Phyre^2

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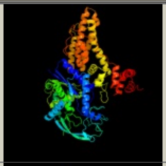
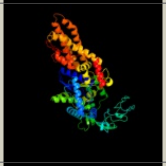
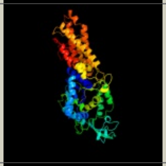
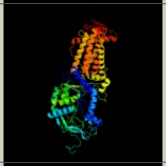
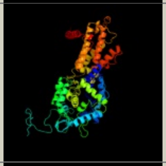
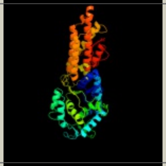
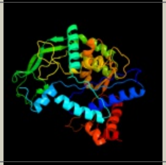
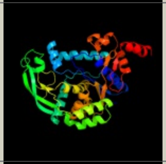
Description	P00959
Date	Thu Jan 5 10:57:21 GMT 2012
Unique Job ID	590fc0eec7767e03

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rqgA_	Alignment		100.0	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
2	c1pfuA_	Alignment		100.0	100	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
3	c3kflA_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
4	c1gaxB_	Alignment		100.0	21	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**valyl-trna synthetase; **PDBTitle:** crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
5	c1woyA_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
6	c1qu2A_	Alignment		100.0	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
7	c1ileA_	Alignment		100.0	23	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
8	c1wz2B_	Alignment		100.0	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
9	c2ct8A_	Alignment		100.0	28	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
10	c2x1lC_	Alignment		100.0	27	**PDB header:**ligase **Chain:** C: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
11	c1wkbA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation

12	c1obhA_	Alignment		100.0	24	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
13	d1h3na3	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	d1ffya3	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	d1pfva2	Alignment		100.0	99	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
16	d1ilea3	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
17	d1rqga2	Alignment		100.0	35	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
18	d1ivsa4	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
19	d2d5ba2	Alignment		100.0	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	c1u0bB_	Alignment		100.0	21	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
21	c3c8zB_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
22	c3tqoA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
23	c3sp1B_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
24	c3fnrA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
25	c1iq0A_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
26	d1li5a2	Alignment	not modelled	100.0	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
27	c2zufA_	Alignment	not modelled	100.0	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
28	d1iq0a2	Alignment	not modelled	100.0	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
29	c1f7uA_	Alignment	not modelled	100.0	21	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of the arginyl-trna synthetase

						complexed with the2 trna(arg) and l-arg
30	d1f7ua2	Alignment	not modelled	100.0	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	d1irxa2	Alignment	not modelled	100.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
32	d1ntga_	Alignment	not modelled	100.0	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
33	d1fl0a_	Alignment	not modelled	100.0	34	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
34	d1pfva1	Alignment	not modelled	100.0	100	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
35	d1gd7a_	Alignment	not modelled	100.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
36	c2q2iA_	Alignment	not modelled	99.9	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**secretion chaperone; **PDBTitle:** crystal structure of the protein secretion chaperone csaa from2 agrobacterium tumefaciens.
37	d1rqga1	Alignment	not modelled	99.9	26	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
38	d1mkha_	Alignment	not modelled	99.9	41	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
39	d1pyba_	Alignment	not modelled	99.9	48	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
40	d1pxfa_	Alignment	not modelled	99.9	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
41	c2cwpA_	Alignment	not modelled	99.9	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**metrs related protein; **PDBTitle:** crystal structure of metrs related protein from pyrococcus horikoshii
42	c2nzoD_	Alignment	not modelled	99.9	32	**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
43	c2e8gB_	Alignment	not modelled	99.9	17	**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
44	d2d5ba1	Alignment	not modelled	99.9	20	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
45	c1g59A_	Alignment	not modelled	99.8	18	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
46	c1irxA_	Alignment	not modelled	99.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
47	c3afhA_	Alignment	not modelled	99.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
48	c2ja2A_	Alignment	not modelled	99.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
49	c2cfoA_	Alignment	not modelled	99.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
50	c2o5rA_	Alignment	not modelled	99.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 1; **PDBTitle:** crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
51	d1gtra2	Alignment	not modelled	99.7	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
52	d1ivsa2	Alignment	not modelled	99.7	17	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
53	d1qu3a1	Alignment	not modelled	99.6	13	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases

						Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
54	d1ilea1	Alignment	not modelled	99.6	17	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
55	d1ffya1	Alignment	not modelled	99.6	13	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
56	d1jjcb3	Alignment	not modelled	99.6	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
57	c3bu2B_	Alignment	not modelled	99.6	19	**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
58	c3al0C_	Alignment	not modelled	99.5	17	**PDB header:**ligase/rna **Chain:** C: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c, glutamyl- **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
59	c1exdA_	Alignment	not modelled	99.4	16	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
60	c2hz7A_	Alignment	not modelled	99.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
61	d1h3na1	Alignment	not modelled	99.4	20	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
62	d1j09a2	Alignment	not modelled	99.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
63	c3pcoD_	Alignment	not modelled	99.2	21	**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
64	c3aiiA_	Alignment	not modelled	99.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
65	c2akwB_	Alignment	not modelled	99.0	29	**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
66	d1nzja_	Alignment	not modelled	98.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
67	c2cybA_	Alignment	not modelled	98.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
68	c3a05A_	Alignment	not modelled	98.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
69	c3hzrD_	Alignment	not modelled	98.2	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
70	c3focB_	Alignment	not modelled	98.2	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
71	c1h3eA_	Alignment	not modelled	98.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
72	c2rhsB_	Alignment	not modelled	98.0	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
73	c2quiB_	Alignment	not modelled	98.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
74	d1pfva3	Alignment	not modelled	97.9	100	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
75	d1r6ta2	Alignment	not modelled	97.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
76	d1iq0a1	Alignment	not modelled	97.6	18	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I

						aminoacyl-tRNA synthetases
77	d1f7ua1	Alignment	not modelled	97.4	19	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
78	c3jxeB_	Alignment	not modelled	97.2	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
79	c2g36A_	Alignment	not modelled	97.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution
80	d1h3fa1	Alignment	not modelled	97.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
81	c3hv0A_	Alignment	not modelled	96.8	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
82	d1j1ua_	Alignment	not modelled	96.6	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
83	c2dlcX_	Alignment	not modelled	96.5	11	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
84	d1n3la_	Alignment	not modelled	96.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
85	c2ip1A_	Alignment	not modelled	96.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
86	c2j5bA_	Alignment	not modelled	96.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
87	c2janD_	Alignment	not modelled	96.2	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
88	c2el7A_	Alignment	not modelled	96.1	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
89	d1i6la_	Alignment	not modelled	96.1	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
90	c3m5wB_	Alignment	not modelled	96.1	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
91	c1jiiA_	Alignment	not modelled	96.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
92	c3prhB_	Alignment	not modelled	96.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
93	c3i05B_	Alignment	not modelled	95.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
94	c1q11A_	Alignment	not modelled	95.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
95	c1yi8C_	Alignment	not modelled	95.9	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl trrna synthetase ii from deinococcus2 radiodurans in complex with l-trp
96	c1r6uB_	Alignment	not modelled	95.8	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
97	c2rkjM_	Alignment	not modelled	95.7	14	**PDB header:**ligase/rna **Chain:** M: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** cocrystal structure of a tyrosyl-trna synthetase splicing2 factor with a group i intron rna
98	d1jila_	Alignment	not modelled	95.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
99	c3sz3A_	Alignment	not modelled	95.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
100	c2cyaA_	Alignment	not modelled	95.6	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
101	c1x8xA_	Alignment	not modelled	95.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
						PDB header:ligase

102	c3p0jD_	Alignment	not modelled	95.4	17	**Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
103	c3n9iA_	Alignment	not modelled	95.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
104	c2yy5C_	Alignment	not modelled	95.2	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
105	c2cycB_	Alignment	not modelled	95.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
106	c2pidB_	Alignment	not modelled	94.1	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
107	d1u0bb1	Alignment	not modelled	94.0	21	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
108	d1li5a1	Alignment	not modelled	91.9	24	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
109	d2ts1a_	Alignment	not modelled	91.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
110	c2ts1A_	Alignment	not modelled	91.0	14	**PDB header:**ligase (synthetase) **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of tyrosyl-t/rna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
111	c2iyaB_	Alignment	not modelled	87.3	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
112	d1f0ka_	Alignment	not modelled	83.3	24	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
113	c1dvbA_	Alignment	not modelled	71.4	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
114	c3dzcA_	Alignment	not modelled	69.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
115	c3cp0A_	Alignment	not modelled	66.0	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
116	d1ccwa_	Alignment	not modelled	65.6	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
117	c2hr5B_	Alignment	not modelled	62.9	17	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
118	d1qmga2	Alignment	not modelled	62.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
119	c3f3mA_	Alignment	not modelled	60.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
120	d1od6a_	Alignment	not modelled	58.5	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase