Phyre2

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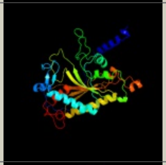
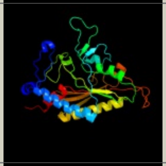
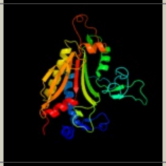
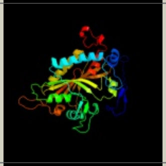
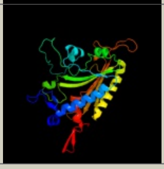
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lssA_	Alignment		100.0	34	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
2	c2dq0A_	Alignment		100.0	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
3	c1wleB_	Alignment		100.0	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
4	c2dq3A_	Alignment		100.0	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
5	c1sryB_	Alignment		100.0	38	**PDB header:**ligase(synthetase) **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
6	c3qo8A_	Alignment		100.0	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
7	c3errB_	Alignment		100.0	36	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
8	d1seta2	Alignment		100.0	39	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
9	c2cj9A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of methanosarcina barkeri seryl-trna2 synthetase complexed with an analog of seryladenylate
10	d1qf6a4	Alignment		100.0	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
11	d1nyra4	Alignment		100.0	20	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain

12	d1nj8a3	Alignment		100.0	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
13	d1nj1a3	Alignment		100.0	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
14	c3mf2B_	Alignment		100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
15	d1hc7a2	Alignment		100.0	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
16	c1nyqA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
17	c3ialB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
18	c1qf6A_	Alignment		100.0	16	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
19	d1b76a2	Alignment		100.0	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
20	d1atia2	Alignment		100.0	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
21	c1nj8C_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
22	c1h4tD_	Alignment	not modelled	100.0	17	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
23	c1nj2A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
24	c1fyfB_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
25	c2j3mA_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
26	c2i4lC_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
27	c1ggmB_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
28	c1atiA_	Alignment	not modelled	100.0	17	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
						PDB header:ligase

29	c3a32A_	Alignment	not modelled	100.0	17	**Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1; **PDBTitle:** crystal structure of putative threonyl-trna synthetase2 thrrs-1 from aeropyrum pernix
30	c1g5hA_	Alignment	not modelled	100.0	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit; **PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
31	d1g5ha2	Alignment	not modelled	100.0	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
32	c2pmfA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
33	d2g4ca2	Alignment	not modelled	100.0	12	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
34	c3ikmC_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna polymerase subunit gamma-2; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
35	d1seta1	Alignment	not modelled	99.9	30	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
36	c2el9B_	Alignment	not modelled	99.8	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of e.coli histidyl-trna synthetase2 complexed with a histidyl-adenylate analogue
37	c1adyA_	Alignment	not modelled	99.8	20	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
38	c3hriF_	Alignment	not modelled	99.8	21	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
39	c1qe0B_	Alignment	not modelled	99.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase
40	c1wu7A_	Alignment	not modelled	99.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
41	c3netB_	Alignment	not modelled	99.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
42	c3od1A_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
43	c2zimA_	Alignment	not modelled	99.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
44	c2znjB_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
45	d1kmma2	Alignment	not modelled	99.5	13	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
46	d1wu7a2	Alignment	not modelled	99.5	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
47	c1z7nB_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate
48	d1h4vb2	Alignment	not modelled	99.2	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	d1z7ma1	Alignment	not modelled	99.1	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
50	c3racA_	Alignment	not modelled	99.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidine-trna ligase; **PDBTitle:** crystal strucutre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
51	c1b70A_	Alignment	not modelled	99.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
52	c2du4B_	Alignment	not modelled	99.1	16	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
53	c3l4gI_	Alignment	not modelled	99.1	14	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
						Fold: Class II aaRS and biotin synthetases

54	d1jjca_	Alignment	not modelled	99.1	15	**Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
55	c2du7C_	Alignment	not modelled	98.9	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
56	d1nnha_	Alignment	not modelled	98.9	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
57	c2rhqA_	Alignment	not modelled	98.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
58	d1qe0a2	Alignment	not modelled	98.7	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
59	d1e1oa2	Alignment	not modelled	98.7	16	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
60	c3g1zB_	Alignment	not modelled	98.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
61	d1l0wa3	Alignment	not modelled	98.6	22	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
62	d1c0aa3	Alignment	not modelled	98.6	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
63	d1eova2	Alignment	not modelled	98.6	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
64	c3pcoC_	Alignment	not modelled	98.5	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**phenylalanyl-trna synthetase, alpha subunit; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
65	d1bbua2	Alignment	not modelled	98.5	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
66	d1b8aa2	Alignment	not modelled	98.5	22	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
67	c3e9hB_	Alignment	not modelled	98.4	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
68	c1e22A_	Alignment	not modelled	98.3	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
69	c3bjuB_	Alignment	not modelled	98.3	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
70	c1efwA_	Alignment	not modelled	98.2	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
71	c1eqrC_	Alignment	not modelled	98.2	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
72	d1usya_	Alignment	not modelled	98.2	15	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
73	c1x55A_	Alignment	not modelled	98.1	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
74	c3m4qA_	Alignment	not modelled	98.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
75	c2xgtB_	Alignment	not modelled	98.0	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
76	c1asyA_	Alignment	not modelled	98.0	14	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
77	c1b8aB_	Alignment	not modelled	97.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
78	c1wydB	Alignment	not modelled	97.8	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase;

						PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
79	c3i7fA_	Alignment	not modelled	97.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
80	c3l4gL_	Alignment	not modelled	97.0	14	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
81	c3cmqA_	Alignment	not modelled	97.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine trna2 synthetase
82	c3ig2B_	Alignment	not modelled	97.0	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** the crystal structure of a putative phenylalanyl-trna synthetase2 (phers) beta chain domain from bacteroides fragilis to 2.1a
83	c3icaB_	Alignment	not modelled	96.9	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83
84	d1jjcb5	Alignment	not modelled	95.0	13	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
85	c3hnwB_	Alignment	not modelled	92.7	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
86	d1n9wa2	Alignment	not modelled	91.5	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
87	c1deqO_	Alignment	not modelled	90.9	12	**PDB header:** **PDB COMPND:**
88	c1ei3E_	Alignment	not modelled	89.8	6	**PDB header:** **PDB COMPND:**
89	c2rhsB_	Alignment	not modelled	89.7	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
90	c3ghgK_	Alignment	not modelled	89.0	10	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
91	c2akwB_	Alignment	not modelled	81.7	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
92	c1n9wA_	Alignment	not modelled	81.0	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
93	c1deqF_	Alignment	not modelled	80.9	15	**PDB header:** **PDB COMPND:**
94	c3ojaB_	Alignment	not modelled	78.3	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
95	c3pcoD_	Alignment	not modelled	77.2	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
96	c2ke4A_	Alignment	not modelled	71.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
97	d2f4ma1	Alignment	not modelled	71.1	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
98	c2zdiA_	Alignment	not modelled	69.7	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**prefoldin subunit beta; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
99	c3isrB_	Alignment	not modelled	66.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transglutaminase-like enzymes, putative cysteine protease; **PDBTitle:** the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
100	d12asa_	Alignment	not modelled	64.7	23	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
101	d2f23a1	Alignment	not modelled	64.0	13	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
102	c3sjbC_	Alignment	not modelled	63.1	18	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
103	c1l8dB_	Alignment	not modelled	57.7	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase;

						PDBTitle: rad50 coiled-coil zn hook
104	c3sjaG_	Alignment	not modelled	57.4	19	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
105	c2gl2B_	Alignment	not modelled	56.2	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
106	c3dtpA_	Alignment	not modelled	54.1	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
107	d1grja1	Alignment	not modelled	50.9	19	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
108	d1gqea_	Alignment	not modelled	48.4	15	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
109	c3u59C_	Alignment	not modelled	47.1	15	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**tropomyosin beta chain; **PDBTitle:** n-terminal 98-aa fragment of smooth muscle tropomyosin beta
110	d1fxka_	Alignment	not modelled	45.5	12	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
111	c3hxxA_	Alignment	not modelled	44.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
112	c1ik9B_	Alignment	not modelled	42.2	18	**PDB header:**gene regulation/ligase **Chain:** B: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
113	c3a7pB_	Alignment	not modelled	40.2	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg16
114	c3cwgA_	Alignment	not modelled	38.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
115	c2y3aB_	Alignment	not modelled	36.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit beta; **PDBTitle:** crystal structure of p110beta in complex with icsh2 of p85beta and2 the drug gdc-0941
116	c3na7A_	Alignment	not modelled	36.5	14	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
117	c2p4vA_	Alignment	not modelled	35.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
118	c2etnA_	Alignment	not modelled	33.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
119	c2fxmB_	Alignment	not modelled	33.3	19	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**myosin heavy chain, cardiac muscle beta isoform; **PDBTitle:** structure of the human beta-myosin s2 fragment
120	c1dipA_	Alignment	not modelled	32.8	19	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures