Phyre2

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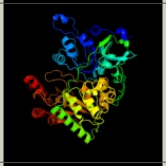
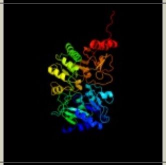
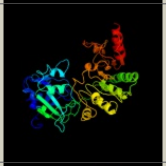
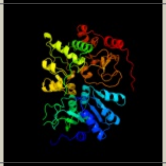
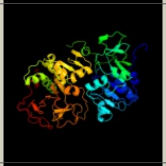
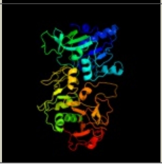
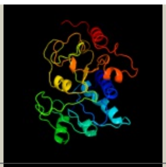
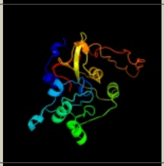
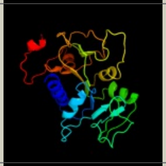
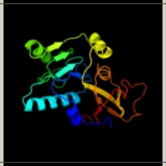
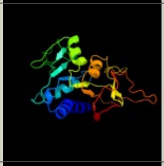
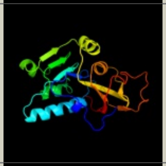
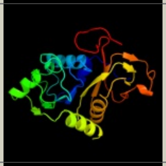
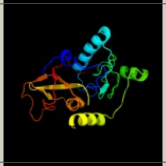
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nvvF_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
2	c2g39A_	Alignment		100.0	45	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
3	c3gk7A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
4	c2oasA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
5	c3eh7A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
6	c3d3uA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
7	d2g39a2	Alignment		100.0	50	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
8	c1xr4B_	Alignment		100.0	21	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**putative citrate lyase alpha chain/citrate-acp transferase; **PDBTitle:** x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
9	c2hj0A_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative citrate lyase, alfa subunit; **PDBTitle:** crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 (casp target).
10	c2ahvC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative enzyme ydif; **PDBTitle:** crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
11	c1ooyA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase, **PDBTitle:** succinyl-coa:3-ketoacid coa transferase from pig heart

12	d1xr4a2	Alignment		100.0	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
13	d2g39a1	Alignment		100.0	40	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
14	d1ooya1	Alignment		100.0	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
15	d1k6da_	Alignment		100.0	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
16	c3cdkD_	Alignment		100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
17	c3cdkA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
18	d2ahua2	Alignment		100.0	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
19	d1ooya2	Alignment		100.0	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
20	d1poia_	Alignment		100.0	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
21	c3rrlC_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
22	d2ahua1	Alignment	not modelled	99.9	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
23	d1poib_	Alignment	not modelled	99.9	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
24	d1xr4a1	Alignment	not modelled	99.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
25	c2f8mB_	Alignment	not modelled	97.3	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
26	c1lk5C_	Alignment	not modelled	96.9	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
27	c3hheA_	Alignment	not modelled	96.8	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
28	c3l7oB_	Alignment	not modelled	96.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159

29	d1m0sa1	Alignment	not modelled	96.7	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
30	c1uj6A_	Alignment	not modelled	96.4	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
31	c3kwmC_	Alignment	not modelled	96.1	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
32	c1m0sA_	Alignment	not modelled	96.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
33	d1lk5a1	Alignment	not modelled	95.8	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
34	c1lkzB_	Alignment	not modelled	95.5	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
35	c1xtzA_	Alignment	not modelled	95.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
36	c2pjmA_	Alignment	not modelled	95.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
37	d1uj4a1	Alignment	not modelled	91.3	10	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
38	d1k8kg_	Alignment	not modelled	55.6	17	**Fold:**alpha-alpha superhelix **Superfamily:**Arp2/3 complex 16 kDa subunit ARPC5 **Family:**Arp2/3 complex 16 kDa subunit ARPC5
39	c1avoA_	Alignment	not modelled	47.0	21	**PDB header:**proteasome activator **Chain:** A: **PDB Molecule:**11s regulator; **PDBTitle:** proteasome activator reg(alpha)
40	d1t5oa_	Alignment	not modelled	45.5	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
41	c1w2wJ_	Alignment	not modelled	43.3	31	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
42	c3ecsD_	Alignment	not modelled	36.2	12	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
43	c2w48D_	Alignment	not modelled	36.1	5	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
44	d3efba1	Alignment	not modelled	33.7	10	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
45	c3u7jA_	Alignment	not modelled	30.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
46	d1vb5a_	Alignment	not modelled	30.2	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
47	d1t9ka_	Alignment	not modelled	29.1	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
48	c3iukB_	Alignment	not modelled	28.7	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
49	c2wpnA_	Alignment	not modelled	26.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
50	d1rz3a_	Alignment	not modelled	25.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
51	c3fgxA_	Alignment	not modelled	25.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rbstp2171; **PDBTitle:** structure of uncharacterised protein rbstp2171 from bacillus2 stearothermophilus
52	c3llmB_	Alignment	not modelled	25.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
53	d1soua_	Alignment	not modelled	24.3	42	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
54	d2gnpa1	Alignment	not modelled	22.4	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like

55	c3dwlG_	Alignment	not modelled	20.1	9	**PDB header:**structural protein **Chain:** G: **PDB Molecule:**actin-related protein 2/3 complex subunit 5; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
56	c3rgwS_	Alignment	not modelled	19.9	15	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
57	d1t3ka_	Alignment	not modelled	19.8	8	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
58	d1ig8a2	Alignment	not modelled	19.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
59	c2yvkA_	Alignment	not modelled	17.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
60	d1qf8a_	Alignment	not modelled	17.3	30	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
61	d1gmxa_	Alignment	not modelled	16.3	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
62	c3myrE_	Alignment	not modelled	15.8	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
63	d1wkca_	Alignment	not modelled	14.8	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
64	d2grea1	Alignment	not modelled	14.5	41	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
65	c1dbgA_	Alignment	not modelled	11.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
66	d1yq9a1	Alignment	not modelled	11.2	30	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
67	c3gxxB_	Alignment	not modelled	11.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
68	d1frfs_	Alignment	not modelled	10.9	26	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
69	c3o0yC_	Alignment	not modelled	10.9	24	**PDB header:**lipid binding protein **Chain:** C: **PDB Molecule:**lipoprotein; **PDBTitle:** the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
70	c2jy9A_	Alignment	not modelled	9.9	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative trna hydrolase domain; **PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
71	d2p7vb1	Alignment	not modelled	9.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
72	c1h2aS_	Alignment	not modelled	9.6	21	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
73	d1wuis1	Alignment	not modelled	9.6	21	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
74	c2zkrv_	Alignment	not modelled	9.6	18	**PDB header:**ribosomal protein/rna **Chain:** V: **PDB Molecule:**rna expansion segment es9 part2; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
75	c3do6B_	Alignment	not modelled	9.5	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**formate--tetrahydrofolate ligase; **PDBTitle:** crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution
76	d1ttya_	Alignment	not modelled	9.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
77	c2jvaA_	Alignment	not modelled	9.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
78	d1tafb_	Alignment	not modelled	9.4	29	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
79	d1cc1s_	Alignment	not modelled	9.4	5	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit

80	d1v4sa2	Alignment	not modelled	9.2	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
81	c3nzeB_	Alignment	not modelled	9.2	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
82	d2coha1	Alignment	not modelled	9.2	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
83	d1g8fa3	Alignment	not modelled	9.2	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
84	c3h75A_	Alignment	not modelled	9.1	15	**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
85	d1ofla_	Alignment	not modelled	9.0	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
86	c2oaq1_	Alignment	not modelled	9.0	21	**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
87	d2f0ca1	Alignment	not modelled	9.0	27	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
88	c2i9uA_	Alignment	not modelled	8.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosine/guanine deaminase related protein; **PDBTitle:** crystal structure of guanine deaminase from c. acetobutylicum with2 bound guanine in the active site
89	c2du9A_	Alignment	not modelled	8.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
90	c2fu2A_	Alignment	not modelled	8.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein spy2152; **PDBTitle:** crystal structure of protein spy2152 from streptococcus pyogenes
91	c1zljE_	Alignment	not modelled	8.2	20	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
92	d1w53a_	Alignment	not modelled	8.1	11	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain
93	c1ydmC_	Alignment	not modelled	8.1	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein yqgn; **PDBTitle:** x-ray structure of northeast structural genomics target sr44
94	c3smaD_	Alignment	not modelled	8.0	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
95	d1vqov1	Alignment	not modelled	7.8	14	**Fold:**Long alpha-hairpin **Superfamily:**Ribosomal protein L29 (L29p) **Family:**Ribosomal protein L29 (L29p)
96	d1eg7a_	Alignment	not modelled	7.7	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
97	d1vcca_	Alignment	not modelled	7.7	33	**Fold:**DNA topoisomerase I domain **Superfamily:**DNA topoisomerase I domain **Family:**Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment
98	c3lzkC_	Alignment	not modelled	7.4	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
99	c1wv9B_	Alignment	not modelled	7.2	10	**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