Phyre^2

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Description	P07118
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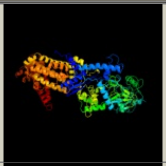
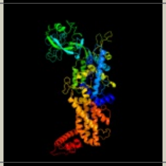
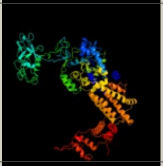
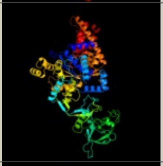
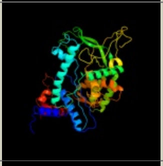
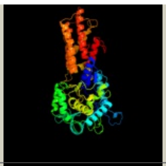
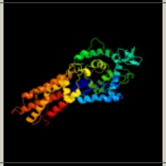
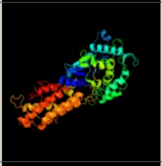
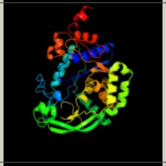
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gaxB_	Alignment		100.0	43	**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
2	c1qu2A_	Alignment		100.0	22	**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
3	c1ileA_	Alignment		100.0	26	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
4	c1wz2B_	Alignment		100.0	23	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
5	c1wkbA_	Alignment		100.0	24	**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
6	c1obhA_	Alignment		100.0	25	**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
7	c1rqgA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
8	d1ffya3	Alignment		100.0	28	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
9	d1h3na3	Alignment		100.0	30	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
10	c1pfuA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
11	d1ilea3	Alignment		100.0	29	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain

12	c3kflA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
13	d1ivsa4	Alignment		100.0	55	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	c1woyA_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
15	c2x1lC_	Alignment		100.0	25	**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
16	c2ct8A_	Alignment		100.0	26	**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
17	d1rqga2	Alignment		100.0	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
18	d2d5ba2	Alignment		100.0	30	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
19	d1pfva2	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	d1ivsa2	Alignment		100.0	35	**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
21	c1u0bB_	Alignment	not modelled	100.0	19	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
22	d1qu3a1	Alignment	not modelled	100.0	15	**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
23	d1wkaa1	Alignment	not modelled	100.0	38	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
24	c3tqoA_	Alignment	not modelled	100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
25	c3sp1B_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
26	c3c8zB_	Alignment	not modelled	100.0	21	**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
27	d1ilea1	Alignment	not modelled	100.0	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
						PDB header:transferase

28	c3fnrA_	Alignment	not modelled	100.0	17	**Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
29	d1ffya1	Alignment	not modelled	100.0	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
30	d1udza_	Alignment	not modelled	100.0	29	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
31	c1iq0A_	Alignment	not modelled	100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
32	d1h3na2	Alignment	not modelled	100.0	29	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
33	c3o0aB_	Alignment	not modelled	100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**leucyl-trna synthetase subunit alpha; **PDBTitle:** crystal structure of the wild type cp1 hydrolitic domain from aquifex2 aeolicus leucyl-trna
34	c2ajhA_	Alignment	not modelled	100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of e. coli leucyl-2 trna synthetase complexes with methionine
35	d1ffya2	Alignment	not modelled	100.0	24	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
36	c2wfdB_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**leucyl-trna synthetase, cytoplasmic; **PDBTitle:** structure of the human cytosolic leucyl-trna synthetase2 editing domain
37	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
38	c2wfgA_	Alignment	not modelled	100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cytosolic leucyl-trna synthetase; **PDBTitle:** structure of the candida albicans cytosolic leucyl-trna2 synthetase editing domain bound to a benzoxaborole-amp3 adduct
39	c3pz6F_	Alignment	not modelled	100.0	24	**PDB header:**ligase **Chain:** F: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** the crystal structure of glleurs-cp1
40	c2zufA_	Alignment	not modelled	99.9	19	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
41	d1iq0a2	Alignment	not modelled	99.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
42	d1h3na1	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
43	d1f7ua2	Alignment	not modelled	99.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
44	d1rqga1	Alignment	not modelled	99.8	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
45	d1irxa2	Alignment	not modelled	99.8	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
46	c1f7uA_	Alignment	not modelled	99.8	18	**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
47	d1pfva1	Alignment	not modelled	99.7	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
48	d2d5ba1	Alignment	not modelled	99.7	15	**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
49	c1g59A_	Alignment	not modelled	99.5	23	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
50	c2ja2A_	Alignment	not modelled	99.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
51	c3afhA_	Alignment	not modelled	99.4	29	**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

52	c2cfoA_	Alignment	not modelled	99.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
53	c2o5rA_	Alignment	not modelled	99.3	24	**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
54	d1gtra2	Alignment	not modelled	99.2	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
55	d1ivsa1	Alignment	not modelled	99.1	26	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
56	c1irxA_	Alignment	not modelled	98.3	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
57	c3aiiA_	Alignment	not modelled	98.3	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
58	c1exdA_	Alignment	not modelled	98.2	24	**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
59	c2hz7A_	Alignment	not modelled	98.2	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
60	d1nzja_	Alignment	not modelled	98.1	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
61	d1j09a2	Alignment	not modelled	98.1	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
62	c3al0C_	Alignment	not modelled	97.8	30	**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.
63	c1h3eA_	Alignment	not modelled	96.9	23	**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
64	c2cybA_	Alignment	not modelled	96.8	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
65	c1jiiA_	Alignment	not modelled	96.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
66	c2janD_	Alignment	not modelled	96.5	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
67	d1h3fa1	Alignment	not modelled	96.5	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
68	d1jila_	Alignment	not modelled	96.3	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
69	c2j5bA_	Alignment	not modelled	96.1	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
70	c1x8xA_	Alignment	not modelled	95.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
71	c2rkjM_	Alignment	not modelled	95.9	20	**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
72	c3focB_	Alignment	not modelled	95.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
73	c3prhB_	Alignment	not modelled	95.8	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
74	c3hv0A_	Alignment	not modelled	95.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
75	c3hzrD_	Alignment	not modelled	95.7	12	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
76	c2dlcX_	Alignment	not modelled	95.5	15	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
77	c2g36A_	Alignment	not modelled	95.4	21	**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
78	d1i6la_	Alignment	not modelled	95.3	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
79	d1n3la_	Alignment	not modelled	95.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
80	c3jxeB_	Alignment	not modelled	95.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
81	c2el7A_	Alignment	not modelled	95.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
82	c2cyaA_	Alignment	not modelled	95.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
83	c2ts1A_	Alignment	not modelled	94.9	13	**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
84	d2ts1a_	Alignment	not modelled	94.9	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
85	c1q11A_	Alignment	not modelled	94.7	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
86	c3i05B_	Alignment	not modelled	94.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
87	c3a05A_	Alignment	not modelled	94.3	19	**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
88	c3m5wB_	Alignment	not modelled	94.2	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
89	c3p0jD_	Alignment	not modelled	94.1	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
90	d1j1ua_	Alignment	not modelled	93.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
91	c1yi8C_	Alignment	not modelled	93.8	20	**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
92	c2quiB_	Alignment	not modelled	93.6	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
93	c2ip1A_	Alignment	not modelled	93.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
94	c2cycB_	Alignment	not modelled	92.8	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
95	c3n9iA_	Alignment	not modelled	92.8	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
96	c2pidB_	Alignment	not modelled	92.4	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
97	d1r6ta2	Alignment	not modelled	89.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
98	c1r6uB_	Alignment	not modelled	87.4	13	**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
99	c3sz3A_	Alignment	not modelled	83.3	20	**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	c2yy5C_	Alignment	not modelled	81.3	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
101	c3lssA_	Alignment	not modelled	70.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
102	d1iq0a1	Alignment	not modelled	64.0	14	**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
103	c3hnwB_	Alignment	not modelled	60.4	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
104	d1f7ua1	Alignment	not modelled	54.7	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
105	c3ojaB_	Alignment	not modelled	54.6	12	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
106	c2opfA_	Alignment	not modelled	48.3	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
107	c2dq0A_	Alignment	not modelled	47.5	16	**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
108	c1nnjA_	Alignment	not modelled	46.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
109	c3d5cX_	Alignment	not modelled	46.4	7	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
110	d1seta1	Alignment	not modelled	46.1	17	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
111	c1k82D_	Alignment	not modelled	45.0	7	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
112	c2f5qA_	Alignment	not modelled	44.9	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
113	c1ee8A_	Alignment	not modelled	42.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
114	c3bmaC_	Alignment	not modelled	41.0	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**d-alanyl-lipoteichoic acid synthetase; **PDBTitle:** crystal structure of d-alanyl-lipoteichoic acid synthetase from2 streptococcus pneumoniae r6
115	c3chfA_	Alignment	not modelled	39.9	24	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of aspergillus fumigatus chitinase b1 in complex2 with tetrapeptide
116	c2dq3A_	Alignment	not modelled	39.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
117	c3cz8A_	Alignment	not modelled	38.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sporulation-specific glycosylase ydhd; **PDBTitle:** crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
118	c1u0iA_	Alignment	not modelled	38.7	48	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
119	c2v2gC_	Alignment	not modelled	38.1	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxiredoxin 6; **PDBTitle:** crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
120	d1k3xa3	Alignment	not modelled	36.5	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins