



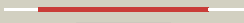



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1f7uA_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
2	<a href="#">c2zufA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
3	<a href="#">c1iq0A_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> thermus thermophilus arginyl-trna synthetase
4	<a href="#">c3fnrA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
5	<a href="#">d1f7ua2</a>	 Alignment		100.0	33	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
6	<a href="#">d1iq0a2</a>	 Alignment		100.0	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
7	<a href="#">c2x1lC_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
8	<a href="#">c2ct8A_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 analogue
9	<a href="#">c1woyA_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
10	<a href="#">c3tqoA_</a>	 Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteiny-trna synthetase; <b>PDBTitle:</b> structure of the cysteiny-trna synthetase (cyss) from coxiella2 burnetii.
11	<a href="#">c1pfuA_</a>	 Alignment		100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate



29	<a href="#">c1wkbA</a>	Alignment	not modelled	100.0	21	<b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
30	<a href="#">c1obhA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> leucyl-trna synthetase; <b>PDBTitle:</b> leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
31	<a href="#">d1h3na3</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
32	<a href="#">d1iq0a1</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
33	<a href="#">d1f7ua1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
34	<a href="#">c1irxA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> lysyl-trna synthetase; <b>PDBTitle:</b> crystal structure of class I lysyl-trna synthetase
35	<a href="#">c1g59A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> glutamyl-trna synthetase complexed with trna(glu).
36	<a href="#">c3gdzA</a>	Alignment	not modelled	99.9	86	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
37	<a href="#">c3afhA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 2; <b>PDBTitle:</b> crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
38	<a href="#">c2cfoA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
39	<a href="#">d1gtra2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
40	<a href="#">c2ja2A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> mycobacterium tuberculosis glutamyl-trna synthetase
41	<a href="#">c2o5rA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase 1; <b>PDBTitle:</b> 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
42	<a href="#">c3al0C</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> ligase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit c, glutamyl- <b>PDBTitle:</b> crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
43	<a href="#">d1iq0a3</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
44	<a href="#">d1j09a2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
45	<a href="#">c2hz7A</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
46	<a href="#">c1exdA</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
47	<a href="#">d1f7ua3</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
48	<a href="#">d1nzja</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
49	<a href="#">c3aiiA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna synthetase; <b>PDBTitle:</b> archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
50	<a href="#">c3hxrD</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase homolog from entamoeba histolytica
51	<a href="#">c2cybA</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
52	<a href="#">d1rqa1</a>	Alignment	not modelled	98.2	9	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I

52	<a href="#">d1ruga1</a>	Alignment	not modelled	98.2	9	aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
53	<a href="#">c2rkjM_</a>	Alignment	not modelled	98.2	14	<b>PDB header:</b> ligase/rna <b>Chain:</b> M: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> cocrystal structure of a tyrosyl-trna synthetase splicing2 factor with a group i intron rna
54	<a href="#">c3a05A_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
55	<a href="#">c2j5bA_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosinol
56	<a href="#">c2cyaA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
57	<a href="#">c3jxeB_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
58	<a href="#">c3focB_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from giardia lamblia
59	<a href="#">d1pfva1</a>	Alignment	not modelled	97.8	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
60	<a href="#">c2ts1A_</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> ligase (synthetase) <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> structure of tyrosyl-tRNA synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
61	<a href="#">d2ts1a_</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
62	<a href="#">d2d5ba1</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
63	<a href="#">c3p0jD_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinc crystal form 1
64	<a href="#">c1h3eA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
65	<a href="#">d1h3fa1</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
66	<a href="#">c1x8xA_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl t-rna synthetase from e.coli complexed with tyrosine
67	<a href="#">c1jiiA_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of s. aureus tyrrs in complex with sb-219383
68	<a href="#">d1jila_</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
69	<a href="#">c2el7A_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
70	<a href="#">c2g36A_</a>	Alignment	not modelled	96.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> 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
71	<a href="#">d1qu3a1</a>	Alignment	not modelled	96.6	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
72	<a href="#">c2janD_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
73	<a href="#">c3m5wB_</a>	Alignment	not modelled	96.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
74	<a href="#">d1ileal</a>	Alignment	not modelled	95.9	15	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
75	<a href="#">c1vi8C_</a>	Alignment	not modelled	95.7	22	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase;

75	<a href="#">c4y8C_</a>	Alignment	not modelled	93.7	42	<b>PDBTitle:</b> crystal structure of tryptophanyl trna synthetase ii from deinococcus2 radiodurans in complex with l-trp <b>PDB header:</b> ligase
76	<a href="#">c2quiB_</a>	Alignment	not modelled	95.3	14	<b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
77	<a href="#">d1ffya1</a>	Alignment	not modelled	94.8	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
78	<a href="#">d1jlua_</a>	Alignment	not modelled	94.3	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
79	<a href="#">d1n3la_</a>	Alignment	not modelled	94.2	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
80	<a href="#">c2dlcX_</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> ligase/trna <b>Chain:</b> X: <b>PDB Molecule:</b> tyrosyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
81	<a href="#">c1q11A_</a>	Alignment	not modelled	94.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
82	<a href="#">d1ivsa2</a>	Alignment	not modelled	93.5	16	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
83	<a href="#">c3i05B_</a>	Alignment	not modelled	91.8	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from trypanosoma brucei
84	<a href="#">c2cycB_</a>	Alignment	not modelled	91.8	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
85	<a href="#">c2pidB_</a>	Alignment	not modelled	90.9	33	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
86	<a href="#">d1r6ta2</a>	Alignment	not modelled	90.9	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
87	<a href="#">c3n9iA_</a>	Alignment	not modelled	89.8	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
88	<a href="#">d1u0bb1</a>	Alignment	not modelled	89.4	20	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
89	<a href="#">c3prhB_</a>	Alignment	not modelled	89.1	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase val144pro mutant from b. subtilis
90	<a href="#">c3sz3A_</a>	Alignment	not modelled	88.9	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
91	<a href="#">d1i6la_</a>	Alignment	not modelled	88.6	9	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
92	<a href="#">c2ip1A_</a>	Alignment	not modelled	88.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
93	<a href="#">c3hv0A_</a>	Alignment	not modelled	87.6	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from cryptosporidium parvum
94	<a href="#">d1h3na1</a>	Alignment	not modelled	87.1	13	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
95	<a href="#">c2yy5C_</a>	Alignment	not modelled	87.0	14	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
96	<a href="#">d1li5a1</a>	Alignment	not modelled	79.8	20	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
97	<a href="#">c1r6uB_</a>	Alignment	not modelled	78.4	23	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
98	<a href="#">d2vgna2</a>	Alignment	not modelled	75.1	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Translational machinery components <b>Family:</b> ERF1/Dom34 middle domain-like
						<b>PDB header:</b> cell cycle



99	<a href="#">c2vgmA</a>	Alignment	not modelled	67.5	11	<b>Chain:</b> A: <b>PDB Molecule:</b> dom34; <b>PDBTitle:</b> structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
100	<a href="#">d1jmkc</a>	Alignment	not modelled	67.2	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
101	<a href="#">c2cbgA</a>	Alignment	not modelled	61.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fengycin synthetase; <b>PDBTitle:</b> crystal structure of the pmsf-inhibited thioesterase domain2 of the fengycin biosynthesis cluster
102	<a href="#">c2iyaB</a>	Alignment	not modelled	60.6	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
103	<a href="#">d2dexx3</a>	Alignment	not modelled	57.0	18	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Peptidylarginine deiminase Pad4, catalytic C-terminal domain
104	<a href="#">c2vsqA</a>	Alignment	not modelled	56.7	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
105	<a href="#">d1f0ka</a>	Alignment	not modelled	50.6	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
106	<a href="#">d2qwxal</a>	Alignment	not modelled	50.3	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
107	<a href="#">d1qrda</a>	Alignment	not modelled	45.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
108	<a href="#">c3mcaB</a>	Alignment	not modelled	43.7	18	<b>PDB header:</b> translation regulation/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein dom34; <b>PDBTitle:</b> structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
109	<a href="#">c3d0qB</a>	Alignment	not modelled	40.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
110	<a href="#">d1sw5a</a>	Alignment	not modelled	39.4	18	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
111	<a href="#">c2ekdD</a>	Alignment	not modelled	38.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0250; <b>PDBTitle:</b> structural study of project id ph0250 from pyrococcus horikoshii ot3
112	<a href="#">c3ia7A</a>	Alignment	not modelled	33.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
113	<a href="#">d1dxqa</a>	Alignment	not modelled	32.1	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
114	<a href="#">c2gk4A</a>	Alignment	not modelled	31.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
115	<a href="#">d1lw7a1</a>	Alignment	not modelled	30.2	30	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenyltransferase
116	<a href="#">c1yunB</a>	Alignment	not modelled	28.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenyltransferase from pseudomonas aeruginosa
117	<a href="#">d1u7za</a>	Alignment	not modelled	27.9	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
118	<a href="#">d1a9xa3</a>	Alignment	not modelled	26.5	26	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
119	<a href="#">d1xd7a</a>	Alignment	not modelled	26.3	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Transcriptional regulator Rrf2
120	<a href="#">d1y88a2</a>	Alignment	not modelled	25.9	18	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like