
































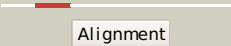
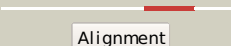

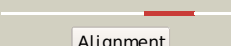
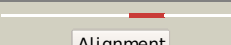
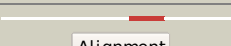
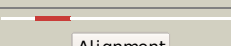
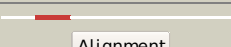
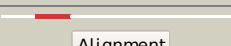
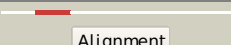
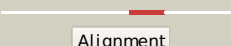
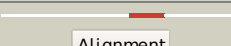
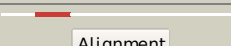
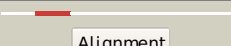

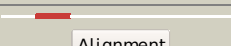
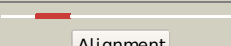
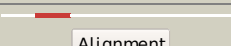
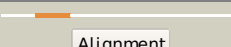
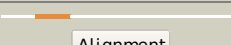
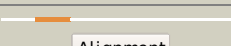
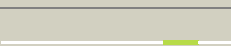
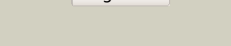



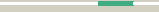



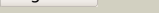


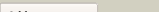
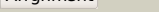

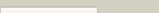



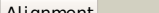



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qu2A_	 Alignment		100.0	43	PDB header: ligase/rna Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
2	c1ileA_	 Alignment		100.0	30	PDB header: aminoacyl-trna synthetase Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: isoleucyl-trna synthetase
3	c1gaxB_	 Alignment		100.0	24	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
4	c1wz2B_	 Alignment		100.0	18	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	18	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	21	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	d1ffya3	 Alignment		100.0	50	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
8	c1rqgA_	 Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from pyrococcus abyssi
9	d1h3na3	 Alignment		100.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
10	d1ileA3	 Alignment		100.0	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
11	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

12	c3kflA_	Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
13	c1woyA_	Alignment		100.0	23	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
14	d1ivsA4	Alignment		100.0	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	c2x1lC_	Alignment		100.0	26	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	24	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 analogue
17	d1ffya1	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
18	d1rqga2	Alignment		100.0	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
19	d2d5ba2	Alignment		100.0	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	d1pfva2	Alignment		100.0	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
21	d1qu3a1	Alignment	not modelled	100.0	33	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
22	c1u0bB_	Alignment	not modelled	100.0	26	PDB header: ligase/rna Chain: B: PDB Molecule: cysteinyln trna; PDBTitle: crystal structure of cysteinyln-trna synthetase binary2 complex with trnacs
23	d1udza_	Alignment	not modelled	100.0	34	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
24	d1ffya2	Alignment	not modelled	100.0	41	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
25	c3tqoA_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: structure of the cysteinyln-trna synthetase (cyss) from coxiella2 burnetii.
26	c3c8zB_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: B: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
27	d1h3na2	Alignment	not modelled	100.0	24	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
28	c3sp1B_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: cysteinyln-trna synthetase; PDBTitle: crystal structure of cysteinyln-trna synthetase (cyss) from

						borrelia2 burgdorferi
29	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;
30	c3o0aB_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase subunit alpha; PDBTitle: crystal structure of the wild type cp1 hydrolytic domain from aquifex2 aeolicus leucyl-trna
31	c2wfdB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase, cytoplasmic; PDBTitle: structure of the human cytosolic leucyl-trna synthetase2 editing domain
32	c2wfgA_	Alignment	not modelled	100.0	21	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
33	dlwkaa1	Alignment	not modelled	100.0	28	Fold: ValRS/IleRS/LeuRS editing domain Superfamily: ValRS/IleRS/LeuRS editing domain Family: ValRS/IleRS/LeuRS editing domain
34	c2ajhA_	Alignment	not modelled	100.0	22	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	dlivsa2	Alignment	not modelled	100.0	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
36	d1li5a2	Alignment	not modelled	100.0	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
37	cliq0A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: thermus thermophilus arginyl-trna synthetase
38	c3pz6F_	Alignment	not modelled	100.0	19	PDB header: ligase Chain: F: PDB Molecule: leucyl-trna synthetase; PDBTitle: the crystal structure of glleuRS-cp1
39	dlileal	Alignment	not modelled	100.0	23	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
40	c2zufA_	Alignment	not modelled	99.9	22	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	dliq0a2	Alignment	not modelled	99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
42	dlirxa2	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
43	dlf7ua2	Alignment	not modelled	99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
44	dlh3na1	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	c1f7uA_	Alignment	not modelled	99.8	20	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
46	dlrqga1	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
47	c1g59A_	Alignment	not modelled	99.7	16	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: glutamyl-trna synthetase complexed with trna(glu).
48	dlpfva1	Alignment	not modelled	99.6	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	c2ja2A_	Alignment	not modelled	99.6	19	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: mycobacterium tuberculosis glutamyl-trna synthetase
50	d2d5ba1	Alignment	not modelled	99.5	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
51	c2cfoA_	Alignment	not modelled	99.5	18	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu PDB header: ligase

52	c3afhA_	Alignment	not modelled	99.4	17	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
53	c2o5rA_	Alignment	not modelled	99.4	20	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	c1lrxA_	Alignment	not modelled	99.1	18	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of class i lysyl-trna synthetase
55	d1gtra2	Alignment	not modelled	98.3	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
56	c3aiaA_	Alignment	not modelled	98.2	25	PDB header: ligase Chain: A: PDB Molecule: glutamyl-trna synthetase; PDBTitle: archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
57	c1exdA_	Alignment	not modelled	98.2	23	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
58	c2hz7A_	Alignment	not modelled	98.1	28	PDB header: ligase Chain: A: PDB Molecule: glutaminyl-trna synthetase; PDBTitle: crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
59	d1nzia_	Alignment	not modelled	98.1	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
60	d1j09a2	Alignment	not modelled	98.0	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
61	c1jiiA_	Alignment	not modelled	97.8	27	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of s. aureus tyrrs in complex with sb-219383
62	c1h3eA_	Alignment	not modelled	97.7	28	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
63	d1jila_	Alignment	not modelled	97.7	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
64	c2janD_	Alignment	not modelled	97.7	23	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
65	c2cybA_	Alignment	not modelled	97.7	32	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
66	c3al0C_	Alignment	not modelled	97.6	20	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.
67	d1h3fa1	Alignment	not modelled	97.4	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
68	c2j5bA_	Alignment	not modelled	97.4	19	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
69	c1x8xA_	Alignment	not modelled	97.3	25	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl t-rna synthetase from e.coli complexed with tyrosine
70	c2ts1A_	Alignment	not modelled	97.1	24	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
71	d2ts1a_	Alignment	not modelled	97.1	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
72	c2rkjM_	Alignment	not modelled	97.0	30	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
73	c2el7A_	Alignment	not modelled	97.0	20	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
74	c2cyaA_	Alignment	not modelled	96.9	30	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
75	c2g36A_	Alignment	not modelled	96.9	25	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
76	c3a05A_	Alignment	not modelled	96.4	25	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

77	c2cycB	 Alignment	not modelled	96.2	28	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
78	c3prhB	 Alignment	not modelled	95.9	17	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase val144pro mutant from b. subtilis
79	c3hxrD	 Alignment	not modelled	95.9	9	PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase homolog from entamoeba histolytica
80	c3n9iA	 Alignment	not modelled	95.9	18	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
81	c3m5wB	 Alignment	not modelled	95.8	22	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
82	c2yy5C	 Alignment	not modelled	95.4	18	PDB header: ligase Chain: C: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
83	c2quiB	 Alignment	not modelled	95.4	23	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
84	c1yi8C	 Alignment	not modelled	95.3	25	PDB header: ligase Chain: C: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl trna synthetase ii from deinococcus2 radiodurans in complex with l-trp
85	d1n3la	 Alignment	not modelled	94.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
86	c3hv0A	 Alignment	not modelled	94.8	19	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from cryptosporidium parvum
87	d1i6la	 Alignment	not modelled	94.5	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
88	c3focB	 Alignment	not modelled	94.3	16	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
89	c3p0jD	 Alignment	not modelled	94.3	26	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	c3jxeB	 Alignment	not modelled	93.9	19	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
91	d1j1ua	 Alignment	not modelled	92.8	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
92	c2dlcX	 Alignment	not modelled	92.8	10	PDB header: ligase/trna Chain: X: PDB Molecule: tyrosyl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
93	c3sz3A	 Alignment	not modelled	92.5	25	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
94	d1r6ta2	 Alignment	not modelled	90.5	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
95	c1q11A	 Alignment	not modelled	90.5	9	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
96	c3i05B	 Alignment	not modelled	90.2	13	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from trypanosoma brucei
97	c2pidB	 Alignment	not modelled	89.0	21	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
98	c2ip1A	 Alignment	not modelled	87.2	21	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
99	c1r6uB	 Alignment	not modelled	85.6	18	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
100	d1iq0a1	 Alignment	not modelled	60.1	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
101	d2ey4e1	 Alignment	not modelled	56.6	53	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
102	d2apob1	 Alignment	not modelled	49.0	59	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like

103	d1zt2a1	 Alignment	not modelled	46.1	13	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
104	d1f7ua1	 Alignment	not modelled	45.4	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
105	c2k42A	 Alignment	not modelled	44.0	22	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protein; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehc effector
106	d1imla2	 Alignment	not modelled	42.8	37	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
107	c2opfa	 Alignment	not modelled	41.1	27	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
108	c1k82D	 Alignment	not modelled	40.1	13	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
109	d1vdda	 Alignment	not modelled	40.1	40	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
110	c1nnja	 Alignment	not modelled	38.3	18	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
111	c3bmaC	 Alignment	not modelled	38.3	24	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
112	d1libia1	 Alignment	not modelled	37.8	83	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
113	c1vddC	 Alignment	not modelled	37.0	40	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
114	c1yuzB	 Alignment	not modelled	35.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
115	d1k3xa3	 Alignment	not modelled	34.5	27	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
116	d1v8fa	 Alignment	not modelled	33.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
117	c1ee8A	 Alignment	not modelled	32.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
118	c2f5qA	 Alignment	not modelled	30.8	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
119	c3a46B	 Alignment	not modelled	28.7	8	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of mvnei1/thf complex
120	d1cta1	 Alignment	not modelled	28.2	57	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain