



STRUCTURAL BIOLOGY
COMMUNICATIONS

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Supporting information for article:

**Crystal structures of glutamyl-tRNA synthetase from
Elizabethkingia anopheles and *E. meningosepticum***

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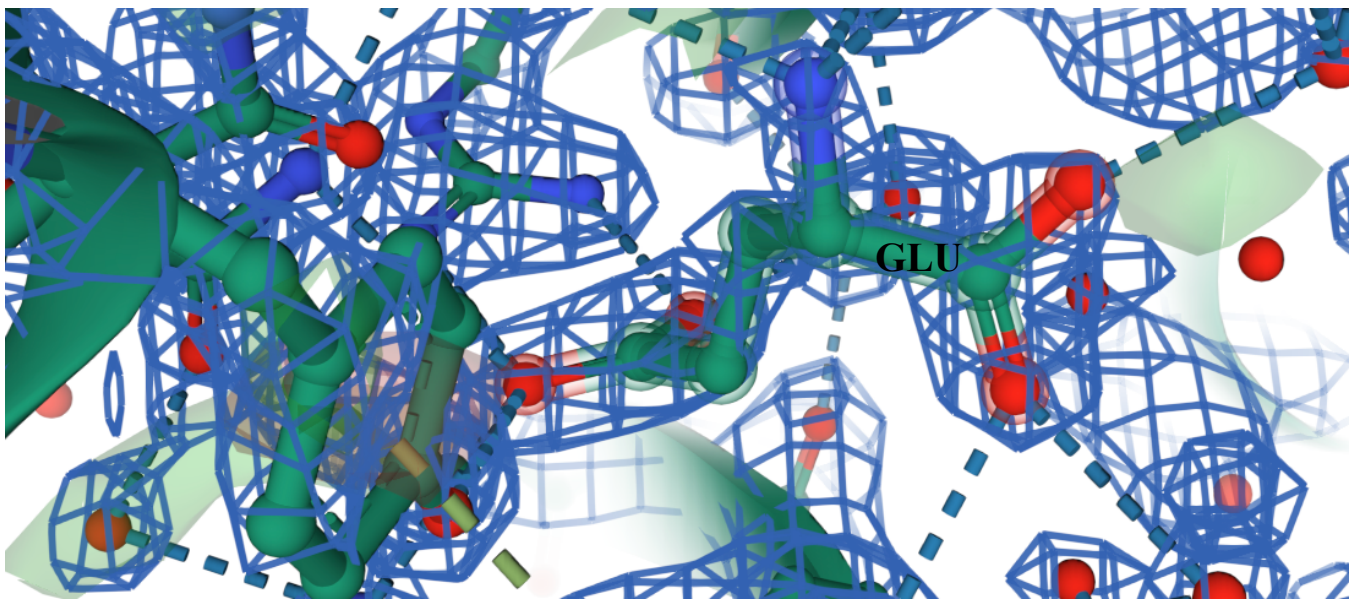


Figure S1 Quality of final 2Fo -Fc electron density map around glutamate in 6BRL contoured at 1.5sigma cutoff

References

- Gouet, P., Robert, X. & Courcelle, E. (2003). *Nucleic Acids Res* **31**, 3320-3323.
- Krissinel, E. & Henrick, K. (2004). *Acta crystallographica. Section D, Biological crystallography* **60**, 2256-2268.
- Robert, X. & Gouet, P. (2014). *Nucleic Acids Res* **42**, W320-324.

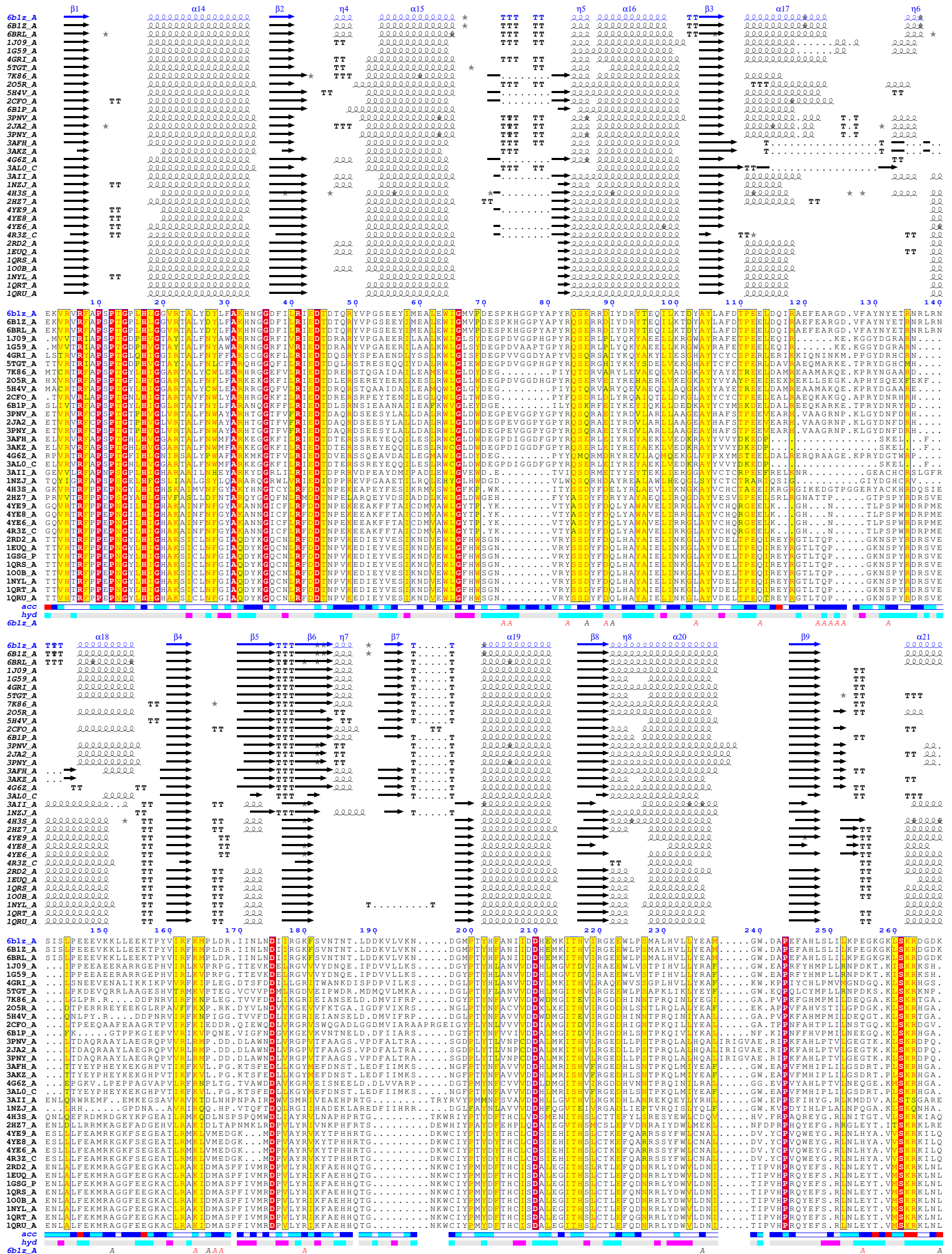
Table S.1 Results from PDBeFold P (<http://www.ebi.ac.uk/msd-srv/ssm/>) analysis (Krissinel & Henrick, 2004)

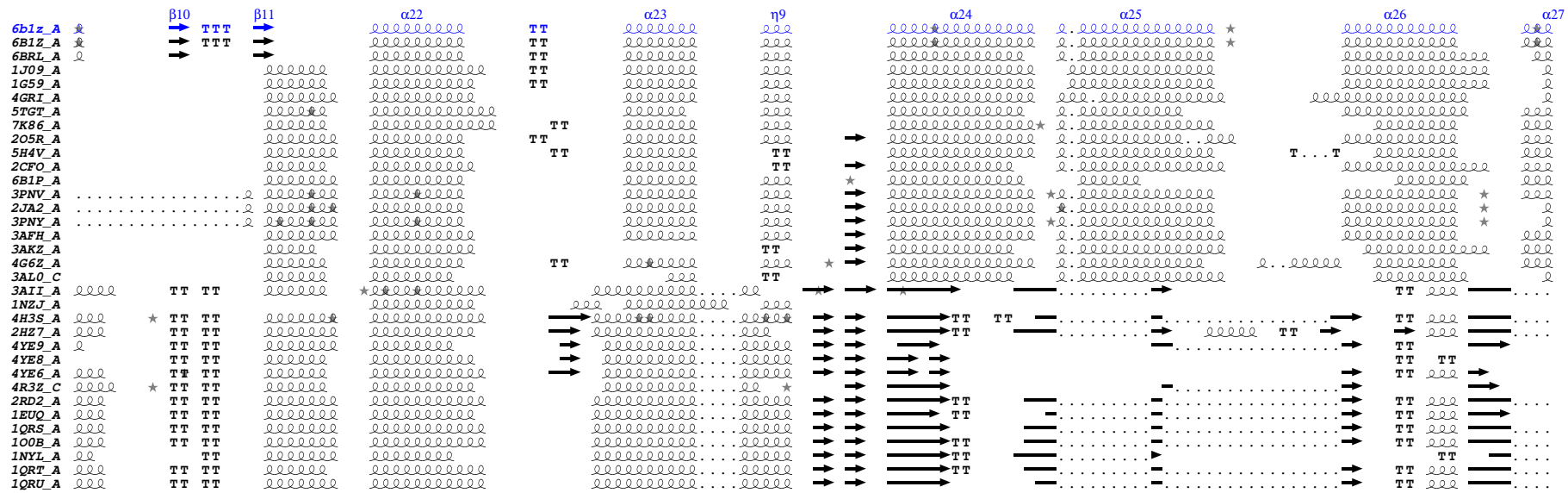
PDBe Fold v2.59. (src3) 14 Apr 2014 result file.

RESULT SUMMARY

##	Q-score	P-score	Z-score	RMSD	Nalgn	Nsse	Ngaps	Seq-%	Nmd	Nres-Q	Nsse-Q	Nres-T	Nsse-T	Query	Target
1	0.8372	55.43	22.5	1.169	490	29	5	0.9673	0	495	31	503	33	PDB 6blz:A	PDB 6brl:A
2	0.5865	25.7	16.52	1.955	440	25	12	0.3841	0	495	31	468	29	PDB 6blz:A	PDB 2cv1:B
3	0.5829	24.7	16.22	1.998	442	27	15	0.3914	0	495	31	469	30	PDB 6blz:A	PDB 1n78:B
4	0.5814	26.29	16.67	1.962	439	27	13	0.385	0	495	31	469	31	PDB 6blz:A	PDB 2cv2:B
5	0.5728	25.58	16.49	1.905	432	25	14	0.3912	0	495	31	469	29	PDB 6blz:A	PDB 2dxi:B
6	0.569	25.28	16.9	1.934	432	25	15	0.3958	0	495	31	468	30	PDB 6blz:A	PDB 2cv0:B
7	0.5473	23.75	15.96	2.031	430	27	17	0.3767	0	495	31	468	31	PDB 6blz:A	PDB 1g59:C
8	0.5445	23.81	16.45	2.002	427	25	16	0.3864	0	495	31	468	29	PDB 6blz:A	PDB 1n77:B
9	0.5313	20.55	15.07	1.997	429	23	21	0.338	0	495	31	485	30	PDB 6blz:A	PDB 2cfo:A
10	0.5305	19.05	14.2	2.078	435	23	18	0.3517	0	495	31	487	30	PDB 6blz:A	PDB 2cfo:B
11	0.5241	19.47	14.68	2.221	434	25	15	0.3825	0	495	31	469	29	PDB 6blz:A	PDB 2dxi:A
12	0.5226	19.17	14.59	2.244	435	25	14	0.3839	0	495	31	469	29	PDB 6blz:A	PDB 2cv2:A
13	0.5218	18.96	14.35	2.362	443	27	16	0.3792	0	495	31	469	29	PDB 6blz:A	PDB 1n78:A
14	0.5208	19.18	14.59	2.262	435	25	14	0.3839	0	495	31	468	29	PDB 6blz:A	PDB 1n77:A
15	0.5206	20.96	14.93	2.321	440	25	15	0.3841	0	495	31	470	28	PDB 6blz:A	PDB 2cv0:A
16	0.5126	18.18	14.28	2.298	435	25	14	0.3839	0	495	31	470	29	PDB 6blz:A	PDB 2cv1:A
17	0.5115	17.8	14.17	2.202	427	27	16	0.3817	0	495	31	468	30	PDB 6blz:A	PDB 1g59:A
18	0.4705	14.57	13.76	2.351	427	23	17	0.3396	0	495	31	485	32	PDB 6blz:A	PDB 3pny:B
19	0.4683	17.64	13.94	2.373	420	27	17	0.3476	0	495	31	468	30	PDB 6blz:A	PDB 2o5r:A
20	0.4654	14.29	13.59	2.297	421	23	19	0.3444	0	495	31	485	31	PDB 6blz:A	PDB 3pnv:B
21	0.4631	13.1	12.6	2.636	436	27	17	0.367	0	495	31	468	31	PDB 6blz:A	PDB 1gln:A
22	0.4522	12.04	12.83	2.430	424	23	20	0.3349	0	495	31	485	30	PDB 6blz:A	PDB 2ja2:A
23	0.4471	12.01	13.11	2.446	421	24	23	0.342	0	495	31	481	31	PDB 6blz:A	PDB 3pnv:A
24	0.4353	14.72	13.2	2.438	417	25	20	0.3645	0	495	31	486	30	PDB 6blz:A	PDB 4gri:B
25	0.4322	16.79	14.09	2.313	400	23	15	0.405	0	495	31	469	30	PDB 6blz:A	PDB 2cuz:A
26	0.4298	10.79	12.69	2.523	418	23	22	0.3349	0	495	31	481	31	PDB 6blz:A	PDB 3pny:A
27	0.4288	16.7	14.26	2.298	397	23	15	0.4081	0	495	31	468	30	PDB 6blz:A	PDB 1n75:A
28	0.4228	14.12	13.53	2.362	403	25	19	0.3747	0	495	31	479	30	PDB 6blz:A	PDB 4gri:A
29	0.4176	14.84	13.64	2.326	394	24	16	0.401	0	495	31	469	30	PDB 6blz:A	PDB 1j09:A
30	0.3354	7.152	10.14	3.131	399	25	21	0.3434	0	495	31	459	28	PDB 6blz:A	PDB 7k86:A
31	0.3124	8.429	10.82	2.891	372	24	28	0.3468	0	495	31	464	29	PDB 6blz:A	PDB 7k86:B

Figure S.2 Results from ENDScript alignment (Gouet et al., 2003, Robert & Gouet, 2014)





Protein	270	280	290	300	310	320	330	340	350	360	370	380	390	
6b1z_A	FGFPVFLNFTDPATGN	SAGYEG	LPPEA	INMAM	GNPAD	NKVF	VSMEM	KE...	FDLNK	HKAGRF	SAEKWF	QOYLQL	SN	EAILPEFKKVLAE
6B1Z_A	FGFPVFLNFTDPATGN	SAGYEG	LPPEA	INMAM	GNPAD	NKVF	VSMEM	KE...	FDLNK	HKAGRF	SAEKWF	QOYLQL	SN	EAILPEFKKVLAE
6BRL_A	FGFPVFLNFTDPATGN	SAGYEG	LPPEA	INMAM	GNPAD	NKVF	VSMEM	KE...	FDLNK	HKAGRF	SAEKWF	QOYLQL	SN	EAILPEFKKVLAE
1J09_A
1G59_A
4GRI_A
5GT_A
7K86_A
205R_A
5H4V_A
2CFO_A
6B1P_A
3PNV_A
2JA2_A
3PNY_A
3AFH_A
3AKZ_A
4G6Z_A
3AL0_C
3AI1_A
1NZJ_A
4H3S_A
2H27_A
4YE9_A
4YE8_A
4YE6_A
4R3Z_C
2RD2_A
1EUQ_A
1QRS_A
100B_A
1NYL_A
1QRT_A
1QRU_A



Protein	400	410	420	430	440	450
6b1z_A	IYNDGKFF	HAPES	DEKASKKAX	...XXXXAVL	...ELTEA	ISSLD
6B1Z_A	IYNDGKFF	HAPES	DEKASKKAW	...SPETAVAL	...ELTEA	ISSLD
6BRL_A	IYNDGKFF	HAPES	DEKASKKAW	...SPETAVAL	...ELTEA	ISSLD
1J09_A
1G59_A
4GRI_A
5GT_A
7K86_A
205R_A
5H4V_A
2CFO_A
6B1P_A
3PNV_A
2JA2_A
3PNY_A
3AFH_A
3AKZ_A
4G6Z_A
3AL0_C
3AI1_A
1NZJ_A
4H3S_A
2H27_A
4YE9_A
4YE8_A
4YE6_A
4R3Z_C
2RD2_A
1EUQ_A
1QRS_A
100B_A
1NYL_A
1QRT_A
1QRU_A

