Phyre^{2}

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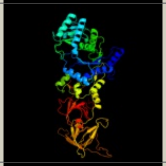
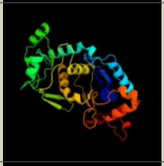
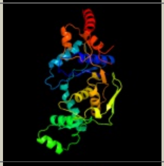
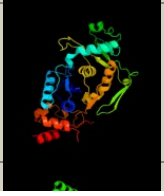
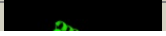
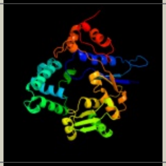
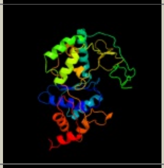
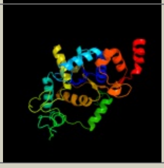
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1exdA_	Alignment		100.0	100	**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
2	c2hz7A_	Alignment		100.0	49	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
3	c3aiiA_	Alignment		100.0	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
4	d1gtra2	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
5	d1j09a2	Alignment		100.0	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
6	c3al0C_	Alignment		100.0	22	**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.
7	d1nzja_	Alignment		100.0	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
8	c2cfoA_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
9	c2ja2A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
10	c1g59A_	Alignment		100.0	25	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
11	c3afhA_	Alignment		100.0	22	**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
						

12	c2o5rA_	Alignment		100.0	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
13	d1gtra1	Alignment		100.0	99	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
14	c1irxA_	Alignment		100.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
15	d1f7ua2	Alignment		100.0	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
16	d1li5a2	Alignment		99.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
17	c3sp1B_	Alignment		99.9	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
18	c1u0bB_	Alignment		99.9	17	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
19	d2d5ba2	Alignment		99.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	d1pfva2	Alignment		99.9	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
21	c3c8zB_	Alignment	not modelled	99.9	14	**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	c2ct8A_	Alignment	not modelled	99.8	16	**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
23	c2x1lC_	Alignment	not modelled	99.8	15	**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
24	d1irxa2	Alignment	not modelled	99.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
25	c1woyA_	Alignment	not modelled	99.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
26	c3tqoA_	Alignment	not modelled	99.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
27	c3fnrA_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
28	d1rqga2	Alignment	not modelled	99.6	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
						Fold: Adenine nucleotide alpha hydrolase-like

29	d1ivsa4	Alignment	not modelled	99.5	19	**Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
30	c1pfuA_	Alignment	not modelled	99.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
31	c3kflA_	Alignment	not modelled	99.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
32	d1ilea3	Alignment	not modelled	99.4	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
33	c1rqgA_	Alignment	not modelled	99.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
34	d1ffya3	Alignment	not modelled	99.3	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
35	d1h3na3	Alignment	not modelled	99.2	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
36	d1iq0a2	Alignment	not modelled	99.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
37	c1f7uA_	Alignment	not modelled	99.1	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
38	c2zufA_	Alignment	not modelled	99.1	16	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
39	c1iq0A_	Alignment	not modelled	99.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
40	c2g36A_	Alignment	not modelled	98.4	18	**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
41	c1gaxB_	Alignment	not modelled	98.3	29	**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
42	c1wkbA_	Alignment	not modelled	98.3	27	**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
43	c1wz2B_	Alignment	not modelled	98.3	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
44	c2j5bA_	Alignment	not modelled	98.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
45	c1obhA_	Alignment	not modelled	98.1	19	**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
46	c1qu2A_	Alignment	not modelled	98.1	28	**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
47	c2cybA_	Alignment	not modelled	98.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
48	c1ileA_	Alignment	not modelled	98.0	18	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
49	c3focB_	Alignment	not modelled	98.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
50	c2cyaA_	Alignment	not modelled	97.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
51	c3hzrD_	Alignment	not modelled	97.8	13	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
52	c3prhB_	Alignment	not modelled	97.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
53	c3p0jD_	Alignment	not modelled	97.6	17	**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
54	c2el7A_	Alignment	not modelled	97.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus

55	c1h3eA_	Alignment	not modelled	97.5	19	**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
56	c3a05A_	Alignment	not modelled	97.5	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
57	c3jxeB_	Alignment	not modelled	97.3	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
58	c3m5wB_	Alignment	not modelled	97.3	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
59	d1h3fa1	Alignment	not modelled	97.3	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
60	d1i6la_	Alignment	not modelled	97.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
61	c1jiiA_	Alignment	not modelled	97.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
62	c2yy5C_	Alignment	not modelled	97.1	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
63	c2quiB_	Alignment	not modelled	97.1	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
64	c3hv0A_	Alignment	not modelled	96.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
65	c2ip1A_	Alignment	not modelled	96.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
66	c3n9iA_	Alignment	not modelled	96.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
67	c3i05B_	Alignment	not modelled	96.8	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
68	c2janD_	Alignment	not modelled	96.7	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
69	c1yi8C_	Alignment	not modelled	96.6	23	**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
70	d1jila_	Alignment	not modelled	96.6	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
71	c3sz3A_	Alignment	not modelled	96.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
72	c2cycB_	Alignment	not modelled	96.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
73	c1x8xA_	Alignment	not modelled	96.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
74	c2dlcX_	Alignment	not modelled	96.4	16	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
75	d1n3la_	Alignment	not modelled	96.1	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
76	c1q11A_	Alignment	not modelled	96.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
77	d1r6ta2	Alignment	not modelled	94.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
78	d1j1ua_	Alignment	not modelled	94.5	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
79	c1r6uB_	Alignment	not modelled	93.6	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
80	d2ts1a_	Alignment	not modelled	92.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain

81	c2ts1A_	Alignment	not modelled	92.9	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
82	c2rkjM_	Alignment	not modelled	91.6	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
83	c2pidB_	Alignment	not modelled	84.5	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
84	c1q1qA_	Alignment	not modelled	67.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase family, cytosolic, 2b, member 1 **PDBTitle:** crystal structure of human pregnenolone sulfotransferase2 (sult2b1a) in the presence of pap
85	d1aqua_	Alignment	not modelled	66.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
86	d2a3ra1	Alignment	not modelled	65.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
87	c2gwhA_	Alignment	not modelled	59.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
88	d1ls6a_	Alignment	not modelled	59.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
89	c3u3oA_	Alignment	not modelled	58.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1a1; **PDBTitle:** crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
90	c3guzB_	Alignment	not modelled	58.5	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
91	d3bfxa1	Alignment	not modelled	56.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
92	d1xv1a_	Alignment	not modelled	52.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
93	d1e5qa2	Alignment	not modelled	52.1	23	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Homoserine dehydrogenase-like
94	c2jd3B_	Alignment	not modelled	50.9	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
95	c2ragB_	Alignment	not modelled	48.7	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
96	c2h8kA_	Alignment	not modelled	45.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
97	c2zvpX_	Alignment	not modelled	44.0	10	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
98	d1jhfa1	Alignment	not modelled	43.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
99	d1q20a_	Alignment	not modelled	41.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
100	d1fmja_	Alignment	not modelled	40.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
101	c1t6zB_	Alignment	not modelled	40.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
102	c3b40A_	Alignment	not modelled	36.8	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidase; **PDBTitle:** crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
103	d1gjja2	Alignment	not modelled	34.9	11	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
104	d1ugpb_	Alignment	not modelled	33.1	14	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
105	d1e6va2	Alignment	not modelled	32.9	45	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
						PDB header:hydrolase

106	c2i5gB_	Alignment	not modelled	29.2	14	**Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
107	d1r9oa_	Alignment	not modelled	26.2	21	**Fold:**Cytochrome P450 **Superfamily:**Cytochrome P450 **Family:**Cytochrome P450
108	c3l4hA_	Alignment	not modelled	25.9	45	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
109	c3sggA_	Alignment	not modelled	25.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
110	d2je8a2	Alignment	not modelled	25.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
111	c3ebsA_	Alignment	not modelled	25.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 2a6; **PDBTitle:** human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin
112	c3nd5D_	Alignment	not modelled	24.0	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
113	d1o94c_	Alignment	not modelled	23.7	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
114	c1zd1B_	Alignment	not modelled	23.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
115	c2oa9B_	Alignment	not modelled	22.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**r.mvai; **PDBTitle:** restriction endonuclease mvai in the absence of dna
116	c3i3aC_	Alignment	not modelled	22.4	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
117	d1vffa1	Alignment	not modelled	22.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
118	d1e6ya2	Alignment	not modelled	22.0	41	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
119	c3e27B_	Alignment	not modelled	21.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate (nicotinamide) nucleotide **PDBTitle:** nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
120	d1hbna2	Alignment	not modelled	21.5	38	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain