Phyre2

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Description	P07395
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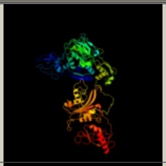
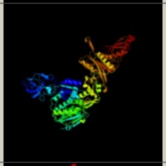
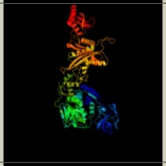
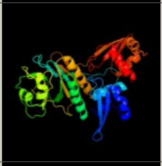
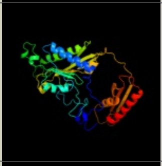
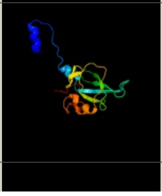
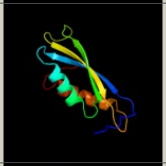
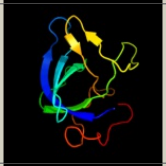
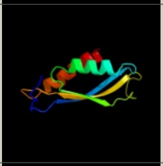
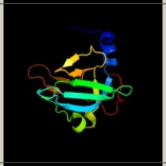
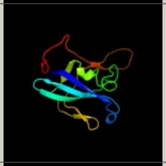
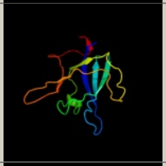
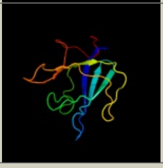
Unique Job ID	0aa962234370b47f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pcoD_	Alignment		100.0	100	**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
2	c2rhsB_	Alignment		100.0	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
3	c2akwB_	Alignment		100.0	37	**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
4	c3l4gL_	Alignment		100.0	20	**PDB header:**ligase **Chain:** L: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
5	c2cxiA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
6	c3cmqA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial phenylalanine trna2 synthetase
7	d1jjcb6	Alignment		100.0	44	**Fold:**PheT/TilS domain **Superfamily:**PheT/TilS domain **Family:**B3/B4 domain of PheRS, PheT
8	d1jjcb5	Alignment		100.0	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
9	c3icaB_	Alignment		100.0	20	**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
10	c3ig2B_	Alignment		100.0	20	**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
11	c3bu2B_	Alignment		100.0	41	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**putative trna-binding protein; **PDBTitle:** crystal structure of a trna-binding protein from2 staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target syr77

12	c2rhqA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
13	d1jjcb3	Alignment		100.0	37	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
14	d1jjcb4	Alignment		99.9	36	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
15	c2e8gB_	Alignment		99.9	38	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**hypothetical protein ph0536; **PDBTitle:** the structure of protein from p. horikoshii at 1.7 angstrom2 resolution
16	d1b7yb4	Alignment		99.9	35	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
17	c2cwpA_	Alignment		99.9	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**metrs related protein; **PDBTitle:** crystal structure of metrs related protein from pyrococcus horikoshii
18	d1gd7a_	Alignment		99.9	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
19	d1pyba_	Alignment		99.9	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
20	d1pxfa_	Alignment		99.9	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
21	d1mkha_	Alignment	not modelled	99.8	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
22	d1jjcb1	Alignment	not modelled	99.8	45	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
23	c2q2iA_	Alignment	not modelled	99.8	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**secretion chaperone; **PDBTitle:** crystal structure of the protein secretion chaperone csaa from2 agrobacterium tumefaciens.
24	d1jjcb2	Alignment	not modelled	99.8	41	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
25	d1fl0a_	Alignment	not modelled	99.8	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
26	d1jjca_	Alignment	not modelled	99.8	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
27	c1b70A_	Alignment	not modelled	99.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase; **PDBTitle:** phenylalanyl trna synthetase complexed with phenylalanine
28	d1ntga_	Alignment	not modelled	99.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
29	c2nzoD_	Alignment	not modelled	99.8	13	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**protein csaa; **PDBTitle:** crystal structure of a secretion chaperone csaa from

						bacillus subtilis2 in the space group p 32 2 1
30	c2du4B_	Alignment	not modelled	99.7	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
31	c3l4gI_	Alignment	not modelled	99.7	16	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase
32	c2du7C_	Alignment	not modelled	99.7	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**o-phosphoseryl-trna synthetase; **PDBTitle:** crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase
33	c3pcoC_	Alignment	not modelled	99.7	17	**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
34	c2zimA_	Alignment	not modelled	99.5	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyrrolysyl-trna synthetase; **PDBTitle:** pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
35	c2znjB_	Alignment	not modelled	99.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
36	d1kmma2	Alignment	not modelled	97.7	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
37	c2el9B_	Alignment	not modelled	97.6	14	**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
38	c3hj7A_	Alignment	not modelled	97.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils c-terminal domain
39	d1wu7a2	Alignment	not modelled	97.5	11	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
40	c3netB_	Alignment	not modelled	97.4	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
41	c3od1A_	Alignment	not modelled	97.4	9	**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
42	c3hriF_	Alignment	not modelled	97.4	9	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
43	c1wu7A_	Alignment	not modelled	97.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
44	c3racA_	Alignment	not modelled	97.4	12	**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.
45	c3g1zB_	Alignment	not modelled	97.2	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative lysyl-trna synthetase; **PDBTitle:** structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
46	c1z7nB_	Alignment	not modelled	97.2	15	**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
47	c1nyqA_	Alignment	not modelled	97.2	14	**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
48	c1adyA_	Alignment	not modelled	97.1	14	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
49	d1h4vb2	Alignment	not modelled	97.1	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
50	d1l0wa3	Alignment	not modelled	97.0	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
51	c2i4lC_	Alignment	not modelled	97.0	10	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
52	d1c0aa3	Alignment	not modelled	96.9	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
53	c2j3mA_	Alignment	not modelled	96.6	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
54	d1nyra4	Alignment	not modelled	96.6	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
55	d1nnha_	Alignment	not modelled	96.5	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
56	d1e1oa2	Alignment	not modelled	96.5	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
57	c1qf6A_	Alignment	not modelled	96.4	13	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
58	d1b8aa2	Alignment	not modelled	96.3	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
59	c2dq3A_	Alignment	not modelled	96.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
60	d1bbua2	Alignment	not modelled	96.2	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
61	c1e22A_	Alignment	not modelled	96.1	17	**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
62	c3e9hB_	Alignment	not modelled	96.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
63	c3a2kB_	Alignment	not modelled	95.9	22	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
64	c1fyfB_	Alignment	not modelled	95.8	12	**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
65	d1seta2	Alignment	not modelled	95.8	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
66	d1eova2	Alignment	not modelled	95.8	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
67	c1sryB_	Alignment	not modelled	95.7	12	**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
68	c1qe0B_	Alignment	not modelled	95.6	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of apo s. aureus histidyl-trna synthetase
69	d1z7ma1	Alignment	not modelled	95.6	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
70	c2dq0A_	Alignment	not modelled	95.5	11	**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
71	d1nj8a3	Alignment	not modelled	95.5	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
72	d1qf6a4	Alignment	not modelled	95.5	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
73	c1atiA_	Alignment	not modelled	95.4	9	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
74	c3bjuB_	Alignment	not modelled	95.4	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
75	c1efwA_	Alignment	not modelled	94.9	16	**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
76	c3a32A_	Alignment	not modelled	94.7	13	**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
77	d1nj1a3	Alignment	not modelled	94.4	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
78	c1ggmB_	Alignment	not modelled	94.3	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
79	c1nj8C_	Alignment	not modelled	94.2	12	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
80	c1eqrC_	Alignment	not modelled	93.8	9	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2

						escherichia coli
81	d1qe0a2	Alignment	not modelled	93.7	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
82	d1hc7a2	Alignment	not modelled	93.6	11	**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	c1x55A_	Alignment	not modelled	93.5	13	**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	c3lssA_	Alignment	not modelled	93.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
85	c3qo8A_	Alignment	not modelled	93.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
86	c1wydB_	Alignment	not modelled	93.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
87	c1wleB_	Alignment	not modelled	92.7	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
88	c3mf2B_	Alignment	not modelled	92.5	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**bll0957 protein; **PDBTitle:** crystal structure of class ii aars homologue (bll0957) complexed with2 amp
89	c1nj2A_	Alignment	not modelled	91.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
90	c1asyA_	Alignment	not modelled	91.1	15	**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
91	c1b8aB_	Alignment	not modelled	91.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
92	c3errB_	Alignment	not modelled	90.9	11	**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
93	c2xgtB_	Alignment	not modelled	87.2	11	**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
94	c1h4tD_	Alignment	not modelled	86.7	12	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
95	d1usya_	Alignment	not modelled	86.1	4	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
96	c3m4qA_	Alignment	not modelled	83.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
97	d1b76a2	Alignment	not modelled	82.2	8	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
98	c2cj9A_	Alignment	not modelled	80.3	15	**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
99	c3mpbA_	Alignment	not modelled	77.6	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
100	c1ni5A_	Alignment	not modelled	77.0	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
101	c2l1nA_	Alignment	not modelled	75.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
102	c3ialB_	Alignment	not modelled	74.0	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
103	c3i7fA_	Alignment	not modelled	73.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
104	d1atia2	Alignment	not modelled	70.2	6	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
105	c3kf6A_	Alignment	not modelled	54.9	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1;

						PDBTitle: crystal structure of s. pombe stn1-ten1 complex
106	c2pmfA_	Alignment	not modelled	47.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant
107	d1cg2a1	Alignment	not modelled	45.9	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
108	d3d3ra1	Alignment	not modelled	42.5	15	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
109	d1j99a_	Alignment	not modelled	40.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
110	d1sb6a_	Alignment	not modelled	39.9	32	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
111	c1t6sB_	Alignment	not modelled	39.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
112	d2pjqa1	Alignment	not modelled	36.9	29	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
113	d1ni5a3	Alignment	not modelled	36.5	18	**Fold:**PheT/TilS domain **Superfamily:**PheT/TilS domain **Family:**tRNA-Ile-lysidine synthetase, TilS, C-terminal domain
114	d2rcfa1	Alignment	not modelled	36.4	14	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
115	d1t6sa1	Alignment	not modelled	36.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ScpB/YpuH-like
116	d1sv6a_	Alignment	not modelled	36.2	19	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
117	c3gw7A_	Alignment	not modelled	35.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yedj; **PDBTitle:** crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
118	d1whza_	Alignment	not modelled	35.1	26	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
119	c1cg2D_	Alignment	not modelled	34.6	25	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
120	c3d3rA_	Alignment	not modelled	33.9	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1