Phyre^2

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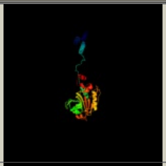
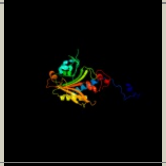
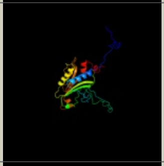
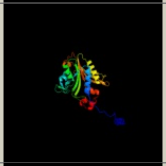
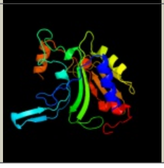
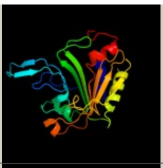
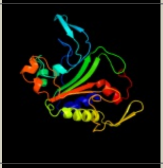
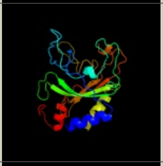
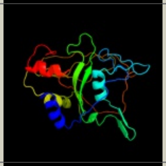
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pcoC_	Alignment		100.0	100	**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
2	c3l4gI_	Alignment		100.0	35	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
3	d1jjca_	Alignment		100.0	51	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
4	c1b70A_	Alignment		100.0	51	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
5	c2du7C_	Alignment		100.0	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
6	c2du4B_	Alignment		100.0	24	**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
7	c3cmqA_	Alignment		100.0	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine trna2 synthetase
8	c2rhqA_	Alignment		100.0	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
9	c2zimA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
10	c2znjB_	Alignment		100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
11	c3bjuB_	Alignment		99.9	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase

12	c1e22A_	Alignment		99.9	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
13	c1eqrC_	Alignment		99.8	25	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
14	c1efwA_	Alignment		99.8	29	**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
15	c3e9hB_	Alignment		99.8	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
16	d1c0aa3	Alignment		99.8	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
17	d1nnha_	Alignment		99.8	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
18	c1b8aB_	Alignment		99.8	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
19	c1asyA_	Alignment		99.8	20	**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
20	c1x55A_	Alignment		99.8	14	**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
21	c3icaB_	Alignment	not modelled	99.8	13	**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
22	d1l0wa3	Alignment	not modelled	99.8	24	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
23	c1wydB_	Alignment	not modelled	99.7	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
24	d1b8aa2	Alignment	not modelled	99.7	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
25	d1eova2	Alignment	not modelled	99.7	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
26	d1jjcb5	Alignment	not modelled	99.7	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
27	c2xgtB_	Alignment	not modelled	99.7	18	**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
28	c3l4gL	Alignment	not modelled	99.7	12	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain;

28	c3l4gL_	Alignment	not modelled	99.7	12	**PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
29	c3g1zB_	Alignment	not modelled	99.7	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
30	c3i7fA_	Alignment	not modelled	99.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
31	c3m4qA_	Alignment	not modelled	99.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
32	c3ig2B_	Alignment	not modelled	99.6	12	**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
33	c3pcoD_	Alignment	not modelled	99.6	18	**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
34	c2rhsB_	Alignment	not modelled	99.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
35	d1kmma2	Alignment	not modelled	99.4	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
36	d1e1oa2	Alignment	not modelled	99.4	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
37	d1bbua2	Alignment	not modelled	99.3	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
38	d1qf6a4	Alignment	not modelled	99.2	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
39	c1fyfB_	Alignment	not modelled	99.2	19	**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
40	c2akwB_	Alignment	not modelled	99.2	21	**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
41	d1eiya1	Alignment	not modelled	99.2	44	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Phenylalanyl-tRNA synthetase (PheRS)
42	c1nyqA_	Alignment	not modelled	99.2	17	**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
43	c1n9wA_	Alignment	not modelled	99.2	32	**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
44	d1n9wa2	Alignment	not modelled	99.2	32	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
45	c1z7nB_	Alignment	not modelled	99.0	11	**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
46	d2iy5a1	Alignment	not modelled	99.0	43	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Phenylalanyl-tRNA synthetase (PheRS)
47	d1hc7a2	Alignment	not modelled	99.0	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
48	c1qf6A_	Alignment	not modelled	99.0	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
49	c2dq0A_	Alignment	not modelled	99.0	15	**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
50	c3qo8A_	Alignment	not modelled	99.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
51	d1nj8a3	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
52	d1seta2	Alignment	not modelled	98.9	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
53	d1wu7a2	Alignment	not modelled	98.9	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
54	c1sryB_	Alignment	not modelled	98.9	17	**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
55	d1nj1a3	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
56	c3racA_	Alignment	not modelled	98.9	18	**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.
57	c2dq3A_	Alignment	not modelled	98.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
58	c1h4tD_	Alignment	not modelled	98.8	15	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
59	c1nj8C_	Alignment	not modelled	98.8	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
60	c2el9B_	Alignment	not modelled	98.8	17	**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
61	c3lssA_	Alignment	not modelled	98.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
62	c1nj2A_	Alignment	not modelled	98.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
63	d1nyra4	Alignment	not modelled	98.8	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	c1atiA_	Alignment	not modelled	98.7	13	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
65	c1adyA_	Alignment	not modelled	98.7	16	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
66	c3hriF_	Alignment	not modelled	98.7	12	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
67	c1wleB_	Alignment	not modelled	98.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
68	d1b76a2	Alignment	not modelled	98.7	9	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
69	d1atia2	Alignment	not modelled	98.7	9	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
70	c3a32A_	Alignment	not modelled	98.7	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1; **PDBTitle:** crystal structure of putative threonyl-trna synthetase2 thrrs-1 from aeropyrum pernix
71	c1ggmB_	Alignment	not modelled	98.6	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
72	c3mf2B_	Alignment	not modelled	98.6	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
73	c3ialB_	Alignment	not modelled	98.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
74	c3od1A_	Alignment	not modelled	98.6	15	**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
75	c1wu7A_	Alignment	not modelled	98.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
76	d1h4vb2	Alignment	not modelled	98.6	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
77	c2i4lC_	Alignment	not modelled	98.6	9	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
78	c1qe0B_	Alignment	not modelled	98.4	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase
						PDB header:ligase

79	c3netB_	Alignment	not modelled	98.4	17	**Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
80	c3errB_	Alignment	not modelled	98.4	16	**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
81	c2j3mA_	Alignment	not modelled	98.3	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
82	d1qe0a2	Alignment	not modelled	98.3	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
83	c2cj9A_	Alignment	not modelled	98.2	13	**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
84	d1z7ma1	Alignment	not modelled	98.1	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
85	d1g5ha2	Alignment	not modelled	98.1	7	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
86	d2g4ca2	Alignment	not modelled	98.0	7	**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	c1g5hA_	Alignment	not modelled	98.0	7	**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
88	d1usya_	Alignment	not modelled	97.9	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
89	c2pmfA_	Alignment	not modelled	97.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
90	c3ikmC_	Alignment	not modelled	97.7	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna polymerase subunit gamma-2; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
91	d1riqa2	Alignment	not modelled	96.8	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
92	c3hxxA_	Alignment	not modelled	96.7	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
93	c1yfsB_	Alignment	not modelled	96.6	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
94	d1j5wa_	Alignment	not modelled	96.2	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
95	c2ztgA_	Alignment	not modelled	93.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
96	c2zzfA_	Alignment	not modelled	93.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
97	c2phmA_	Alignment	not modelled	81.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
98	d1phza2	Alignment	not modelled	80.9	17	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
99	d1toha_	Alignment	not modelled	79.0	17	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
100	d1j8ua_	Alignment	not modelled	77.9	17	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
101	c3e2tA_	Alignment	not modelled	76.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophan 5-hydroxylase 1; **PDBTitle:** the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
102	c3rf1B_	Alignment	not modelled	70.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glycyl-trna synthetase alpha subunit; **PDBTitle:** the crystal structure of glycyl-trna synthetase subunit

						alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
103	c3ls1A_	Alignment	not modelled	45.7	15	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
104	c2lhuA_	Alignment	not modelled	43.5	53	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
105	c1vraA_	Alignment	not modelled	42.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
106	c3it4C_	Alignment	not modelled	41.4	44	**PDB header:**transferase **Chain:** C: **PDB Molecule:**arginine biosynthesis bifunctional protein argj **PDBTitle:** the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
107	c2v4iA_	Alignment	not modelled	40.1	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate n-acetyltransferase 2 alpha chain; **PDBTitle:** structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
108	d12asa_	Alignment	not modelled	39.1	28	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
109	c3n6oB_	Alignment	not modelled	38.8	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide exchange factor; **PDBTitle:** crystal structure of the gef and p4m domain of drra/sidm from2 legionella pneumophila
110	d1uoya_	Alignment	not modelled	36.9	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Bubble protein **Family:**Bubble protein
111	d1h05a_	Alignment	not modelled	31.4	18	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
112	d1vz6a_	Alignment	not modelled	31.2	44	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**ArgJ-like
113	d1vr3a1	Alignment	not modelled	23.0	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase