTSKLGEDADKLQAILPNTKIDY	203
		IKKTSKLGEDA KLQAILPN KIDY	
Sbjct	193	IKKTSKLGEDAGKLQAILPNAKIDY	217

>EMF79993.1 leucine rich repeat protein [Leptospira weilii serovar Topaz

str. LT2116]
Length=185

Score = 294 bits (753), Expect = 1e-98, Method: Compositional matrix adjust.
Identities = 167/185 (90%), Positives = 177/185 (96%), Gaps = 0/185 (0%)

```
Query 19  LG EAKAKPELVQTLD FGMQKLSTVPEE VCGFPNLTKDLRLNSLTFLPEFIGECKRLEQL 78
          +GEAKAKPE +QTLD FGMQKLST+PE VCGFPNLTKDLRLNSLT LPEFIGEC+RLEQL
Sbjct 1  MGEAKAKPESIQTLDFGMQKLSTIPEGVCGFPNLTKDLRLNSLTSLPEFIGECRRLEQL 60

Query 79  NLFGNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDV 138
          NLFGNDL TFPSTFSKLK NLKVLLAG+NDF+ILPSELLFLPLIKILYVD+NKLTLTETDV
Sbjct 61  NLFGNDLATFPSTFSKLK NLKVLLAGSNDFSILPSELLFLPLIKILYVDQNKLTLTETDV 120

Query 139 eilaslsleeeldslslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDADKLQAILPN 198
          EILASLS+LEELD L+LN GIK+LPFNYEKL NL NLKRLNIKKTSLKGEDA KLQAILPN
Sbjct 121 EILASLSNLEELD LNLNLGIKSLPFNYEKLGNLTNLKRLNIKKTSLKGEDAYKLQAILPN 180

Query 199 TKIDY 203
          TKIDY
Sbjct 181 TKIDY 185
```

>EMY13797.1 leucine rich repeat protein [Leptospira weilii str. Ecochallenge]
Length=185

Score = 290 bits (742), Expect = 4e-97, Method: Compositional matrix adjust.
Identities = 167/185 (90%), Positives = 175/185 (95%), Gaps = 0/185 (0%)

```
Query 19  LG EAKAKPELVQTLD FGMQKLSTVPEE VCGFPNLTKDLRLNSLTFLPEFIGECKRLEQL 78
          +GEAKAK E ++TLDFGMQKLSTVPE VCGFPNLTKDLRLNSLT LPEFIG+CK LEQL
Sbjct 1  MGEAKAKSESIRTLD FGMQKLSTVPEGVCGFPNLTKDLRLNSLTSLPEFIGDCKNLEQL 60

Query 79  NLFGNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDV 138
          NLFGNDL TFP TFSKLK NLKVLLAG+NDF+ILPSELLFLPLIKILYVDRNKLTLTETDV
Sbjct 61  NLFGNDLATFPPTFSKLK NLKVLLAGSNDFILPSELLFLPLIKILYVDRNKLTLTETDV 120

Query 139 eilaslsleeeldslslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDADKLQAILPN 198
          EILASLS+LEELD L+LN GIK+LPFNYEKL NL NLKRLNIKKTSLKGEDADKLQAILPN
Sbjct 121 EILASLSNLEELD LNLNLGIKSLPFNYEKLGNLTNLKRLNIKKTSLKGEDADKLQAILPN 180

Query 199 TKIDY 203
          TKIDY
Sbjct 181 TKIDY 185
```

>WP_100761136.1 leucine-rich repeat domain-containing protein [Leptospira barantonii]
PJZ59167.1 hypothetical protein CH367_03875 [Leptospira barantonii]
Length=217

Score = 289 bits (739), Expect = 4e-96, Method: Compositional matrix adjust.
Identities = 165/195 (85%), Positives = 176/195 (90%), Gaps = 0/195 (0%)

```
Query 9  FDCKKNAEEILGEAKAKPELVQTLD FGMQKLSTVPEE VCGFPNLTKDLRLNSLTFLPEF 68
          DCKKNAEEIL EAKAKPE VQ LD GMQKL+ VPE VCGFP+LTKDLRLNSLT LPEF
```


Sbjct	23	IDCKKNAEEILEEAKAKPESVQVLDLGMQKLTAVPESVCGFPSLTKDLRLNSLTSLPEF	82
Query	69	IGECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR	128
		IGECK LEQLNLFGNDLT+ PS+FSKLKLNKVLLAG+ND T+LPSELLFLPLIK LY+D+	
Sbjct	83	IGECKNLEQLNLFGNDLTSIPSSFSKLKLNKVLLAGSNDLTVLPSELLFLPLIKTLYLDQ	142
Query	129	NKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGED	188
		NKL L ETDVEILASLS LEELDL+LNSGIKALP NYEKL +L LKRLNIKKTSLKGED	
Sbjct	143	NKLVLNETDVEILASLSGLEELDLNLSGIKALPSNYEKLKSLTRLKRLNIKKTSLKGED	202
Query	189	ADKLQAILPNTKIDY 203	
		ADKLQA+LPNTKIDY	
Sbjct	203	ADKLQALLPNTKIDY 217	

>WP_123179347.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]
AYV55126.1 hypothetical protein EFP84_06105 [Leptospira kmetyi]
Length=217

Score = 280 bits (716), Expect = 1e-92, Method: Compositional matrix adjust.
Identities = 160/195 (82%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

Query	9	FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEF	68
		DCKKNA E+L EAKAKPE VQTLG GMQKL+ VPE VC FPNLTCLDLRLNSLT LP+	
Sbjct	23	IDCKKNAGEVLEEAKAKPESVQTLDFGMQKLTAVPEGVCAFPNLTCLDLRLNSLTVLPDS	82
Query	69	IGECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR	128
		IGECK LEQLNLFGNDLT+ PS+FSKLKLNKVLLAG+ND T+LPSELLFLP I+ LY+D+	
Sbjct	83	IGECKNLEQLNLFGNDLTSIPSSFSKLKLNKVLLAGSNDLTVLPSELLFLPSIRTLYLDQ	142
Query	129	NKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGED	188
		NKL L ETDVEILASL LEELDL+LNSGIKALP NYEKL +L LKRLNIKKTSLKGED	
Sbjct	143	NKLVLNETDVEILASLPGLEELDLNLSGIKALPSNYEKLKSLTRLKRLNIKKTSLKGED	202
Query	189	ADKLQAILPNTKIDY 203	
		ADKLQAILPNTKIDY	
Sbjct	203	ADKLQAILPNTKIDY 217	

>WP_100755326.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]
PJZ30273.1 hypothetical protein CH378_08580 [Leptospira kmetyi]
Length=217

Score = 280 bits (715), Expect = 1e-92, Method: Compositional matrix adjust.
Identities = 161/195 (83%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

Query	9	FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEF	68
		DCKKNA E+L EAKAKPE VQTLG GMQKL+ VPE VC FPNLTCLDLRLNSLT LP+	
Sbjct	23	IDCKKNAGEVLEEAKAKPESVQTLDFGMQKLTAVPEGVCAFPNLTCLDLRLNSLTVLPDS	82
Query	69	IGECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR	128
		IGECK LEQLNLFGNDLT+ PS+FSKLKLNKVLLAG+ND T+LPSELLFLP IK LY+D+	
Sbjct	83	IGECKNLEQLNLFGNDLTSIPSSFSKLKLNKVLLAGSNDLTVLPSELLFLPSIKTLYLDQ	142
Query	129	NKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGED	188

```

          NKL L ETDVEILASLS LEELDL+LNSGIK LP NYEKL +L LKRLNIKKTSLKGED
Sbjct  143 NKLALNETDVEILASLSGLEELDLNLNSGIKVLPSNYEKLKSLTRLKRLNIKKTSLKGED  202

Query  189 ADKLQAILPNTKIDY  203
          ADKLQAILPNTKIDY
Sbjct  203 ADKLQAILPNTKIDY  217

```

>WP_135607718.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]
 TGK19466.1 hypothetical protein EH062_05620 [Leptospira kmetyi]
 TGK32832.1 hypothetical protein EH066_03605 [Leptospira kmetyi]
 Length=217

Score = 279 bits (713), Expect = 3e-92, Method: Compositional matrix adjust.
 Identities = 160/195 (82%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

```

Query   9   FDCKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEF  68
          DCKKNA E+L EAKAKPE VQTLG GMQKL+ VPE VC FPNLTCLDLRLNSLT LP+
Sbjct  23   IDCKKNAGEVLEEAKAKPESVQTLDLGMQKLTAPEGVCAFPNLTCLDLRLNSLTVLPDS  82

Query   69   IGECKRLEQLNLFGNLDTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR  128
          IGECK LEQLNLFGNLDT+ PS+FSKLKLNKVLLAG+ND T+LPSELLFLP I+ LY+D+
Sbjct  83   IGECKNLEQLNLFGNLDTSIPSSFSLKLNKVLLAGSNDLTVLPSELLFLPSIRTLYLDQ  142

Query   129  NKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINKRLNIKKTSLKGED  188
          NKL L ETDVEILASLS LEELDL+LNSGIK LP NYEKL +L LKRLNIKKTSLKGED
Sbjct  143  NKLVLNETDVEILASLSGLEELDLNLNSGIKVLPSNYEKLKSLTRLKRLNIKKTSLKGED  202

Query   189  ADKLQAILPNTKIDY  203
          ADKLQAILPNTKIDY
Sbjct  203  ADKLQAILPNTKIDY  217

```

>WP_020775386.1 leucine-rich repeat domain-containing protein [Leptospira alstonii]
 EMJ90581.1 leucine rich repeat protein [Leptospira alstonii serovar Sichuan
 str. 79601]
 EQA82096.1 leucine rich repeat protein [Leptospira alstonii serovar Pingchang
 str. 80-412]
 Length=217

Score = 278 bits (712), Expect = 6e-92, Method: Compositional matrix adjust.
 Identities = 163/195 (84%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

```

Query   9   FDCKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEF  68
          DCKKNAAEIL EA KPE V+ LD GMQKLS+VP+ VCGFPNLT LDLRLNSLT LPEF
Sbjct  23   IDCKKNAAEILREANTKPESVRVLDLGMQKLSSVPDGVCGFPNLTNLDLRLNSLTSLPEF  82

Query   69   IGECKRLEQLNLFGNLDTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR  128
          IGECK LEQLNLFGNLDT TFP++ SKLKLNKVLLAGNNDF LPSELLFLP IK LY+DR
Sbjct  83   IGECKNLEQLNLFGNLDTGTFPASISKLNKVLLAGNNDFAALPSELLFLPSIKTLYLDR  142

Query   129  NKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINKRLNIKKTSLKGED  188
          NKLTLTETDVEILASLS LEELDL+LNS IKALP NY+KL NL LKRLNIKKTSLKGED
Sbjct  143  NKLTLTETDVEILASLSGLEELDLNLNSDIKALPSNYKKLNLTRKRLNIKKTSLKGED  202

```

Query 189 ADKLQAILPNTKIDY 203
A+KLQAILPNTKIDY
Sbjct 203 AEKLQAILPNTKIDY 217

>WP_010574016.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]
EQA55239.1 leucine rich repeat protein [Leptospira kmetyi serovar Malaysia
str. Bejo-Iso9]
Length=217

Score = 278 bits (711), Expect = 6e-92, Method: Compositional matrix adjust.
Identities = 160/195 (82%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

Query 9 FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLT KD LRLNSLTFLPEF 68
DCKKNA E+L EAKAKPE VQ LD GMQKL+ VPE VC FPNLT+LDLRLNSLT LP+
Sbjct 23 IDCKKNAGEVLEEAKAKPESVQNLDLGMQKLTA VPEGVCAFPNLTQLDLRLNSLT VLPDS 82

Query 69 IGECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDR 128
IGECK LEQLNLF GNDLT+ PS+FSKLK NLKVLLAG+ND T+LPSELLFLP IK LY+D+
Sbjct 83 IGECKNLEQLNLF GNDLTSIPSSFSKLK NLKVLLAGSNDLTVLPSELLFLPSIKTLYLDQ 142

Query 129 NKLT LTETDVeilas lssleeldlslns GIKALPFNYEKL VNLINL KRLNIKKTSLKGED 188
NKL L ETDVEILASLS LEELDL+LNSGIKALP NYEKL +L LKRLNIKKTSLKGED
Sbjct 143 NKLV LNETDVEILASLSGLEELDLNLNSGIKALPSNYEKLKSLTRLKRLNIKKTSLKGED 202

Query 189 ADKLQAILPNTKIDY 203
ADKLQAILPNTKIDY
Sbjct 203 ADKLQAILPNTKIDY 217

>WP_135653950.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]
TGL70325.1 hypothetical protein EHQ67_05935 [Leptospira kmetyi]
Length=217

Score = 278 bits (711), Expect = 7e-92, Method: Compositional matrix adjust.
Identities = 159/195 (82%), Positives = 171/195 (88%), Gaps = 0/195 (0%)

Query 9 FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLT KD LRLNSLTFLPEF 68
DCKKNA E+L EAKAKPE VQTL D GMQKL+ VPE VC FPNLT KD LRLNSLT LP+
Sbjct 23 IDCKKNAGEVLEEAKAKPESVQTL D LGMQKLTA VPEGVCAFPNLT KD LRLNSLT VLPDS 82

Query 69 IGECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDR 128
IGECK LEQLNLF GNDLT+ PS+FSKLK NLKVLLAG+ND T+LPSELLFLP I+ LY+D+
Sbjct 83 IGECKNLEQLNLF GNDLTSIPSSFSKLK NLKVLLAGSNDLTVLPSELLFLPSIRTLYLDQ 142

Query 129 NKLT LTETDVeilas lssleeldlslns GIKALPFNYEKL VNLINL KRLNIKKTSLKGED 188
NKL L ETDVEILASL LEELDL+LNSGIKALP NYEKL +L LKRLNIKKTSLKGED
Sbjct 143 NKLV LNETDVEILASLPGLEELDLNLNSGIKALPSNYEKLKSLTRLKRLNIKKTSLKGED 202

Query 189 ADKLQAILPNTKIDY 203
ADKLQ ILPNTKIDY
Sbjct 203 ADKLQ TILPNTKIDY 217

>WP_100738364.1 leucine-rich repeat domain-containing protein [Leptospira kmetyi]

PJZ40049.1 hypothetical protein CH370_17970 [Leptospira kmetyi]
Length=217

Score = 278 bits (711), Expect = 7e-92, Method: Compositional matrix adjust.
Identities = 159/195 (82%), Positives = 171/195 (88%), Gaps = 0/195 (0%)

```
Query   9      FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEF  68
          DCKKNA E+L EAKAKPE VQTLG GMQKL+ VPE VC FPNLTCLDLRLNSLT LP+
Sbjct   23      IDCKKNAGEVLEEAKAKPESVQTLGGMQKLTA VPEGVCAFPNLTCLDLRLNSLT VLPDS  82

Query   69      IGECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDR  128
          IGECK LEQLNLF GNDLT+ PS+FSKLKLNKVLLAG+ND T+LPSELLFLP I+ LY+D+
Sbjct   83      IGECKNLEQLNLF GNDLTSIPSSFSKLKLNKVLLAGSNDLTVLPSELLFLPSIRTLYLDQ  142

Query   129     NKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNINLKRLNIKKTSKLGED  188
          NKL L ETDVEILASL LEELDL+LNSGIK LP NYEKL +L LKRLNIKKTSKLGED
Sbjct   143     NKLVLNETDVEILASLPGLEELDLNLSGIKVLPSNYEKLKSLTRLKRLNIKKTSKLGED  202

Query   189     ADKLQAILPNTKIDY  203
          ADKLQAILPNTKIDY
Sbjct   203     ADKLQAILPNTKIDY  217
```

>MBW0432169.1 hypothetical protein [Leptospira yasudae]
Length=217

Score = 277 bits (709), Expect = 1e-91, Method: Compositional matrix adjust.
Identities = 158/193 (82%), Positives = 174/193 (90%), Gaps = 0/193 (0%)

```
Query   11      CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEFIG  70
          CKKN+ EIL EAKAKPE VQ LD GMQKLS++P+ VC FPNLT+LDLRLNSLT LP+FIG
Sbjct   25      CKKNSAEILEEAKAKPESVQILDGGMQKLSSIPDGVCAPNLTCLDLRLNSLTALPDFIG  84

Query   71      ECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNK  130
          +C +LEQLN+FGNDL FPS+FSKLKLNKVLLAG+ND TILPSELLFLPLIK LYVD+NK
Sbjct   85      DCTKLEQLNVFGNDLNAFPSSFSKLKLNKVLLAGSNDLTVLPSELLFLPLIKTLYVDQNK  144

Query   131     LTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNINLKRLNIKKTSKLGEDAD  190
          LTLTETDVEILASLS+LEELDL+LNS I ALP NY+KL +L LKRLNIKKTSKLGEDAD
Sbjct   145     LTLTETDVEILASLSALEELDLNLSKIAALPSNYQKLKSLTRLKRLNIKKTSKLGEDAD  204

Query   191     KLQAILPNTKIDY  203
          KLQAILPNTKIDY
Sbjct   205     KLQAILPNTKIDY  217
```

>TGN02502.1 hypothetical protein EHR10_00815 [Leptospira yasudae]
Length=217

Score = 277 bits (709), Expect = 2e-91, Method: Compositional matrix adjust.
Identities = 158/193 (82%), Positives = 174/193 (90%), Gaps = 0/193 (0%)

```
Query   11      CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLTCLDLRLNSLTFLPEFIG  70
          CKKN+ EIL EAKAKPE VQ LD GMQKLS++P+ VC FPNLT+LDLRLNSLT LP+FIG
Sbjct   25      CKKNSAEILEEAKAKPESVQILDGGMQKLSSIPDGVCAPNLTCLDLRLNSLTALPDFIG  84
```

Query	71	ECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK	130
		+C +LEQLN+FGNDL FPS+FSKLKNLKVLLAG+ND TILPSELLFLPLIK LYVD+NK	
Sbjct	85	DCTKLEQLNVFGNDLNAFPSSFSKLKNLKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK	144
Query	131	LTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRNIKKTSLKGEDAD	190
		LTLTETDVEILASLS+LEELDL+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDAD	
Sbjct	145	LTLTETDVEILASLSALEELDLNLNSKIAALPSNYQKLKSLTRLKRLNIKKTSLKGEDAD	204
Query	191	KLQAILPNTKIDY	203
		KLQAILPNTKIDY	
Sbjct	205	KLQAILPNTKIDY	217

>WP_118964127.1 hypothetical protein [Leptospira yasudae]
 RHX95586.1 hypothetical protein DLM76_00905 [Leptospira yasudae]
 Length=217

Score = 276 bits (707), Expect = 2e-91, Method: Compositional matrix adjust.
 Identities = 159/193 (82%), Positives = 174/193 (90%), Gaps = 0/193 (0%)

Query	11	CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG	70
		CKKNA EIL EAKAKPE VQ LD GMQKLS++P+ VC FPNLT+LDLRLNSLT LP+FIG	
Sbjct	25	CKKNAEEILEEAKAKPESVQILD LGMQKLSSIPDGVC AFPNLTRLDLRLNSLTTLPDFIG	84
Query	71	ECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK	130
		+C +LEQLN+FGNDL FPS+FSKLKNLKVLLAG+ND TILPSELLFLPLIK LYVD+NK	
Sbjct	85	DCTKLEQLNVFGNDLNAFPSSFSKLKNLKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK	144
Query	131	LTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRNIKKTSLKGEDAD	190
		LTLTETDVEILASLS+LEELDL+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDAD	
Sbjct	145	LTLTETDVEILASLSALEELDLNLNSKITALPSNYQKLKSLTRLKRLNIKKTSLKGEDAD	204
Query	191	KLQAILPNTKIDY	203
		KLQAILPNTKIDY	
Sbjct	205	KLQAILPNTKIDY	217

>WP_061249228.1 leucine-rich repeat domain-containing protein [Leptospira alstonii]
 Length=217

Score = 276 bits (707), Expect = 3e-91, Method: Compositional matrix adjust.
 Identities = 162/195 (83%), Positives = 172/195 (88%), Gaps = 0/195 (0%)

Query	9	FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEF	68
		DCKKNAEEIL EA KPE V+ LD GMQKLS+VP+ VCGFPNLT LDLRLNSLT LPEF	
Sbjct	23	IDCKKNAEEILREANTKPESVRVLD LGMQKLSSVPDGVCGFPNLTNLDLRLNSLTSLPEF	82
Query	69	IGECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDR	128
		IGECK LEQLNLFGNDL TFP++ SKLKNLKVLLAGNNDF LPSELLFLP IK LY+DR	
Sbjct	83	IGECKNLEQLNLFGNDLGTFPASISKLKNLKVLLAGNNDFAALPSELLFLPSIKTLYLDR	142
Query	129	NKLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRNIKKTSLKGED	188
		NKLTLTETDVEILASLS LEELDL+LNS IKALP NY+KL NL LK+LNIKKTSLKGED	
Sbjct	143	NKLTLTETDVEILASLSGLEELDLNLNSDIKALPSNYKKLKNLTRLKKLNIKKTSLKGED	202

Query 189 ADKLQAILPNTKIDY 203
A+KLQAILPNTKIDY
Sbjct 203 AEKLQAILPNTKIDY 217

>EMY77189.1 leucine rich repeat protein [Leptospira weilii serovar Ranarum
str. ICFT]
Length=241

Score = 277 bits (708), Expect = 4e-91, Method: Compositional matrix adjust.
Identities = 160/205 (78%), Positives = 178/205 (87%), Gaps = 2/205 (1%)

Query 1 GFVCFTASF--DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKDLR 58
G++ F + F DCKK AEEILGEAKA P V LD GMQKLS++PE +C FPNLT KDLR
Sbjct 37 GWLFFASIFWIDCKKTAEEILGEAKASPSSVLLLDLGMQKLSSIPEGICSFPNLTKDLR 96

Query 59 LNSLTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFL 118
LNSLT LPE +GECK LEQLNLF GNDLTTFP++FSKLKNLKVLLAGNND T+LPSELLFL
Sbjct 97 LNSLTSLPESVGECKNLEQLNLF GNDLTTFPASFSKLKNLKVLLAGNNDLTVLPSELLFL 156

Query 119 PLIKILYVDRNKLTLTETDVeilaslsleeIdlslnsGIKALPFNYEKL VNLINLKRLN 178
P IK LY+D+NK+TLTETDVEILASLS LEELDL+LN+GIK LP NY KL +L LK+LN
Sbjct 157 PRIKTLYLDQNKITLTETDVEILASLSELEELDLNLNTGIKTLPSNYGKLKSLARLKKLN 216

Query 179 IKKTSLKGEDADKLQAILPNTKIDY 203
IKKTSLKGEDA+KLQAILPNTKIDY
Sbjct 217 IKKTSLKGEDAEKLQAILPNTKIDY 241

>WP_238730679.1 hypothetical protein [Leptospira sanjuanensis]
MCG6194236.1 hypothetical protein [Leptospira sanjuanensis]
Length=217

Score = 276 bits (706), Expect = 4e-91, Method: Compositional matrix adjust.
Identities = 158/193 (82%), Positives = 173/193 (90%), Gaps = 0/193 (0%)

Query 11 CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
CKKNA EIL EAKAKPE VQ LD GMQKLS +PE VC +PNLT+LDLRLNSLT LP+FIG
Sbjct 25 CKKNAEEILEEAKAKPESVQILD LGMQKLSAIEPEGVCAYPNLTRLDLRLNSLTLPDFIG 84

Query 71 ECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
+C +LEQLN+FGNDL+ FPS+FSKLKNLKVLLAG+ND TILPSELLFLPLIK LYVD+NK
Sbjct 85 DCTKLEQLNVFGNDLSGFPSSFSKLKNLKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK 144

Query 131 LTLTETDVeilaslsleeIdlslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDAD 190
LTLTETDVEILASLS LEELDL+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDA+
Sbjct 145 LTLTETDVEILASLSVLEELDLNLSKITALPSNYQKLKSLTRLKRLNIKKTSLKGEDAE 204

Query 191 KLQAILPNTKIDY 203
KLQAILPNTKIDY
Sbjct 205 KLQAILPNTKIDY 217

>WP_238747060.1 hypothetical protein [Leptospira sanjuanensis]

MCG6168822.1 hypothetical protein [Leptospira sanjuanensis]
Length=217

Score = 276 bits (705), Expect = 6e-91, Method: Compositional matrix adjust.
Identities = 158/193 (82%), Positives = 173/193 (90%), Gaps = 0/193 (0%)

```
Query 11  CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KDLRLNSLTFLPEFIG 70
          CKKNA EIL EAKAKPE VQ LD GMQKLS +PE VC +PNLT+LDLRLNSLT LP+FIG
Sbjct 25  CKKNAEEILEEAKAKPESVQILD LGMQKLSAIPEGVCAYPNLTRLDLRLNSLTTLPDFIG 84

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          +C +LEQLN+FGNDL+ FPS+FSKLKLNKVLLAG+ND TILPSELLFLPLIK LYVD+NK
Sbjct 85  DCTKLEQLNVFGNDLSGFPSSFSKLKLNKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK 144

Query 131 LTLTETDVeilaslssleeldslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDAD 190
          LTLTETDVEILASLS LEELDL+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDA+
Sbjct 145 LTLTETDVEILASLSVLEELDLNLSKITALPSNYQKLKSLTRLKRLNIKKTSLKGEDAE 204

Query 191 KLQAILPNTKIDY 203
          KLQAILPNTKIDY
Sbjct 205 KLQAILPNTKIDY 217
```

>WP_135574399.1 hypothetical protein [Leptospira yasudae]
TGL76867.1 hypothetical protein EH077_17875 [Leptospira yasudae]
TGL79657.1 hypothetical protein EH072_08705 [Leptospira yasudae]
TGL83601.1 hypothetical protein EH083_12525 [Leptospira yasudae]
Length=217

Score = 275 bits (704), Expect = 9e-91, Method: Compositional matrix adjust.
Identities = 161/202 (80%), Positives = 176/202 (87%), Gaps = 1/202 (0%)

```
Query 2  FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLT KDLRLNS 61
          V F A CKKNA EIL EAKAKPE VQ LD GMQKLS++P+ VC FPNLT+LDLRLNS
Sbjct 17  LVSFLA-VACKKNAEEILEEAKAKPESVQILD LGMQKLSSIPDGVCAPNLT RLDLRLNS 75

Query 62  LTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLI 121
          LT LP+FIG+C +LEQLN+FGNDL FPS+FSKLKLN VLLAG+ND TILPSELLFLPLI
Sbjct 76  LTTLPDFIGDCTKLEQLNVFGNDLNAFPSSFSKLKLNVLVLAGSNDLTILPSELLFLPLI 135

Query 122 KILYVDRNKLTLTETDVeilaslssleeldslnsGIKALPFNYEKLVLNINLKRLNIKK 181
          K LYVD+NKLTLTETDVEILASLS+LEELDL+LNS I ALP NY+KL +L LKRLNIKK
Sbjct 136 KTLYVDQNKLTLTETDVEILASLSALEELDLNLSKIAALPSNYQKLKSLTRLKRLNIKK 195

Query 182 TSLKGEDADKLQAILPNTKIDY 203
          TSLKGEDADKLQAILPNTKIDY
Sbjct 196 TSLKGEDADKLQAILPNTKIDY 217
```

>WP_135581985.1 hypothetical protein [Leptospira yasudae]
TGK27116.1 hypothetical protein EH005_09670 [Leptospira yasudae]
TGM08091.1 hypothetical protein EH086_03500 [Leptospira yasudae]
Length=217

Score = 273 bits (698), Expect = 7e-90, Method: Compositional matrix adjust.

Identities = 157/193 (81%), Positives = 172/193 (89%), Gaps = 0/193 (0%)

```
Query 11  CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
          CKKNA EIL EAKAK E VQ LD GMQKLS++P+ VC FPNLT+LDLRLNSLT LP+FIG
Sbjct 25  CKKNAEEILEEAKAKSESVQILD LGMQKLSSIPDGVCAFPNLTRDLRLNSLTALPDFIG 84

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          +C +LEQLN+FGNDL FPS+FSKLK NLKVLLAG+ND TILPSELLFLPLIK LYVD+NK
Sbjct 85  DCTKLEQLNVFGNDLNAFPSSFSKLK NLKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK 144

Query 131 LTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDAD 190
          LTLTETDVEILASL +LEELD L+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDAD
Sbjct 145 LTLTETDVEILASLPAL EELD LNLNSKITALPSNYQKLKSLTRLKRNLNIKKTSLKGEDAD 204

Query 191 KLQAILPNTKIDY 203
          KLQAILPNTKIDY
Sbjct 205 KLQAILPNTKIDY 217
```

>WP_118956310.1 hypothetical protein [Leptospira yasudae]
RHX79626.1 hypothetical protein DLM77_12155 [Leptospira yasudae]
Length=217

Score = 271 bits (694), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 156/193 (81%), Positives = 171/193 (89%), Gaps = 0/193 (0%)

```
Query 11  CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
          CKKNA EIL EAKAK E VQ LD GMQKLS++P+ VC FPNLT+LDLRLNSLT LP+FIG
Sbjct 25  CKKNAEEILEEAKAKSESVQILD LGMQKLSSIPDGVCAFPNLTRDLRLNSLTALPDFIG 84

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          +C +LEQLN+FGNDL FPS+FSKLK NLKVLLAG+ND TILPSELLFLPLIK LYVD+NK
Sbjct 85  DCTKLEQLNVFGNDLNAFPSSFSKLK NLKVLLAGSNDLTILPSELLFLPLIKTLYVDQNK 144

Query 131 LTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDAD 190
          LTLTE DVEILASL +LEELD L+LNS I ALP NY+KL +L LKRLNIKKTSLKGEDAD
Sbjct 145 LTLTEADVEILASLPAL EELD LNLNSKITALPSNYQKLKSLTRLKRNLNIKKTSLKGEDAD 204

Query 191 KLQAILPNTKIDY 203
          KLQAILPNTKIDY
Sbjct 205 KLQAILPNTKIDY 217
```

>WP_004767299.1 hypothetical protein [Leptospira kirschneri]
EKR10488.1 leucine rich repeat protein [Leptospira kirschneri serovar Valbuzzi
str. 200702274]
Length=217

Score = 270 bits (689), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 158/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10  DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct 24  DCKKNAVEILEEAKRKSESVQILD LGMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWI 83
```



```

Query 70  GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct 84  GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKMLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217

```

```

>WP_004759233.1 hypothetical protein [Leptospira kirschneri]
  EKP03838.1 leucine rich repeat protein [Leptospira kirschneri str. 2008720114]
  EMK16725.1 leucine rich repeat protein [Leptospira kirschneri serovar Bim
str. PUO 1247]
  EMN03438.1 leucine rich repeat protein [Leptospira kirschneri serovar Bim
str. 1051]
  EMN24755.1 leucine rich repeat protein [Leptospira kirschneri serovar Sokoine
str. RM1]
  EPG48343.1 leucine rich repeat protein [Leptospira kirschneri serovar Cynopteri
str. 3522 CT]
Length=217

```

Score = 270 bits (689), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 158/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```

Query 10  DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EECVGFPNLT KDLRLNSLTLFPEFI 69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct 24  DCKKNAVEILEEAKRKSESQVILD LGMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWI 83

Query 70  GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct 84  GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217

```

```

>WP_004750770.1 MULTISPECIES: hypothetical protein [Leptospira]
  EJ071711.1 leucine rich repeat protein [Leptospira kirschneri serovar Grippytyphosa
str. RM52]
  EK050626.1 leucine rich repeat protein [Leptospira kirschneri str. 200802841]
  EMK05056.1 leucine rich repeat protein [Leptospira kirschneri str. MMD1493]
  EMK06448.1 leucine rich repeat protein [Leptospira kirschneri]
  EM080710.1 leucine rich repeat protein [Leptospira kirschneri str. 200801774]
Length=217

```

Score = 269 bits (687), Expect = 3e-88, Method: Compositional matrix adjust.

Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct 24 DCKKNAVEILEEAKRKSESQILDGLMQKLTSIPEGICSFPNLTLQLDLRLNSLNSLPDWI 83

Query 70 GECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct 84 GTCKNLEQINLFGNDLATIPSSFSLKLNKVLVGNNDFAFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL LKRLNIKKTS+GEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLRGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217
```

>WP_004779378.1 hypothetical protein [Leptospira kirschneri]
EK060426.1 leucine rich repeat protein [Leptospira kirschneri str. H2]
EMK25402.1 leucine rich repeat protein [Leptospira kirschneri serovar Bulgarica str. Nikolaevo]
Length=217

Score = 269 bits (687), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EI+ EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct 24 DCKKNAVEIIIEAKRKSESQILDGLMQKLTSIPEGICSFPNLTLQLDLRLNSLNSLPDWI 83

Query 70 GECKRLEQLNLFGNLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct 84 GTCKNLEQINLFGNDLATIPSSFSLKLNKVLVGNNDFAFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217
```

>WP_016752856.1 hypothetical protein [Leptospira kirschneri]
Length=217

Score = 268 bits (686), Expect = 4e-88, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EI+ EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct 24 DCKKNAVEIIIEAKRKSESQILDGLMQKLTSIPEGICSFPNLTLQLDLRLNSLNSLPDWI 83
```

```

Query   70   GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN   129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct   84   GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN   143

Query   130  KLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA   189
          KLTLTETDVEILASLSSLEELD L+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct   144  KLTLTETDVEILASLSSLEELD LNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA   203

Query   190  DKLQAILPNTKIDY   203
          DKLQAILPNTKIDY
Sbjct   204  DKLQAILPNTKIDY   217

```

>WP_020778543.1 hypothetical protein [Leptospira kirschneri]
 EMJ94579.1 leucine rich repeat protein [Leptospira kirschneri str. JB]
 Length=217

Score = 268 bits (685), Expect = 7e-88, Method: Compositional matrix adjust.
 Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```

Query   10   DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EEVCGFPNLTKLDLRLNSLTFLPEFI   69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct   24   DCKKNAVEIIEEAKRKSESQILD LGMQKLTSIPEGICSFPNLTLQLDLRLNSLNSLPDWI   83

Query   70   GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN   129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct   84   GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN   143

Query   130  KLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA   189
          KLTLTETDVEIL+SLSSLEELD L+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct   144  KLTLTETDVEILSSSLSSLEELD LNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA   203

Query   190  DKLQAILPNTKIDY   203
          DKLQAILPNTKIDY
Sbjct   204  DKLQAILPNTKIDY   217

```

>WP_082292870.1 hypothetical protein [Leptospira kirschneri]
 OOV43912.1 hypothetical protein B1J93_06785 [Leptospira kirschneri serovar
 Pomona]
 Length=217

Score = 268 bits (684), Expect = 1e-87, Method: Compositional matrix adjust.
 Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```

Query   10   DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EEVCGFPNLTKLDLRLNSLTFLPEFI   69
          DCKKNA EI+ EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I
Sbjct   24   DCKKNAVEIIEEAKRKSESQILD LGMQKLTSIPEGICSFPNLTLQLDLRLNSLNSLPDWI   83

Query   70   GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN   129
          G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N
Sbjct   84   GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN   143

Query   130  KLTLTETDVeilaslssleeldlslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA   189
          KLTLTETDVEIL+SLSSLEELD L+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA

```

Sbjct 144 KLTLTETDVEILSSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
DKLQAILPNTKIDY

Sbjct 204 DKLQAILPNTKIDY 217

>WP_004768364.1 hypothetical protein [Leptospira kirschneri]
EM067317.1 leucine rich repeat protein [Leptospira kirschneri str. 200803703]
Length=217

Score = 267 bits (682), Expect = 2e-87, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI 69
DCK+NA EI+ EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL LP++I

Sbjct 24 DCKENAVEIIEEAKRKSESVQILD LGMQKLTSIPEGICSFPNLT QDLRLNSLNSLPDWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
G CK LEQ+NLF GNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N

Sbjct 84 GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldlslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDA 189
KLTLTETDVEILASLSSLEELD L+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA

Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
DKLQAILPNTKIDY

Sbjct 204 DKLQAILPNTKIDY 217

>WP_004760926.1 hypothetical protein [Leptospira kirschneri]
EKQ84072.1 leucine rich repeat protein [Leptospira kirschneri serovar Grippotyphosa
str. Moskva]
O0V50381.1 hypothetical protein B1J94_00195 [Leptospira kirschneri serovar
Grippotyphosa]
Length=217

Score = 266 bits (681), Expect = 2e-87, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 169/194 (87%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI 69
DCKKNA EIL EAK K E VQ LD GMQKL+++PE +C FPNLT+LDLRLNSL L ++I

Sbjct 24 DCKKNAVEIIEEAKRKSESVQILD LGMQKLTSIPEGICSFPNLT QDLRLNSLNSLTDWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
G CK LEQ+NLF GNDL T PS+FSKLKNLKVLL GNNDF LPSELLFLPLIKILY+D+N

Sbjct 84 GTCKNLEQINLFGNDLATIPSSFSKLKNLKVLLVGNNDF AFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldlslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDA 189
KLTLTETDVEILASLSSLEELD L+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA

Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKTLPSNYNKLKLNRLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
DKLQAILPNTKIDY

Sbjct 204 DKLQAILPNTKIDY 217

>WP_069608131.1 hypothetical protein [Leptospira tipperaryensis]
AOP34913.1 hypothetical protein A0128_14300 [Leptospira tipperaryensis]
Length=217

Score = 261 bits (667), Expect = 4e-85, Method: Compositional matrix adjust.
Identities = 151/193 (78%), Positives = 165/193 (85%), Gaps = 0/193 (0%)

Query	11	CKKNAAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLT	70
		CKKNAAEEIL EAKA P V LD GMQKL+ +PE CGFPNL +LDLRLNSL LP+ +G	
Sbjct	25	CKKNAAEEILNEAKANPASVTILDLMQKLTAIPEGACGFNLT	84
		CKKNAAEEILNEAKANPASVTILDLMQKLTAIPEGACGFNLT	
Query	71	ECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNK	130
		ECK +EQLN+FGNDLTTFPS SKLKLNKVLLAGNND T LPSELLFLP IK +Y+D+NK	
Sbjct	85	ECKSVEQLNVFGNDLTTFPSELSKLKLNKVLLAGNNDLTNLPSELLFLPEIKTIYMDQNK	144
		ECKSVEQLNVFGNDLTTFPSELSKLKLNKVLLAGNNDLTNLPSELLFLPEIKTIYMDQNK	
Query	131	LTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDAD	190
		LTLTETDV+ILASLS+LEELDL+LNSGIK LP NY KL NL LKRLNIKKTSLKGEDA+	
Sbjct	145	LTLTETDVIDILASLSNLEELDLNLNSGIKLPANYTKLNLT	204
		LTLTETDVIDILASLSNLEELDLNLNSGIKLPANYTKLNLT	
Query	191	KLQAILPNTKIDY 203	
		KLQAILP TKIDY	
Sbjct	205	KLQAILPKTKIDY 217	
		KLQAILPKTKIDY	

>WP_205279762.1 hypothetical protein [Leptospira ainlahdjerensis]
MBM9577638.1 hypothetical protein [Leptospira ainlahdjerensis]
Length=217

Score = 261 bits (667), Expect = 4e-85, Method: Compositional matrix adjust.
Identities = 150/193 (78%), Positives = 164/193 (85%), Gaps = 0/193 (0%)

Query	11	CKKNAAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFNLT	70
		CKKNAAEEIL EAKA P V LD GMQKL+ +PE CGFPNL +LDLRLNSL LP+ +G	
Sbjct	25	CKKNAAEEILNEAKANPASVTILDLMQKLTAIPEGACGFNLT	84
		CKKNAAEEILNEAKANPASVTILDLMQKLTAIPEGACGFNLT	
Query	71	ECKRLEQLNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNK	130
		ECK +EQLN+FGNDLTTFPS SKLKLNKVLLAGNND T LPSELLFLP IK +Y+D+NK	
Sbjct	85	ECKSVEQLNVFGNDLTTFPSALS	144
		ECKSVEQLNVFGNDLTTFPSALS	
Query	131	LTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDAD	190
		LTLTETDV+ILASLS+LEELDL+LN GIK LP NY KL NL LKRLNIKKTSLKGEDA+	
Sbjct	145	LTLTETDVIDILASLSNLEELDLNLNVGIKILPANYTKLNLT	204
		LTLTETDVIDILASLSNLEELDLNLNVGIKILPANYTKLNLT	
Query	191	KLQAILPNTKIDY 203	
		KLQAILP TKIDY	
Sbjct	205	KLQAILPKTKIDY 217	
		KLQAILPKTKIDY	

>WP_232371773.1 hypothetical protein [Leptospira ainazelensis]
Length=199

Score = 258 bits (658), Expect = 5e-84, Method: Compositional matrix adjust.

Identities = 149/193 (77%), Positives = 166/193 (86%), Gaps = 0/193 (0%)

```
Query 11  CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
          CKKN EEIL EA AK + V LD GMQKL+++P+ VC FPNL +LDLRLNSL LP+FIG
Sbjct 7   CKKNVEEILNEANAKADSVTILD LGMQKLTSIPDGVCKFPNLKRLDLRLNSLASLPDFIG 66

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          ECK +EQLN+FGNDLTTFPS SKLKNLKV LAGNND T LPSELLFLP IK +Y+D+NK
Sbjct 67  ECKSVEQLNVFGNDLTTFPSALS KLK NLKVFLAGNNDLTNLPSELLFLPEIKTIYMDQNK 126

Query 131  LTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDAD 190
          LTLTETDV+ILASLS+LEELDL+LNSGIK+LP NY KL NL LKRLNIKKTSLKGEDA+
Sbjct 127  LTLTETDVIDILASLSNLEELDLNLNSGIKSLPSNYTKLKNLTRLKRLNIKKTSLKGEDAE 186

Query 191  KLQAILPNTKIDY 203
          KLQAILP TKIDY
Sbjct 187  KLQAILPKTKIDY 199
```

>MBM9502464.1 hypothetical protein [Leptospira ainazelensis]
Length=217

Score = 258 bits (659), Expect = 6e-84, Method: Compositional matrix adjust.
Identities = 149/193 (77%), Positives = 166/193 (86%), Gaps = 0/193 (0%)

```
Query 11  CKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
          CKKN EEIL EA AK + V LD GMQKL+++P+ VC FPNL +LDLRLNSL LP+FIG
Sbjct 25  CKKNVEEILNEANAKADSVTILD LGMQKLTSIPDGVCKFPNLKRLDLRLNSLASLPDFIG 84

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          ECK +EQLN+FGNDLTTFPS SKLKNLKV LAGNND T LPSELLFLP IK +Y+D+NK
Sbjct 85  ECKSVEQLNVFGNDLTTFPSALS KLK NLKVFLAGNNDLTNLPSELLFLPEIKTIYMDQNK 144

Query 131  LTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDAD 190
          LTLTETDV+ILASLS+LEELDL+LNSGIK+LP NY KL NL LKRLNIKKTSLKGEDA+
Sbjct 145  LTLTETDVIDILASLSNLEELDLNLNSGIKSLPSNYTKLKNLTRLKRLNIKKTSLKGEDAE 204

Query 191  KLQAILPNTKIDY 203
          KLQAILP TKIDY
Sbjct 205  KLQAILPKTKIDY 217
```

>WP_004443975.1 hypothetical protein [Leptospira noguchii]
EM090500.1 leucine rich repeat protein [Leptospira noguchii str. 2001034031]
Length=217

Score = 255 bits (652), Expect = 7e-83, Method: Compositional matrix adjust.
Identities = 158/202 (78%), Positives = 174/202 (86%), Gaps = 0/202 (0%)

```
Query 2   FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNS 61
          F+          DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNS
Sbjct 16  FLISIFWIDCKKNAIEILEEAKKKSESVQILD LGMQKLTSIPEGVCSFPNLQLDLRLNS 75

Query 62  LTFLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLI 121
          L+FLP++IG CK LEQ+NLF GNDLTT PS+FSKLK NLKVLL GNNDFT LPSELLFLPLI
```

Sbjct	76	LSFLPDWIGTCKNLEQVNLFGNDLTTVPSSFSKLNKLVLLGNNDFTFLPSELLFLPLI	135
Query	122	KILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKK	181
		K LY+D+NKLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NLI+LKRLNIKK	
Sbjct	136	KTLYLDQNKLTLTETDIEILSSLSGLEELDNLNPGIKILPSNYNKLKNLIHLKRLNIKK	195
Query	182	TSLKGEDADKLQAILPNTKIDY	203
		T LKGEDADKLQAILPNTKIDY	
Sbjct	196	TLLKGEDADKLQAILPNTKIDY	217

>WP_004449517.1 hypothetical protein [Leptospira noguchii]
 EMI70452.1 leucine rich repeat protein [Leptospira noguchii str. Bonito]
 TQE73030.1 hypothetical protein FF021_12990 [Leptospira noguchii]
 UOG31535.1 hypothetical protein MAL06_05855 [Leptospira noguchii]
 UOG35182.1 hypothetical protein MAL02_05610 [Leptospira noguchii]
 UOG46091.1 hypothetical protein MAL01_05745 [Leptospira noguchii]
 Length=217

Score = 254 bits (650), Expect = 1e-82, Method: Compositional matrix adjust.
 Identities = 157/194 (81%), Positives = 172/194 (89%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKLDLRLNSLTFLEPFI	69
		DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I	
Sbjct	24	DCKKNAVEILEEAKKSESQVILDLGMQKLTSIPEGVCSFPNLTKLDLRLNSLSFLPDWI	83
Query	70	GECKRLEQLNLF GNDLTTFPSTFSKLNKLVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDLTT PS+FSKLNKLVLL GNNDFT LPSELLFLPLIK LY+D+N	
Sbjct	84	GTCKNLEQVNLFGNDLTTVPSSFSKLNKLVLLGNNDFTFLPSELLFLPLIKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETD+EIL+SLS LEELDL+LNSGIK LP NY KL NL +LKRLNIKKT LKGEDA	
Sbjct	144	KLTLTETDIEILSSLSGLEELDNLNLSGIKMLPSNYNKLKNLTHLKRLNIKKTLKGEDA	203
Query	190	DKLQAILPNTKIDY	203
		DKLQAILPNTKIDY	
Sbjct	204	DKLQAILPNTKIDY	217

>WP_004422093.1 hypothetical protein [Leptospira noguchii]
 EKR73675.1 leucine rich repeat protein [Leptospira noguchii str. 2006001870]
 UOG49773.1 hypothetical protein MAL00_05865 [Leptospira noguchii]
 Length=217

Score = 254 bits (650), Expect = 2e-82, Method: Compositional matrix adjust.
 Identities = 157/194 (81%), Positives = 172/194 (89%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKLDLRLNSLTFLEPFI	69
		DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I	
Sbjct	24	DCKKNAVEILEEAKKSESQVILDLGMQKLTSIPEGVCSFPNLTKLDLRLNSLSFLPDWI	83
Query	70	GECKRLEQLNLF GNDLTTFPSTFSKLNKLVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDLTT PS+FSKLNKLVLL GNNDFT LPSELLFLPLIK LY+D+N	
Sbjct	84	GTCKNLEQVNLFGNDLTTVPSSFSKLNKLVLLGNNDFTFLPSELLFLPLIKTLYLDQN	143

```

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSKGEDA 189
          KLTLTETD+EIL+SLS LEELDL+LNSGIK LP NY KL NL +LKRLNIKKT LKGEDA
Sbjct 144 KLTLTETDIEILSSSLGLEELDNLNLSGIKILPSNYNKLKLNTHLKRLNIKKTLLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217

```

>WP_004455400.1 hypothetical protein [Leptospira noguchii]
 EMS87372.1 leucine rich repeat protein [Leptospira noguchii str. Hook]
 UOG61555.1 hypothetical protein MAL07_06005 [Leptospira noguchii]
 Length=217

Score = 254 bits (648), Expect = 2e-82, Method: Compositional matrix adjust.
 Identities = 157/194 (81%), Positives = 172/194 (89%), Gaps = 0/194 (0%)

```

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KLDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I
Sbjct 24 DCKKNAIEILEEAKKKSESVQILD LGMQKLTSIPEGVCSFPNLTQLDLRLNSLSFLPDWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLF GNDLTT PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GTCKNLEQVNLFGNDLTTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSKGEDA 189
          KLTLTETD+EIL+SLS LEELDL+LNSGIK LP NY KL NL +LKRLNIKKT LKGEDA
Sbjct 144 KLTLTETDIEILSSSLGLEELDNLNLSGIKILPSNYNKLKLNTHLKRLNIKKTLLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217

```

>WP_243817925.1 hypothetical protein [Leptospira noguchii]
 UOG36928.1 hypothetical protein MAL08_12575 [Leptospira noguchii]
 Length=217

Score = 254 bits (648), Expect = 3e-82, Method: Compositional matrix adjust.
 Identities = 156/194 (80%), Positives = 171/194 (88%), Gaps = 0/194 (0%)

```

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KLDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I
Sbjct 24 DCKKNAVEILEEAKKKSESVQILD LGMQKLTSIPEGVCSFPNLTQLDLRLNSLSFLPDWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLF GNDLTT PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GTCKNLEQVNLFGNDLTTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSKGEDA 189
          KLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRLNIKKT LKGEDA
Sbjct 144 KLTLTETDIEILSSSLGLEELDNLNLP GIKMLPSNYNKLKLNTHLKRLNIKKTLLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY

```


Sbjct 204 DKLQAILPNTKIDY 217

>WP_053522720.1 hypothetical protein [Leptospira noguchii]
Length=217

Score = 254 bits (648), Expect = 3e-82, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 172/194 (89%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EECVGFNLT KDLRLNSLTLPEFI 69
          DCKK+A EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I
Sbjct 24 DCKKSAVEILEEAKKSESQILD LGMQKLTSIPEGVCSFPNLTQLDLRLNSLSFLPDWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+N FGNDLTT PS+FSKLK NLKVLL GNNDFT LPSELLFLPLIKILY+D+N
Sbjct 84 GTCKNLEQVNF F GNDLTTVPSSFSKLK NLKVLLGNNDFTFLPSELLFLPLIKILYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKR LNIKKTSLKGEDA 189
          KLTLTETD+EIL+SLS LEELDL+LNSGIK LP NY KL NL +LKRLNIKKT LKGEDA
Sbjct 144 KLTLTETDIEILSSLSGLEELDLNLNSGIKMLPSNYNKLK NLTHLKR LNIKKTLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217
```

>WP_004452014.1 hypothetical protein [Leptospira noguchii]
EMS89273.1 leucine rich repeat protein [Leptospira noguchii str. Cascata]
UOG57651.1 hypothetical protein MAL03_05830 [Leptospira noguchii]
Length=217

Score = 253 bits (647), Expect = 4e-82, Method: Compositional matrix adjust.
Identities = 157/202 (78%), Positives = 173/202 (86%), Gaps = 0/202 (0%)

```
Query 2 FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EECVGFNLT KDLRLNS 61
          F+ DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNS
Sbjct 16 FLISIFWIDCKKNAVEILEEAKKSESQILD LGMQKLTSIPEGVCSFPNLTQLDLRLNS 75

Query 62 LTLPEFIGECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLI 121
          L+FLP++IG CK LEQ+NLFGNDLTT PS+FSKLK NLKVLL GNNDFT LPSELLFLPLI
Sbjct 76 LSFLPDWIGTCKNLEQVNLFGNDLTTVPSSFSKLK NLKVLLGNNDFTFLPSELLFLPLI 135

Query 122 KILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKR LNIKK 181
          K LY+D+NKLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRLNIKK
Sbjct 136 KTLYLDQNKLTLTETDIEILSSLSGLEELDLNLNPGIKILPSNYNKLK NLTHLKR LNIKK 195

Query 182 TSLKGEDADKLQAILPNTKIDY 203
          T LKGEDADKLQAILPNTKIDY
Sbjct 196 TLLKGEDADKLQAILPNTKIDY 217
```

>WP_243827912.1 hypothetical protein [Leptospira noguchii]
UOG42562.1 hypothetical protein MAL05_05795 [Leptospira noguchii]
Length=217

Score = 253 bits (646), Expect = 5e-82, Method: Compositional matrix adjust.
Identities = 157/202 (78%), Positives = 173/202 (86%), Gaps = 0/202 (0%)

```
Query 2 FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFPNLTKDLRLNS 61
F+ DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNS
Sbjct 16 FLISIFWIDCKKNAIEILEEAKKKSESQILDGLGMQKLTSIPEGVCSFPNLTQLDLRLNS 75

Query 62 LTFLPEFIGECKRLEQLNLFGNLDTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLI 121
L+FLP++IG CK LEQ+NLFGNDLTT PS+FSKLKLNKVLL GNNDFT LPSELLFLPLI
Sbjct 76 LSFLPDWIGTCKNLEQVNLFGNDLTTVPSSFSKLKLNKVLLGNNDFTFLPSELLFLPLI 135

Query 122 KILYVDRNKLTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKK 181
K LY+D+NKLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRLNIKK
Sbjct 136 KTLYLDQNKLTLTETDIEILSSLSGLEELDLNLPGIKILPSNYNKLKLNTHLKRLNIKK 195

Query 182 TSLKGEDADKLQAILPNTKIDY 203
T LKGEDADKLQAILPNTKIDY
Sbjct 196 TLLKGEDADKLQAILPNTKIDY 217
```

>WP_061233070.1 hypothetical protein [Leptospira noguchii]
Length=217

Score = 253 bits (645), Expect = 8e-82, Method: Compositional matrix adjust.
Identities = 157/202 (78%), Positives = 173/202 (86%), Gaps = 0/202 (0%)

```
Query 2 FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFPNLTKDLRLNS 61
F+ DCKK+A EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNS
Sbjct 16 FLISIFWIDCKKSAIEILEEAKRKSESQILDGLGMQKLTSIPEGVCSFPNLTQLDLRLNS 75

Query 62 LTFLPEFIGECKRLEQLNLFGNLDTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLI 121
L FLP++IG CK LEQ+NLFGNDLTT PS+FSKLKLNKVLL GNNDFT LPSELLFLPLI
Sbjct 76 LNFLPDWIGTCKNLEQVNLFGNDLTTVPSSFSKLKLNKVLLGNNDFTFLPSELLFLPLI 135

Query 122 KILYVDRNKLTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKK 181
KILY+D+NKLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRLNIKK
Sbjct 136 KILYLDQNKLTLTETDIEILSSLSGLEELDLNLPGIKILPSNYNKLKLNTHLKRLNIKK 195

Query 182 TSLKGEDADKLQAILPNTKIDY 203
T LKGEDADKLQAILPNTKIDY
Sbjct 196 TLLKGEDADKLQAILPNTKIDY 217
```

>WP_017852233.1 hypothetical protein [Leptospira interrogans]
Length=217

Score = 252 bits (643), Expect = 1e-81, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 171/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFPNLTKDLRLNSLTFLPEFI 69
DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGLGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLFGNLDTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
G CK LEQ+NLFGNDL T PS+FSKLKLNKVLL GNNDFT LPSELLFLPLIK LY+D+N
```

Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNDFTFLPSELLFLPLIKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSSLEELD+LNSGIKALP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKALPSNYNKLKLNTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY 203	
		DKLQA+LPNT+IDY	
Sbjct	204	DKLQAVLPNTRIDY 217	

>WP_061241709.1 hypothetical protein [Leptospira interrogans]
Length=217

Score = 251 bits (641), Expect = 3e-81, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLRLNSLTFLPEFI	69
		DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I	
Sbjct	24	DCKKNAVEILEEAKRKSESIQILDGGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N	
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNDFTFLPSELLFLPLIKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY 203	
		DKLQA+LPNTKIDY	
Sbjct	204	DKLQAVLPNTKIDY 217	

>WP_001010180.1 hypothetical protein [Leptospira interrogans]
EMJ57593.1 leucine rich repeat protein [Leptospira interrogans serovar Valbuzzi str. Duyster]
EN074053.1 leucine rich repeat protein [Leptospira interrogans serovar Valbuzzi str. Valbuzzi]
Length=217

Score = 251 bits (641), Expect = 3e-81, Method: Compositional matrix adjust.
Identities = 157/194 (81%), Positives = 171/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLRLNSLTFLPEFI	69
		DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I	
Sbjct	24	DCKKNAVEILEEAKRKSESIQILDGGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N	
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNDFTFLPSELLFLPLIKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NLI+LKRLNIKKTSLKGD+DA	
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLKLNLIHLKRLNIKKTSLKGD+DA	203

Query 190 DKLQAILPNTKIDY 203
 DKLQA+LPNTKIDY
 Sbjct 204 DKLQAVLPNTKIDY 217

>WP_001011126.1 MULTISPECIES: hypothetical protein [Leptospira]
 EJP05270.1 leucine rich repeat protein [Leptospira interrogans serovar Bulgarica str. Mallika]
 EK005519.1 leucine rich repeat protein [Leptospira interrogans str. C10069]
 EK013588.1 leucine rich repeat protein [Leptospira kirschneri str. H1]
 UID84470.1 hypothetical protein J9305_05680 [Leptospira interrogans]
 UML79483.1 hypothetical protein FH602_14425 [Leptospira kirschneri]
 Length=217

Score = 251 bits (641), Expect = 3e-81, Method: Compositional matrix adjust.
 Identities = 157/194 (81%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFI 69
 DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
 Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTLQLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
 G CK LEQ+NLF GNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N
 Sbjct 84 GACKNLEQINLF GNDLNTVPSSFSLKLNKVL LLAGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDA 189
 KLTLTETDVEILASLSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
 Sbjct 144 KLTLTETDVEILASLSLEELDNLNSGIKVLPSNYNKLNLTHLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
 DKLQA+LPNTKIDY
 Sbjct 204 DKLQAVLPNTKIDY 217

>WP_118981207.1 hypothetical protein [Leptospira stimsonii]
 RHX88693.1 hypothetical protein DLM78_07170 [Leptospira stimsonii]
 TGK22822.1 hypothetical protein EH098_05955 [Leptospira stimsonii]
 TGM14994.1 hypothetical protein EH090_11000 [Leptospira stimsonii]
 Length=217

Score = 251 bits (640), Expect = 4e-81, Method: Compositional matrix adjust.
 Identities = 145/195 (74%), Positives = 162/195 (83%), Gaps = 0/195 (0%)

Query 9 FDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEF 68
 +CKKN EEIL EA A + + LD GMQKL+++PE C FPNL +LDLRLNSL LPE
 Sbjct 23 VECKKNVEEILNEANASADSI AVL DLGMQKLTSIPEGACKFPNLKRLDLRLNSLASLPES 82

Query 69 IGECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDR 128
 +GECK +EQLN+FGNDL TFPS SKLKNLKVLLAGNND LPSELLFLP IK +Y+D+
 Sbjct 83 LGECKSVEQLNVFGNDLKT FPSALS KLKLNKVL LLAGNNDLANLPSELLFLPEIKTIYLDQ 142

Query 129 NKLTLETETDVeilaslsleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGED 188
 NKL LTETDV+ILASLSLEELDLSLN+GIK+LP NY KL NL LKRLNIKKTSLKGED
 Sbjct 143 NKLILTETDVIDILASLSLEELDLSLNTGIKSLPANYTKLKNLTRLKRLNIKKTSLKGED 202

Query 189 ADKLQAILPNTKIDY 203
A+KLQAILP TKIDY
Sbjct 203 AEKLQAILPKTKIDY 217

>WP_004427427.1 hypothetical protein [Leptospira noguchii]
EMN02249.1 leucine rich repeat protein [Leptospira noguchii str. 2007001578]
EPE81746.1 leucine rich repeat protein [Leptospira noguchii str. 1993005606]
Length=217

Score = 251 bits (640), Expect = 4e-81, Method: Compositional matrix adjust.
Identities = 154/194 (79%), Positives = 171/194 (88%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFPNLTCLDLRLNSLTFLPEFI 69
DCKK+A EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL+FLP++I
Sbjct 24 DCKKSAIEILEEAKRKSESVQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLSFLPDWI 83

Query 70 GECKRLEQLNLFQNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
G CK LEQ+NLFQNDLTT PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GTCKNLEQVNLFGNDLTTVPSSFSLKNLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRNLNIKKTSKGEDA 189
KLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRNLNIKK L+GEDA
Sbjct 144 KLTLTETDIEILSSLSGLEELDLNLPNGIKMLPSNYNKLKNLTHLKRNLNIKKTLRGEDA 203

Query 190 DKLQAILPNTKIDY 203
DKLQAILPNTKIDY
Sbjct 204 DKLQAILPNTKIDY 217

>WP_004438578.1 hypothetical protein [Leptospira noguchii]
EM040832.1 leucine rich repeat protein [Leptospira noguchii serovar Autumnalis
str. ZUN142]
Length=217

Score = 251 bits (640), Expect = 5e-81, Method: Compositional matrix adjust.
Identities = 156/202 (77%), Positives = 172/202 (85%), Gaps = 0/202 (0%)

Query 2 FVCFTASFDCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVCGFPNLTCLDLRLNS 61
F+ DCKKNA EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNS
Sbjct 16 FLISIFWIDCKKNAVEILEEAKKKSESVQILDGMQKLTSIPEGVCSFPNLTQLDLRLNS 75

Query 62 LTFLPEFIGECKRLEQLNLFQNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLI 121
L+FLP++IG CK LEQ+NLFQNDLTT PS+FSKLKNLKVLL GNNDFT LPSELLFLPLI
Sbjct 76 LSFLPDWIGTCKNLEQVNLFGNDLTTVPSSFSLKNLKVLLGNNDFTFLPSELLFLPLI 135

Query 122 KILYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRNLNIKK 181
K LY+D+NKLTLTETD+EIL+SLS LEELDL+LN GIK LP NY KL NL +LKRNLNIKK
Sbjct 136 KTLYLDQNKLTLTETDIEILSSLSGLEELDLNLPNGIKILPSNYNKLKNLTHLKRNLNIKK 195

Query 182 TSLKGEDADKLQAILPNTKIDY 203
T LKGEDA KLQAILPNTKIDY
Sbjct 196 TLLKGEDAGKLQAILPNTKIDY 217

>EMN50877.1 leucine rich repeat protein [Leptospira interrogans str. L1207]
Length=217

Score = 250 bits (639), Expect = 6e-81, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDG MQKLTSIPEGVCSFPNLTKDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLK NLKVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GACKNLEQINLF GNDLNTVPSSFSKLK NLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKRNLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD L+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELD LNLNSGIKVLPSNYNKLK NLTHLKRNLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQA+LPNT+IDY
Sbjct 204 DKLQAVLPNTRIDY 217
```

>WP_001010181.1 MULTISPECIES: hypothetical protein [Leptospira]
KAA1269663.1 hypothetical protein C5473_18355 [Leptospira interrogans serovar Weerasinghe]
ASV07105.1 hypothetical protein B2G47_15925 [Leptospira interrogans serovar Canicola]
EJ080485.1 leucine rich repeat protein [Leptospira interrogans serovar Pomona str. Kennewicki LC82-25]
EJP16928.1 leucine rich repeat protein [Leptospira interrogans str. FPW2026]
EKN96857.1 leucine rich repeat protein [Leptospira interrogans serovar Pomona str. Pomona]
Length=217

Score = 250 bits (638), Expect = 7e-81, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVP EEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDG MQKLTSIPEGVCSFPNLTKDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLK NLKVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GACKNLEQINLF GNDLNTVPSSFSKLK NLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKL VNLINLKRNLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD L+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELD LNLNSGIKVLPSNYNKLK NLTHLKRNLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQA+LPNT+IDY
Sbjct 204 DKLQAVLPNTRIDY 217
```

>WP_001010177.1 hypothetical protein [Leptospira interrogans]
 KAA1287472.1 hypothetical protein C4X99_23350 [Leptospira interrogans serovar Geyawera]
 MCR8646250.1 hypothetical protein [Leptospira interrogans serovar Bataviae]
 OAM85608.1 hypothetical protein A1343_17415 [Leptospira interrogans serovar Bataviae]
 QC036829.1 hypothetical protein E4412_06120 [Leptospira interrogans]
 QOI37956.1 hypothetical protein Lepto1548_06450 [Leptospira interrogans serovar Bataviae]
 Length=217

Score = 250 bits (638), Expect = 8e-81, Method: Compositional matrix adjust.
 Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI	69
		DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I	
Sbjct	24	DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY+D+N	
Sbjct	84	GACKNLEQINLF GNDLNTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLIKTLYLDQN	143
Query	130	KLTLTETDVeilaslsleeeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSLEEELDL+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEILASLSLEEELDLNLNSGIKVLPSNYNKLKLNTHLKRNLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY 203	
		DKLQA+LPNT+IDY	
Sbjct	204	DKLQAVLPNTRIDY 217	

>WP_002177142.1 hypothetical protein [Leptospira noguchii]
 EM054849.1 leucine rich repeat protein [Leptospira noguchii]
 EQA71632.1 leucine rich repeat protein [Leptospira noguchii serovar Panama str. CZ214]
 MCH1912101.1 hypothetical protein [Leptospira noguchii]
 MCH1915762.1 hypothetical protein [Leptospira noguchii]
 UOG63215.1 hypothetical protein MAL04_12845 [Leptospira noguchii]
 Length=217

Score = 250 bits (638), Expect = 1e-80, Method: Compositional matrix adjust.
 Identities = 155/194 (80%), Positives = 169/194 (87%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI	69
		DCKK+A EIL EAK K E VQ LD GMQKL+++PE VC FPNLT+LDLRLNSL FLP++I	
Sbjct	24	DCKKSAIEILEEAKRKSESVQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNLFPDWI	83
Query	70	GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDLTT PS+FSKLKNLKVLL GNNDFT LPSELLFLPLIK LY D+N	
Sbjct	84	GTCKNLEQVNLFGNDLTTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLIKTLYFDQN	143
Query	130	KLTLTETDVeilaslsleeeldslslnsGIKALPFNYEKLVLNLINLKRNLNIKKTSLKGEDA	189
		KLTLTETD+EIL+SLS LEEELDL+LN GIK LP NY KL NL +LKRLNIKKT LKGEDA	
Sbjct	144	KLTLTETDIEILSSLSGLEELDLNLNPGIKILPSNYNKLKLNTHLKRNLNIKKTLLKGEDA	203

Query 190 DKLQAILPNTKIDY 203
 DKLQAILPNTKIDY
 Sbjct 204 DKLQAILPNTKIDY 217

>WP_100785841.1 hypothetical protein [Leptospira adleri]
 PJZ53367.1 hypothetical protein CH380_10810 [Leptospira adleri]
 PJZ64012.1 hypothetical protein CH376_00300 [Leptospira adleri]
 Length=218

Score = 249 bits (637), Expect = 1e-80, Method: Compositional matrix adjust.
 Identities = 144/193 (75%), Positives = 162/193 (84%), Gaps = 0/193 (0%)

Query 11 CKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
 CKKN EEIL EA A + + LD GMQKL+++PE VC FPNL +LDLRLNSL LP+ +G
 Sbjct 26 CKKNTEEILNEANANADSI AVL DLGMQKLTSIPEGVCKFPNLKRLDLRLNSLASLPDSL G 85

Query 71 ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
 +CK +EQLN+FGNDL TFPS SKLKNLKVLLAGNND T LPSELLFLP IK +Y+D+NK
 Sbjct 86 DCKSVEQLNVFGNDLKT FPSALS KLK NLKVLLAGNNDLTNLPSELLFLPEIKTIYMDQNK 145

Query 131 LTLTETDVeilaslssleeldslnsG IKALPFNYEKL VNLINLKR LNIKKTS LKGEDAD 190
 LTLTE DV+ILASLS+LEELD L+LNSGIK+LP NY KL NL LKRLNIKKTS LKGEDAD
 Sbjct 146 LTLTEADVILASLSNLEELD LNLNSGIKSLPTNYAKLKNLTRLKR LNIKKTS LKGEDAD 205

Query 191 KLQAILPNTKIDY 203
 KLQ ILP TKIDY
 Sbjct 206 KLQTILPKTKIDY 218

>WP_135691680.1 hypothetical protein [Leptospira adleri]
 TGM52779.1 hypothetical protein EHQ97_12710 [Leptospira adleri]
 Length=218

Score = 249 bits (635), Expect = 2e-80, Method: Compositional matrix adjust.
 Identities = 144/193 (75%), Positives = 162/193 (84%), Gaps = 0/193 (0%)

Query 11 CKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
 CKKN EEIL EA A + + LD GMQKL+++PE VC FPNL +LDLRLNSL LP+ +G
 Sbjct 26 CKKNTEEILNEANANADSI AVL DLGMQKLTSIPEGVCKFPNLKRLDLRLNSLASLPDSL G 85

Query 71 ECKRLEQLNLF GNDLTTFPSTFSKLK NLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
 +CK +EQLN+FGNDL TFPS SKLKNLKVLLAGNND T LPSELLFLP IK +Y+D+NK
 Sbjct 86 DCKSVEQLNVFGNDLKT FPSALS KLK NLKVLLAGNNDLTNLPSELLFLPEIKTIYMDQNK 145

Query 131 LTLTETDVeilaslssleeldslnsG IKALPFNYEKL VNLINLKR LNIKKTS LKGEDAD 190
 LTLTETDV+ILASLS+LEELD L+LNSGIK+LP NY KL NL LKR NIKKTS LKGEDAD
 Sbjct 146 LTLTETDVILASLSNLEELD LNLNSGIKSLPSNYAKLKNLTRLKRFNIKKTS LKGEDAD 205

Query 191 KLQAILPNTKIDY 203
 KLQ ILP TKIDY
 Sbjct 206 KLQTILPKTKIDY 218

>PJZ91020.1 hypothetical protein CH379_21015 [Leptospira ellisii]
PKA03647.1 hypothetical protein CH375_15745 [Leptospira ellisii]
Length=217

Score = 248 bits (633), Expect = 4e-80, Method: Compositional matrix adjust.
Identities = 143/200 (72%), Positives = 164/200 (82%), Gaps = 0/200 (0%)

```
Query 4 CFTASFDCCKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLT 63
      C + DCKKNAEEIL EA+ K E + LD GMQKLS++PE +C FPNL +LDLRLNSL+
Sbjct 18 CMLSLSDCCKNAEEILTEAEKKTETITVLDLGMQKLSSLPEGICSFPNLQRLDLRLNSLS 77

Query 64 FLPEFIGECKRLEQLNLFGNDLTTFPSTFSKLNKLVLLAGNNDFTILPSELLFLPLIKI 123
      L E IG+C LEQ+NLFGNDL+T PSTFSKLNK L+VLL G+NDF LPSELLFLP I+
Sbjct 78 TLAETIGDCGNLEQINLFGNDLSTLPSTFSKLNKRLRVLLMGSNDFKTLPESELLFLPEIRT 137

Query 124 LYVDRNKLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTS 183
      +Y D+NKL+L ETDVEILASL+ LEELDL+LNS IK LP NY KL NL LKRLNIKKTS
Sbjct 138 IYADQNKLSLAETDVEILASLTGLEELDLNLNSNIKTLPPNYTKLNKRLKRLNIKKTS 197

Query 184 LKGEDADKLQAILPNTKIDY 203
      LKGEDA+KLQAILP+TKIDY
Sbjct 198 LKGEDAELQAILPSTKIDY 217
```

>WP_002188945.1 hypothetical protein [Leptospira interrogans]
ALE38687.1 leucine-rich-repeat protein [Leptospira interrogans serovar Hardjo str. Norma]
ALN99945.1 hypothetical protein LIH_06205 [Leptospira interrogans serovar Hardjo-prajitno]
EK095373.1 leucine rich repeat protein [Leptospira interrogans str. Brem 329]
MCD1166362.1 hypothetical protein [Leptospira interrogans]
MCH1885836.1 hypothetical protein [Leptospira interrogans]
Length=217

Score = 248 bits (633), Expect = 5e-80, Method: Compositional matrix adjust.
Identities = 155/194 (80%), Positives = 169/194 (87%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFI 69
      DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDLMQKLTSIPEGVCSFPNLQLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLFGNDLTTFPSTFSKLNKLVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
      G CK LEQ+NLFGNDL PS+FSKLNKLVLL GNNDFT LPSELLFLPLIK LY+D+N
Sbjct 84 GACKNLEQINLFGNDLNMVPSSFSLKLNKLVLLGNNDFTFLPSELLFLPLIKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLSKGEDA 189
      KLTLTETDVEILASLSSLEELDL+LNSGIK LP NY KL NL +LKRLNIKKTSLSKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDLNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLSKGEDA 203

Query 190 DKLQAILPNTKIDY 203
      DKLQA+LPNT+IDY
Sbjct 204 DKLQAVLPNTRIDY 217
```

>WP_118970865.1 hypothetical protein [Leptospira stimsonii]
RHX84273.1 hypothetical protein DLM75_23045 [Leptospira stimsonii]
Length=217

Score = 248 bits (632), Expect = 6e-80, Method: Compositional matrix adjust.
Identities = 145/193 (75%), Positives = 160/193 (83%), Gaps = 0/193 (0%)

```
Query   11   CKKNAAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG   70
          CKKN EEIL EA A  + +  LD GMQKL+++PE C FPNL +LDLRLNSL LPE G
Sbjct   25   CKKNVEEILNEANASADSI AVL DLGMQKLTSIPEGACKFPNLKRLDLRLNSLASLPESFG   84

Query   71   ECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRNK   130
          ECK +EQLN+FGNDL TFPS SKLKNLKVLLAGNND LPSSELLFLP IK +Y+D+NK
Sbjct   85   ECKSVEQLNVFGNDLKT FPSALS KLKNLKVLLAGNNDLANLPSELLFLPEIKTIYLDQNK   144

Query   131  LTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRNLNIKKTSLKGEDAD   190
          L LTETDV+ILASLSSLEELDLSLN+GIK+LP NY KL NL LKRLNIKKTSLKGEDA+
Sbjct   145  LILTETDVIDILASLSSLEELDLSLNTGIKSLPANYTKLKNLTLLKRLNIKKTSLKGEDAE   204

Query   191  KLQAILPNTKIDY   203
          KLQAILP TKIDY
Sbjct   205  KLQAILPKTKIDY   217
```

>WP_243399589.1 hypothetical protein [Leptospira ellisii]
Length=199

Score = 246 bits (627), Expect = 2e-79, Method: Compositional matrix adjust.
Identities = 142/194 (73%), Positives = 162/194 (84%), Gaps = 0/194 (0%)

```
Query   10   DCKKNAAEEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFI   69
          DCKKNAAEEIL EA+ K E +  LD GMQKLS++PE +C FPNL +LDLRLNSL+ L E I
Sbjct    6   DCKKNAAEEILTEAEKKTETITVLDLGMQKLSSSLPEGICSFPNLQRLDLRLNSLSTLAETI   65

Query   70   GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN   129
          G+C LEQ+NLFGNDL+T PSTFSKLK L+VLL G+NDF LPSSELLFLP I+ +Y D+N
Sbjct   66   GDCGNLEQINLFGNDLSTLPSTFSKLKRLRVLLMGSNDFKTLPSSELLFLPEIRTIYADQN   125

Query   130  KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRNLNIKKTSLKGEDA   189
          KL+L ETDVEILASL+ LEELD+LNS IK LP NY KL NL LKRLNIKKTSLKGEDA
Sbjct   126  KLSLAETDVEILASLTGLEELDNLNSNIKTLPPNYTKLKNLRLKRLNIKKTSLKGEDA   185

Query   190  DKLQAILPNTKIDY   203
          +KLQAILP+TKIDY
Sbjct   186  EKLQAILPSTKIDY   199
```

>WP_135589926.1 leucine-rich repeat domain-containing protein [Leptospira gomenensis]
TGK28958.1 leucine-rich repeat domain-containing protein [Leptospira gomenensis]
TGK35419.1 leucine-rich repeat domain-containing protein [Leptospira gomenensis]
TGK40717.1 leucine-rich repeat domain-containing protein [Leptospira gomenensis]
TGK68439.1 leucine-rich repeat domain-containing protein [Leptospira gomenensis]
Length=217

Score = 244 bits (622), Expect = 2e-78, Method: Compositional matrix adjust.

Identities = 136/193 (70%), Positives = 160/193 (83%), Gaps = 0/193 (0%)

```
Query 11  CKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFIG 70
          CKKNAAEIL +A+A PE V LD GMQKL++ P +C FPNL++LDLRLNSL+ L E IG
Sbjct 25  CKKNAAEILKDAEASPETVTVLDLGMQKLSTPNGICSFPNLSRLDLRLNSLSSLAETIG 84

Query 71  ECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNK 130
          +CK LEQ+NLFGNDL+ FPS+FSKLK L+V+L G+NDF PSE LFLP I+ +Y D+N+
Sbjct 85  DCKNLEQINLFGNDLSAFPSSFSKLKRLRVILMGSNDFKTFPSEFLFLPEIRTIYADQNQ 144

Query 131  LTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDAD 190
          L+LTETDVEILASL+ LEELDL+LN IK+LP NY KL NL LKRLNIKKTSL+GEDAD
Sbjct 145  LSLTETDVEILASLTGLEELDLNLRNISKSLPSNYTKLKNLTRLKRLNIKKTSLRGEDAD 204

Query 191  KLQAILPNTKIDY 203
          KLQAILP TKIDY
Sbjct 205  KLQAILPKTKIDY 217
```

>WP_250180949.1 hypothetical protein [Leptospira interrogans]
MCL8309742.1 hypothetical protein [Leptospira interrogans]
Length=217

Score = 232 bits (591), Expect = 1e-73, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10  DCKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24  DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI 83

Query 70  GECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKLNKVLL GNNDFT LPSELLFLPL+K LY+D+N
Sbjct 84  GACKNLEQINLFGNDLNTVPSSFSKLKLNKVLLGNNDFTFLPSELLFLPLLKTLYLDQN 143

Query 130  KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELDL+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144  KLTLTETDVEILASLSSLEELDLNLSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDA 203

Query 190  DKLQAILPNTKIDY 203
          DKLQA+LPNTKIDY
Sbjct 204  DKLQAVLPNTKIDY 217
```

>WP_061272825.1 hypothetical protein [Leptospira interrogans]
Length=217

Score = 231 bits (590), Expect = 2e-73, Method: Compositional matrix adjust.
Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10  DCKKNAAEILGEAKAKPELVQTLDFGMQKLSTVPEEVC GFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24  DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI 83

Query 70  GECKRLEQLNLF GNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKLNKVLL GNNDFT LPSELLFLPL+K LY+D+N
```

Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNNDFTFLPSELLFLPLLKTYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY	203
		DKLQA+LPNTKIDY	
Sbjct	204	DKLQAVLPNTKIDY	217

>WP_002127204.1 hypothetical protein [Leptospira interrogans]
 EMN78462.1 leucine rich repeat protein [Leptospira interrogans serovar Grippotyphosa str. UI 12764]
 EM095466.1 leucine rich repeat protein [Leptospira interrogans str. UI 13372]
 Length=217

Score = 231 bits (590), Expect = 2e-73, Method: Compositional matrix adjust.
 Identities = 156/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLRLNSLTFLPEFI	69
		DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I	
Sbjct	24	DCKKNAVEILEEAKRKSESIQILDGLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N	
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNNDFTFLPSELLFLPLLKTYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY	203
		DKLQA+LPNTKIDY	
Sbjct	204	DKLQAVLPNTKIDY	217

>WP_061286495.1 hypothetical protein [Leptospira interrogans]
 Length=217

Score = 231 bits (589), Expect = 2e-73, Method: Compositional matrix adjust.
 Identities = 154/194 (79%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEEVCGFPNLTKLDLRLNSLTFLPEFI	69
		DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I	
Sbjct	24	DCKKNAVEILEEAKRKSESIQILDGLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN	129
		G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N	
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSKLKNLKVLLLGNNDFTFLPSELLFLPLLKTYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA	189
		KLTLTETDVEI+ASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	
Sbjct	144	KLTLTETDVEIIASLSSLEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDA	203

Query 190 DKLQAILPNTKIDY 203
 DKLQA+LPNT+IDY
 Sbjct 204 DKLQAVLPNTRIDY 217

>WP_001010185.1 hypothetical protein [Leptospira interrogans]
 EMN29390.1 leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. L0374]
 EMP06413.1 leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. 200701872]
 EMN63541.1 leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. R168]
 QC033794.1 hypothetical protein E4414_12465 [Leptospira interrogans]
 QOI35068.1 hypothetical protein LeptoLang_13150 [Leptospira interrogans serovar Icterohaemorrhagiae]
 Length=217

Score = 231 bits (589), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 155/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKLDLRLNSLTFLPEFI 69
 DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
 Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGMLQKLSIPEGVCSFPNLTKLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLFQNDLTTFPSTFSKLNKLVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
 G CK LEQ+NLFGNDL T PS+FSKLNKLVLL GNNDFT LPSELLFLPL+K LY+D+N
 Sbjct 84 GACKNLEQINLFGNDLNTVPSSFSLKLNKLVLLGNNDFTFLPSELLFLPLKTLTYLDQN 143

Query 130 KLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNINLKRNLNIKKTSLKGEDA 189
 KLTLTETDVEILASLSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
 Sbjct 144 KLTLTETDVEILASLSLEELDNLNSGIKVLPSNYNKLNLTHLKRNLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
 DKLQA+LPNT+IDY
 Sbjct 204 DKLQAVLPNTRIDY 217

>WP_001010184.1 MULTISPECIES: hypothetical protein [Leptospira]
 EMF71629.1 leucine rich repeat protein [Leptospira interrogans serovar Canicola str. LT1962]
 EMG20762.1 leucine rich repeat protein [Leptospira interrogans serovar Copenhageni str. LT2050]
 EM002625.1 leucine rich repeat protein [Leptospira interrogans serovar Icterohaemorrhagiae str. Verdun HP]
 OCA00011.1 Leucine rich repeat protein [Leptospira interrogans serovar Copenhageni/Icterohaemorrhagiae]
 AAN48523.1 leucine-rich-repeat protein [Leptospira interrogans serovar Lai str. 56601]
 Length=217

Score = 231 bits (588), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 155/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKLDLRLNSLTFLPEFI 69

Sbjct	24	DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N	129
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSLKLNKVLLLGNNDFTFLPSELLFLPLLKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	189
Sbjct	144	KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLNLTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY 203 DKLQA+LPNT+IDY	
Sbjct	204	DKLQAVLPNTRIDY 217	

>WP_001010182.1 hypothetical protein [Leptospira interrogans]
 EMY06628.1 leucine rich repeat protein [Leptospira interrogans str. 2002000626]
 EMY23346.1 leucine rich repeat protein [Leptospira interrogans serovar Australis str. 200703203]
 EKN86156.1 leucine rich repeat protein [Leptospira interrogans str. 2002000624]
 EKQ39337.1 leucine rich repeat protein [Leptospira interrogans str. 2002000621]
 EKQ45586.1 leucine rich repeat protein [Leptospira interrogans str. 2002000623]
 Length=217

Score = 231 bits (588), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 154/194 (79%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

Query	10	DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKLDLRLNSLTLFPEFI	69
Sbjct	24	DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I DCKKNAVEILEEAKRKSESIQILDGMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI	83
Query	70	GECKRLEQLNLFGNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN G CK LEQ+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N	129
Sbjct	84	GACKNLEQINLFGNDLNTVPSSFSLKLNKVLLLGNNDFTFLPSELLFLPLLKTLYLDQN	143
Query	130	KLTLTETDVeilaslssleeldslslnSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDA KLTLTETDVEI+ASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA	189
Sbjct	144	KLTLTETDVEIIASLSSLEELDNLNSGIKVLPSNYNKLNLTHLKRLNIKKTSLKGEDA	203
Query	190	DKLQAILPNTKIDY 203 DKLQA+LPNT+IDY	
Sbjct	204	DKLQAVLPNTRIDY 217	

>WP_001010178.1 hypothetical protein [Leptospira interrogans]
 EMF44105.1 leucine rich repeat protein [Leptospira interrogans serovar Lora str. TE 1992]
 EMG10292.1 leucine rich repeat protein [Leptospira interrogans serovar Grippotyphosa str. LT2186]
 EMN70889.1 leucine rich repeat protein [Leptospira interrogans serovar Bataviae str. UI 08561]
 AJR13823.1 hypothetical protein LIL_11221 [Leptospira interrogans serovar Linhai str. 56609]
 AKH76669.1 leucine rich repeat protein [Leptospira interrogans serovar Bratislava]

Length=217

Score = 231 bits (588), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 155/194 (80%), Positives = 170/194 (88%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDGFMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGFMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLF GNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N
Sbjct 84 GACKNLEQINLF GNDLNTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLLKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDA 189
          KLTLTETDVEILASLSSLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLSSLEELDNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQA+LPNT+IDY
Sbjct 204 DKLQAVLPNTRIDY 217
```

>WP_001010183.1 hypothetical protein [Leptospira interrogans]

AKP26578.1 leucine rich repeat protein [Leptospira interrogans serovar Manilae]

AKP30357.1 leucine rich repeat protein [Leptospira interrogans serovar Manilae]

EYU63041.1 hypothetical protein CI00_16890 [Leptospira interrogans serovar

Manilae]

SOR62694.1 Leucine rich repeat protein [Leptospira interrogans serovar Manilae]

Length=217

Score = 231 bits (588), Expect = 4e-73, Method: Compositional matrix adjust.
Identities = 155/194 (80%), Positives = 169/194 (87%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDGFMQKLSTVPPEEVC GFPNLT KDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGFMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLF GNDLTTFPSTFSKLKNLKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLF GNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+N
Sbjct 84 GACKNLEQINLF GNDLNTVPSSFSKLKNLKVLLGNNDFTFLPSELLFLPLLKTLYLDQN 143

Query 130 KLTLTETDVeilaslssleeldslnsGIKALPFNYEKL VNLINLKRLNIKKTSLKGEDA 189
          KLTLTETDVEILASL SLEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144 KLTLTETDVEILASLFSLEELDNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQA+LPNTKIDY
Sbjct 204 DKLQAVLPNTKIDY 217
```

>WP_192505591.1 hypothetical protein [Leptospira interrogans]

QOI42007.1 hypothetical protein Lepto782_06840 [Leptospira interrogans serovar Canicola]

Length=217

Score = 229 bits (584), Expect = 1e-72, Method: Compositional matrix adjust.
Identities = 154/194 (79%), Positives = 169/194 (87%), Gaps = 0/194 (0%)

```
Query 10 DCKKNAEEILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFI 69
          DCKKNA EIL EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +I
Sbjct 24 DCKKNAVEILEEAKRKSESIQILDGMLQKLSIPEGVCSPNLTLQDLRLNSLNSLPGWI 83

Query 70 GECKRLEQLNLFNGDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRN 129
          G CK LEQ+NLFGNDL T PS+FSKLKLNKVLL GNNDFT LPSELLFLPL+K LY+D+N
Sbjct 84 GACKNLEQINLFNGDLNTPSSFSKLKLNKVLLGNNDFTFLPSELLFLPLLKTYLDQN 143

Query 130 KLTLTETDVeilaslsleeldlslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDA 189
          K TLTLTETDVEILASLSSEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDA
Sbjct 144 KFTLTETDVEILASLSSEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDA 203

Query 190 DKLQAILPNTKIDY 203
          DKLQA+LPNT+IDY
Sbjct 204 DKLQAVLPNTRIDY 217
```

>EMM97254.1 leucine rich repeat protein [*Leptospira interrogans* serovar Zanon]
str. LT2156]
Length=188

Score = 218 bits (555), Expect = 1e-68, Method: Compositional matrix adjust.
Identities = 147/187 (79%), Positives = 164/187 (88%), Gaps = 0/187 (0%)

```
Query 17 EILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFIGECKRLE 76
          EIL +AK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +IG CK LE
Sbjct 2 EILEAKARKSESIQILDGMLQKLSIPEGVCSPNLTLQDLRLNSLNSLPGWIGACKNLE 61

Query 77 QLNLFNGDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNKLTLTET 136
          Q+NLFGNDL T PS+FSKLKLNKVLL GNNDFT LPSELLFLPL+K LY+D+NKLTTLTET
Sbjct 62 QINLFNGDLNTPSSFSKLKLNKVLLGNNDFTFLPSELLFLPLLKTYLDQNKLTLTET 121

Query 137 DVeilaslsleeldlslnsGIKALPFNYEKLVLNINLKRLNIKKTSLKGEDADKLQAIL 196
          DVEI+ASLSSEELD+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDADKLQA+L
Sbjct 122 DVEIIASLSSEELDNLNSGIKVLPSNYNKLKLNTHLKRLNIKKTSLKGEDADKLQAVL 181

Query 197 PNTKIDY 203
          PNT+IDY
Sbjct 182 PNTRIDY 188
```

>MBW9228790.1 hypothetical protein [*Leptospira interrogans*]
Length=186

Score = 216 bits (551), Expect = 5e-68, Method: Compositional matrix adjust.
Identities = 147/186 (79%), Positives = 163/186 (88%), Gaps = 0/186 (0%)

```
Query 18 ILGEAKAKPELVQTLDFGMQKLSTVPPEVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQ 77
          +L EAK K E +Q LD GMQKL+++PE VC FPNLT+LDLRLNSL LP +IG CK LEQ
Sbjct 1 MLEEAKRKSESIQILDGMLQKLSIPEGVCSPNLTLQDLRLNSLNSLPGWIGACKNLEQ 60

Query 78 LNLFGNDLTTFPSTFSKLKLNKVLLAGNNDFTILPSELLFLPLIKILYVDRNKLTLTETD 137
```


Sbjct	61	+NLFGNDL T PS+FSKLKNLKVLL GNNDFT LPSELLFLPL+K LY+D+NKLTLTETD INLFGNDLNTVPSSFSKLKNLKVLLLGNNDFTFLPSELLFLPLLKTLYLDQNKLTLTETD	120
Query	138	VeilaslsleeeldlslnsGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILP VEILASLSLEEELDL+LNSGIK LP NY KL NL +LKRLNIKKTSLKGEDADKLQA+LP	197
Sbjct	121	VEILASLSLEEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLP	180
Query	198	NTKIDY 203 NT+IDY	
Sbjct	181	NTRIDY 186	

Multiple sequence alignment of the protein rhKU_Sej_LRR_2271 (Genbank: AFV46188.1) and the amino sequences of *Leptospira* that has the same serovars with rabbit hyperimmune sera in this study using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>: access on 11 November 2022)

```

OCA00011.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
EM002625.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
EMF71629.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
QOI35068.1      -----MN-----F-LSLKKIFKLYFFLWSFFVIDCKKNAVEILEEA 36
EMN63541.1      -----MN-----F-LSLKKIFKLYFFLWSFFVIDCKKNAVEILEEA 36
EMP06413.1      -----MN-----F-LSLKKIFKLYFFLWSFFVIDCKKNAVEILEEA 36
EMN29390.1      -----MN-----F-LSLKKIFKLYFFLWSFFVIDCKKNAVEILEEA 36
EMN70889.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
EMN78462.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
AKH76669.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
EMG10292.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
EMY23346.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
QOI42007.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
ASV07105.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
EJ080485.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
EKN96857.1      -----MN-----F-LSLKKIFKLYFFLWSFFGIDCKKNAVEILEEA 36
MCR8646250.1    -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
OAM85608.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
QOI37956.1      -----MN-----F-LSLKKIFKIYFFLWSFFGIDCKKNAVEILEEA 36
OOV43912.1      -----MN-----F-VFLKKIFRIYFFFWISIFGIDCKKNAVEIIEEA 36

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EKQ84072.1	-----MN-----F-LFLKKIFRIYFFFWISIFGIDCKKNAVEILEEA	36
EPG48343.1	-----MN-----F-LFLKKIFRIYFFFWISIFGIDCKKNAVEILEEA	36
EJ071711.1	-----MN-----F-LFLKKIFRIYFFFWISIFGIDCKKNAVEILEEA	36
EM040832.1	-----MN-----S-LSLKKIFRIYFFFLISIFWIDCKKNAVEILEEA	36
EQA71632.1	-----MN-----S-LSLKKIFRIYFFFLISIFWIDCKKSAIEILEEA	36
EMY77189.1	MQVKSMILVGTLEKFAFLILFIPKTFQLVGKVMIAIGWLFFASIFWIDCKKTAEIILGEA	60
EMJ90581.1	-----MN-----F-PSLKKFVTIGSLFLAPIFWIDCKKNAAEILREA	36
EQA82096.1	-----MN-----F-PSLKKFVTIGSLFLAPIFWIDCKKNAAEILREA	36
EKT85788.2	-----MIEGVERMN-----F-PLLKRFLTIGFICFTASLEIDCKKNTEEILEEA	43
EMN21750.1	-----MN-----F-PLLKRFLTIGFICFTASLEIDCKKNTEEILEEA	36
EQA64549.1	-----MREGVKRMN-----F-PLLKEFLAIGFICFTAS--FDCKKNAAEILGEA	41
AFV46185.1	-----GFLCFTAS--FDCKKNAAEILGEA	22
PTM44326.1	-----MREGAKRMN-----F-PLLKEFLVIGFVCFTAS--FDCKKNAAEILGEA	41
AFV46188.1	-----GFVCFTAS--FDCKKNAAEILGEA	22
ALO26640.1	-----MREGAKRMN-----F-PLLKEFLVIGFVCFTAS--FDCKKNAAEILGEA	41
AFV46187.1	-----GFVCFTAS--FDCKKNAAEILGEA	22
AFV46186.1	-----GFVCFTAS--FDCKKNAAEILGEA	22
AXX17321.1	-----MN-----F-PLLKEFLVIGFVCFTAS--FDCKKNAAEILGEA	34
EM062774.1	-----MN-----F-PLLKEFLVIGFVCFTAS--FNCKKNAAEILGEA	34
ABJ76745.1	-----MN-----F-PLLKEFLVIGFVCFTAS--FNCKKNAAEILGEA	34

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OCA00011.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EM002625.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMF71629.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
QOI35068.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMN63541.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMP06413.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMN29390.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMN70889.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMN78462.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
AKH76669.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMG10292.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EMY23346.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
QOI42007.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
ASV07105.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EJ080485.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
EKN96857.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
MCR8646250.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
OAM85608.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
QOI37956.1	KRKSESIQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNSLPGWIGACKNLEQINLFG 96
OOV43912.1	KRKSESVQILDLMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWIGTCKNLEQINLFG 96
EKQ84072.1	KRKSESVQILDLMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWIGTCKNLEQINLFG 96
EPG48343.1	KRKSESVQILDLMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWIGTCKNLEQINLFG 96
EJ071711.1	KRKSESVQILDLMQKLTSIPEGICSFPNLTQLDLRLNSLNSLPDWIGTCKNLEQINLFG 96

EM040832.1	KKKSESVQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLSFLPDWIGTCKNLEQVNLFG 96
EQA71632.1	KRKSESVQILDLMQKLTSIPEGVCSFPNLTQLDLRLNSLNFLPDWIGTCKNLEQVNLFG 96
EMY77189.1	KASPSSVLLLDLMQKLSSIEGICSFPNLTKDLRLNSLTSLPESVGECKNLEQLNLFG 120
EMJ90581.1	NTKPESVRVLDLMQKLSSVPDGVCGFPNLTNLDLRLNSLTSLPEFIGECKNLEQLNLFG 96
EQA82096.1	NTKPESVRVLDLMQKLSSVPDGVCGFPNLTNLDLRLNSLTSLPEFIGECKNLEQLNLFG 96
EKT85788.2	KARPESVQTLDFGMRKLSAVPEGVCGFPNLTKDLRLNSLTSLPEFIGECKSLEQLNLFG 103
EMN21750.1	KARPESVQTLDFGMRKLSAVPEGVCGFPNLTKDLRLNSLTSLPEFIGECKSLEQLNLFG 96
EQA64549.1	KAKPELVQTLDFGMQKLSTVPEGVCGFPNLTKDLRLNSLSSLPDEIGDCKNLEQLNLFG 101
AFV46185.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 82
PTM44326.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 101
AFV46188.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 82
ALO26640.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 101
AFV46187.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 82
AFV46186.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 82
AXX17321.1	KAKPELVQTLDFGMQKLSTVPEEVCVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 94
EM062774.1	KAKPELVQTLDFGMQKLSTVPEGVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 94
ABJ76745.1	KAKPELVQTLDFGMQKLSTVPEGVCGFPNLTKDLRLNSLTFLPEFIGECKRLEQLNLFG 94

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OCA00011.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EM002625.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMF71629.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
QOI35068.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMN63541.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMP06413.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMN29390.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMN70889.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMN78462.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
AKH76669.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMG10292.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEILA 156
EMY23346.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKLT LTETDVEIIA 156
QOI42007.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLLKTL YLDQNKFT LTETDVEILA 156
ASV07105.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
EJ080485.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
EKN96857.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
MCR8646250.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
OAM85608.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
QOI37956.1	NDLNTVPSSF SKLKNLKVLLLGNNDFTF LPSSELLFLPLIKTL YLDQNKLT LTETDVEILA 156
OOV43912.1	NDLATIPSSF SKLKNLKVLLVGNNDFAF LPSSELLFLPLIKIL YLDQNKLT LTETDVEILS 156
EKQ84072.1	NDLATIPSSF SKLKNLKVLLVGNNDFAF LPSSELLFLPLIKIL YLDQNKLT LTETDVEILA 156
EPG48343.1	NDLATIPSSF SKLKNLKVLLVGNNDFAF LPSSELLFLPLIKIL YLDQNKLT LTETDVEILA 156
EJ071711.1	NDLATIPSSF SKLKNLKVLLVGNNDFAF LPSSELLFLPLIKIL YLDQNKLT LTETDVEILA 156

EM040832.1	NDLTTVPSSF SKLKNLKVLL LGNNDFTFLPSELLFLPLIKTLYLDQNKLTLTETDIEILS 156
EQA71632.1	NDLTTVPSSF SKLKNLKVLL LGNNDFTFLPSELLFLPLIKTLYFDQNKLTLTETDIEILS 156
EMY77189.1	NDLTTFPASF SKLKNLKVLL AGNNDLTVLPSELLFLPRIKTLYLDQNKITLTETDVEILA 180
EMJ90581.1	NDLGTFPASIS KLKNLKVLL AGNNDFAALPSELLFLPSIKTLYLDRNKLTLTETDVEILA 156
EQA82096.1	NDLGTFPASIS KLKNLKVLL AGNNDFAALPSELLFLPSIKTLYLDRNKLTLTETDVEILA 156
EKT85788.2	NDLTTLPSTF SKLKNLKVLL AGSNDFTVLPSELLFLPSIKTLYVDRNRLTLTETDVEILA 163
EMN21750.1	NDLTTLPSTF SKLKNLKVLL AGSNDFTVLPSELLFLPSIKTLYVDRNRLTLTETDVEILA 156
EQA64549.1	NDLTTFPAALS KLKKLRILL AGNNDLKFLPSELLFLPEIKTIYMDQNKLTLTETDVEILA 161
AFV46185.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 142
PTM44326.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 161
AFV46188.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 142
ALO26640.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 161
AFV46187.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 142
AFV46186.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 142
AXX17321.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 154
EM062774.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 154
ABJ76745.1	NDLTTFPSTF SKLKNLKVLL AGNNDFTILPSELLFLPLIKILYVDRNKLTLTETDVEILA 154

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OCA00011.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EM002625.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMF71629.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
QOI35068.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMN63541.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMP06413.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMN29390.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMN70889.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMN78462.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTKID 216
AKH76669.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMG10292.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EMY23346.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
QOI42007.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
ASV07105.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EJ080485.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
EKN96857.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
MCR8646250.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
OAM85608.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
QOI37956.1	SLSSLEELDLNLNSGIKVLPSNYNKLKNLTHLKRLNIKKTSLKGEDADKLQAVLPNTRID 216
OOV43912.1	SLSSLEELDLNLNSGIKTLPSNYNKLKNLNRLKRLNIKKTSLKGEDADKLQAILPNTKID 216
EKQ84072.1	SLSSLEELDLNLNSGIKTLPSNYNKLKNLNRLKRLNIKKTSLKGEDADKLQAILPNTKID 216
EPG48343.1	SLSSLEELDLNLNSGIKTLPSNYNKLKNLNRLKRLNIKKTSLKGEDADKLQAILPNTKID 216
EJ071711.1	SLSSLEELDLNLNSGIKTLPSNYNKLKNLNRLKRLNIKKTSLRGEDADKLQAILPNTKID 216

EM040832.1	SLSGLEELDLNLPNGIKILPSNYNKLKNLTHLKRLNIKKTLKGEDAGKLQAILPNTKID 216
EQA71632.1	SLSGLEELDLNLPNGIKILPSNYNKLKNLTHLKRLNIKKTLKGEDADKLQAILPNTKID 216
EMY77189.1	SLSELEELDLNLTGIKTLPSNYGKLKSLARLKKLNIKKTSLKGEDAEKLQAILPNTKID 240
EMJ90581.1	SLSGLEELDLNLSNDIKALPSNYKKLKNLTRLKRLNIKKTSLKGEDAEKLQAILPNTKID 216
EQA82096.1	SLSGLEELDLNLSNDIKALPSNYKKLKNLTRLKRLNIKKTSLKGEDAEKLQAILPNTKID 216
EKT85788.2	SLSSLEELDLNQNSGIGTLPFNYEKLRLNLTGLKRLNIKKTSLKGEDAGKLQAILPNAKID 223
EMN21750.1	SLSSLEELDLNQNSGIGTLPFNYEKLRLNLTGLKRLNIKKTSLKGEDAGKLQAILPNAKID 216
EQA64549.1	SLSSLEELDLNLTGIKTLPFNYEKLGNLTNLKRLNIKKTSLKGEDADKLQAILPNTKID 221
AFV46185.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILRNTKID 202
PTM44326.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 221
AFV46188.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 202
ALO26640.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 221
AFV46187.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 202
AFV46186.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 202
AXX17321.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 214
EM062774.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 214
ABJ76745.1	SLSSLEELDLSLNSGIKALPFNYEKLVLNLINLKRLNIKKTSLKGEDADKLQAILPNTKID 214

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OCA00011.1	Y 217
EM002625.1	Y 217
EMF71629.1	Y 217
QOI35068.1	Y 217
EMN63541.1	Y 217
EMP06413.1	Y 217
EMN29390.1	Y 217
EMN70889.1	Y 217
EMN78462.1	Y 217
AKH76669.1	Y 217
EMG10292.1	Y 217
EMY23346.1	Y 217
QOI42007.1	Y 217
ASV07105.1	Y 217
EJ080485.1	Y 217
EKN96857.1	Y 217
MCR8646250.1	Y 217
OAM85608.1	Y 217
QOI37956.1	Y 217
OOV43912.1	Y 217
EKQ84072.1	Y 217
EPG48343.1	Y 217
EJ071711.1	Y 217

EM040832.1	Y 217
EQA71632.1	Y 217
EMY77189.1	Y 241
EMJ90581.1	Y 217
EQA82096.1	Y 217
EKT85788.2	Y 224
EMN21750.1	Y 217
EQA64549.1	Y 222
AFV46185.1	Y 203
PTM44326.1	Y 222
AFV46188.1	Y 203
ALO26640.1	Y 222
AFV46187.1	Y 203
AFV46186.1	Y 203
AXX17321.1	Y 215
EM062774.1	Y 215
ABJ76745.1	Y 215

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Accession	Accession from 100 Hit	Description	Max Score	Total Score	Query Cover	E value	Per. Ident
ALO26640.1	ALO26640.1	leucine rich repeat protein [Leptospira borgpetersenii serovar Ballum]	359	359	100%	8E-124	100.00%
PTM44326.1	ALO26640.1	leucine rich repeat (LRR) protein [Leptospira borgpetersenii serovar Javanica]	359	359	100%	8E-124	100.00%
AFV46187.1	AFV46186.1	leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Mini]	358	358	100%	6.00E-124	100.00%
AFV46186.1	AFV46186.1	leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Ballum]	358	358	100%	6E-124	100.00%
AFV46188.1	AFV46186.1	leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Sejroe]	358	358	100%	6E-124	100.00%
AXX17321.1	WP_002731979.1	hypothetical protein C4Q31_14790 [Leptospira borgpetersenii serovar Ceylonica]	358	358	100%	1E-123	100.00%
EMO62774.1	EMO62774.1	leucine rich repeat protein [Leptospira borgpetersenii serovar Pomona str. 200901868]	354	354	100%	7.00E-122	99.01%
AFV46185.1	AFV46185.1	leucine-rich repeat protein, partial [Leptospira borgpetersenii serovar Javanica]	354	354	100%	3E-122	99.01%
ABJ76745.1	WP_011669694.1	Leucine-rich-repeat protein [Leptospira borgpetersenii serovar Hardjo-bovis str. JB197]	352	352	100%	4E-121	98.52%
EQA64549.1	EQA64549.1	leucine rich repeat protein [Leptospira alexanderi serovar Manhao 3 str. L60]	312	312	100%	2E-105	86.70%
EKT85788.2	EKT85788.2	hypothetical protein LSS_15741 [Leptospira santarosai serovar Shermani str. LT 821]	305	305	100%	1E-102	85.85%
EMN21750.1	WP_004471631.1	leucine rich repeat protein [Leptospira santarosai serovar Arenal str. MAVJ 401]	305	305	100%	2E-102	85.85%
EMJ90581.1	WP_020775386.1	leucine rich repeat protein [Leptospira alstonii serovar Sichuan str. 79601]	278	278	96%	6E-92	83.59%
EQA82096.1	WP_020775386.1	leucine rich repeat protein [Leptospira alstonii serovar Pingchang str. 80-412]	278	278	96%	6E-92	83.59%
EMY77189.1	EMY77189.1	leucine rich repeat protein [Leptospira weilii serovar Ranarum str. ICFT]	277	277	100%	4E-91	78.05%
EPG48343.1	WP_004759233.1	leucine rich repeat protein [Leptospira kirschneri serovar Cynopteri str. 3522 CT]	270	270	95%	2E-88	81.44%
EJO71711.1	WP_004750770.1	leucine rich repeat protein [Leptospira kirschneri serovar Grippotyphosa str. RM52]	269	269	95%	3E-88	80.93%
OOV43912.1	WP_082292870.1	hypothetical protein B1J93_06785 [Leptospira kirschneri serovar Pomona]	268	268	95%	1.00E-87	80.41%
EKQ84072.1	WP_004760926.1	leucine rich repeat protein [Leptospira kirschneri serovar Grippotyphosa str. Moskva]	266	266	95%	2E-87	80.93%
EMO40832.1	WP_004438578.1	leucine rich repeat protein [Leptospira noguchii serovar Autumnalis str. ZUN142]	251	251	99%	5E-81	77.23%
ASV07105.1	WP_001010181.1	hypothetical protein B2G47_15925 [Leptospira interrogans serovar Canicola]	250	250	95%	7.00E-81	80.41%
EJO80485.1	WP_001010181.1	leucine rich repeat protein [Leptospira interrogans serovar Pomona str. Kennewicki LC82-25]	250	250	95%	7.00E-81	80.41%
EKN96857.1	WP_001010181.1	leucine rich repeat protein [Leptospira interrogans serovar Pomona str. Pomona]	250	250	95%	7.00E-81	80.41%
MCR8646250.1	WP_001010177.1	hypothetical protein [Leptospira interrogans serovar Bataviae]	250	250	95%	8.00E-81	80.41%
OAM85608.1	WP_001010177.1	hypothetical protein A1343_17415 [Leptospira interrogans serovar Bataviae]	250	250	95%	8.00E-81	80.41%
QOI37956.1	WP_001010177.1	hypothetical protein Lepto1548_06450 [Leptospira interrogans serovar Bataviae]	250	250	95%	8.00E-81	80.41%
EQA71632.1	WP_002177142.1	leucine rich repeat protein [Leptospira noguchii serovar Panama str. CZ214]	250	250	95%	1E-80	79.90%
QOI35068.1	WP_001010185.1	hypothetical protein LeptoLang_13150 [Leptospira interrogans serovar Icterohaemorrhagiae]	231	231	95%	3.00E-73	79.90%
EMF71629.1	WP_001010184.1	leucine rich repeat protein [Leptospira interrogans serovar Canicola str. LT1962]	231	231	95%	3.00E-73	79.90%
EMO02625.1	WP_001010184.1	leucine rich repeat protein [Leptospira interrogans serovar Icterohaemorrhagiae str. Verdun]	231	231	95%	3.00E-73	79.90%
OCA00011.1	WP_001010184.1	Leucine rich repeat protein [Leptospira interrogans serovar Copenhageni/Icterohaemorrhagiae]	231	231	95%	3.00E-73	79.90%
EMY23346.1	WP_001010182.1	leucine rich repeat protein [Leptospira interrogans serovar Australis str. 200703203]	231	231	95%	3.00E-73	79.38%
EMN70889.1	WP_001010178.1	leucine rich repeat protein [Leptospira interrogans serovar Bataviae str. UI 08561]	231	231	95%	3.00E-73	79.90%
EMN78462.1	WP_002127204.1	leucine rich repeat protein [Leptospira interrogans serovar Grippotyphosa str. UI 12764]	231	231	95%	2E-73	80.41%
EMN29390.1	WP_001010185.1	leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. L0374]	231	231	95%	3E-73	79.90%
EMP06413.1	WP_001010185.1	leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. 200701872]	231	231	95%	3E-73	79.90%
EMN63541.1	WP_001010185.1	leucine rich repeat protein [Leptospira interrogans serovar Pyrogenes str. R168]	231	231	95%	3E-73	79.90%
EMG10292.1	WP_001010178.1	leucine rich repeat protein [Leptospira interrogans serovar Grippotyphosa str. LT2186]	231	231	95%	3E-73	79.90%
AKH76669.1	WP_001010178.1	leucine rich repeat protein [Leptospira interrogans serovar Bratislava]	231	231	95%	3E-73	79.90%
QOI42007.1	WP_192505591.1	hypothetical protein Lepto782_06840 [Leptospira interrogans serovar Canicola]	229	229	95%	1.00E-72	79.38%