Phyre^2

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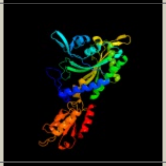
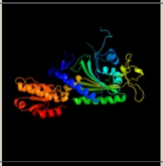
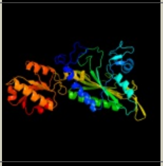
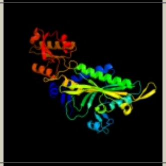
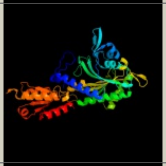
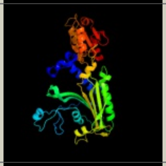
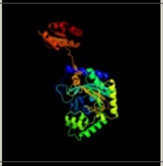
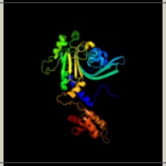
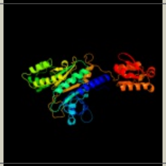
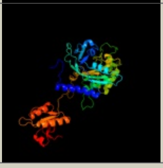
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j3mA_	Alignment		100.0	46	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
2	c2i4lC_	Alignment		100.0	51	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
3	c1ggmB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
4	c3ialB_	Alignment		100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
5	c1nyqA_	Alignment		100.0	23	**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
6	c2pmfA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
7	c1qf6A_	Alignment		100.0	23	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
8	c1atiA_	Alignment		100.0	20	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
9	c1nj8C_	Alignment		100.0	27	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
10	c1h4tD_	Alignment		100.0	25	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
11	c1nj2A_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus

12	c3a32A_	Alignment		100.0	18	**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
13	c1fyfB_	Alignment		100.0	23	**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
14	c3ikmC_	Alignment		100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna polymerase subunit gamma-2; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
15	c1g5hA_	Alignment		100.0	22	**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
16	c1adyA_	Alignment		100.0	18	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
17	c2el9B_	Alignment		100.0	18	**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
18	c1wu7A_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
19	c3netB_	Alignment		100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
20	c3hriF_	Alignment		100.0	18	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
21	c1qe0B_	Alignment	not modelled	100.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase
22	d1nj1a3	Alignment	not modelled	100.0	25	**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	d1nj8a3	Alignment	not modelled	100.0	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
24	c3od1A_	Alignment	not modelled	100.0	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
25	d1qf6a4	Alignment	not modelled	100.0	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
26	d1hc7a2	Alignment	not modelled	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
27	d1nyra4	Alignment	not modelled	100.0	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
28	c2cj9A_	Alignment	not modelled	100.0	27	**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
29	d1atia2	Alignment	not modelled	100.0	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
30	d1b76a2	Alignment	not modelled	100.0	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
31	d1seta2	Alignment	not modelled	100.0	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
32	c3mf2B_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
33	c1wleB_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
34	c1sryB_	Alignment	not modelled	100.0	21	**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
35	c3lssA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
36	c3qo8A_	Alignment	not modelled	100.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
37	c2dq0A_	Alignment	not modelled	100.0	23	**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
38	c2dq3A_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
39	c3errB_	Alignment	not modelled	100.0	22	**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
40	d1wu7a2	Alignment	not modelled	100.0	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
41	d1z7ma1	Alignment	not modelled	100.0	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
42	d1kmma2	Alignment	not modelled	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
43	d1g5ha2	Alignment	not modelled	100.0	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
44	c1z7nB_	Alignment	not modelled	100.0	14	**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
45	c3racA_	Alignment	not modelled	100.0	15	**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.
46	d1h4vb2	Alignment	not modelled	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
47	d2g4ca2	Alignment	not modelled	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
48	d1qe0a2	Alignment	not modelled	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
49	d1nj1a1	Alignment	not modelled	100.0	33	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
50	d1nj8a1	Alignment	not modelled	100.0	32	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
51	c3g1zB_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
52	d1usya_	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
53	d1bbua2	Alignment	not modelled	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

54	d1hc7a1	Alignment	not modelled	100.0	38	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
55	d1e1oa2	Alignment	not modelled	99.9	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
56	d1nyra1	Alignment	not modelled	99.9	29	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
57	d1qf6a1	Alignment	not modelled	99.9	26	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
58	d1g5ha1	Alignment	not modelled	99.9	17	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
59	d1atia1	Alignment	not modelled	99.9	19	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
60	d2g4ca1	Alignment	not modelled	99.9	20	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
61	d1eova2	Alignment	not modelled	99.9	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
62	c2zimA_	Alignment	not modelled	99.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
63	d1kmma1	Alignment	not modelled	99.9	19	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
64	d1wu7a1	Alignment	not modelled	99.8	17	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
65	d1qe0a1	Alignment	not modelled	99.8	30	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
66	d1h4vb1	Alignment	not modelled	99.8	16	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
67	d1b8aa2	Alignment	not modelled	99.8	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
68	c2znjB_	Alignment	not modelled	99.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
69	d1l0wa3	Alignment	not modelled	99.8	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
70	d1nnha_	Alignment	not modelled	99.7	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
71	d1c0aa3	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
72	c1e22A_	Alignment	not modelled	99.7	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
73	c1b70A_	Alignment	not modelled	99.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
74	d1jjca_	Alignment	not modelled	99.6	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
75	c3l4gI_	Alignment	not modelled	99.6	14	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
76	c3bjuB_	Alignment	not modelled	99.5	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
77	c3e9hB_	Alignment	not modelled	99.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
78	c1asyA_	Alignment	not modelled	99.3	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
79	c1eqrC_	Alignment	not modelled	99.1	21	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
						PDB header:ligase

80	c2rhqA_	Alignment	not modelled	99.1	8	**Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
81	c1efwA_	Alignment	not modelled	99.1	19	**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
82	c2xgtB_	Alignment	not modelled	99.1	22	**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
83	c1x55A_	Alignment	not modelled	99.0	17	**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
84	c1b8aB_	Alignment	not modelled	99.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
85	c1wydB_	Alignment	not modelled	98.9	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
86	c3m4qA_	Alignment	not modelled	98.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
87	c2du4B_	Alignment	not modelled	98.8	14	**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
88	c3i7fA_	Alignment	not modelled	98.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
89	c2du7C_	Alignment	not modelled	98.6	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
90	c1n9wA_	Alignment	not modelled	98.5	19	**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
91	c3pcoC_	Alignment	not modelled	98.5	9	**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
92	c3ig2B_	Alignment	not modelled	98.5	15	**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
93	d1v95a_	Alignment	not modelled	98.4	15	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
94	c3icaB_	Alignment	not modelled	98.4	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
95	c3l4gL_	Alignment	not modelled	98.2	14	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
96	d1jjcb5	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
97	d1wdva_	Alignment	not modelled	97.8	25	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
98	d1n9wa2	Alignment	not modelled	97.7	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
99	c2rhsB_	Alignment	not modelled	97.5	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
100	c2dxaA_	Alignment	not modelled	97.4	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein ybak; **PDBTitle:** crystal structure of trans editing enzyme prox from e.coli
101	d1dbxa_	Alignment	not modelled	97.2	22	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
102	d1vkia_	Alignment	not modelled	97.1	19	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
103	c2cx5B_	Alignment	not modelled	97.1	26	**PDB header:**translation **Chain:** B: **PDB Molecule:**a putative trans-editing enzyme; **PDBTitle:** crystal structure of a putative trans-editing enzyme for2 prolyl trna synthetase
104	c3cmqA_	Alignment	not modelled	96.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine

						trna2 synthetase
105	d1vjfa_	Alignment	not modelled	96.1	17	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
106	c3pcoD_	Alignment	not modelled	96.1	12	**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
107	c2akwB_	Alignment	not modelled	95.9	15	**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
108	c3op6B_	Alignment	not modelled	87.9	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an oligo-nucleotide binding protein (lpg1207)2 from legionella pneumophila subsp. pneumophila str. philadelphia 1 at3 2.00 a resolution
109	d1mkza_	Alignment	not modelled	79.5	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
110	c3h16A_	Alignment	not modelled	61.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
111	c1zejA_	Alignment	not modelled	56.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
112	c3pfnB_	Alignment	not modelled	52.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
113	d1y5ea1	Alignment	not modelled	46.9	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
114	c3mogA_	Alignment	not modelled	45.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
115	d1f0ya1	Alignment	not modelled	40.9	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
116	d2cvba1	Alignment	not modelled	39.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
117	c2is8A_	Alignment	not modelled	35.0	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
118	c3rfqC_	Alignment	not modelled	28.4	8	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
119	c3oziB_	Alignment	not modelled	27.6	17	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**l6tr; **PDBTitle:** crystal structure of the tir domain from the flax disease resistance2 protein l6
120	d1m5wa_	Alignment	not modelled	27.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase