Phyre^2

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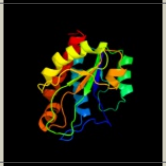
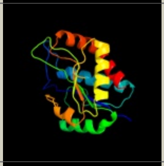
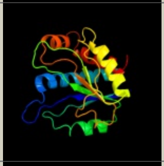
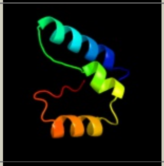
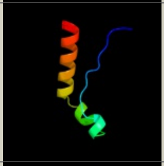
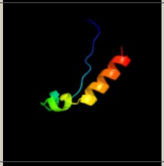
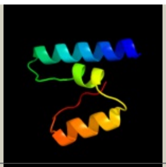
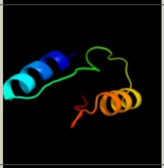
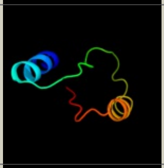
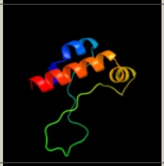
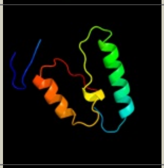
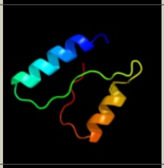
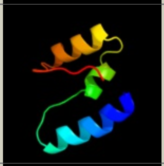
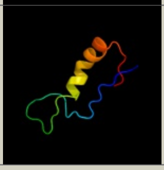
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ne8A_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
2	d1jwqa_	Alignment		100.0	37	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
3	c1xovA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ply protein; **PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
4	c3czxA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
5	d1xova2	Alignment		100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
6	c3qayC_	Alignment		100.0	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
7	c2qvpC_	Alignment		86.8	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative metallopeptidase (sama_0725) from2 shewanella amazonensis sb2b at 2.00 a resolution
8	d1nyra1	Alignment		77.7	10	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
9	c2gfqC_	Alignment		72.2	25	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
10	d1yqea1	Alignment		64.1	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
11	c2fuvB_	Alignment		62.7	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.

12	d1nj1a1	Alignment		61.3	22	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
13	c3l2nA_	Alignment		60.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m14, carboxypeptidase a; **PDBTitle:** crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
14	d1wu7a1	Alignment		59.6	20	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
15	d2g4ca1	Alignment		59.5	9	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
16	d2gfqa1	Alignment		58.9	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
17	c1nj2A_	Alignment		57.2	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
18	d1qf6a1	Alignment		56.9	8	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
19	d1qe0a1	Alignment		50.7	22	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
20	c2vefB_	Alignment		50.1	35	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
21	c3bghB_	Alignment	not modelled	49.6	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative neuraminyllactose-binding hemagglutinin homolog; **PDBTitle:** crystal structure of putative neuraminyllactose-binding hemagglutinin2 homolog from helicobacter pylori
22	d1nj8a1	Alignment	not modelled	48.3	16	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
23	c1b74A_	Alignment	not modelled	47.3	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
24	c1u83A_	Alignment	not modelled	45.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
25	d1u83a_	Alignment	not modelled	45.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
26	c1y80A_	Alignment	not modelled	44.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
27	c2jfoB_	Alignment	not modelled	43.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
28	c2dlnA_	Alignment	not modelled	43.4	26	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution

29	c3outC_	Alignment	not modelled	43.4	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
30	d1g5ha1	Alignment	not modelled	43.3	10	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
31	c2i4lC_	Alignment	not modelled	43.1	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
32	d1b74a1	Alignment	not modelled	42.7	23	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
33	c3i3wB_	Alignment	not modelled	42.1	28	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
34	d1ccwa_	Alignment	not modelled	41.8	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
35	c3na6A_	Alignment	not modelled	41.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
36	c2yxbA_	Alignment	not modelled	40.3	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
37	d3bula2	Alignment	not modelled	39.7	18	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
38	c2jfqA_	Alignment	not modelled	39.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
39	c3fs2A_	Alignment	not modelled	36.9	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
40	c3nh8A_	Alignment	not modelled	36.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartoacylase-2; **PDBTitle:** crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
41	d2naca2	Alignment	not modelled	35.7	25	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
42	d1fmfa_	Alignment	not modelled	34.9	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
43	c2jfzB_	Alignment	not modelled	34.5	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
44	c3netB_	Alignment	not modelled	34.5	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
45	c1fyfB_	Alignment	not modelled	34.0	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
46	c2gzmB_	Alignment	not modelled	33.8	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
47	c3hriF_	Alignment	not modelled	33.2	18	**PDB header:**ligase **Chain:** F: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase (apo) from trypanosoma brucei
48	c1wwpA_	Alignment	not modelled	32.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
49	c2e85B_	Alignment	not modelled	32.7	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
50	c2j3mA_	Alignment	not modelled	32.1	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
51	c2vavL_	Alignment	not modelled	31.1	13	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
52	c1atiA_	Alignment	not modelled	30.0	13	**PDB header:**protein biosynthesis **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** crystal structure of glycyl-trna synthetase from thermus thermophilus
53	c1g5hA_	Alignment	not modelled	29.0	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit; **PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
						PDB header:ligase

54	c1wu7A_	Alignment	not modelled	28.9	20	**Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
55	c3l80A_	Alignment	not modelled	28.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
56	c3k2kA_	Alignment	not modelled	28.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxypeptidase; **PDBTitle:** crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
57	c2hkoA_	Alignment	not modelled	27.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
58	c2ronA_	Alignment	not modelled	26.7	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
59	d1ad1a_	Alignment	not modelled	26.6	63	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
60	c1ggmB_	Alignment	not modelled	26.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (glycyl-trna synthetase); **PDBTitle:** glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
61	c2an1D_	Alignment	not modelled	26.2	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
62	c3hfrA_	Alignment	not modelled	26.1	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
63	c3rfqC_	Alignment	not modelled	25.4	18	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
64	c3i1iA_	Alignment	not modelled	25.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
65	c3s29C_	Alignment	not modelled	25.1	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sucrose synthase 1; **PDBTitle:** the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
66	d1kfia2	Alignment	not modelled	23.9	29	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
67	d1iowa1	Alignment	not modelled	23.3	30	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
68	c3a32A_	Alignment	not modelled	22.6	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable threonyl-trna synthetase 1; **PDBTitle:** crystal structure of putative threonyl-trna synthetase2 thrrs-1 from aeropyrum pernix
69	c2ohoA_	Alignment	not modelled	22.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
70	c3ezxA_	Alignment	not modelled	22.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
71	d1ztca1	Alignment	not modelled	21.7	25	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
72	c1nyqA_	Alignment	not modelled	21.2	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
73	c2y5sA_	Alignment	not modelled	21.1	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
74	c3ibtA_	Alignment	not modelled	20.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; **PDBTitle:** structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
75	c2dwuA_	Alignment	not modelled	19.8	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
76	c2vf7B_	Alignment	not modelled	19.8	29	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
77	c2dzaA_	Alignment	not modelled	19.5	88	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
78	d1atia1	Alignment	not modelled	18.9	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
79	c1qe0B_	Alignment	not modelled	18.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase;

						PDBTitle: crystal structure of apo s. aureus histidyl-trna synthetase
80	c1nj8C_	Alignment	not modelled	18.3	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from2 methanocaldococcus janaschii
81	c2dkdA_	Alignment	not modelled	18.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoacetylglucosamine mutase; **PDBTitle:** crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
82	c1qf6A_	Alignment	not modelled	18.3	10	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
83	c2jfnA_	Alignment	not modelled	17.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
84	d1rz3a_	Alignment	not modelled	17.6	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
85	d1mdah_	Alignment	not modelled	17.5	16	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
86	c2vp8A_	Alignment	not modelled	17.3	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
87	d2vata1	Alignment	not modelled	17.1	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
88	d1eyea_	Alignment	not modelled	17.0	75	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
89	d2grea2	Alignment	not modelled	16.8	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
90	c2i80B_	Alignment	not modelled	16.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
91	d1c4xa_	Alignment	not modelled	16.5	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
92	c1tx2A_	Alignment	not modelled	16.3	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
93	d1tx2a_	Alignment	not modelled	16.3	63	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
94	d1vixa1	Alignment	not modelled	16.3	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
95	c2i9iA_	Alignment	not modelled	16.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of helicobacter pylori protein hp0492
96	d2i9ia1	Alignment	not modelled	16.3	10	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**NLBH-like
97	c1k8wA_	Alignment	not modelled	16.2	55	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
98	c2i2xO_	Alignment	not modelled	15.9	16	**PDB header:**transferase **Chain:** O: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
99	c2pmfA_	Alignment	not modelled	15.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glycyl-trna synthetase; **PDBTitle:** the crystal structure of a human glycyl-trna synthetase mutant