Phyre²

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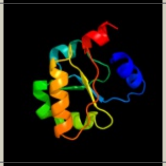
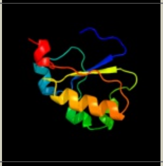
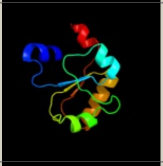
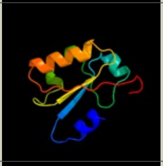
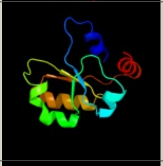
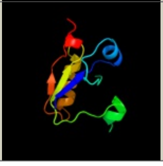
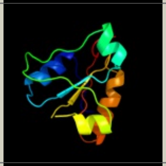
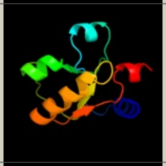
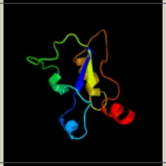
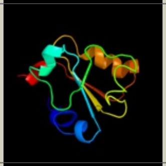
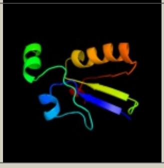
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jtqA_	Alignment		99.9	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
2	c3icrA_	Alignment		99.8	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
3	c3tp9B_	Alignment		99.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
4	c3ntaA_	Alignment		99.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
5	c3ilmD_	Alignment		99.8	26	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr3790 protein; **PDBTitle:** crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
6	d1yt8a4	Alignment		99.8	17	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
7	c1yt8A_	Alignment		99.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
8	c2k0zA_	Alignment		99.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp1203; **PDBTitle:** solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
9	d1yt8a2	Alignment		99.8	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
10	c3fojA_	Alignment		99.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
11	c3d1pA_	Alignment		99.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase yor285w; **PDBTitle:** atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae

12	d1yt8a1	Alignment		99.8	25	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
13	c2fsxA_	Alignment		99.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase; **PDBTitle:** crystal structure of rv0390 from m. tuberculosis
14	c3k9rA_	Alignment		99.7	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**alr3790 protein; **PDBTitle:** x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anabaena sp. northeast structural genomics consortium target3 nsr437c.
15	c3i2vA_	Alignment		99.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase and sulfurtransferase mocs3; **PDBTitle:** crystal structure of human mocs3 rhodanese-like domain
16	c2hhgA_	Alignment		99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa3614; **PDBTitle:** structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
17	d1uara2	Alignment		99.7	27	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
18	d1qxna_	Alignment		99.7	21	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
19	d1tq1a_	Alignment		99.7	32	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
20	c3g5jA_	Alignment		99.7	30	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
21	c3r2uC_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
22	c3emeA_	Alignment	not modelled	99.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rhodanese-like domain protein; **PDBTitle:** crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
23	c2dcqA_	Alignment	not modelled	99.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
24	d1okga2	Alignment	not modelled	99.7	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
25	c3gk5A_	Alignment	not modelled	99.7	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized rhodanese-related protein **PDBTitle:** crystal structure of rhodanese-related protein (tvg0868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
26	d1yt8a3	Alignment	not modelled	99.7	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
27	d1gmxa_	Alignment	not modelled	99.7	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
28	c3olhA_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase;

						PDBTitle: human 3-mercaptopyruvate sulfurtransferase
29	c3ippA_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
30	d1c25a_	Alignment	not modelled	99.6	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
31	d1ymka1	Alignment	not modelled	99.6	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
32	c1boiA_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
33	c3f4aA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ygr203w; **PDBTitle:** structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
34	c2uzqE_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m-phase inducer phosphatase 2; **PDBTitle:** protein phosphatase, new crystal form
35	c1e0cA_	Alignment	not modelled	99.6	18	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
36	c3nhvE_	Alignment	not modelled	99.6	20	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**bh2092 protein; **PDBTitle:** crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
37	c2j6pF_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
38	c3aaxB_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
39	c1urhA_	Alignment	not modelled	99.6	25	**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
40	c3hzuA_	Alignment	not modelled	99.6	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
41	c1uarA_	Alignment	not modelled	99.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
42	c2eg4B_	Alignment	not modelled	99.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase
43	c3op3A_	Alignment	not modelled	99.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**m-phase inducer phosphatase 3; **PDBTitle:** crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
44	d1e0ca1	Alignment	not modelled	99.5	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
45	d1t3ka_	Alignment	not modelled	99.5	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
46	c1wv9B_	Alignment	not modelled	99.5	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
47	c1okgA_	Alignment	not modelled	99.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
48	d1e0ca2	Alignment	not modelled	99.5	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
49	d1rhsa1	Alignment	not modelled	99.5	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
50	d1rhsa2	Alignment	not modelled	99.4	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
51	d1okga1	Alignment	not modelled	99.4	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
52	d1urha1	Alignment	not modelled	99.3	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
53	c2vswB_	Alignment	not modelled	99.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 16; **PDBTitle:** the structure of the rhodanese domain of the human dual2 specificity phosphatase 16

54	d1urha2	Alignment	not modelled	99.3	17	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
55	c2oucB_	Alignment	not modelled	99.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the map kinase binding domain of mkp5
56	d1uara1	Alignment	not modelled	99.2	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
57	d1hzma_	Alignment	not modelled	99.2	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
58	d1whba_	Alignment	not modelled	99.2	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
59	d2gwfa1	Alignment	not modelled	99.1	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
60	c2f46A_	Alignment	not modelled	90.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
61	c3flhC_	Alignment	not modelled	85.4	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1913; **PDBTitle:** crystal structure of lp_1913 protein from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr140b
62	d1ywfa1	Alignment	not modelled	85.3	19	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
63	c3gxgA_	Alignment	not modelled	83.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase (duf442); **PDBTitle:** crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
64	d1xria_	Alignment	not modelled	76.9	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
65	d1nkta4	Alignment	not modelled	71.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
66	d1oywa3	Alignment	not modelled	63.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
67	c3i32A_	Alignment	not modelled	59.9	10	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
68	c2jgnB_	Alignment	not modelled	59.8	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** ddx3 helicase domain
69	d1hv8a2	Alignment	not modelled	54.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
70	d1fuka_	Alignment	not modelled	52.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
71	d2g2ja1	Alignment	not modelled	50.7	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
72	d1a1va2	Alignment	not modelled	50.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
73	c2v1xB_	Alignment	not modelled	46.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
74	d7reqb2	Alignment	not modelled	41.9	21	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
75	c1oywA_	Alignment	not modelled	41.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
76	d1k92a1	Alignment	not modelled	41.1	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
77	d1ecfa1	Alignment	not modelled	40.4	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
78	d1ydha_	Alignment	not modelled	40.1	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
79	d1t5la2	Alignment	not modelled	40.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

80	d1gph11	Alignment	not modelled	40.0	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
81	d2j0sa2	Alignment	not modelled	38.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
82	c2f55C_	Alignment	not modelled	37.4	19	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
83	c2hjvB_	Alignment	not modelled	37.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase dbpa; **PDBTitle:** structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
84	c2vxoB_	Alignment	not modelled	36.6	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
85	d1tf5a4	Alignment	not modelled	36.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
86	c3rh0A_	Alignment	not modelled	35.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
87	d1t35a_	Alignment	not modelled	35.6	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
88	c3o2sB_	Alignment	not modelled	33.3	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
89	d1t5ia_	Alignment	not modelled	32.5	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
90	c2i6oA_	Alignment	not modelled	32.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
91	c3o2qB_	Alignment	not modelled	32.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
92	c2kbfA_	Alignment	not modelled	31.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of carboxyl-terminal domain of dbp5p
93	c2oz5A_	Alignment	not modelled	30.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphotyrosine protein phosphatase ptpb; **PDBTitle:** crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
94	c2omkB_	Alignment	not modelled	30.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
95	c2p6nA_	Alignment	not modelled	28.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx41; **PDBTitle:** human dead-box rna helicase ddx41, helicase domain
96	d1c4oa2	Alignment	not modelled	28.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
97	c6reqB_	Alignment	not modelled	28.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein (methylmalonyl-coa mutase); **PDBTitle:** methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
98	d1jl3a_	Alignment	not modelled	28.2	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
99	c1tvmA_	Alignment	not modelled	27.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
100	d1ru8a_	Alignment	not modelled	27.1	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
101	d1u9ya2	Alignment	not modelled	27.1	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
102	c2hmaA_	Alignment	not modelled	26.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
103	c2c4kD_	Alignment	not modelled	26.7	11	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)

104	c1k97A_	Alignment	not modelled	26.7	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
105	c1a1vA_	Alignment	not modelled	25.8	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
106	c3bxzA_	Alignment	not modelled	25.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**preprotein translocase subunit seca; **PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca
107	d1vl2a1	Alignment	not modelled	25.7	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
108	d1iiba_	Alignment	not modelled	25.1	9	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
109	d1npya1	Alignment	not modelled	24.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
110	c3d3jA_	Alignment	not modelled	23.9	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
111	d8ohma2	Alignment	not modelled	23.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
112	c2dg2D_	Alignment	not modelled	23.5	26	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
113	c3ohgA_	Alignment	not modelled	23.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein from duf2233 family; **PDBTitle:** crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
114	c2q4dB_	Alignment	not modelled	23.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
115	c1gpjA_	Alignment	not modelled	22.9	23	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
116	c3fdfA_	Alignment	not modelled	22.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
117	c2l18A_	Alignment	not modelled	22.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
118	c3nbmA_	Alignment	not modelled	21.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
119	d1gpja2	Alignment	not modelled	21.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
120	c3lm8D_	Alignment	not modelled	21.2	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine pyrophosphokinase; **PDBTitle:** crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677