

Supporting Information for the article:

**A Peptidomimetic Antibiotic Interacts with the Periplasmic Domain of LptD
from *Pseudomonas aeruginosa***

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- 1. PCR primers**
- 2. Homology modelling of *P. aeruginosa* LptD**
- 3. List of LptD/E peptides quantified by MS**

1. PCR primers

List of primers used to amplify *Pa* LptD and LptE from strain PAO1, with restriction sites underlined.

lptDfor atctacatatggcagtgaaatccctcg
lptDrev acaatggatccttacatagcttgatcttcacg
lptEfor ttacaccatgggcaaacgtatcctgaccagcgccgcgc
lptEhis6rev tacgtctcgagtcgaatggtgatgatggtgatgcggggtggggaactcgatcggcgactgc

2. Homology modelling of *P. aeruginosa* LptD

The full-length *P. aeruginosa* LptD (res. 34–924) comprises a C-terminal β -barrel domain (res. 324–924), a β jellyroll domain (res. 145–323), and an N-terminal insert domain (res. 45–144) characteristic of *Pseudomonas* spp. (Figure 2A). The recently solved X-ray structure of truncated *Pa* LptD/E (PDB 5IVA, residues 317–895) contains only the β -barrel domain.¹ A homology model of the conserved β jellyroll domain was generated after sequence alignment with the jellyroll domain in *Shigella flexneri* LptD (PDB 4Q35) (Figure S1).² The *Pa* jellyroll shows a sequence similarity of 47% (28% identity) with the aligned *Sf* LptD region (Table S1). An additional loop insertion between R165–K170 was adjusted manually and was energy minimized. The relative orientation of the β -jellyroll and the β -barrel domain in *Pa* LptD is likely to be very similar to that in the full-length *Sf* LptD structure based on a sequence alignment. In particular, the sequences of the region linking the β -jellyroll to the barrel in LptD from *P. aeruginosa* (I317–L326) and *Shigella flexneri* (V220–L229) contain highly conserved residues, indicating a similar fold in this region.

Attempts to identify secondary structure motifs or a protein homology template for the insert domain in *Pa* LptD using protein structure prediction methods (I-Tasser, MODELLER, PredictProtein, PSIPRED, JPRED, SwissModel) were unsuccessful. However, a sequence motif search in the PDB database with selected parts of the sequence provided similarities with a human V_H immunoglobulin (Ig) domain (PDB 1T2J) (Table S1 and Figure S2 and S3). After sequence alignment (25% sequence identity) a homology model was generated for the insert domain, with a truncated V_H-like fold. Interestingly, this model allows a disulfide to form between C49 and C134, which resembles an intra-domain disulfide commonly found in the Ig V_H fold, including bacterial Ig-like domains.³

Table S1. Sequence and structure comparisons of the jellyroll domain of *Pa* LptD with that of *Sf* LptD; and the N-terminal insert domain with the Ig-like domain (1T2J).

Alignment with <i>S. flexneri</i> LptD (PDB 4Q35)	Sequence identity	Sequence similarity	RMSD
jelly roll domain (G145–L326)	28 %	47 %	0.9 Å
Alignment with Ig-like domain PDB 1T2J			
Insert domain	25 %	34 %	1.1 Å

Figure S1. Sequence alignment of full-length *P. aeruginosa* LptD and *Shigella flexneri* LptD (signal peptides are not shown).

PaLPTD SiLPTD	34 - 25	ADQFDCKV S ADLASQCMLG	ATGGWDCSPL -----	QNANANLPPR -----	PAHTATSVST -----	AAAGSSVSGS -----	82 34
PaLPTD SiLPTD	83 35	GGETVEAEPT -----	QRLVTESGGR -----	ALKSR SADYS -----	HLDWIPREKL -----	TAAQLAEIGP -----	132 34
PaLPTD SiLPTD	133 35	YCGGSYIEPV - - VPSYDRPL	RPGMDDGAPS VQGD TNDLPV	DESPTYVSAK TINADHAKGD	ASRYEQEKQI YP - - - - - DD	ATLAGDVVLR AVFTGSVDIM	182 76
PaLPTD SiLPTD	183 77	QGSMQVEGDE QQNSRQLQADE	ANLHQLE - - - VQLHQKEAPG	- - - - - NRGEL QPEPVRTVDA	VGNVKLRDKG LGNVHYDDNQ	MLVVGDHAQV VILKGPKGWA	221 126
PaLPTD SiLPTD	225 127	QLDNGEAQVD NLNTKDTNVW	NAEYVIHKAH EGDYQMVGRQ	ARGSA - LYAK GRGKADLMKQ	RSENAIIMLK RGENRYTILD	DGTYTRCEPS NGSFTSCLPG	273 176
PaLPTD SiLPTD	274 177	SNAWTLKGNN SDTWSVVGSE	VKLN PATGFG I IHDREEQVA	TATNATLRVK EIWNARFKVG	DFPVFYTPYI PVP I FYSPYL	YFPIDRRRQS QLPVGDKRRS	323 226
PaLPTD SiLPTD	324 227	GFLPPSFSST GFLIPNAKYT	SDTGFTLVTP TTNYFEFYLP	YYFN LAPNYD YYWNIAPNMD	ATLYPRYMAK ATITPHYMHR	R - GMMLEGEF RGNIMWENEF	372 276
PaLPTD SiLPTD	373 277	RYLTHSSEGI RYLSQAGAGL	VNAAYLNDKD MELDYLP SDK	- - DHREGFPD VYEDEHPNDD	YSKDRWLYGL -SSRRWLFYW	KNTTGLDSRW NHSGVMDQVW	420 325
PaLPTD SiLPTD	421 326	LAEVDYTRIS RFNV DYT KVS	DPYYFQDLDT DPSYFNDFDN	DLGVGSTTYV KYGSSTDGYA	NQRGTLTYRG TQKFSVG YAV	DTFTGRLNAQ QNFNATVSTK	470 375
PaLPTD SiLPTD	471 376	AYQLATTTDV QFQVFSEQNT	TPYDRLPQIT SSYSAEPQLD	FDGFLPYNPG VNY YQ - NDVG	GMQFTYGTEF PF DTRIYGQA	VRFD RDLDEN VHFVNTRDD -	520 423
PaLPTD SiLPTD	521 424	IYFNDDGSIR - - - - - - - -	GKRPDASLQG - - - - - - - -	LARATGDRMH - - MPEATRVH	LEPGMSLPM T LEPTILPLKS	RSWGYVTPTL NNWGSINTEA	570 451
PaLPTD SiLPTD	571 452	KYLYTKYDLD KFLATHYQQT	LDSQGKTDLN NLDWYNS - - -	KRDESFD SNQ RNTTKLDES V	DL SPLNLKVD NRVMPQFKVD	SGLYFD RDTT GKMVF ERDME	620 498
PaLPTD SiLPTD	621 499	FAGTPFRQTL MLAPGYTQTL	EPRAMYLYVP EPRAQYLYVP	YKDQDSL PVF YRDQSDIYNY	DTSEPSFSYD DSSL LQSDYS	SLWREN RFTG GLFRDRTYGG	670 548
PaLPTD SiLPTD	671 549	KDRIGDANQL LDRIASANQV	SLGVTSRFIE TTGVT SRIYD	ENGFERASIS DAAVERFNIS	AGQIYYFRDR VGQIYYFTES	RVQLPGLTEK RTGDDNITWE	720 598
PaLPTD SiLPTD	721 599	DLKRLNLDPS N - - - - - - -	GLDNDSWRSP - - DDKTGSLV	YAFAGQYRFN WAGDTYWRIS	RDWRINSDFN ERWGLRGGIQ	WNPNTSRTES YDTRLDNVAT	770 637
PaLPTD SiLPTD	771 638	GSAIFHYQPE SNSSIEYRR -	VDPGKVVNVG - DEDRLVQLN	YRYRADARRF YHYASPEYIQ	DSSRGTFRYG ATLPKYYSTA	NE - NDI IKQH EQYKNGISQV	819 685
PaLPTD SiLPTD	820 686	DFSVIWPLVP GAVASRP IAD	QWSVLARWQY RWSIVGAYYY	DYNKNRTLEA DTNANKQADS	FGGFEYDSCC MLGVQYSSCC	WKLRLINRYW YAIRVGYERK	869 735
PaLPTD SiLPTD	870 736	LDVDDDAFLV LNGWDND - - K	QSEKADRGIF QHAVYDNAIG	LQIVLKGLGG FNIELRGLSS	IVGNKTEMFL NYGLGTQEML	DKG IQGYRQR RSN ILPYQNT	919 783
PaLPTD SiLPTD	920 784	EDQAM L - - - - 784					

Figure S2. The sequence alignment of the insert domain (res. 45–146) of *P. aeruginosa* LptD and the Ig-like V_H domain (PDB file 1T2J). The β -strands (A1–G) in the V_H domain (1T2J) are indicated, with only the seven predicted β -strands B–F present in the model of the insert domain.

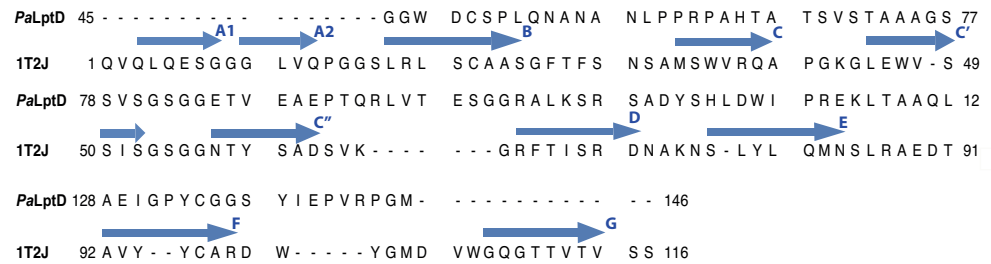
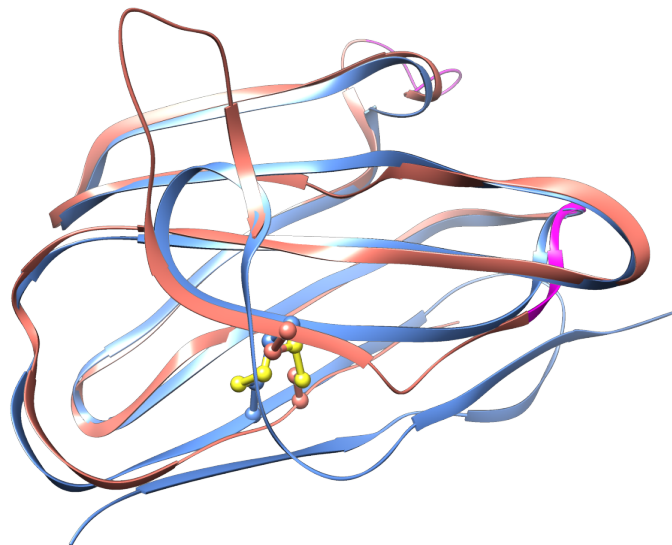


Figure S3. Superposition of a homology model of the N-terminal insert domain of *Pa* LptD (*red*, res. 45–144) with the Ig V_H domain (*blue*, 1T2J). The disulfide bridge in both proteins is displayed in ball-and-stick representation.



3. List of LptD/E peptides quantified by MS

Table S2. List of LptD/E peptides quantified by MS with measured abundance fold change upon photo-crosslinking with photoprobe **PAL6**. Peptides are sorted according to protein domain (insert orange; jellyroll purple; β -barrel green; LptE light blue), green and red arrows indicate biologically significant up- and downregulation ($\log_2$ fold change $> \pm 0.58$) and stars indicate statistically significant abundance changes (q-value < 0.05). The ETV (res. 85-87) and ENR (res. 199-201) sequence motifs of LptD insert and jellyroll domain, respectively, are highlighted in bold.

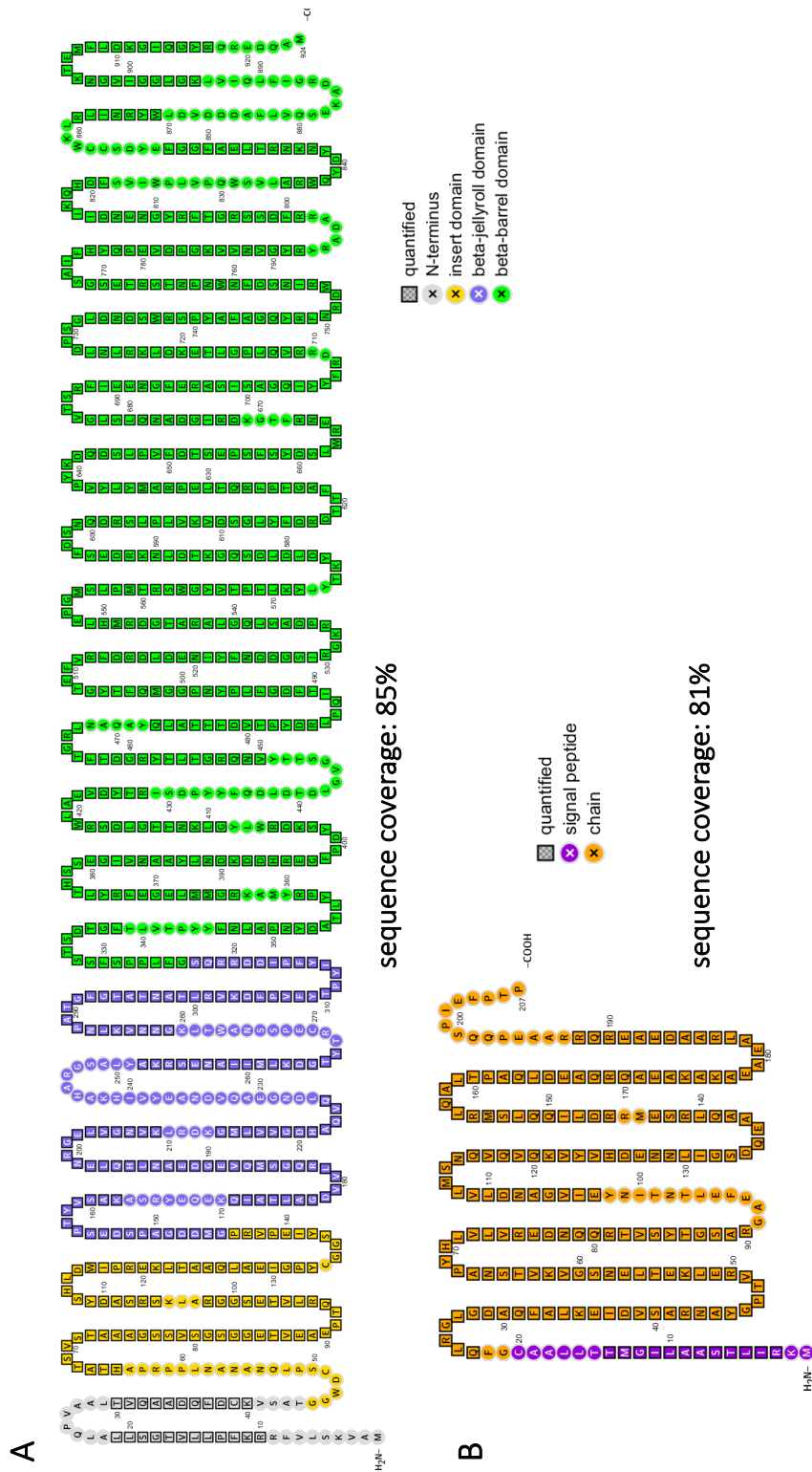
Protein_Entry	Protein_Domain	Sequence	log2 peptide abundance ratio (labeled vs unlabeled)	q-value	res. start	res. end	res. mid
LptD_Q915U2	LptD_N-term	RKFPLLVTG	↓	-2.040997028	0.115974819	10	18
LptD_Q915U2	LptD_N-term	KFPLLVTGSL	↓	-1.882098794	0.117390029	11	21
LptD_Q915U2	LptD_N-term	TVQAADQFDCK	↓	-3.214735508	0.051356677	30	40
LptD_Q915U2	LptD_N-term	ADQFDCK	↓	-0.630928218	0.214706988	34	40
LptD_Q915U2	LptD_insert	HTATSVSTAAAGSSVSGSGGETVEAEPTQR	↓	-0.217327505	0.354243686	65	94
LptD_Q915U2	LptD_insert	ATSVSTAAAGSSVSGSGGETVEAEPTQR	↓	-0.59875536	0.217521852	67	94
LptD_Q915U2	LptD_insert	TSVSTAAAGSSVSGSGGETVEAEPTQR	↓	-0.444552869	0.214665569	68	94
LptD_Q915U2	LptD_insert	SVSTAAAGSSVSGSGGETVEAEPTQR	↓	-0.983084142	0.047897219	69	94
LptD_Q915U2	LptD_insert	STAAAGSSVSGSGGETVEAEPTQR	↓	-0.550596356	0.027008595	71	94
LptD_Q915U2	LptD_insert	TAAAGSSVSGSGGETVEAEPTQR	↓	-0.329122514	0.066812974	72	94
LptD_Q915U2	LptD_insert	AAAGSSVSGSGGETVEAEPTQR	↓	-1.136440396	0.010446344	73	94
LptD_Q915U2	LptD_insert	AAGSSVSGSGGETVEAEPTQR	↓	-0.678272367	0.017491654	74	94
LptD_Q915U2	LptD_insert	AGSSVSGSGGETVEAEPTQR	↓	-1.164577842	0.003100856	75	94
LptD_Q915U2	LptD_insert	GSSVSGSGGETVEAEPTQR	↓	-0.854492605	0.009896912	76	94
LptD_Q915U2	LptD_insert	SVSVDGSGGETVEAEPTQR	↓	-1.291841507	0.027850968	77	94
LptD_Q915U2	LptD_insert	SVSVDGSGGETVEAEPTQR	↓	-1.12938714	0.003100856	78	94
LptD_Q915U2	LptD_insert	VSGSGGETVEAEPTQR	↓	-1.547986388	0.028230588	79	94
LptD_Q915U2	LptD_insert	SGSGGETVEAEPTQR	↓	-2.279568911	0.018926199	80	94
LptD_Q915U2	LptD_insert	GSGETVEAEPTQR	↓	-2.481119394	0.010446344	81	94
LptD_Q915U2	LptD_insert	SGGETVEAEPTQR	↓	-1.491169095	0.012765388	82	94
LptD_Q915U2	LptD_insert	GGETVEAEPTQR	↓	-1.692623854	0.018926199	83	94
LptD_Q915U2	LptD_insert	GETVEAEPTQR	↓	-0.910798073	0.027850968	84	94
LptD_Q915U2	LptD_insert	ETVEAEPTQR	↓	-1.175467849	0.048035412	85	94
LptD_Q915U2	LptD_insert	LVTESGGR	↓	0.463142902	0.214706988	95	102
LptD_Q915U2	LptD_insert	SADYSHLD	↓	-0.176817909	0.354243686	108	115
LptD_Q915U2	LptD_insert	RSADYSHLDWIPR	↓	-0.092073843	0.355569525	106	119
LptD_Q915U2	LptD_insert	RSADYSHLDWIPR	↓	-0.430961996	0.166074273	107	119
LptD_Q915U2	LptD_insert	SADYSHLDWIP	↑	0.612305164	0.300707638	108	118
LptD_Q915U2	LptD_insert	SADYSHLDWIPR	↓	0.350829512	0.048035412	108	119
LptD_Q915U2	LptD_insert	RSADYSHLDWIPREK	↓	-1.690024734	0.207438575	106	121
LptD_Q915U2	LptD_insert	RSADYSHLDWIPREK	↓	-1.340161443	0.008871141	107	121
LptD_Q915U2	LptD_insert	ADYSHLDWIPR	↓	-0.331701308	0.185066874	109	119
LptD_Q915U2	LptD_insert	SADYSHLDWIPREK	↓	-0.8045609	0.012765388	108	121
LptD_Q915U2	LptD_insert	DYSHLDWIPR	↓	-0.448816329	0.122743975	110	119
LptD_Q915U2	LptD_insert	SHLDWIPR	↓	-0.563129544	0.19170552	112	119
LptD_Q915U2	LptD_insert	SHLDWIPREK	↓	-1.572404981	0.048035412	112	121
LptD_Q915U2	LptD_insert	LTAQLAEIGPY	↓	-1.046897054	0.075861777	122	133
LptD_Q915U2	LptD_insert	TAAQLAEIGPY	↓	-1.038890004	0.192342847	123	133
LptD_Q915U2	LptD_jellyroll	GGSYIEPVRPGMDDGAPSDSPYVSAS	↓	-0.521354496	0.039970343	135	162
LptD_Q915U2	LptD_jellyroll	IEPVRPGMDDGAPSDSPYVSAS	↓	-0.491692424	0.105502071	139	162
LptD_Q915U2	LptD_jellyroll	EPVRPGMDDGAPSDSPYVSAS	↓	-0.023788407	0.414187506	140	162
LptD_Q915U2	LptD_jellyroll	VRPGMDDGAPSDSPYVSAS	↓	-0.130741015	0.246634107	142	162
LptD_Q915U2	LptD_jellyroll	APSDSPYVSAS	↑	0.633911848	0.127877563	150	162
LptD_Q915U2	LptD_jellyroll	SDSPYVSAS	↓	-0.426079661	0.192196407	152	162
LptD_Q915U2	LptD_jellyroll	DESPYVSAS	↓	-1.902620554	0.033886088	153	162
LptD_Q915U2	LptD_jellyroll	ESPTYVSAS	↓	-0.173785254	0.298631471	154	162
LptD_Q915U2	LptD_jellyroll	QIATLAGDVVLR	↑	1.048849225	0.075861777	171	182
LptD_Q915U2	LptD_jellyroll	IATLAGDVVLR	↓	-0.932461739	0.069464716	172	182
LptD_Q915U2	LptD_jellyroll	QIATLAGDVVLRQ	↓	-0.607531548	0.135494965	171	183
LptD_Q915U2	LptD_jellyroll	ATLAGDVVLR	↓	-0.270619184	0.227557489	173	182
LptD_Q915U2	LptD_jellyroll	TLAGDVVLR	↓	-2.642323971	0.021529266	174	182
LptD_Q915U2	LptD_jellyroll	QGSMDQVEGEANLH	↓	-0.963671088	0.010446344	183	196
LptD_Q915U2	LptD_jellyroll	QGSMDQVEGEANLHQL	↓	-1.067395926	0.091345866	183	198
LptD_Q915U2	LptD_jellyroll	QGSMDQVEGEANLHQLENR	↓	-0.573159099	0.012765388	183	201
LptD_Q915U2	LptD_jellyroll	GSMQVEGEANLHQLENR	↓	-2.675170183	0.000192023	184	201
LptD_Q915U2	LptD_jellyroll	QVEGEANLHQLENR	↓	-3.816850424	0.000208482	187	201
LptD_Q915U2	LptD_jellyroll	RQGSMDQVEGEANLHQLENRGELVGNVK	↓	-1.801071405	0.215741445	182	209
LptD_Q915U2	LptD_jellyroll	DEANLHQLENR	↓	-3.769959927	0.075861777	191	201
LptD_Q915U2	LptD_jellyroll	QGSMDQVEGEANLHQLENRGELVGNVK	↓	-1.521563172	0.225693443	183	209
LptD_Q915U2	LptD_jellyroll	GSMQVEGEANLHQLENRGELVGNVK	↓	-2.532865047	0.055274521	184	209
LptD_Q915U2	LptD_jellyroll	SMQVEGEANLHQLENRGELVGNVK	↓	-1.673057318	0.061870683	185	209
LptD_Q915U2	LptD_jellyroll	QVEGEANLHQLENRGELVGNVK	↓	-3.490809441	2.77E-05	187	209
LptD_Q915U2	LptD_jellyroll	VEGEANLHQLENRGELVGNVK	↓	-2.8448174	0.048252212	188	209
LptD_Q915U2	LptD_jellyroll	GDEANLHQLENRGELVGNVK	↓	-3.346674442	0.005553289	190	209
LptD_Q915U2	LptD_jellyroll	DEANLHQLENRGELVGNVK	↓	-3.348915577	0.000192023	191	209
LptD_Q915U2	LptD_jellyroll	NLHQLENRGELVGNVK	↓	-0.813192546	0.098444485	194	209
LptD_Q915U2	LptD_jellyroll	HQLENRGELVGNVK	↓	-0.315098852	0.289724484	196	209
LptD_Q915U2	LptD_jellyroll	QLENRGELVGNVK	↓	-1.553606391	0.002792038	197	209
LptD_Q915U2	LptD_jellyroll	ENRGELVGNVK	↓	-1.958863497	0.002792038	199	209
LptD_Q915U2	LptD_jellyroll	NRGELVGNVK	↓	-0.720071316	0.03871991	200	209
LptD_Q915U2	LptD_jellyroll	RGELVGNVK	↓	-1.138474107	0.065972922	201	209
LptD_Q915U2	LptD_jellyroll	GELVGNVK	↓	-0.1405541	0.234545679	202	209
LptD_Q915U2	LptD_jellyroll	GMLVVGDDHA	↓	-1.391724944	0.091345866	214	222
LptD_Q915U2	LptD_jellyroll	GMLVVGDDHAQ	↓	-1.489968777	0.079018305	214	223
LptD_Q915U2	LptD_jellyroll	GMLVVGDDHAQVQ	↓	-2.466878891	0.008871141	214	225
LptD_Q915U2	LptD_jellyroll	RSENAIM	↓	-0.806384921	0.030361387	254	261
LptD_Q915U2	LptD_jellyroll	AKRSENAIIMLK	↓	-1.457039475	0.069464716	252	263
LptD_Q915U2	LptD_jellyroll	KRSENAIIMLK	↓	-2.371243715	0.081530898	253	263
LptD_Q915U2	LptD_jellyroll	RSENAIIMLK	↓	-0.94785738	0.012765388	254	263
LptD_Q915U2	LptD_jellyroll	SENAIIMLK	↓	-0.62841481	0.018926199	255	263
LptD_Q915U2	LptD_jellyroll	ENAIIMLK	↓	-0.825141668	0.026849047	256	263

LptD_Q9ISU2	LptD_jellyroll	NAIIMLK		-0.487929344	0.217521852	257	263	260
LptD_Q9ISU2	LptD_jellyroll	RSENAIMLKDGTY	↓	-0.769421577	0.079018305	254	267	260.5
LptD_Q9ISU2	LptD_jellyroll	GNNVKLNPA	↓	-0.783953428	0.144246783	281	289	285
LptD_Q9ISU2	LptD_jellyroll	GNNVKLNPAATGF		0.022684852	0.430059779	281	292	286.5
LptD_Q9ISU2	LptD_jellyroll	GNNVKLNPAATGFGTATNATLR	↓	-1.307109237	0.066812974	281	301	291
LptD_Q9ISU2	LptD_jellyroll	LNPATGFGTATN	↑	0.585244715	0.096036725	286	296	291
LptD_Q9ISU2	LptD_jellyroll	LNPATGFGTATN		-0.23924762	0.075861777	286	297	291.5
LptD_Q9ISU2	LptD_jellyroll	LNPATGFGTATNA	↑	1.226473212	0.069474162	286	298	292
LptD_Q9ISU2	LptD_jellyroll	LNPATGFGTATNATLR		-0.404132217	0.06854365	286	301	293.5
LptD_Q9ISU2	LptD_jellyroll	NPATGFGTATNATLR	↓	-0.688337505	0.161737201	287	301	294
LptD_Q9ISU2	LptD_jellyroll	PATGFGTATNATLR		-0.441622168	0.200664428	288	301	294.5
LptD_Q9ISU2	LptD_jellyroll	TGFGTATNATLR		-0.133532733	0.109326548	290	301	295.5
LptD_Q9ISU2	LptD_jellyroll	GFGTATNATLR		0.110644333	0.406497531	291	301	296
LptD_Q9ISU2	LptD_jellyroll	FGTATNATLR	↑	0.998711467	0.097532897	292	301	296.5
LptD_Q9ISU2	LptD_jellyroll	GDTATNATLR	↓	-1.038866639	0.239044509	293	301	297
LptD_Q9ISU2	LptD_jellyroll	RVKDFPVFY		-0.148955762	0.378170193	301	309	305
LptD_Q9ISU2	LptD_jellyroll	VKDFPVFY		-0.506918132	0.160427482	302	309	305.5
LptD_Q9ISU2	LptD_jellyroll	RVKDFPVFYTPY		-0.472384959	0.261463431	301	312	306.5
LptD_Q9ISU2	LptD_jellyroll	DFPVFYTPY	↑	0.708630741	0.18427368	304	312	308
LptD_Q9ISU2	LptD_jellyroll	TPYIFYPIDDR		0.01044932	0.4331092	310	320	315
LptD_Q9ISU2	LptD_jellyroll	TPYIFYPIDRR		0.5734846	0.298788162	310	321	315.5
LptD_Q9ISU2	LptD_jellyroll	IYFIDDR		0.08093337	0.14060694	313	320	316.5
LptD_Q9ISU2	LptD_jellyroll	IYFIDRR		0.239288807	0.204875249	313	321	317
LptD_Q9ISU2	LptD_jellyroll	FPIDRR	↑	3.687490463	0.072933362	315	321	318
LptD_Q9ISU2	LptD_beta-barrel	RQSGFLPPSFSSSDTGF	↑	0.90501821	0.248415794	321	338	329.5
LptD_Q9ISU2	LptD_beta-barrel	QSGFLPPSFSSSDTGF	↑	2.571289301	0.192342847	322	338	330
LptD_Q9ISU2	LptD_beta-barrel	NLAPNYDATLY	↓	-2.847301722	0.069375849	347	357	352
LptD_Q9ISU2	LptD_beta-barrel	FNLPAPNYDATLYPR		-0.055968951	0.406497531	346	359	352.5
LptD_Q9ISU2	LptD_beta-barrel	NLAPNYDATLYPR		0.000874972	0.433766395	347	359	353
LptD_Q9ISU2	LptD_beta-barrel	LAPNYDATLYPR		0.272662222	0.079528178	348	359	353.5
LptD_Q9ISU2	LptD_beta-barrel	APNYDATLYPR		0.111144736	0.354243686	349	359	354
LptD_Q9ISU2	LptD_beta-barrel	YDATLYPR	↑	0.923169136	0.075861777	352	359	355.5
LptD_Q9ISU2	LptD_beta-barrel	DATLYPR	↑	0.707713187	0.039891336	353	359	356
LptD_Q9ISU2	LptD_beta-barrel	RGMMLGEF	↓	-2.374005556	0.200664428	364	372	368
LptD_Q9ISU2	LptD_beta-barrel	RGMMLGEFR	★	0.375829458	0.025274617	364	373	368.5
LptD_Q9ISU2	LptD_beta-barrel	GMMLEGEFR		-0.340908647	0.299953527	365	373	369
LptD_Q9ISU2	LptD_beta-barrel	MMLEGEFR		0.191819623	0.298631471	366	373	369.5
LptD_Q9ISU2	LptD_beta-barrel	MLEGEFR	↑	0.940959215	0.047897219	367	373	370
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVN		-0.049647253	0.257278096	374	384	379
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVNA		0.239104569	0.278682655	374	385	379.5
LptD_Q9ISU2	LptD_beta-barrel	RYLTHSSEGIVNAAY	↓	-2.281217098	0.197228722	373	387	380
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVNAA		0.005476057	0.430540477	374	386	380
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVNAAY		0.337806761	0.121031084	374	387	380.5
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVNAAYL		-0.272196084	0.355569525	374	388	381
LptD_Q9ISU2	LptD_beta-barrel	THSSEGIVNAAY	↓	-0.726057649	0.265578305	376	387	381.5
LptD_Q9ISU2	LptD_beta-barrel	YLTHSSEGIVNAAYLNK		-0.006207973	0.431316847	374	391	382.5
LptD_Q9ISU2	LptD_beta-barrel	LNKDDHREGFPDYK	↑	1.466746926	0.012765388	388	403	395.5
LptD_Q9ISU2	LptD_beta-barrel	DDHREGFPDYK		0.145248413	0.353549019	392	403	397.5
LptD_Q9ISU2	LptD_beta-barrel	EGFPDYK	↓	-0.588537693	0.108957314	396	403	399.5
LptD_Q9ISU2	LptD_beta-barrel	EGFPDYKDR		-0.539537191	0.075861777	396	405	400.5
LptD_Q9ISU2	LptD_beta-barrel	GLKNTTGLDSR	↓	-0.654536903	0.225693443	409	419	414
LptD_Q9ISU2	LptD_beta-barrel	NTTGLDSRW		0.123312972	0.354243686	412	420	416
LptD_Q9ISU2	LptD_beta-barrel	WLAEVDYTR	↑	2.441585541	0.091529665	420	428	424
LptD_Q9ISU2	LptD_beta-barrel	LAEDVYTR	↑	1.691240549	0.075861777	421	428	424.5
LptD_Q9ISU2	LptD_beta-barrel	AEVDYTR		0.371827334	0.284772388	422	428	425
LptD_Q9ISU2	LptD_beta-barrel	VNQRGTLTY	↓	-1.155394673	0.298631471	450	458	454
LptD_Q9ISU2	LptD_beta-barrel	GTLTYRGDTF	↓	-0.969043791	0.248920816	454	463	458.5
LptD_Q9ISU2	LptD_beta-barrel	TYRGDTF		-0.056044251	0.295769172	457	463	460
LptD_Q9ISU2	LptD_beta-barrel	GTLTYRGDTFTGR		0.072179228	0.420965192	454	466	460
LptD_Q9ISU2	LptD_beta-barrel	TYRGDTFTGR	↓	-0.925630748	0.151070422	457	466	461.5
LptD_Q9ISU2	LptD_beta-barrel	RGDTFTGR	↑	0.707967997	0.144246783	459	467	463
LptD_Q9ISU2	LptD_beta-barrel	GDTFTGR	↑	2.219792128	0.133036388	460	467	463.5
LptD_Q9ISU2	LptD_beta-barrel	QLATTTDVTVPYDR		0.536112726	0.244270274	473	485	479
LptD_Q9ISU2	LptD_beta-barrel	DRLPQITF	★	0.216809675	0.030765467	484	491	487.5
LptD_Q9ISU2	LptD_beta-barrel	DGFLPYPGGMQF		0.474513501	0.276982421	492	504	498
LptD_Q9ISU2	LptD_beta-barrel	NPGGMQFTY		-0.074114792	0.410431973	498	506	502
LptD_Q9ISU2	LptD_beta-barrel	TYGTEFVR	↑	1.079380631	0.088746937	505	512	508.5
LptD_Q9ISU2	LptD_beta-barrel	YGTTEFVR	↓	-1.605264664	0.19170552	506	512	509
LptD_Q9ISU2	LptD_beta-barrel	TYGTEFVR		-0.468804568	0.225693443	505	513	509
LptD_Q9ISU2	LptD_beta-barrel	GTEFVR	↓	-1.138354421	0.075861777	507	513	510
LptD_Q9ISU2	LptD_beta-barrel	TYGTEFVRFOR		-0.160229325	0.298788162	505	515	510
LptD_Q9ISU2	LptD_beta-barrel	GTEFVRFOR		-0.198910326	0.278682655	507	515	511
LptD_Q9ISU2	LptD_beta-barrel	FDRDLDENIY		0.264987707	0.298788162	513	522	517.5
LptD_Q9ISU2	LptD_beta-barrel	DRDLDENIY		-0.468898296	0.248099014	514	522	518
LptD_Q9ISU2	LptD_beta-barrel	IYFNDDGSIR	↑	1.085234284	0.119013716	521	530	525.5
LptD_Q9ISU2	LptD_beta-barrel	YFNDDGSIR		0.107036799	0.35671197	522	530	526
LptD_Q9ISU2	LptD_beta-barrel	FNDDGSIR		0.252874345	0.243319698	523	530	526.5
LptD_Q9ISU2	LptD_beta-barrel	FNDDGSIRGK		0.043595772	0.403778287	523	532	527.5
LptD_Q9ISU2	LptD_beta-barrel	GKRPDASLQ		-0.037007317	0.415039126	531	539	535
LptD_Q9ISU2	LptD_beta-barrel	GKRPDASLQGLA	↑	0.727592051	0.018926199	531	542	536.5
LptD_Q9ISU2	LptD_beta-barrel	GKRPDASLQGLAR	↑	0.651716709	0.082048537	531	543	537
LptD_Q9ISU2	LptD_beta-barrel	RPDASLQGL		-0.341858953	0.117390029	533	541	537
LptD_Q9ISU2	LptD_beta-barrel	RPDASLQGLA	↑	0.753582358	0.127877563	533	542	537.5
LptD_Q9ISU2	LptD_beta-barrel	RPDASLQGLAR		-0.398887753	0.134910573	533	543	538
LptD_Q9ISU2	LptD_beta-barrel	DASLQGLAR		-0.107186846	0.358931697	535	543	539
LptD_Q9ISU2	LptD_beta-barrel	ASLQGLAR	↓	-2.034970045	0.096036725	536	543	539.5
LptD_Q9ISU2	LptD_beta-barrel	ATGDRMHLEPGMSLPM	★	-0.510388732	0.048035412	544	559	551.5
LptD_Q9ISU2	LptD_beta-barrel	ATGDRMHLEPGMSLPMTR	★	-0.637015283	0.002792038	544	561	552.5
LptD_Q9ISU2	LptD_beta-barrel	MHLEPGMSL		0.206453219	0.416886736	549	557	553
LptD_Q9ISU2	LptD_beta-barrel	GDRMHLEPGMSLPMTR	★	1.428945541	0.002792038	546	561	553.5
LptD_Q9ISU2	LptD_beta-barrel	MHLEPGMSLPM		-0.30479753	0.248415794	549	559	554

LptD_Q9ISU2	LptD_beta-barrel	MHLEPGMSLPMTR		0.206948146	0.188853129	549	561	555
LptD_Q9ISU2	LptD_beta-barrel	HLEPGMSLPMTR		0.255927503	0.1687179	550	561	555.5
LptD_Q9ISU2	LptD_beta-barrel	LEPGMSLPMTR		1.073154807	0.109630865	551	561	556
LptD_Q9ISU2	LptD_beta-barrel	EPGMSLPMTR	↑	-1.078237295	0.246634107	552	561	556.5
LptD_Q9ISU2	LptD_beta-barrel	SWGYYTPTLK	↓	-0.172339231	0.266531118	562	571	566.5
LptD_Q9ISU2	LptD_beta-barrel	WGYVTPTLK	↑	2.716914654	0.027850968	563	571	567
LptD_Q9ISU2	LptD_beta-barrel	SWGYYTPTLKY	↑	0.835783064	0.277942369	562	572	567
LptD_Q9ISU2	LptD_beta-barrel	GYVTPTLK	↑	0.919792354	0.044414233	564	571	567.5
LptD_Q9ISU2	LptD_beta-barrel	TKYDLDLDSQGK	↑	1.155433774	0.048252212	575	586	580.5
LptD_Q9ISU2	LptD_beta-barrel	YDLDLDSQGK	↑	0.633354008	0.314604159	577	586	581.5
LptD_Q9ISU2	LptD_beta-barrel	DLDLDSQGK	↑	0.561847329	0.15421787	578	586	582
LptD_Q9ISU2	LptD_beta-barrel	YDLDLDSQGKTDLNK	↓	-1.016589046	0.028230588	577	591	584
LptD_Q9ISU2	LptD_beta-barrel	YDLDLDSQGKTDLNKR	↑	1.500206947	0.014652501	577	592	584.5
LptD_Q9ISU2	LptD_beta-barrel	DLDLDSQGKTDLNK		-0.197909981	0.349417546	578	591	584.5
LptD_Q9ISU2	LptD_beta-barrel	DLDLDSQGKTDLNKR		0.112526841	0.342027627	578	592	585
LptD_Q9ISU2	LptD_beta-barrel	TDLNKRDESFDSNQDR		0.38822031	0.091529665	587	602	594.5
LptD_Q9ISU2	LptD_beta-barrel	DLNKRDESFDSNQDR		-0.022067849	0.402069255	588	602	595
LptD_Q9ISU2	LptD_beta-barrel	NKRDESFDSNQDR		-0.362311244	0.179343952	590	602	596
LptD_Q9ISU2	LptD_beta-barrel	KRDESFDSNQDR	↓	-0.599866033	0.225693443	591	602	596.5
LptD_Q9ISU2	LptD_beta-barrel	RDESFDSNQDR	↓	-0.593821168	0.07261745	592	602	597
LptD_Q9ISU2	LptD_beta-barrel	DESFDSNQDR		0.471219301	0.19170552	593	602	597.5
LptD_Q9ISU2	LptD_beta-barrel	SLPLVKVDSGL		0.391217202	0.278682655	603	613	608
LptD_Q9ISU2	LptD_beta-barrel	SLPLVKVDSGLY	↓	-1.299883723	0.079018305	603	614	608.5
LptD_Q9ISU2	LptD_beta-barrel	VDSGLYFDR		0.332601011	0.234545679	609	617	613
LptD_Q9ISU2	LptD_beta-barrel	VDSGLYFDRDITTF		-0.141655058	0.24214517	609	621	615
LptD_Q9ISU2	LptD_beta-barrel	VDSGLYFDRDITFA		0.401721507	0.225344221	609	622	615.5
LptD_Q9ISU2	LptD_beta-barrel	YFDRDITTF		-0.093545012	0.376287671	614	621	617.5
LptD_Q9ISU2	LptD_beta-barrel	FDRDITTF		0.152773067	0.04183989	615	621	618
LptD_Q9ISU2	LptD_beta-barrel	VDSGLYFDRDITTFAGTTPFR	↑	1.050641179	0.266531118	609	627	618
LptD_Q9ISU2	LptD_beta-barrel	FDRDITTFAGTFF		0.144447193	0.359456689	615	626	620.5
LptD_Q9ISU2	LptD_beta-barrel	FDRDITTFAGTTPFR	↓	-0.768832564	0.1687179	615	627	621
LptD_Q9ISU2	LptD_beta-barrel	DTTFAGTTPFR		-0.091173127	0.355569525	618	627	622.5
LptD_Q9ISU2	LptD_beta-barrel	QTLPEPRA	↑	0.630236089	0.155460968	628	634	631
LptD_Q9ISU2	LptD_beta-barrel	AMLYLVPPYK	↑	0.844182789	0.180575133	634	642	638
LptD_Q9ISU2	LptD_beta-barrel	YLYVPPYK	↑	1.00317347	0.048035412	636	642	639
LptD_Q9ISU2	LptD_beta-barrel	KDQDSLPLVFDITSEPSFSY	↑	2.35209322	0.168944987	642	659	650.5
LptD_Q9ISU2	LptD_beta-barrel	DSLWRENR		0.312277585	0.354243686	660	667	663.5
LptD_Q9ISU2	LptD_beta-barrel	DRIGDANQL		0.415964037	0.07110223	672	680	676
LptD_Q9ISU2	LptD_beta-barrel	DRIGDANQLSL		-0.094817623	0.225693443	672	682	677
LptD_Q9ISU2	LptD_beta-barrel	DRIGDANQLSLGVTSR	↑	0.676760554	0.079018305	672	687	679.5
LptD_Q9ISU2	LptD_beta-barrel	IGDANQLSLGVTSR		-0.034312196	0.419732568	674	687	680.5
LptD_Q9ISU2	LptD_beta-barrel	ANQLSLGVTSR	↑	0.716999233	0.248415794	677	687	682
LptD_Q9ISU2	LptD_beta-barrel	SRFIEENGFER	↓	-1.146912098	0.069464716	686	696	691
LptD_Q9ISU2	LptD_beta-barrel	FIEENGFER		-0.245429292	0.31133005	688	696	692
LptD_Q9ISU2	LptD_beta-barrel	IEENGFER	↑	0.623226643	0.047321439	689	696	692.5
LptD_Q9ISU2	LptD_beta-barrel	FIEENGFERA		-0.01076164	0.427493701	688	697	692.5
LptD_Q9ISU2	LptD_beta-barrel	ASISAGQIY		-0.323325276	0.265707509	697	705	701
LptD_Q9ISU2	LptD_beta-barrel	ASISAGQIYY	↓	-3.084347486	0.168944987	697	706	701.5
LptD_Q9ISU2	LptD_beta-barrel	ASISAGQIYYFR		-0.454708338	0.217521852	697	708	702.5
LptD_Q9ISU2	LptD_beta-barrel	RVQLPGLTEK	↓	-1.442379355	0.227557489	711	720	715.5
LptD_Q9ISU2	LptD_beta-barrel	VQLPGLTEK		0.451734364	0.060953824	712	720	716
LptD_Q9ISU2	LptD_beta-barrel	QLPGLTEK	↑	0.82327944	0.075105573	713	720	716.5
LptD_Q9ISU2	LptD_beta-barrel	RVQLPGLTEKDLK		-0.21536617	0.301540116	711	723	717
LptD_Q9ISU2	LptD_beta-barrel	VQLPGLTEKDLK		-0.165921167	0.146472426	712	723	717.5
LptD_Q9ISU2	LptD_beta-barrel	VQLPGLTEKDLKR		-0.168745965	0.349417546	712	724	718
LptD_Q9ISU2	LptD_beta-barrel	RLNLDPGLDNDNSWR	↑	1.07182014	0.051356677	724	738	731
LptD_Q9ISU2	LptD_beta-barrel	LNLDPSGLDNDNSW	↑	1.160336852	0.214706988	725	737	731
LptD_Q9ISU2	LptD_beta-barrel	LNLDPSGLDNDNSWR		0.542779803	0.168911375	725	738	731.5
LptD_Q9ISU2	LptD_beta-barrel	NLDPSGLDNDNSWR		-0.113032863	0.393820025	726	738	732
LptD_Q9ISU2	LptD_beta-barrel	LDPSGLDNDNSWR	↑	0.611316085	0.051356677	727	738	732.5
LptD_Q9ISU2	LptD_beta-barrel	RLNLDPGLDNDNSWRSPY		-0.288519323	0.298788162	724	741	732.5
LptD_Q9ISU2	LptD_beta-barrel	DPSGLDNDNSWR	↓	-0.725672483	0.094479441	728	738	733
LptD_Q9ISU2	LptD_beta-barrel	PSGLDNDNSWR	↑	0.769068062	0.248099014	729	738	733.5
LptD_Q9ISU2	LptD_beta-barrel	SPYAFAGQYR	↑	0.861299038	0.260512643	739	748	743.5
LptD_Q9ISU2	LptD_beta-barrel	YAFAGQYR		0.42359972	0.234545679	741	748	744.5
LptD_Q9ISU2	LptD_beta-barrel	AFAGQYR		0.52125144	0.109326548	742	748	745
LptD_Q9ISU2	LptD_beta-barrel	RFNDRWR		0.227481306	0.383116072	748	753	750.5
LptD_Q9ISU2	LptD_beta-barrel	FNRDWR	↑	1.026957035	0.018926199	749	754	751.5
LptD_Q9ISU2	LptD_beta-barrel	RINSDFNWNPNNTSR	↓	-0.695811272	0.185066874	754	767	760.5
LptD_Q9ISU2	LptD_beta-barrel	INSDFNWNPNNTSR		0.183201849	0.143716644	755	767	761
LptD_Q9ISU2	LptD_beta-barrel	NSDFNWNPNNTSR		0.28691569	0.310351479	756	767	761.5
LptD_Q9ISU2	LptD_beta-barrel	SDFNWNPNNTSR		0.043111909	0.382344886	757	767	762
LptD_Q9ISU2	LptD_beta-barrel	NWNPNNTSR	↑	0.605584383	0.19170552	760	767	763.5
LptD_Q9ISU2	LptD_beta-barrel	INSDFNWNPNNTSRTESGS		0.484191418	0.246634107	755	772	763.5
LptD_Q9ISU2	LptD_beta-barrel	NWNPNNTSRTESGSAIF	↓	-1.430130124	0.108957314	760	775	767.5
LptD_Q9ISU2	LptD_beta-barrel	AIFHYQPEVDPGK	↑	3.290810585	0.103415096	773	785	779
LptD_Q9ISU2	LptD_beta-barrel	HYQPEVDPGK		0.333617598	0.107408623	776	785	780.5
LptD_Q9ISU2	LptD_beta-barrel	HYQPEVDPGKVVNVGY		0.561069608	0.091345866	776	791	783.5
LptD_Q9ISU2	LptD_beta-barrel	HYQPEVDPGKVVNVGYR		0.373797894	0.021513377	776	792	784
LptD_Q9ISU2	LptD_beta-barrel	DPGKVVNVGYR		0.150778919	0.314604159	782	792	787
LptD_Q9ISU2	LptD_beta-barrel	PGKVVNVGYR	↑	1.039623857	0.109326548	783	792	787.5
LptD_Q9ISU2	LptD_beta-barrel	GKVVNVGYR		0.510811508	0.225693443	784	792	788
LptD_Q9ISU2	LptD_beta-barrel	VNVNVGYR	↑	1.341169119	0.109326548	786	792	789
LptD_Q9ISU2	LptD_beta-barrel	RFDSRGTF		-0.150891796	0.406497531	799	807	803
LptD_Q9ISU2	LptD_beta-barrel	RFDSRGTFTR	↓	-1.024472475	0.090460135	799	808	803.5
LptD_Q9ISU2	LptD_beta-barrel	FDSRGTF	↓	-0.855354726	0.319324646	800	807	803.5
LptD_Q9ISU2	LptD_beta-barrel	RYGNENDIIK		-0.508812964	0.234545679	808	817	812.5
LptD_Q9ISU2	LptD_beta-barrel	YGNENDIIK		0.382027537	0.109326548	809	817	813
LptD_Q9ISU2	LptD_beta-barrel	YGNENDIIKQ		0.436732888	0.225693443	809	818	813.5
LptD_Q9ISU2	LptD_beta-barrel	GNENDIIKQHDF	↓	-0.68250984	0.21024202	810	821	815.5
LptD_Q9ISU2	LptD_beta-barrel	WQYDYNK	↑	0.843273818	0.051356677	837	843	840

LptD_Q9I5U2	LptD_beta-barrel	ARWQYDYNKNR	↑	0.881101847	0.217521852	835	845	840
LptD_Q9I5U2	LptD_beta-barrel	WQYDYNKNR	↑	2.012160778 ★	0.026849047	837	845	841
LptD_Q9I5U2	LptD_beta-barrel	NRTLEAFGGF		-0.430461735	0.246634107	844	853	848.5
LptD_Q9I5U2	LptD_beta-barrel	RLINRY		0.523261726	0.205204127	863	868	865.5
LptD_Q9I5U2	LptD_beta-barrel	LINRYW	↑	0.823237956	0.065496864	864	869	866.5
LptD_Q9I5U2	LptD_beta-barrel	KGLGGIVGNK		-0.036972288	0.410768798	895	904	899.5
LptD_Q9I5U2	LptD_beta-barrel	GLGGIVGNK	↑	0.803203404 ★	0.03871991	896	904	900
LptD_Q9I5U2	LptD_beta-barrel	GLGGIVGNKTEM	↑	0.912104011	0.07261745	896	907	901.5
LptD_Q9I5U2	LptD_beta-barrel	GLGGIVGNKTEMF	↑	0.803023815 ★	0.018926199	896	908	902
LptD_Q9I5U2	LptD_beta-barrel	KGLGGIVGNKTEMFDDK		0.158829018	0.355569525	895	911	903
LptD_Q9I5U2	LptD_beta-barrel	GLGGIVGNKTEMFDDK	↑	0.644001722	0.055274521	896	911	903.5
LptD_Q9I5U2	LptD_beta-barrel	GGIVGNKTEMFDDK		0.119273081	0.33924152	898	911	904.5
LptD_Q9I5U2	LptD_beta-barrel	KTEMFDDK		0.577573717 ★	0.047897219	904	911	907.5
LptD_Q9I5U2	LptD_beta-barrel	TEMFDDK	↑	1.476521969 ★	0.021485715	905	911	908
LptD_Q9I5U2	LptD_beta-barrel	TEMFDDKGIQGYR	↑	1.106205583	0.19170552	905	917	911
LptD_Q9I5U2	LptD_beta-barrel	FLDKGIQGYR		0.264457405	0.161737201	908	917	912.5
LptD_Q9I5U2	LptD_beta-barrel	LDKGIQGYR		0.547606051	0.094479441	909	917	913
LptE_Q9HX32	LptE_signal peptide	RILTSAAUGMT	↓	-5.870284081	0.269511868	3	14	8.5
LptE_Q9HX32	LptE_chain	QLRGLGDAQF	↑	1.027638316	0.121031084	23	32	27.5
LptE_Q9HX32	LptE_chain	ALKEIDVSAR	↑	1.231087446	0.075861777	33	42	37.5
LptE_Q9HX32	LptE_chain	EIDVSARN	↑	0.763617396	0.072163074	36	43	39.5
LptE_Q9HX32	LptE_chain	NAYGPTVR	↑	1.207088709	0.075861777	43	50	46.5
LptE_Q9HX32	LptE_chain	ELKETLENSGVK	↑	1.194216967 ★	0.002792038	51	62	56.5
LptE_Q9HX32	LptE_chain	LKETLENSGVK		-0.450332135	0.096036725	52	62	57
LptE_Q9HX32	LptE_chain	ELKETLENSGVKVT	↑	1.239287853	0.117390029	51	64	57.5
LptE_Q9HX32	LptE_chain	ELTENSGVKVT	↓	-2.371899843 ★	0.048252212	54	64	59
LptE_Q9HX32	LptE_chain	ELKETLENSGVKVTSNAPY	↑	0.759512365	0.217521852	51	69	60
LptE_Q9HX32	LptE_chain	VTSNAPYHLVLR		0.040338036	0.420420043	63	75	69
LptE_Q9HX32	LptE_chain	HLVLVREDNQQR		-0.020183044	0.393820025	70	81	75.5
LptE_Q9HX32	LptE_chain	VLVREDNQQR		-0.546850204	0.055274521	72	81	76.5
LptE_Q9HX32	LptE_chain	VSYTGSAR		-0.02596996	0.430059779	82	90	86
LptE_Q9HX32	LptE_chain	VSYTGSAR		0.34624666	0.349795519	83	90	86.5
LptE_Q9HX32	LptE_chain	EIVGANDLVLMNSQVQVQK	↑	1.351752996 ★	0.012765388	103	121	112
LptE_Q9HX32	LptE_chain	VLMNSQVQVQK	↑	0.872299373 ★	0.018926199	111	121	116
LptE_Q9HX32	LptE_chain	MSNQVQVQK	↑	1.072729468 ★	0.03871991	113	121	117
LptE_Q9HX32	LptE_chain	MSNQVQVQKVYVHDENNL	↑	1.897056341	0.267952649	113	130	121.5
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQ	↑	1.194699645	0.110275497	122	139	130.5
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQQLR	↑	1.227746964 ★	0.027850968	122	141	131.5
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQQLR		0.346918851	0.265578305	123	141	132
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQQL	↓	-1.564569831	0.205774239	124	140	132
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQQLRSE	↑	1.20427525 ★	0.018926199	122	143	132.5
LptE_Q9HX32	LptE_chain	VYVHDENNLIGSDQEAQQLR		-0.196592867	0.1687179	124	141	132.5
LptE_Q9HX32	LptE_chain	HDENNLIGSDQEAQQLR		0.158003435	0.327472688	125	141	133
LptE_Q9HX32	LptE_chain	DENNLIGSDQEAQQLR		0.470982403	0.248920816	126	141	133.5
LptE_Q9HX32	LptE_chain	NLIGSDQEAQQLR	↓	-1.040130258	0.160427482	129	141	135
LptE_Q9HX32	LptE_chain	IGSDQEAQQLR		0.446872681	0.107408623	130	141	135.5
LptE_Q9HX32	LptE_chain	GSDQEAQQLR	↑	1.130748749	0.096970269	132	141	136.5
LptE_Q9HX32	LptE_chain	RDLIQQL		-0.146960422	0.146953423	146	152	149
LptE_Q9HX32	LptE_chain	DLIQQLSM	↑	2.393887997	0.096461635	147	154	150.5
LptE_Q9HX32	LptE_chain	DLIQQLSMR	↓	-1.328466654	0.074846657	147	155	151
LptE_Q9HX32	LptE_chain	RLQALTPAQLDEAQR		0.52057147	0.123873576	155	169	162
LptE_Q9HX32	LptE_chain	LQALTPAQLDEAQR		0.117787793	0.19170552	156	169	162.5
LptE_Q9HX32	LptE_chain	QALTPAQLDEAQR	↑	0.915397823 ★	0.027850968	157	169	163
LptE_Q9HX32	LptE_chain	ALTPAQLDEAQR	↑	0.675958455 ★	0.047897219	158	169	163.5
LptE_Q9HX32	LptE_chain	LTPAQLDEAQR		0.07412982	0.399831839	159	169	164
LptE_Q9HX32	LptE_chain	TPAQLDEAQR		0.170436874	0.260512643	160	169	164.5
LptE_Q9HX32	LptE_chain	RLQALTPAQLDEAQRQAEAK		-0.129322007	0.248415794	155	174	164.5
LptE_Q9HX32	LptE_chain	LQALTPAQLDEAQRQAEAK		-0.254166782	0.234545679	156	174	165
LptE_Q9HX32	LptE_chain	QALTPAQLDEAQRQAEAK		-0.359755039	0.088746937	157	174	165.5
LptE_Q9HX32	LptE_chain	ALTPAQLDEAQRQAEAK		0.115570195	0.378205953	158	174	166
LptE_Q9HX32	LptE_chain	QLDEAQRQAEAK		-0.018595796	0.420420043	163	174	168.5
LptE_Q9HX32	LptE_chain	AKAEAEAL		0.301512808	0.299122762	175	182	178.5
LptE_Q9HX32	LptE_chain	AKAEAEALR		-0.281902552	0.255624397	175	183	179
LptE_Q9HX32	LptE_chain	AKAEAEALRA	↑	1.546369195 ★	0.018926199	175	184	179.5
LptE_Q9HX32	LptE_chain	AKAEAEALRAADEAER		0.430291444	0.065496864	175	190	182.5
LptE_Q9HX32	LptE_chain	KAEEALRAADEAER	↑	0.733445227 ★	0.044414233	176	190	183
LptE_Q9HX32	LptE_chain	AEAEALRAADEAER		0.031132117	0.380267337	177	190	183.5
LptE_Q9HX32	LptE_chain	EAELRAADEAER		0.407705933	0.292279534	178	190	184
LptE_Q9HX32	LptE_chain	AEALRAADEAER		0.341715336	0.146953423	179	190	184.5
LptE_Q9HX32	LptE_chain	AEAEALRAADEAERQR		-0.189107805	0.170819546	177	192	184.5
LptE_Q9HX32	LptE_chain	EALRAADEAER	↑	0.612682521	0.107408623	180	190	185
LptE_Q9HX32	LptE_chain	ALRAADEAERQR	↓	-0.597052515	0.134388672	181	192	186.5

Figure S4. MS identified peptide fragments of recombinant *Pa* LptD (A) and LptE (B) colored according to annotated protein domains and visualized using Protter webtool. MS detectable peptides are uniformly distributed across all domains of LptD/E with >80% of protein sequence covered by MS.



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