Phyre2

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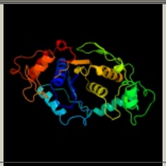
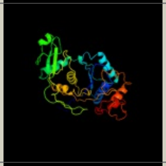
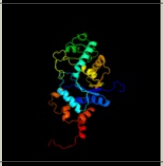
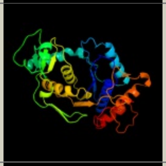
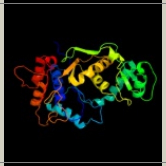
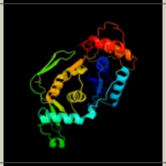
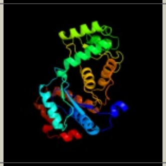
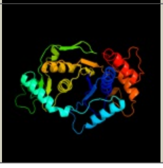
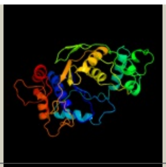
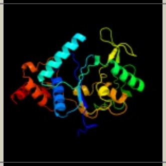
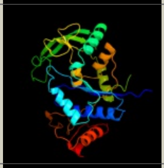
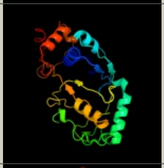
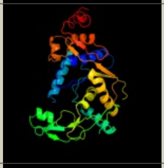
Description	P27305
Date	Thu Jan 5 11:43:51 GMT 2012
Unique Job ID	ac7e387dee9df9ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nzja_	Alignment		100.0	98	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
2	d1j09a2	Alignment		100.0	35	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
3	c3al0C_	Alignment		100.0	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.
4	c2hz7A_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
5	c1exdA_	Alignment		100.0	21	**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
6	d1gtra2	Alignment		100.0	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
7	c2cfoA_	Alignment		100.0	34	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
8	c2ja2A_	Alignment		100.0	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
9	c3afhA_	Alignment		100.0	33	**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
10	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
11	c2o5rA_	Alignment		100.0	31	**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

12	c1g59A_	Alignment		100.0	34	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
13	c1irxA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
14	d1f7ua2	Alignment		100.0	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	d1li5a2	Alignment		99.9	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
16	d2d5ba2	Alignment		99.9	19	**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	d1pfva2	Alignment		99.9	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
19	c1u0bB_	Alignment		99.9	13	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
20	d1irxa2	Alignment		99.8	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
21	c3c8zB_	Alignment	not modelled	99.8	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	c3fnrA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
23	c2x1lC_	Alignment	not modelled	99.7	18	**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	c1woyA_	Alignment	not modelled	99.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
25	c3tqoA_	Alignment	not modelled	99.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
26	c2ct8A_	Alignment	not modelled	99.6	14	**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
27	c1f7uA_	Alignment	not modelled	99.4	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
28	c1pfuA_	Alignment	not modelled	99.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli

						complexed2 with methionine phosphinate
29	c2zufA_	Alignment	not modelled	99.3	23	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
30	d1ivsa4	Alignment	not modelled	99.3	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
31	d1ilea3	Alignment	not modelled	99.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
32	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
33	c1iq0A_	Alignment	not modelled	99.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
34	c2g36A_	Alignment	not modelled	99.0	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
35	d1rqga2	Alignment	not modelled	99.0	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
36	c3hzrD_	Alignment	not modelled	98.8	10	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
37	c1rqgA_	Alignment	not modelled	98.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
38	c3kflA_	Alignment	not modelled	98.8	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
39	c2j5bA_	Alignment	not modelled	98.8	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
40	c2cybA_	Alignment	not modelled	98.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
41	c2cyaA_	Alignment	not modelled	98.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
42	c3a05A_	Alignment	not modelled	98.7	21	**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
43	c3focB_	Alignment	not modelled	98.7	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
44	d1ffya3	Alignment	not modelled	98.6	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
45	c3jxeB_	Alignment	not modelled	98.6	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
46	d1h3na3	Alignment	not modelled	98.6	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
47	c2el7A_	Alignment	not modelled	98.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
48	d1h3fa1	Alignment	not modelled	98.4	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
49	c3prhB_	Alignment	not modelled	98.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
50	c1gaxB_	Alignment	not modelled	98.3	26	**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
51	c1wkbA_	Alignment	not modelled	98.3	26	**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
52	d1i6la_	Alignment	not modelled	98.3	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
53	c3m5wB_	Alignment	not modelled	98.2	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
54	c1wz2B_	Alignment	not modelled	98.2	26	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**leucyl-trna synthetase;

54	c1wz2B_	Alignment	not modelled	98.2	20	**PDBTitle:** the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
55	c1qu2A_	Alignment	not modelled	98.2	19	**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
56	c2cycB_	Alignment	not modelled	98.1	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
57	c2quiB_	Alignment	not modelled	98.1	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
58	c3p0jD_	Alignment	not modelled	98.1	23	**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
59	c2ip1A_	Alignment	not modelled	98.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
60	c1obhA_	Alignment	not modelled	98.0	26	**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
61	c1h3eA_	Alignment	not modelled	98.0	15	**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
62	c1yi8C_	Alignment	not modelled	98.0	18	**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
63	c3i05B_	Alignment	not modelled	98.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
64	c3hv0A_	Alignment	not modelled	97.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
65	c1ileA_	Alignment	not modelled	97.9	21	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
66	c2dlcX_	Alignment	not modelled	97.9	14	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
67	d1r6ta2	Alignment	not modelled	97.9	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
68	c2yy5C_	Alignment	not modelled	97.9	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
69	c1q11A_	Alignment	not modelled	97.8	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
70	c1jiiA_	Alignment	not modelled	97.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
71	d1n3la_	Alignment	not modelled	97.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
72	d1jila_	Alignment	not modelled	97.7	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
73	c1x8xA_	Alignment	not modelled	97.5	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
74	d2ts1a_	Alignment	not modelled	97.4	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
75	c2ts1A_	Alignment	not modelled	97.4	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
76	c3n9iA_	Alignment	not modelled	97.2	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
77	c2janD_	Alignment	not modelled	97.2	23	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
78	c3sz3A_	Alignment	not modelled	97.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
79	c2rkjM_	Alignment	not modelled	97.0	21	**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
						PDB header:ligase

80	c1r6uB_	Alignment	not modelled	96.9	16	**Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
81	d1j1ua_	Alignment	not modelled	96.1	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
82	c2pidB_	Alignment	not modelled	86.1	18	**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
83	d1e5qa2	Alignment	not modelled	58.6	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Homoserine dehydrogenase-like
84	d1aqua_	Alignment	not modelled	55.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
85	c2h8kA_	Alignment	not modelled	53.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
86	c1zd1B_	Alignment	not modelled	53.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
87	d1gjja2	Alignment	not modelled	50.6	36	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
88	d1r9oa_	Alignment	not modelled	48.9	9	**Fold:**Cytochrome P450 **Superfamily:**Cytochrome P450 **Family:**Cytochrome P450
89	c3guzB_	Alignment	not modelled	46.2	28	**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
90	c1q1qA_	Alignment	not modelled	43.3	17	**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
91	c2r5wA_	Alignment	not modelled	41.8	25	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
92	d2a3ra1	Alignment	not modelled	38.5	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
93	c3ebsA_	Alignment	not modelled	36.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 2a6; **PDBTitle:** human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin
94	c1t6zB_	Alignment	not modelled	35.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
95	d3bfxa1	Alignment	not modelled	34.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
96	d1fmja_	Alignment	not modelled	34.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
97	c3u3oA_	Alignment	not modelled	32.7	19	**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
98	d1ls6a_	Alignment	not modelled	30.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
99	d1xv1a_	Alignment	not modelled	30.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
100	c2zvpX_	Alignment	not modelled	29.2	17	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
101	d1q20a_	Alignment	not modelled	28.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
102	c1vq0A_	Alignment	not modelled	27.9	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
103	c1vzyA_	Alignment	not modelled	27.2	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33
104	d1xjha_	Alignment	not modelled	23.0	38	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
						PDB header:transferase

105	c2gwhA_	Alignment	not modelled	22.5	19	**Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
106	c2x0kB_	Alignment	not modelled	22.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
107	d1xmpa_	Alignment	not modelled	21.2	13	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
108	c2hq3A_	Alignment	not modelled	20.7	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nosl protein; **PDBTitle:** solution nmr structure of the apo-nosl protein from2 achromobacter cycloclastes