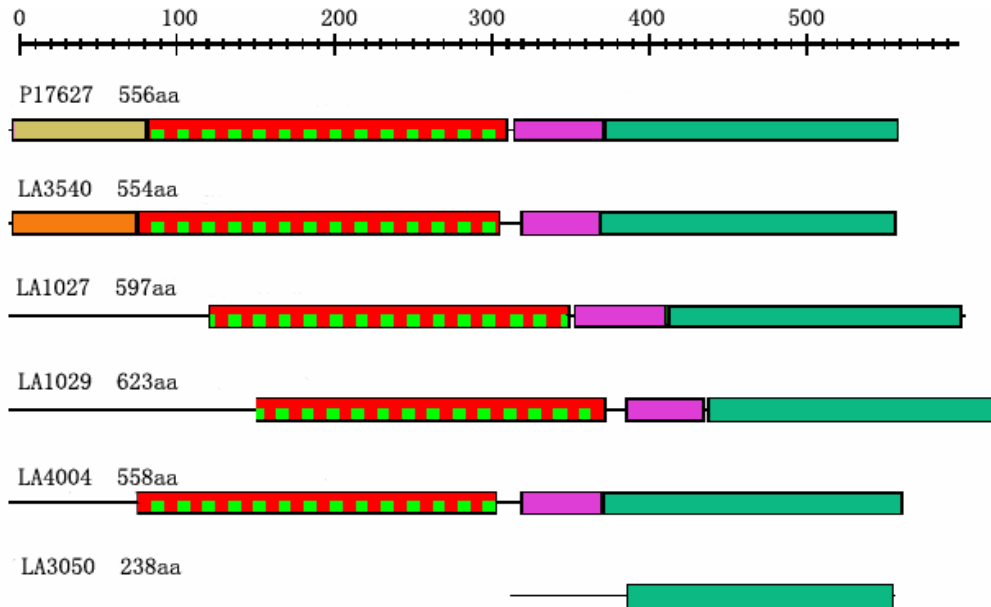


Supplementary information 7: Hemolysin genes of *L. interrogans* serovar lai.

A. Sphingomyelinase-like hemolysins from *L. interrogans* serovar lai

Relevant genes: *sph1-4*: LA1027, LA1029, LA4004, LA3050; *sphH**, LA3540

1. Domain analysis of predicted sphingomyelinase-like hemolysins from *L. interrogans* serovar lai



Conserved structure domains illustrated in the figure:

ProDom ID	Illustration	Domain
PD133144		sphingomyelinase C precursor SMASE
PD133145		hemolytic
PD011673		precursor hydrolase signal
PD447657		precursor hydrolase signal
PD041204		sphingomyelinase C precursor SMASE

Domain homology comparison (% of identities, similarities) for the predicted sphingomyelinase-like hemolysins from *L. interrogans* strain Lai and SP/P17627 (*L. interrogans* serovar hardijo)

ID	PD133144	PD 133145	PD011673	PD447657	PD041204
P17627	100,100	—	100,100	100,100	100,100
LA3540	—	100,100	100,100	100,100	90,90
LA1027	—	—	61, 76	71, 78	60, 74
LA1029	—	—	68, 83	82, 89	57, 70
LA4004	—	—	56, 72	74, 82	54, 68
LA3050	—	—	—	—	53, 67

2. Sequence similarity comparison of predicted sphingomyelinase-like hemolysins from *L. interrogans* serovar lai with that from *L. interrogans* serovar hardijo (sp|P17627):

P17627	1	-----MRIKK ^Y TKVRL ^L VN ^C CL ^L LF ^F LD ^C GAD ^R QSLYKD ^L AS ^L IYISDNK	47
LA1027	1	MITKRNIPPC ^K KNW ^K YK ^K KSISLT ^L ITICYMFL ^L FLTS ^C KPG ^K KNSIN ^L LL ^L LLNTLDNK	59
LA1029	1	-----MINK ^I TKPKL ^L I ^G YLL ^L FLSL ^L IR ^C LPE ^K ESSYKD ^L FTS ^L LLFLPNQT	46
LA4004	1	MKTKRNPLLNK ^C KPK ^K FKYRNL ^L I ^G LL ^L CL ^F PLN ^C TFK ^D SLVYN ^K F ^L MY ^L ISFSHKNL	58
LA3540	1	---MRN ^I FRK ^K KN ^G IRN ^T YK ^K SK ^S L ^I GFY ^C LF ^M FF ^L LN ^C LP ^D KQ ^K EHAD ^L MS ^L LLFSKDQ	57
LA3050	1	-----	1
P17627	48	^N IG ^L -----ST ^N SD ^L LTGSGSV	62
LA1027	60	NVNEK ^I EDSTNTDP-----SS ^N VNEEDENSI	85
LA1029	47	^N SNQVNSVSINNDPANPNPVPNPASANNQVNAVPE ^N DDPANLNPVNPASAN ^S NQVNAAPE	106
LA4004	59	^N FE-----LEN ^I NS ^T RK---	70
LA3540	58	^N IQ-----FAN ^I SAERIG--	70
LA3050	1	-----	1
P17627	63	SSSPA ^D AAP ^E -----NSILAN-----SIP-----ENMG ^T K ^I L ^T H ^N V ^F LLP	97
LA1027	86	NANAND ^N AP ^S SDSDSSNPRSPDKNPVN-----PTSPNS-SSADIG ^I K ^I L ^S HS ^I FMAP	135
LA1029	107	NGSPA ^D PN ^P ANLASANNQVNAVANNYFTKEDSSNIPK ^K VNSKNVE ^L K ^V LS ^H N ^V FMLP	166
LA4004	70	-----TLL ^P K-----SEIDL ^N LS ^Y N ^L FLYS	91
LA3540	70	-----I ^D AQVS-----SEVD ^T K ^I LS ^Y N ^L FM ^Y H	92
LA3050	1	-----	1
P17627	98	KT ^L PG ^W GN ^W GQ ^N ERA ^R Q ^R IV ^S SN ^Y I ^Q NQ ^D V ^I V ^F DEA ^F DT ^D ARK ^I LLD ^G V ^R SE ^Y YP ^Q TD ^V I ^G	157
LA1027	136	TN ^L SS ^W GD ^L GQ ^E ERA ^R Q ^R IAS ^S SY ^I KNQ ^D V ^I V ^F EGL ^S H ^N NA ^E K ^I LL ^E K ^I RS ^E YP ^Q TN ^V VG	195
LA1029	167	TN ^L PR ^W GN ^L GH ^D ERA ^R K ^I SK ^S D ^Y V ^K NQ ^D V ^I V ^F EAA ^F DT ^S ARK ^I LLD ^N LRE ^E YP ^Q TD ^V I ^G	226
LA4004	92	KED ^I YF ^G Y ^W E ^E K ^R A ^L LL ^G K ^S K ^F T ^K NQ ^D V ^I V ^L SRV ^F DT ^N AR ^N T ^L LD ^N L ^N L ^E Y ^P D ^Q TD ^V I ^G	151
LA3540	93	KG ^L FN ^S GN ^W GQ ^E K ^R A ^R LL ^V D ^S K ^Y V ^K D ^Q D ^V V ^L LEGV ^F DT ^S K ^S KN ^L LM ^N GL ^R S ^Y PN ^Q TD ^V I ^G	152
LA3050	1	-----MK ^M I ^Q N ^I LR ^K E-	11
P17627	158	RT ^K K ^G W ^D A ^T L ^G L ^Y RT---DAFT ^N GGV ^I V ^S K ^W P ^I E ^E K ^I Q ^H V ^F K ^E K ^G CG ^A D ^V FS ^N K ^G F ^A YV	214
LA1027	196	RT ^K K ^G W ^N A ^T L ^G A ^Y IT---SPM ^A GGV ^I V ^S K ^W P ^I E ^E K ^V Q ^Y I ^F N ^N S ^N CG ^Q D ^Q Y ^Y N ^K G ^F A ^Y V	252
LA1029	227	RT ^K K ^N W ^D A ^S L ^G N ^F RS---YSLV ^N GGV ^I V ^S K ^W P ^I E ^E K ^I Q ^Y I ^F N ^D S ^G CG ^A D ^W F ^A N ^K G ^F V ^Y V	283
LA4004	152	K ^T K ^Y G ^W D ^Q T ^L G ^D FR---QQIN ^N GGV ^I V ^S K ^W P ^I E ^E K ^I Q ^Y I ^F K ^N H ^G CG ^N D ^F Y ^Y N ^K G ^F A ^Y V	207
LA3540	153	R ^A T ^Y G ^W N ^Q T ^L G ^D FR ^A F ^L LD ^N D ^Y GGV ^I V ^L S ^K W ^P I ^E E ^K I ^Q Y ^I F ^E N ^H G ^G N ^D Y ^Y N ^K G ^F V ^Y V	212
LA3050	12	K ^V K ^T W ^N QL ^K G-----SK ^F FR ^C CL ^F I-----I ^L F ^F D---CL ^P D-----	42
P17627	215	R ^I D ^K N ^G R ^K F ^H I ^G T ^H V ^Q A ^D S ^G CAN ^L G ^V VS ^R V ^N Q ^F NE ^T RD ^F IDS ^K K ^I P ^K NE ^M V ^L IAG ^D LN	274
LA1027	253	K ^I N ^K D ^G K ^K F ^H V ^I GT ^Q LQ ^A RE ^P DC ^F NS ^G ET ^I R ^K L ^Q L ^N D ^I KS ^F IDS ^K D ^I P ^K DE ^T V ^L I ^T G ^D LN	312
LA1029	284	K ^I N ^K E ^G K ^K F ^H V ^I GT ^H A ^Q S ^D Q ^N C ^S N ^L G ^I PN ^R AN ^Q F ^D IR ^N F ^I Y ^S KN ^I P ^K DE ^T V ^L I ^V G ^D LN	343
LA4004	208	K ^I K ^G S ^Q I ^H I ^H V ^G T ^D Q ^S ED ^S T ^C S ^D L ^G YN ^A R ^I N ^Q L ^T E ^K KE ^I DS ^K R ^I SN ^K E ^V L ^I AG ^A LN	267
LA3540	213	K ^I N ^K H ^G R ^K Y ^H I ^G T ^D V ^Q N--T ^S C ^S D ^L G ^Q N ^A R ^K H ^Q F ^V E ^I KN ^F IN ^L K ^Q V ^P KN ^E T ^I FL ^A GS ^F N	270
LA3050	42	-----L ^Q S-----S ^E NN ^L FL ^S LL ^S L ^P K ^N GG ^I L ^I LR ^N D ^K S	70
P17627	275	V ^I I ^K GS-REY ^H Q ^M L ^C I ^N V ^N N ^P K ^Y V ^G V ^P FT ^W D ^T K ^T NE ^I AA ^F Y ^Y K---K ^V EP ^A Y ^L D ^Y I ^F VS	329
LA1027	313	I ^I I ^K GSNEY ^F D ^M ISK ^L N ^V NE ^P RY ^V G ^V P ^F T ^L D ^T K ^T NA ^L AA ^Y Y ^E ---KE ^K P ^I Y ^L D ^Y I ^L VS	367
LA1029	344	V ^I I ^K ESNEY ^Y D ^M ISR ^L N ^V NE ^P RY ^V G ^V P ^F T ^W DA ^K T ^N E ^I AA ^Y Y ^E ---NE ^E P ^V Y ^L D ^Y I ^F VS	398
LA4004	268	V ^D KS ^N Q ^S EY ^K N ^M L ^N I ^L EV ^N EP ^N Y ^A G ^I P ^F T ^W D ^T K ^K NA ^A Y ^N I ^Y SW ^N Q ^T S ^N Y ^G E ^I Y ^L VS	327
LA3540	271	V ^N K ^G S-TEY ^Q D ^I L ^M I ^L G ^V D ^E PH ^Y A ^G I ^S FT ^W D ^P K ^K NA ^I AS ^Y T---S ^G T ^N Q ^V SS ^Y L ^E Y ^I F ^V V	326
LA3050	71	I ^A K ^S -----K-----	75
P17627	330	K ^S H ^F Q ^P P ^I W ^Q N ^L A ^Y D ^P I ^S AK ^T W ^T A ^K -G ^Y T ^S D ^E F ^S D ^H Y ^P Y ^G F ^I Y ^A D ^S ST ^P T ^K S ^G R ^K R ^K Y ^D	388
LA1027	368	KL ^H A ^Q PP ^V W ^Q N ^L A ^Y D ^P I ^S NT ^T W ^K R ^S D ^G Y ^T S ^E F ^S D ^R Y ^P Y ^G F ^I Y ^A D ^S ST ^P T ^K S ^G H ^K R ^K Y ^D	427
LA1029	399	K ^S H ^A Q ^P P ^V W ^Q N ^L A ^Y D ^P I ^S K ^Q T ^W T ^V S-G ^Y T ^S D ^E F ^S D ^H Y ^P Y ^G F ^V Y ^A D ^P ST ^P T ^K S ^G H ^K K ^K Y ^D	457
LA4004	328	K ^S H ^A Q ^P P ^I W ^Q N ^L A ^Y D ^P I ^S PT ^T W ^K R ^K N ^G Y ^T S ^E F ^S D ^H F ^I Y ^G F ^V Y ^A D ^P ST ^P T ^K S ^G H ^K R ^K Y ^D	387
LA3540	327	G ^T H ^F G ^P Q ^V W ^Q N ^L A ^Y D ^P I ^T P ^T W ^N -V ^V G ^Y T ^G Y ^E F ^S D ^R Y ^P Y ^G F ^I Y ^A D ^S N ^I P ^T Q ^S A ^H R ^R K ^Y D	385
LA3050	75	-----T--TR ^K Y ^G	81
P17627	389	R ^V S ^F V ^S V ^A T ^G K ^K I ^Q AN ^S E ^K S ^N A ^W L ^K V ^N --ATT ^E T ^D L ^T K ^F N ^L V ^Q T ^N D ^P D ^S N ^P S ^C M ^K S ^G H ^V	445
LA1027	428	Q ^V S ^F Q ^S T ^F N ^R K ^F I ^Q AD ^H N ^K D ^G W ^L K ^A D---TR ^I K ^T D ^F T ^K F ^N L ^L Q ^E N ^V S ^E N ^P S ^C M ^N S ^G S ^V	484
LA1029	458	Q ^V S ^F Q ^S AA ^N G ^K Y ^I Q ^A D ^P N ^R K ^N G ^W L ^K A ^D ---AV ^I E ^T D ^F T ^K F ^N L ^L Q ^E G ^N --L ^N D ^S C ^I K ^N G ^L V	512
LA4004	388	Q ^V S ^L I ^A K ^Y T ^G K ^A I ^Q V ^D H ^N R ^P D ^G W ^L K ^A D ^G T ^A K ^E K ^G T ^E F ^T K ^F N ^L L ^Q E ^Y D ^P D ^S T ^F C ^M L ^G G ^R V	447
LA3540	386	Q ^V S ^F E ^S M ^S T ^G K ^K I ^Q AD ^P K ^Q A ^N G ^W L ^Q V ^N --AS ^D E ^T E ^F T ^K F ^N L ^L Q ^E AD ^P K ^S D ^T N ^C L ^K S ^G Y ^T	442
LA3050	82	W ^V T ^F T ^S Q ^V T ^G K ^K I ^Q AD ^P ER ^P D ^G W ^L RV ^N --AS ^S N ^T D ^F T ^F T ^L Y ^Q D ^G K---D ^P D ^C I ^K G ^G P ^I	135
P17627	446	R ^I ESS ^H S ^L N ^Y F ^W N ^W W ^L G ^G G ^K G ^N Y ^A Y ^P K ^F N ^D G ^S N ^R I ^Q T ^I N ^L D ^G G-CL ^Q D ^G S ^R V ^A F ^K D ^Y D ^T	504
LA1027	485	R ^I ESS ^Y Y ^L N ^Y Y ^W N ^W F ^I G ^A AS ^G D ^Y G ^Y T ^K F ^N NG ^S D ^S L ^G I ^K N ^L D ^N G-CL ^K D ^G S ^R V ^A F ^Y D ^W D ^T	543
LA1029	513	R ^I ESS ^R L ^N Y ^F W ^N W ^L G ^G S ^G N ^Y G ^Y S ^K F ^N DA ^S N ^Q L ^E I ^N LS ^D E-CL ^E NG ^S L ^V F ^K D ^Y D ^T	571
LA4004	448	R ^I ESS ^Q Y ^L N ^Y F ^W T ^W W ^L R ^G G ^G G ^N Y ^A Y ^P K ^F D ^D SS ^K L ^L E ^M I ^I IR ^Q G-CL ^E D ^E S ^L V ^F K ^D F ^D T	506
LA3540	443	R ^I E ^P S ^Y Y ^L N ^Y Y ^W N ^W W ^L G ^G G ^K G ^N Y ^A Y ^P K ^F N ^D AS ^N N ^L Q ^T H ^V L ^D E ^E E ^C I ^K D ^G S ^R I ^V F ^K D ^Y D ^G	502
LA3050	136	R ^V E ^P T ^A Y ^R N ^Y Y ^W N ^W W ^L G ^G A ^G N ^Y A ^Y P ^K Y ^K D ^G S ^N K ^L Q ^I Y ^V L ^K V ^S G ^C L ^E S ^G D ^R V ^L F ^S D ^Y D ^T	195
P17627	505	I ^S RR ^Q Y ^F L ^T V ^W E ^G G ^N W ^D K ^Y L ^Y L ^W RS-HI ^G L ^R E ^I F ^Y L ^K L ^D SS ^P E ^M N ^W S ^K L ^I Y ^R -	556
LA1027	544	I ^G GG ^Y Y ^L T ^V W ^D K ^G S ^W K ^E H ^L FL ^W V ^Q S ^F L ^S S ^R E ^I F ^Y L ^H L ^D S ^N P ^P K ^D W ^S K ^D L ^I Y ^H H	597
LA1029	572	Y ^S R ^N H ^Y Y ^L T ^V W ^D K ^G N ^W E ^H L ^Y L ^W K ^D -S ^I S ^Q R ^E I ^F Y ^L K ^L N ^S T ^P V ^R N ^W S ^A D ^L I ^Y R-	623
LA4004	507	Y ^S R ^N H ^Y Y ^L AV ^W ENG ^S W ^K D ^Y I ^L Y ^W T-NA ^Q P ^N S ^Y F ^I A ^K L ^N T ^S P ^E R ^D W ^S K ^D L ^I Y ^R -	558
LA3540	503	A ^T L ^D Y ^Y Y ^L T ^I W ^D G ^G N ^W D ^G Y ^L Y ^L W ^N K-TY ^N L ^R E ^T F ^K V ^R L ^N T ^K P ^E R ^D W ^K D ^L I ^Y R-	554
LA3050	196	I ^T Q ^D D ^Y F ^V I ^D W ^D G ^G S ^W N ^E Y ^L FL ^W Y ^K F ^P K ^V Q ^R G ^Y F ^Y V ^Q L ^N E ^G P ^E -----	239

B. Domain and amino acid sequence similarity analysis of predicted non-sphingomyelinase hemolysins

Relevant genes: *tlyA*, LA0327; *hlyX*, LA0378; *hlpA*, LA1650; *hlyC*, LA3937

1. LA0327 (*tlyA*)

Domain analysis

PD007579



LA0327

PD007579: hemolysin A from *Treponema hyodysenteriae*

Sequence similarity analysis: Identities:0.36; Similarities:0.51

LA0327_LEPIN	1	LFPQKKNKHSFRSFRFTLAR---	EMIRLDVLLFERGFADSL	EKAKSL	ILSGSVLVNEQKV	57		
Q06803_TREHY	1	-----	MRLDEYVHSEGYTESRS	SKAQDI	LAGCVFVNGVKV	35		
Q9X1R2_THEMA	1	-----	MAD---	KKRLDQLVLERGLV	SREKAKVL	LAGKVLVNGERV	39	
P19672_BACSU	1	-----	MTS---	KKERLDVLLVERGLA	ETREKAKRA	IMAGIVYSNENRL	40	
Q9K972_BACHA	1	-----	MS---	KKERVDVLLVERGLM	ETREKAKRS	IMAGLVFSGHERV	39	
Q8XJE2_CLOPE	1	-----	MAEKKEKERLDVLLV	EOGIAESREKAKRY	IMAGMVFIGEKRV	43		
Q92BY9_LISIN	1	-----	MTI---	KKERADILLVEQGLF	ETREKAKRA	IMAGIVYRKEERV	40	
Q8Y7C0_LISMO	1	-----	MTI---	KKERADILLVEQGLF	ETREKAKRA	IMAGIVYRKEERV	40	
Q9F6Y3_CHLAU	1	-----	MP---	RORLDQVLLVSRGLA	ETARRAQAL	IMAGQVLVNGQVQ	38	
LA0327_LEPIN	58	TKVGFKFPKDS	SEIRILNI	IPEYVSRGVYKLLKA	FVFPLOVDGKLC	LDLGASTGGFTQVL	117	
Q06803_TREHY	36	TSKAHKIKD	TDNIEVQN	IKYVSRAGEKLEKA	FVEFGISVENKIC	LDIGASTGGFTDCL	94	
Q9X1R2_THEMA	40	TKASKLVPE	DANVELLEE	PKYVSRGGYKLESA	FESFKIDVSGK	VACDIGASTGGFTDFL	98	
P19672_BACSU	41	DKPGEKIDRD	LPLTVKGNPLR	YVSRGGKLEKALKE	FPVSVKDKIM	LDIGASTGGFTDCA	100	
Q9K972_BACHA	40	DKPGKLVDRD	TPLSVKGEVLP	YVSRGGKLEKALRA	FDLHLDTRVVD	LDIGASTGGFTDCA	99	
Q8XJE2_CLOPE	44	DKAGEKVPVSSNI	IFRGEKLP	YVSRGGFKLDKAVKS	FGIDLKGGKRC	LDIGASTGGFTDCM	103	
Q92BY9_LISIN	41	DKPGEKIPAD	SELOVKGKOMP	YVSRGGKLEKALQV	FNFVDKDKLMD	LDIGASTGGFTDCA	100	
Q8Y7C0_LISMO	41	DKPGEKIPAD	SELOVKGKOMP	YVSRGGKLEKALQV	FNFVDKDKLMD	LDIGASTGGFTDCA	100	
Q9F6Y3_CHLAU	39	TKAGTLIAD	DASVEVRTG	LPYVSRGGFKLAHA	LDDQFALDPTGLTA	LDVIGASTGGFTDVL	97	
LA0327_LEPIN	118	LEKGAWKVEA	CDVGYGQLAEKLRN	HSSVIVKDRFHLKNLS	SALEIDWENNR	FQTPHPEAIV	177	
Q06803_TREHY	95	LKHGAKKYAL	LDVGHNLVYKLRND	NRVVSIEDFN	AKDINKEMFNDE	-----	IPSV	145
Q9X1R2_THEMA	99	LQRGAKKYAV	DDVGYGQLHKKLRND	PRVVMEKVNARYLN	PDDLGE	-----	KVDV	148
P19672_BACSU	101	LQNGAKQSYA	VDDVGYQLAWKLRD	ERVVMERTNFRYA	TPADFTKG	-----	MPEF	151
Q9K972_BACHA	100	LQNGATFYA	VDDVGYQLAWKLRD	ERVVMERTNFRYLK	PEVLERG	-----	LPNM	150
Q8XJE2_CLOPE	104	LONDASKVFS	IDVGYGQFAWKLRVD	PRVVCERTNFRYV	TPAQIGE	-----	LCDF	153
Q92BY9_LISIN	101	LQNGARHSYAL	DDVGYQLAWKLRND	ERVVMERTNFRHV	TPADFTG	-----	LAEF	151
Q8Y7C0_LISMO	101	LQNGARHSYAL	DDVGYQLAWKLRND	ERVVMERTNFRHV	TPADFAEG	-----	LADF	151
Q9F6Y3_CHLAU	98	LQRGAGRVA	VDDVGYGTLDRHLRND	PRVVALERTNIRHL	TALPANT	-----	LADC	147
LA0327_LEPIN	178	IVMDLSFISL	RSVFPVIQKLRKEK	IPKLECVSLIKPQFEA	NRNDLVKGI	LKDKSKIRFQ	236	
Q06803_TREHY	146	IVSDVSFISL	TKIAPIIFKELN	-----	NLEFVWTLIKPQFEA	ERGDVSKGGI	IRDDILREK	201
Q9X1R2_THEMA	149	VTCVDSFISL	KKIIPAI	SRILK-----	NIGDALLVKPQFEA	PRKFFL	KKGIVKDPGVHLE	203
P19672_BACSU	152	ATIDVSFISL	RLLPVLRTLLV	-----	PGSDCMALVKPQFEA	GRSVGKKGI	IVRDPKVHAD	207
Q9K972_BACHA	151	ATIDVSFISL	KLLPVLKTMLL	-----	ENSDVVALVKPQFEA	GREVVGKGI	IVRDKSVHQA	206
Q8XJE2_CLOPE	154	ASIDVSFISL	TTVLPVAVLNLLN	-----	DNGEVMALIKPQFEA	GREKVGKGI	VVREASTHKE	209
Q92BY9_LISIN	152	ATIDVSFISL	KLLPVLRTVLLV	-----	TGGDVMTLIKPQFEA	GREVVGKGI	IRDPAVHEA	207
Q8Y7C0_LISMO	152	ATIDVSFISL	KLLPVLRTVLLV	-----	TGGDVMTLIKPQFEA	GREVVGKGI	IRDPAVHES	207
Q9F6Y3_CHLAU	148	AVIDVSFISL	RLLVPAVQRLVT	-----	PTAWIVALIKPQFEA	GPKHVGGV	VVRDPAVHAQ	203
LA0327_LEPIN	237	IVLSLCRYL	KKKEIGGFVLEWSP	IEGRDGNKEILLFWNL	-----	-----	276	
Q06803_TREHY	202	ILNNAISKI	IDCGFKEVNRTISP	IKGAKGNTEYLAHF	II-----	-----	240	
Q9X1R2_THEMA	204	VLEEIRKSL	IENGFVVKGCCFSK	IKGTEGNIEYFFWVK	KEGENAEID---	LRKIV	VEEAW	259
P19672_BACSU	208	VLKRMISFS	AAEGYICKGLSFS	ITGGDGNIEFL	LQFALAGRGTGR	-----	PGTAGR-RD	261
Q9K972_BACHA	207	VLSTIVEFA	LKEGYAVGGLDFSP	ITGGEGNIEFL	LHLMMWRKDKESF	IS--	QEMIRDTVE	263
Q8XJE2_CLOPE	210	VIKKIVDFA	LSHKNILGLDFSP	ITGGEGNIEFL	IYLKKDNNTTEFDY	-----	NIIDVV	265
Q92BY9_LISIN	208	VVENIALFA	LDNGYDLMGLDFSP	ITGGEGNIEFL	IAHLKWTGKETGENH	LEPAA	ITKLI	266
Q8Y7C0_LISMO	208	VVEHIVQFA	LDNGYDLMGLDYSP	ITGGEGNIEFL	IAHLKWTGEETG	ISHLEPDA	ITKLI	266
Q9F6Y3_CHLAU	204	VTRDILSFA	RDCGLNPAALTRSP	ITGPAGNVEFL	LALFHPARPTLDSE	-----	RAIAS-VV	257
LA0327_LEPIN	276	-----	276	-----	-----	-----	-----	
Q06803_TREHY	240	-----	240	-----	-----	-----	-----	
Q9X1R2_THEMA	260	RFFGERER	-	267	-----	-----	-----	
P19672_BACSU	262	HARCRRST	-	269	-----	-----	-----	
Q9K972_BACHA	264	RAHLELKKG	-	272	-----	-----	-----	
Q8XJE2_CLOPE	266	KSHSDL	-	271	-----	-----	-----	
Q92BY9_LISIN	267	KAHTKLDK	-	274	-----	-----	-----	
Q8Y7C0_LISMO	267	KAHTKLDK	-	274	-----	-----	-----	
Q9F6Y3_CHLAU	258	HTH	-----	260	-----	-----	-----	

2. LA0378 (*hlyX*) Domain analysis

PD314750



LA0378

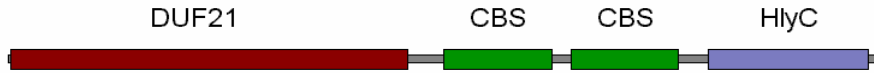
PD314750: hemolysinX from *Leptospira borgpetersenii*

Sequence similarity analysis: Identities:0.90; Similarities:0.94

LA0378_LEPIN	1	LVEALSVSDLRRKSMNRSII	ITGFLFICAGLLTAVYQITIQDEDSKRKNVLEKIKEGEE	60		
Q9RMG4_LEPBO	1	-----MNRSII	ITGFLFICAGLLIGVYQTTVQDEDSKRTSVLERIKEGEE	46		
LA0378_LEPIN	61	YLKQTN	SKAAEKAVDIFSELSAREIPEEH	SFRVKYDMGRALERNQDSSLALGIYRELNQK	120	
Q9RMG4_LEPBO	47	YLKQIN	PSATEKAVDIFSELSAKEIPEEY	SFRVKYDMGRALERNQDSSLALGIYRELNQK	106	
LA0378_LEPIN	121	EGLSRDERSKVAYS	SMGNLLQLNRDEEGKGHLEEVLRISADSK	LRSNALSAIADYYMKKG	180	
Q9RMG4_LEPBO	107	EGLSRDERSKVAYS	SMGNLLQLNRDEEGKGHLEEVLRISADSK	FRSNALSAIADYYMKKG	166	
LA0378_LEPIN	181	NYDLSRKNYVLALQEDPENVKARV	RWGKSLRRMGKDSAYD	VYDDYAQAGFYDPEKEKV	240	
Q9RMG4_LEPBO	167	NYDLSRKNYVLALQEDPENVKARV	RWGKSLRRMGKDSAYE	VYDDYAQAGFYDPEKEKV	226	
LA0378_LEPIN	241	SSEFRSGILEKARQLYVRKQYYGA	IDTFKKALDMGVSS	KAAEQALFYIAESYEAIGKSDS	300	
Q9RMG4_LEPBO	227	TSEFRSGILEKARQLYVRKQYYGA	IDTFKKALEMGI	SPKAAEQALFYIAESYEAIVGKSDS	286	
LA0378_LEPIN	301	ALQYLN	RVLGNQDGS	LDQTALFRKGTIYFKSGKYEKAAALFQEA	TDKYPDSPVGRKASAW	360
Q9RMG4_LEPBO	287	ALQYLN	RVLGNQDGS	LDQTALFRKGTIYFKSGKYEKAAALFQEA	SDRYPDSPVGRKASAW	346
LA0378_LEPIN	361	KKESLDQVEDNLHYKQEDKE	KKSKEDLETEKLD	392		
Q9RMG4_LEPBO	347	KKESLDQIEDNLHYKESDKA	KKSKEDLETERLD	378		

4. LA3937 (hlyC)

Domain analysis



LA3937

DUF21: Domain of unknown function

CBS (cystathionine-beta-synthase): unknown function

HlyC: involved in Magnesium and cobalt efflux

Sequence similarity analysis Identities:0.34; Similarities:0.56

LA3937_LEPIN	1	-----ME-----LIGFFIVLILFANGFFVSAEFALVSRP	SRLEELIKE	40
Q9PIU6_CAMJE	1	MDPSQVLDLNQSTASFDAGYSILMVVVALVFLNGFFVLS	EFVVKVRRSKLEEMVKE	60
Q9ZJC9_HELPY	1	-----MDPSESILMLMVAFLLVFLNAFFVLS	EFALVKVRKTRLEELVKI	44
Q97J64_CLOAC	1	-----MDN-----LLNIVIIILLVFMNAFFVAAEF	SMVKIRKSRILETLVLD	41
O26023_CAMPY	1	-----MGRNQGAYLDPSESILMLMVAFLLVFLNAFFVLS	EFALVKVRKTRLEELVKI	52
O07585_BACSU	1	-----MD-----LVNLIIVAVLIALTAFFVAS	EFVIRIRGSRIDQLIAE	40
P54428_BACSU	1	-----MT-----TINLIIFTLLIVLTAFFVAT	EFVIRKRSKIDQLILE	40
LA3937_LEPIN	41	NKPLAFITKRAAQKNDMLSVCCQVGTITIASLLGWGGE	GYVSRWLFLEMFYGYSANEAT	100
Q9PIU6_CAMJE	61	KKAGAKKALEVTSRLODTYLSACQLGITLSSLAGWIGEP	AIKMLLEIPLINLGFSS--TVI	118
Q9ZJC9_HELPY	45	GNSNAKLALEMSQRDITYLSATQLGITLSSLAGWGE	PAIAKLLAALFESMDLRENPIF	104
Q97J64_CLOAC	42	GDKNAKYLGVINNSYLSACQLGITLSSLAGWGE	PAVSKMLSPFLNLLKIP--KQI	99
O26023_CAMPY	53	GNSNAKLALKMSQRDITYLSATQLGITLSSLAGWGE	PAIAKLLAALFESMDLRENPIF	112
O07585_BACSU	41	GNKAAIAVKKVTHLDEYLSACQLGITLSSLAGVLGEST	IERLLHPLFVQMNVP--GSL	98
P54428_BACSU	41	GKKGAISAKKVIITHLDEYLSACQLGITVTA	LGIWVGESTFEVILHPLFAHFHVS--ETV	98
LA3937_LEPIN	101	VHGLAITTSFTITFLHLLGELLPKTVANTETIALFIS	PLFFFYLYFPIITFFLNE	160
Q9PIU6_CAMJE	119	IHTMAFIIFASIIITLHVVLGELVPKSI	IAVADKAVLFARPLHWVMMFLPCIKIFDF	178
Q9ZJC9_HELPY	105	IHSMSVVIAFLSITFLHVVLGELVPKSLA	AKSEKATLFAARPLHVFWVVFYPVVRFLDV	164
Q97J64_CLOAC	100	IGSISVVVGFIIITGRHIVLGEAPK	SVAI LNTE SIAKATAIPLTLFYKFTYPIVAFNK	159
O26023_CAMPY	113	IHSMSVVIAFLSITFLHVVLGELVPKSLA	AKSEKATLFAARPLHVFWVVFYPVVRFLDV	172
O07585_BACSU	99	SHVISFIEAYAITFLHVVLGELAPKTV	AIKQAEAVSMLFAKPLIWFYRIAFPFIWLLNN	158
P54428_BACSU	99	SHVLIIVLAFVMAITLHVVLGELAPKTL	AIKQAEITITLTAKPIIWFYRIELFPFIWFLNG	158
LA3937_LEPIN	161	MTSFLKLIIGIEA-NKSRMMHSPFELMIIIE	EQNKQKIDQEEFQIQNTFQFSEHQAKD	219
Q9PIU6_CAMJE	179	LAAISLKLFGIKPAKESLTHSEEEKI	IASESQKGGVLEDEFETEIIRNAVDFSOTVAKE	238
Q9ZJC9_HELPY	165	IAHFFLKKMGVNP-KHEEGMHSEELKI	IVGESLREGIIDSVEGEIKNNAVDFSOTSAKE	223
Q97J64_CLOAC	160	STDLVKLFGIKQVDHEEAHTDEEIRMLV	ESYKHGLIDKTELTFVDNVDFSEKTVKE	219
O26023_CAMPY	173	IAHFFLKKMGINP-KHDGTHSEELKI	IVGESLREGIIDSVEGEIKNNAVDFSOTSAKE	231
O07585_BACSU	159	SARLLTKAFGLTETSENGLAHSEELRI	ILSESYKSGEINQSEFKYVNNIFEFDDRLAKE	218
P54428_BACSU	159	SARFIVGLFGLKPASHEGLAHSEELRI	ILSESYKSGEINQNELKYVNNIFEFDERIAKE	218
LA3937_LEPIN	220	VMTHRLSIIIGIPHDTSMDSLISII	IAEHHSRYPIYEGSIDKIGIITHVQTYLTWLSNS--	277
Q9PIU6_CAMJE	239	IMTPRKDMICLNKQKSYEENMQI	ICEHKHTREPYIDGSKDITLGMHHRDIIQN-ELN-	295
Q9ZJC9_HELPY	224	IMTPRKDMVCLDEENSYEENID	VLKSHFTRYPYCKGSKDNIGMVHHRDILLSRSIFT-	281
Q97J64_CLOAC	220	IMVPRDMKCFVDESFDDIVGVT	IDIEHFTRYPVCEESKDNIGLITHKDLYKLNK--	277
O26023_CAMPY	232	IMTPRKDMVCLDEENSYEENID	VLKGFHTRYPYCKGSKDNIGMVHHRDILLSRSIFT-	289
O07585_BACSU	219	IMIPRTEIVSLPHDIKISEMMD	IIGIEKYTRYPVEEGDKDNIGVNIKEVLTACISG--	276
P54428_BACSU	219	IMIPRREIVAISSEDSYETIVK	IKTESYTRYPVLNGDKDSIGFINAKEFLSAYIDTDQ	278
LA3937_LEPIN	278	KKGRKEKVTAIMQPPIFVPEGLS	EKVMQKLRNKKQHMALVIDEYGGVAGLLTLEDIIEE	337
Q9PIU6_CAMJE	295	--HKSQLDITFVKPLILVPENIS	SKVLVMNKNERSHTALVVDEYGGTAGLITMEDIMEE	353
Q9ZJC9_HELPY	281	--PKMHDFKQIVRKMIVPESAS	ISQILIKMKKEQIHTALVIDEYGGTAGLLTMEIIEE	339
Q97J64_CLOAC	277	---EDEKIESIIREIKFVPESMS	SELFERMEQKERMQMALVIDEYGGTAGLVTIEDILEE	334
O26023_CAMPY	289	--PKMHDFNQIVRKMIVPESAS	ISQILIKMKKEQIHTALVIDEYGGTAGLLTMEIIEE	347
O07585_BACSU	277	EVSVDSTISQFVNPILHVI	ESAPQDLVKKMOKERVHMAILSDEYGGTAGLVTVEDIIEE	336
P54428_BACSU	279	KIKEDFKLENHINPVHVI	ESVPHDVLVKKMOKERTHIALVIDEYGGTAGLVTAEIIEE	338
LA3937_LEPIN	338	IFGQIRDETDHETDPFPTQHSDSFT	IDGEAELDDLKEILVGVQEEIKDIRTTAGFILG	397
Q9PIU6_CAMJE	354	IIGEIKSEHE--EDSYKKLAENI	YEFQGRCDIETVEEMLVINYDEDL-EQVTIGGYVFN	409
Q9ZJC9_HELPY	340	IMGEISDEYDL-KQEGVKLEEGVFE	LEGMLDLESVEEVLIHQFDKCE-EQVTLGGYVFS	397
Q97J64_CLOAC	335	IVGEIQDEFD-EEMEEIKKTENG	SYVVDGKVLIEDINELDIEIYEE--NIDTIGGWIYS	391
O26023_CAMPY	348	IMGEISDEYDL-KQEGINKLEEGVFE	LEGMLDLESVEEAHQHIEFDKCE-EQVTLGGYVFS	405
O07585_BACSU	337	IVGEIRDEFDIDKIEISEIRK	IGEGHYILDGKVLIDQVNDLGIHLENE--EVDTIGGWFLT	394
P54428_BACSU	339	IVGEIRDEFDKDEVPNIRK	IGENHYILDSKVLIEDVNDLGLTTLASD--EVDTIGGWFLT	396
LA3937_LEPIN	398	RIEDMPPEEGSTISLQGTTLT	VEKMEGNKILSVRFTRVSLNNRAQSKK----	444
Q9PIU6_CAMJE	410	LLGRLPMVGDRIEDELICY	EVKMKDGNSEIRVKVVKTKNKDEE-----	452
Q9ZJC9_HELPY	398	LLKERP	IEGDTIVSHGYAFEVLSVDGARIKRLKAVKQDQGENEA-----	441
Q97J64_CLOAC	392	KLKKYPKTNEKINYGNYQ	FIIILKCDRRRIEKILIKNL-----	428
O26023_CAMPY	406	LLKERP	MEGDTIVSHGYAFEVLSVDGARIKRLKAVKQDQGENEA-----	449
O07585_BACSU	395	KQYDVEKDSDILEEG-CE	FINEIDGHHVAYIEVKKLQEEELLETANQEA	444
P54428_BACSU	397	QQIDAAVGSVIEADG-YI	FKVHETVGRHINYLEIVRKK-----	434

Abbreviation used for sequences from relevant microorganisms:

Treponema hyodysenteriae, TREHY;

Thermotoga maritime, THEMA;

Bacillus subtilis, BACSU;

Bacillus halodurans, BACHA;

Clostridium perfringens, CLOPE;

Listeria innocua, LISIN;

Listeria monocytogenes, LISMO;

Chloroflexus aurantiacus, CHLAU;

Campylobacter jejuni, CAMJE;

Helicobacter pylori J99, HELPY;

Clostridium acetobutylicum, CLOAC;

Leptospira interrogans, LEPIN;

Leptospira borgpetersenii, LEPBO;

Anabaena sp. (strain PCC 7120), ANABA;

Mycobacterium avium, MYCAV.

* Lee, S. H., Kim, S., Park, S. C. & Kim, M. J. Cytotoxic activities of *Leptospira interrogans* hemolysin SphH as a pore-forming protein on mammalian cells. *Infect Immun* **70**, 315-22 (2002).