Phyre^2

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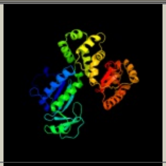
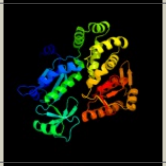
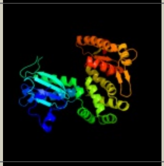
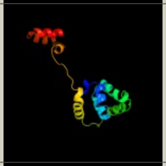
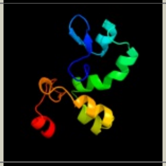
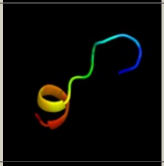
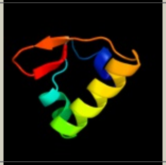
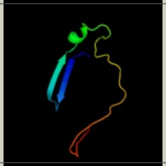
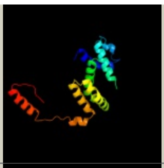
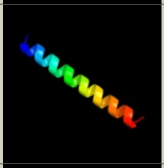
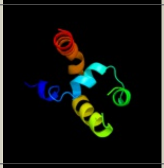
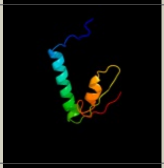
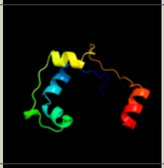
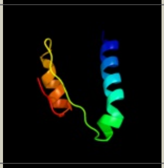
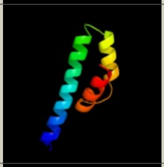
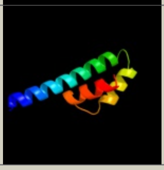
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a5iB_	Alignment		100.0	32	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha
2	c3mydA_	Alignment		100.0	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
3	c2x49A_	Alignment		100.0	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**invasion protein inva; **PDBTitle:** crystal structure of the c-terminal domain of inva
4	c3mixA_	Alignment		100.0	31	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
5	c3lw9B_	Alignment		100.0	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**invasion protein inva; **PDBTitle:** structure of a cytoplasmic domain of salmonella inva
6	c3pl4A_	Alignment		53.7	10	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein; **PDBTitle:** crystal structure of flig (residue 116-343) from h. pylori
7	d1lm5a_	Alignment		49.0	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Plakin repeat **Family:**Plakin repeat
8	c2jobA_	Alignment		41.8	38	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
9	d1wi9a_	Alignment		36.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
10	d1jhna4	Alignment		35.2	11	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Calnexin/calreticulin
11	c3t6kB_	Alignment		32.8	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator receiver; **PDBTitle:** crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution

12	c1vj7B_	Alignment		30.7	17	**PDB header:**hydrolase, transferase **Chain:** B: **PDB Molecule:**bifunctional rela/spot; **PDBTitle:** crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
13	c3mtuD_	Alignment		29.6	23	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**tropomyosin alpha-1 chain, microtubule-associated protein **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
14	d2f2ea1	Alignment		28.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
15	d1pvda1	Alignment		26.6	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
16	d2fswa1	Alignment		26.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
17	c3bhwA_	Alignment		26.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from magnetospirillum2 magneticum
18	d1zpda1	Alignment		26.1	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
19	c2peoA_	Alignment		24.4	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rbcx protein; **PDBTitle:** crystal structure of rbcx from anabaena ca
20	d2peoa1	Alignment		24.4	19	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
21	c4a5mH_	Alignment	not modelled	24.2	14	**PDB header:**transcription **Chain:** H: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yybr; **PDBTitle:** redox regulator hypr in its oxidized form
22	c3hjlA_	Alignment	not modelled	23.9	15	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** the structure of full-length flig from aquifex aeolicus
23	c2o2fA_	Alignment	not modelled	23.8	12	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
24	c2lkyA_	Alignment	not modelled	23.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
25	c2q2kA_	Alignment	not modelled	22.8	41	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
26	c3pihA_	Alignment	not modelled	22.1	14	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
27	c3rg0A_	Alignment	not modelled	21.0	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**calreticulin; **PDBTitle:** structural and functional relationships between the lectin and arm2 domains of calreticulin
28			not modelled	20.6	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis

28	c2kvcA_	Alignment	not modelled	20.6	19	protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
29	c3kmgE_	Alignment	not modelled	20.0	28	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator-1; **PDBTitle:** the x-ray crystal structure of ppar-gamma in complex with an indole2 derivative modulator, gsk538, and an src-1 peptide
30	d1orna_	Alignment	not modelled	19.9	12	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
31	c1t98B_	Alignment	not modelled	19.7	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of mukf(1-287)
32	c1zcjA_	Alignment	not modelled	19.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
33	c1t6sB_	Alignment	not modelled	19.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
34	c3pkrA_	Alignment	not modelled	19.0	10	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar motor switch protein; **PDBTitle:** crystal structure of flig (residue 86-343) from h. pylori
35	c1b35D_	Alignment	not modelled	17.2	22	**PDB header:**virus **Chain:** D: **PDB Molecule:**protein (cricket paralysis virus, vp4); **PDBTitle:** cricket paralysis virus (crpv)
36	d1qhma_	Alignment	not modelled	16.7	44	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
37	c2z99A_	Alignment	not modelled	15.3	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis
38	d2h9fa2	Alignment	not modelled	15.3	18	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PA0793-like
39	c3a11D_	Alignment	not modelled	15.0	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
40	c2hfpB_	Alignment	not modelled	14.9	38	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
41	c3cfyA_	Alignment	not modelled	14.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
42	d1ovma1	Alignment	not modelled	14.8	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
43	c2cdqB_	Alignment	not modelled	14.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
44	c3df8A_	Alignment	not modelled	14.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible hxlr family transcriptional factor; **PDBTitle:** the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
45	c1k74E_	Alignment	not modelled	14.7	38	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.3 angstrom resolution crystal structure of the2 heterodimer of the human ppargamma and rxralpha ligand3 binding domains respectively bound with gw409544 and 9-cis4 retinoic acid and co-activator peptides.
46	c1fm6E_	Alignment	not modelled	14.7	38	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
47	c1fm9E_	Alignment	not modelled	14.7	38	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and gi262570 and co-activator peptides.
48	c1fm6V_	Alignment	not modelled	14.4	38	**PDB header:**transcription **Chain:** V: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
49	d1wpga4	Alignment	not modelled	14.3	22	**Fold:**Calcium ATPase, transmembrane domain M **Superfamily:**Calcium ATPase, transmembrane domain M **Family:**Calcium ATPase, transmembrane domain M
50	c3s93B_	Alignment	not modelled	14.0	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
51	c3m65A_	Alignment	not modelled	13.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease la 1; **PDBTitle:** crystal structure of bacillus subtilis lon n-terminal domain
52	d1h16a_	Alignment	not modelled	13.6	44	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes

						Family:PFL-like
53	d1j6ra_	Alignment	not modelled	12.4	10	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Hypothetical protein TM0269
54	c1p8dC_	Alignment	not modelled	12.2	31	**PDB header:**membrane protein/protein binding **Chain:** C: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
55	d1niga_	Alignment	not modelled	12.2	18	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
56	d1a68a_	Alignment	not modelled	12.2	25	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
57	c3dnfB_	Alignment	not modelled	12.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
58	c3ol4B_	Alignment	not modelled	12.0	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
59	c2ka1A_	Alignment	not modelled	12.0	86	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
60	c2ka2B_	Alignment	not modelled	12.0	86	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
61	c2ka1B_	Alignment	not modelled	12.0	86	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
62	c2ka2A_	Alignment	not modelled	12.0	86	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
63	c2oviA_	Alignment	not modelled	11.7	13	**PDB header:**ligand binding protein, metal transport **Chain:** A: **PDB Molecule:**hypothetical protein chux; **PDBTitle:** structure of the heme binding protein chux
64	c2prgC_	Alignment	not modelled	11.5	38	**PDB header:**complex (thiazolidinedione/receptor) **Chain:** C: **PDB Molecule:**nuclear receptor coactivator src-1; **PDBTitle:** ligand-binding domain of the human peroxisome proliferator2 activated receptor gamma
65	c1cpbA_	Alignment	not modelled	11.3	24	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** A: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
66	d1wfra_	Alignment	not modelled	11.1	27	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**Sterol carrier protein, SCP
67	c1nw3A_	Alignment	not modelled	11.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase
68	d1nw3a_	Alignment	not modelled	11.1	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
69	c2q9qF_	Alignment	not modelled	11.0	12	**PDB header:**replication **Chain:** F: **PDB Molecule:**gins complex subunit 4; **PDBTitle:** the crystal structure of full length human gins complex
70	d1ugpa_	Alignment	not modelled	11.0	16	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
71	c3ke8A_	Alignment	not modelled	10.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
72	d1ckqa_	Alignment	not modelled	10.6	13	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRI
73	d1zh2a1	Alignment	not modelled	10.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	d2a9ha1	Alignment	not modelled	10.6	19	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
75	d3b60a2	Alignment	not modelled	10.4	5	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
76	d1r2za1	Alignment	not modelled	10.3	12	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins

77	d1dsxa_	Alignment	not modelled	10.0	27	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
78	c3gz6A_	Alignment	not modelled	9.9	15	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
79	d2iuba2	Alignment	not modelled	9.7	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
80	c3nvtA_	Alignment	not modelled	9.5	15	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
81	d1r3jc_	Alignment	not modelled	9.2	17	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
82	d2e9xd1	Alignment	not modelled	9.0	10	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**SLD5 N-terminal domain-like
83	c2yujA_	Alignment	not modelled	8.9	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
84	c2rmrA_	Alignment	not modelled	8.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
85	c2f3oB_	Alignment	not modelled	8.8	31	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
86	d1jm6a1	Alignment	not modelled	8.7	7	**Fold:**Bromodomain-like **Superfamily:**alpha-ketoacid dehydrogenase kinase, N-terminal domain **Family:**alpha-ketoacid dehydrogenase kinase, N-terminal domain
87	c1p8dD_	Alignment	not modelled	8.7	45	**PDB header:**membrane protein/protein binding **Chain:** D: **PDB Molecule:**nuclear receptor coactivator 1 isoform 3; **PDBTitle:** x-ray crystal structure of lxr ligand binding domain with 24(s),25-2 epoxycholesterol
88	c2bbjB_	Alignment	not modelled	8.7	20	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
89	c1j8yF_	Alignment	not modelled	8.6	10	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
90	c3d4uA_	Alignment	not modelled	8.5	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**carboxypeptidase b2; **PDBTitle:** bovine thrombin-activatable fibrinolysis inhibitor (tafia) in complex2 with tick-derived carboxypeptidase inhibitor.
91	c1mhsA_	Alignment	not modelled	8.4	17	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
92	c2ejaB_	Alignment	not modelled	8.4	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
93	d1b0na1	Alignment	not modelled	8.4	25	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
94	c2k1oA_	Alignment	not modelled	8.3	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative; **PDBTitle:** nmr structure of helicobacter pylori jhp0511 (hp0564).
95	c1zc1A_	Alignment	not modelled	8.2	13	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
96	c3k5wA_	Alignment	not modelled	8.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
97	c4ktqA_	Alignment	not modelled	8.2	15	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (large fragment of dna polymerase i); **PDBTitle:** binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
98	d1lvaa3	Alignment	not modelled	8.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
99	d1iuka_	Alignment	not modelled	7.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain