Phyre^2

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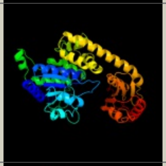
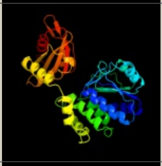
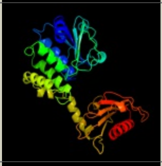
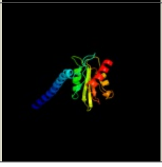
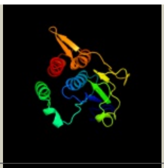
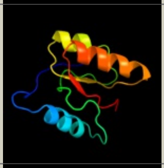
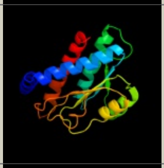
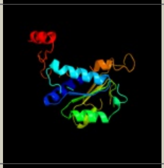
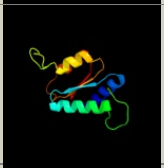
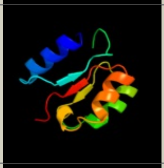
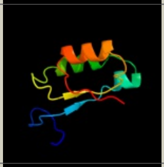
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zxrA_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj; **PDBTitle:** crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
2	d1ir6a_	Alignment		100.0	38	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
3	c1ir6A_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
4	c3dmaA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
5	c3devB_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sh1221; **PDBTitle:** crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
6	d1wpna_	Alignment		98.0	13	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
7	d1i74a_	Alignment		98.0	19	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
8	d1k20a_	Alignment		97.7	15	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
9	d2hawa1	Alignment		97.6	11	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
10	c2eb0B_	Alignment		97.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**manganese-dependent inorganic pyrophosphatase; **PDBTitle:** crystal structure of methanococcus jannaschii putative family ii2 inorganic pyrophosphatase
11	c2zvfG_	Alignment		95.8	14	**PDB header:**ligase **Chain:** G: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain

12	c2qb6A_	Alignment		94.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** saccharomyces cerevisiae cytosolic exopolyphosphatase, sulfate complex
13	d2fywa1	Alignment		91.9	19	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
14	d1x94a_	Alignment		91.7	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
15	c1nriA_	Alignment		91.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
16	d1nria_	Alignment		91.3	20	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
17	c2yvaB_	Alignment		89.8	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
18	d1nmpa_	Alignment		89.6	21	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
19	d1qo2a_	Alignment		88.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
20	d2gx8a1	Alignment		85.4	19	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
21	d1h5ya_	Alignment	not modelled	85.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
22	c3g98B_	Alignment	not modelled	85.2	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
23	c2nydB_	Alignment	not modelled	84.4	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
24	c2ihfA_	Alignment	not modelled	84.0	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
25	d2jfga1	Alignment	not modelled	83.4	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
26	c3trjC_	Alignment	not modelled	83.3	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
27	d1tk9a_	Alignment	not modelled	82.1	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
28	c1ecjB_	Alignment	not modelled	81.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer

29	c2gx8B_	Alignment	not modelled	81.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
30	c2w6rA_	Alignment	not modelled	80.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
31	c3cvjB_	Alignment	not modelled	79.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
32	d1vzwa1	Alignment	not modelled	78.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
33	c3pdiG_	Alignment	not modelled	78.4	11	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
34	c3kf6A_	Alignment	not modelled	78.1	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
35	c2iheA_	Alignment	not modelled	78.0	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
36	d1y5ia2	Alignment	not modelled	77.9	14	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
37	d1p3da1	Alignment	not modelled	77.5	21	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
38	c3q98A_	Alignment	not modelled	77.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
39	d1m3sa_	Alignment	not modelled	77.4	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
40	c3ippA_	Alignment	not modelled	76.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
41	c1zq2A_	Alignment	not modelled	76.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
42	d1x92a_	Alignment	not modelled	76.3	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
43	d1u9ya1	Alignment	not modelled	75.9	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
44	d1pvda1	Alignment	not modelled	74.4	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
45	c2p4dA_	Alignment	not modelled	74.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** structure-assisted discovery of variola major h12 phosphatase inhibitors
46	c3tdmD_	Alignment	not modelled	73.8	15	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**computationally designed two-fold symmetric tim-barrel **PDBTitle:** computationally designed tim-barrel protein, halfflr
47	d1dkua1	Alignment	not modelled	73.6	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
48	d1ovma1	Alignment	not modelled	72.6	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
49	c3fhwB_	Alignment	not modelled	72.4	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
50	c3guxA_	Alignment	not modelled	72.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
51	c3ke8A_	Alignment	not modelled	72.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
52	d1a9xb2	Alignment	not modelled	71.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
53	c1keeH_	Alignment	not modelled	71.7	15	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
54	d1pqua1	Alignment	not modelled	70.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

54	d1pqua1	Alignment	not modelled	70.9	15	**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	d1iuka_	Alignment	not modelled	70.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
56	c2decA_	Alignment	not modelled	70.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
57	d1thfd_	Alignment	not modelled	70.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
58	c3k8aA_	Alignment	not modelled	69.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
59	c2ivfA_	Alignment	not modelled	68.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
60	c3izbA_	Alignment	not modelled	68.4	19	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
61	d1vlva2	Alignment	not modelled	68.3	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
62	c3olhA_	Alignment	not modelled	67.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
63	d2ji7a1	Alignment	not modelled	67.4	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
64	c2v45A_	Alignment	not modelled	67.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
65	c2x3yA_	Alignment	not modelled	66.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
66	c3eafA_	Alignment	not modelled	66.3	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
67	c3fxaA_	Alignment	not modelled	66.0	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
68	d2jioa2	Alignment	not modelled	66.0	10	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
69	d1gm5a2	Alignment	not modelled	65.8	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
70	c3gdwA_	Alignment	not modelled	65.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
71	c2xhzC_	Alignment	not modelled	64.6	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
72	c3cwoX_	Alignment	not modelled	64.3	21	**PDB header:**de novo protein **Chain:** X: **PDB Molecule:**beta/alpha-barrel protein based on 1thf and 1tmy; **PDBTitle:** a beta/alpha-barrel built by the combination of fragments2 from different folds
73	d1u9ya2	Alignment	not modelled	64.1	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
74	d1jeoa_	Alignment	not modelled	64.0	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
75	c1z9fA_	Alignment	not modelled	63.6	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
76	d1urha2	Alignment	not modelled	63.2	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
77	c3h75A_	Alignment	not modelled	62.8	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
78	c2y85D_	Alignment	not modelled	62.8	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis

						phosphoribosyl2 isomerase with bound rcdrp
79	d1ka9f_	Alignment	not modelled	62.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
80	d1eyea_	Alignment	not modelled	62.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
81	c1dkrB_	Alignment	not modelled	62.1	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
82	c3shoA_	Alignment	not modelled	61.8	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
83	c3qy6A_	Alignment	not modelled	61.8	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe; **PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
84	d1ml4a2	Alignment	not modelled	61.4	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
85	d1o6ca_	Alignment	not modelled	61.4	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
86	c1urhA_	Alignment	not modelled	60.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
87	c2zkqb_	Alignment	not modelled	60.1	18	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
88	c1s1hB_	Alignment	not modelled	59.8	18	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
89	d1edga_	Alignment	not modelled	59.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
90	c3lpnB_	Alignment	not modelled	59.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
91	c3iz6A_	Alignment	not modelled	59.0	17	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
92	d1ozha1	Alignment	not modelled	58.7	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
93	d2ihta1	Alignment	not modelled	58.5	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
94	c1yz4A_	Alignment	not modelled	58.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
95	c1boiA_	Alignment	not modelled	57.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
96	c2yybA_	Alignment	not modelled	57.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
97	c3nuhB_	Alignment	not modelled	57.8	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
98	d2pi2a1	Alignment	not modelled	57.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
99	d1ybha1	Alignment	not modelled	57.2	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
100	c3outC_	Alignment	not modelled	57.0	12	**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.
101	d1ecfa1	Alignment	not modelled	57.0	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
102	d1c4oa2	Alignment	not modelled	56.9	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
						Fold: Chelatase-like

103	d1pq4a_	Alignment	not modelled	56.6	15	**Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
104	c2puwA_	Alignment	not modelled	56.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
105	c2xznB_	Alignment	not modelled	56.4	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
106	c3dmdA_	Alignment	not modelled	55.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
107	c2pi2A_	Alignment	not modelled	55.7	18	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
108	c3aaxB_	Alignment	not modelled	55.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
109	d1otha2	Alignment	not modelled	55.4	27	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
110	c1y5iA_	Alignment	not modelled	55.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
111	c2ph5A_	Alignment	not modelled	55.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
112	c3rlhA_	Alignment	not modelled	55.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
113	c3eyxB_	Alignment	not modelled	54.9	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
114	c2yz5B_	Alignment	not modelled	54.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol phosphatase; **PDBTitle:** histidinol phosphate phosphatase complexed with phosphate
115	d1duvg2	Alignment	not modelled	53.9	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
116	c3q41B_	Alignment	not modelled	53.7	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
117	d1m65a_	Alignment	not modelled	53.3	28	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
118	c2j17A_	Alignment	not modelled	53.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase yil113w; **PDBTitle:** ptyr bound form of sdp-1
119	c2w3nA_	Alignment	not modelled	53.1	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
120	c3pshA_	Alignment	not modelled	52.7	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)