Phyre^2

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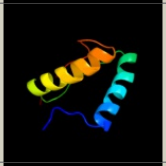
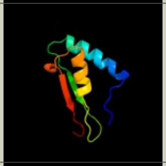
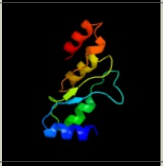
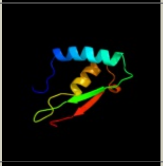
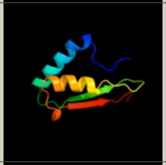
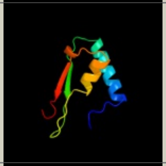
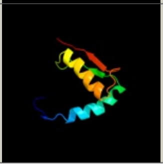
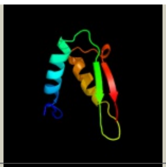
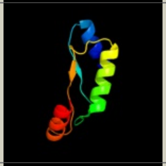
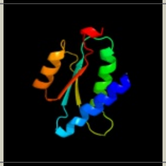
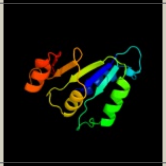
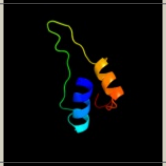
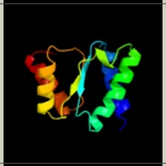
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ca8B_	Alignment		99.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
2	c2zf8A_	Alignment		94.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
3	d2aizp1	Alignment		94.2	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
4	d2hqsc1	Alignment		92.9	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
5	c3k13A_	Alignment		92.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
6	d1r1ma_	Alignment		91.9	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
7	c1r1mA_	Alignment		91.9	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
8	c2kgwA_	Alignment		91.7	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
9	c3khnB_	Alignment		88.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
10	c2k1sA_	Alignment		88.2	18	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
11	c2l26A_	Alignment		87.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains

12	c3oonA_	Alignment		86.8	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
13	c2h9aA_	Alignment		82.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
14	c2h9aB_	Alignment		81.4	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
15	d1p5dx1	Alignment		75.9	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
16	d1c7qa_	Alignment		74.2	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
17	c3td4D_	Alignment		74.0	13	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
18	c3rhgA_	Alignment		71.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
19	c2rgyA_	Alignment		67.1	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
20	d3pmga1	Alignment		66.8	16	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
21	c3m5uA_	Alignment	not modelled	65.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
22	d1ad1a_	Alignment	not modelled	63.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
23	c1zzgB_	Alignment	not modelled	62.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
24	d1f6ya_	Alignment	not modelled	60.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
25	c3e3mA_	Alignment	not modelled	57.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
26	c2q8nB_	Alignment	not modelled	57.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
27	c3c04A_	Alignment	not modelled	56.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
28	c3brqA_	Alignment	not modelled	54.9	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg

29	c3tr9A_	Alignment	not modelled	54.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
30	d2nzug1	Alignment	not modelled	54.5	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
31	c3ldtA_	Alignment	not modelled	53.7	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein; **PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
32	d2nvma1	Alignment	not modelled	52.6	14	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
33	c2r6hC_	Alignment	not modelled	51.4	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
34	d2nlva1	Alignment	not modelled	51.3	24	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
35	c3cs3A_	Alignment	not modelled	50.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
36	c2xmhB_	Alignment	not modelled	50.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
37	c2zvyB_	Alignment	not modelled	49.7	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form ii)
38	d2nwva1	Alignment	not modelled	48.9	19	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
39	d1ru8a_	Alignment	not modelled	48.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
40	c3d8uA_	Alignment	not modelled	48.5	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
41	c2vefB_	Alignment	not modelled	47.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
42	d1xpja_	Alignment	not modelled	47.6	20	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
43	c3d7qB_	Alignment	not modelled	47.5	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
44	c3mn1B_	Alignment	not modelled	47.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
45	d1vm8a_	Alignment	not modelled	47.5	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
46	d2djia3	Alignment	not modelled	45.6	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
47	c3h5oB_	Alignment	not modelled	45.2	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
48	d1vkha_	Alignment	not modelled	44.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
49	c2yqsA_	Alignment	not modelled	43.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
50	d1cqxa3	Alignment	not modelled	42.2	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
51	c3i3wB_	Alignment	not modelled	41.7	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
52	d1ir6a_	Alignment	not modelled	40.4	16	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
53	c1ir6A	Alignment	not modelled	40.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj;

53	c1ir6A_	Alignment	not modelled	40.4	16	**PDBTitle:** crystal structure of exonuclease recj bound to manganese
54	d2gzsa1	Alignment	not modelled	38.7	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**IroE-like
55	d1jv1a_	Alignment	not modelled	38.7	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
56	c3cyqM_	Alignment	not modelled	38.5	19	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
57	d1jqlb_	Alignment	not modelled	35.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
58	d1eyea_	Alignment	not modelled	35.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
59	c2vsnB_	Alignment	not modelled	35.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
60	c3muxB_	Alignment	not modelled	34.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
61	c2x5sB_	Alignment	not modelled	34.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
62	c3m6yA_	Alignment	not modelled	34.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
63	c3clkB_	Alignment	not modelled	33.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
64	d2ji7a1	Alignment	not modelled	33.0	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
65	c3qk7C_	Alignment	not modelled	32.7	14	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
66	c3mmzA_	Alignment	not modelled	32.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
67	c3q41B_	Alignment	not modelled	31.7	7	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
68	c2ecfA_	Alignment	not modelled	31.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
69	d1gvha3	Alignment	not modelled	31.1	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
70	c3ff1B_	Alignment	not modelled	31.0	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
71	d1lzla_	Alignment	not modelled	30.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
72	d1rz3a_	Alignment	not modelled	30.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
73	c3k32D_	Alignment	not modelled	30.6	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
74	c3d6kB_	Alignment	not modelled	30.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative aminotransferase; **PDBTitle:** the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
75	c1t3tA_	Alignment	not modelled	30.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
76	c3en0A_	Alignment	not modelled	30.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
77	c2yciX_	Alignment	not modelled	30.0	12	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
78	d3bofa1	Alignment	not modelled	30.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like

						Family: Methyltetrahydrofolate-utiluzing methyltransferases
79	d1nkta4	Alignment	not modelled	30.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
80	c2r8zC_	Alignment	not modelled	29.9	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
81	c3gnnA_	Alignment	not modelled	29.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
82	c3ed1E_	Alignment	not modelled	29.6	22	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
83	d1tx2a_	Alignment	not modelled	28.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
84	c1tx2A_	Alignment	not modelled	28.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
85	c3gv0A_	Alignment	not modelled	27.6	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
86	d1qopb_	Alignment	not modelled	27.6	11	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
87	c2kpoA_	Alignment	not modelled	27.3	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x2 fold protein; **PDBTitle:** solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
88	c3n07B_	Alignment	not modelled	27.1	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
89	c3ljkA_	Alignment	not modelled	27.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
90	c1x1qA_	Alignment	not modelled	26.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
91	c2vp8A_	Alignment	not modelled	26.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
92	d3bzka5	Alignment	not modelled	26.1	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
93	d1v77a_	Alignment	not modelled	26.1	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30
94	d1gzda_	Alignment	not modelled	25.7	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
95	c3dbiA_	Alignment	not modelled	25.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
96	c3azqA_	Alignment	not modelled	25.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
97	c2cunA_	Alignment	not modelled	25.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
98	c1gvhA_	Alignment	not modelled	25.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
99	c3oc9A_	Alignment	not modelled	24.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
100	c3k4hA_	Alignment	not modelled	24.8	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
101	c3hutA_	Alignment	not modelled	24.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
						PDB header:transferase

102	c3f0hA_	Alignment	not modelled	23.8	12	**Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
103	d1krha2	Alignment	not modelled	23.0	8	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
104	d1iata_	Alignment	not modelled	23.0	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
105	d1o2da_	Alignment	not modelled	22.7	13	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
106	d2g6ta1	Alignment	not modelled	22.6	26	**Fold:**CAC2185-like **Superfamily:**CAC2185-like **Family:**CAC2185-like
107	c2z9wA_	Alignment	not modelled	22.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
108	c3hbmA_	Alignment	not modelled	22.5	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
109	c3pe3D_	Alignment	not modelled	22.4	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
110	c2fzvC_	Alignment	not modelled	22.4	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
111	d1ou0a_	Alignment	not modelled	22.2	17	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
112	c3sg0A_	Alignment	not modelled	21.9	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
113	d2ioja1	Alignment	not modelled	21.7	29	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
114	d1jq5a_	Alignment	not modelled	21.7	11	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
115	c3ez1A_	Alignment	not modelled	21.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase mocr family; **PDBTitle:** crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
116	d1jr3d2	Alignment	not modelled	21.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
117	d1ybha1	Alignment	not modelled	21.1	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
118	c1y88A_	Alignment	not modelled	21.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1548; **PDBTitle:** crystal structure of protein of unknown function af1548
119	d1miob_	Alignment	not modelled	20.9	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
120	d1tvca2	Alignment	not modelled	20.6	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like