Phyre2

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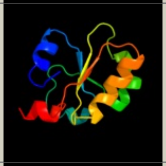
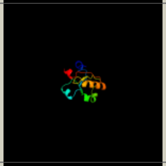
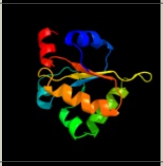
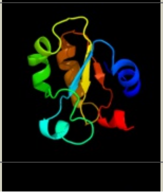
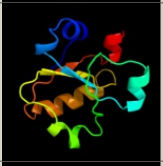
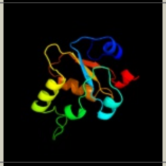
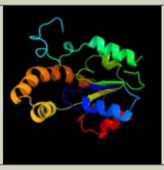
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5jA_	Alignment		100.0	32	**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
2	c3icrA_	Alignment		99.8	24	**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	30	**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	c3i2vA_	Alignment		99.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase and sulfurtransferase mocs3; **PDBTitle:** crystal structure of human mocs3 rhodanese-like domain
5	d1tq1a_	Alignment		99.8	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
6	c3ntaA_	Alignment		99.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
7	c3ilmD_	Alignment		99.8	19	**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
8	c3d1pA_	Alignment		99.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase yor285w; **PDBTitle:** atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
9	c3fojA_	Alignment		99.8	25	**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.
10	d1yt8a4	Alignment		99.8	26	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
11	c1yt8A_	Alignment		99.8	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa

12	c2hhgA_	Alignment		99.8	26	**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
13	c3gk5A_	Alignment		99.8	23	**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
14	c3k9rA_	Alignment		99.8	19	**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	c1e0cA_	Alignment		99.8	14	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
16	c3emeA_	Alignment		99.7	30	**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
17	d1c25a_	Alignment		99.7	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
18	c2j6pF_	Alignment		99.7	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
19	d1yt8a1	Alignment		99.7	32	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
20	c3f4aA_	Alignment		99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ygr203w; **PDBTitle:** structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
21	d1yt8a2	Alignment	not modelled	99.7	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
22	c3aaxB_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
23	d1gmxa_	Alignment	not modelled	99.7	21	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
24	d1qxna_	Alignment	not modelled	99.7	25	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
25	c3nhvE_	Alignment	not modelled	99.7	19	**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
26	d1yt8a3	Alignment	not modelled	99.7	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
27	d1e0ca1	Alignment	not modelled	99.7	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
28	c2fsxA_	Alignment	not modelled	99.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase; **PDBTitle:** crystal structure of rv0390 from m. tuberculosis
						PDB header:unknown function

29	c2dcqA_	Alignment	not modelled	99.7	15	**Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
30	c3hzuA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
31	c1urhA_	Alignment	not modelled	99.7	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
32	c2k0zA_	Alignment	not modelled	99.7	26	**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
33	d1ymka1	Alignment	not modelled	99.7	27	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
34	c3ippA_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
35	d1uara2	Alignment	not modelled	99.7	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
36	c1uarA_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
37	c2uzqE_	Alignment	not modelled	99.6	27	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m-phase inducer phosphatase 2; **PDBTitle:** protein phosphatase, new crystal form
38	d1t3ka_	Alignment	not modelled	99.6	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
39	c2jtqA_	Alignment	not modelled	99.6	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
40	c3olhA_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
41	c1wv9B_	Alignment	not modelled	99.6	29	**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
42	c2oucB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the map kinase binding domain of mkp5
43	d1okga2	Alignment	not modelled	99.6	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
44	c1boiA_	Alignment	not modelled	99.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
45	d1rhsa1	Alignment	not modelled	99.6	11	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
46	d1okga1	Alignment	not modelled	99.6	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
47	c2eg4B_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase
48	d1urha1	Alignment	not modelled	99.6	14	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
49	d1rhsa2	Alignment	not modelled	99.6	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
50	d1e0ca2	Alignment	not modelled	99.5	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
51	d1hzma_	Alignment	not modelled	99.5	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
52	c3op3A_	Alignment	not modelled	99.5	22	**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
53	d1uara1	Alignment	not modelled	99.5	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
54	c3r2uC_	Alignment	not modelled	99.5	15	**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

55	c2vswB_	Alignment	not modelled	99.5	15	**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
56	c1okgA_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
57	d1urha2	Alignment	not modelled	99.4	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
58	d2gwfa1	Alignment	not modelled	99.4	11	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
59	d1whba_	Alignment	not modelled	99.4	12	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
60	d1rkba_	Alignment		97.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
61	d1knqa_	Alignment		97.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Gluconate kinase
62	c3nwjB_	Alignment		97.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atsk2; **PDBTitle:** crystal structure of shikimate kinase from arabidopsis thaliana2 (atsk2)
63	d1viaa_	Alignment		97.0	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
64	c3fdiA_	Alignment		97.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
65	c2pt5D_	Alignment		97.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**shikimate kinase; **PDBTitle:** crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
66	d1jbka_	Alignment	not modelled	96.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
67	d1e6ca_	Alignment	not modelled	96.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
68	c3pvsA_	Alignment	not modelled	96.8	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
69	c2qz4A_	Alignment	not modelled	96.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
70	c2x8aA_	Alignment	not modelled	96.8	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear valosin-containing protein-like; **PDBTitle:** human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
71	d1ywfa1	Alignment	not modelled	96.7	16	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
72	d1kaga_	Alignment	not modelled	96.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
73	d2iyva1	Alignment	not modelled	96.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
74	d1khta_	Alignment	not modelled	96.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Nucleotide and nucleoside kinases
75	c2if2C_	Alignment	not modelled	96.5	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
76	d1sxje2	Alignment	not modelled	96.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	c3h0kA_	Alignment	not modelled	96.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0200 protein sso1041; **PDBTitle:** crystal structure of an adenylated kinase related protein from2 sulfolobus solfataricus to 3.25a
78	c3asyB_	Alignment		96.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine kinase; **PDBTitle:** ligand-free structure of uridine kinase from thermus thermophilus hb8
79	d1ly1a_	Alignment	not modelled	96.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
80	c1ly1A_	Alignment	not modelled	96.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** structure and mechanism of t4 polynucleotide kinase
81	c2cnwF_	Alignment	not modelled	96.4	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
82	d1y63a_	Alignment	not modelled	96.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
83	c3t61A_	Alignment	not modelled	96.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconokinase; **PDBTitle:** crystal structure of a gluconokinase from sinorhizobium meliloti 1021
84	c3gxgA_	Alignment	not modelled	96.2	13	**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
85	c3exaD_	Alignment	not modelled	96.2	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
86	c3fozB_	Alignment	not modelled	96.2	16	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
87	d1ckea_	Alignment	not modelled	96.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
88	d1fnna2	Alignment	not modelled	96.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
89	d1zp6a1	Alignment	not modelled	96.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
90	d2bdta1	Alignment	not modelled	96.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
91	d1e94e_	Alignment	not modelled	96.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
92	c1zuiA_	Alignment	not modelled	96.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
93	c2yvuA_	Alignment	not modelled	96.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
94	d1ki9a_	Alignment	not modelled	95.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
95	d1nksa_	Alignment	not modelled	95.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
96	c3flhC_	Alignment	not modelled	95.9	18	**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
97	c3trfB_	Alignment	not modelled	95.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**shikimate kinase; **PDBTitle:** structure of a shikimate kinase (arok) from coxiella burnetii
						PDB header:protein transport

98	c1xwiA_	Alignment	not modelled	95.8	15	**Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
99	c3hdtB_	Alignment	not modelled	95.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
100	d1in4a2	Alignment	not modelled	95.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
101	c2chgB_	Alignment	not modelled	95.7	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
102	c1in8A_	Alignment	not modelled	95.7	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
103	c3a8tA_	Alignment	not modelled	95.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
104	c3b9qA_	Alignment	not modelled	95.6	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
105	d1ixsb2	Alignment	not modelled	95.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
106	c3crqA_	Alignment	not modelled	95.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
107	d1njfa_	Alignment	not modelled	95.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
108	c2vliB_	Alignment	not modelled	95.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**antibiotic resistance protein; **PDBTitle:** structure of deinococcus radiodurans tunicamycin resistance2 protein
109	c3d3qB_	Alignment	not modelled	95.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
110	c3dm5A_	Alignment	not modelled	95.6	24	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
111	c3eihB_	Alignment	not modelled	95.6	20	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
112	d2ce7a2	Alignment	not modelled	95.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
113	c1hqcB_	Alignment	not modelled	95.5	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
114	c1iqpF_	Alignment	not modelled	95.5	13	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
115	d1yj5a2	Alignment	not modelled	95.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
116	c2oaq1_	Alignment	not modelled	95.4	18	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**type ii secretion system protein; **PDBTitle:** crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
117	d1g6oa_	Alignment	not modelled	95.4	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
118	c2zamA_	Alignment	not modelled	95.4	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
119	c1sxjE_	Alignment	not modelled	95.3	16	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
120	c1r6bX_	Alignment	not modelled	95.3	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa