Phyre^2

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Description	P0ABA4
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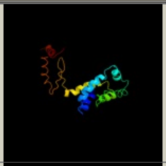
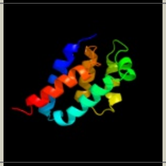
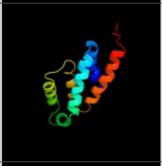
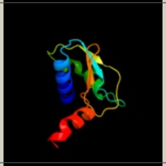
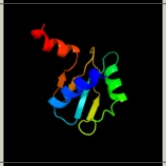
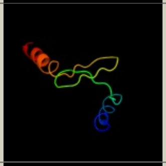
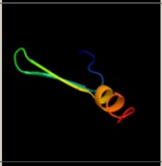
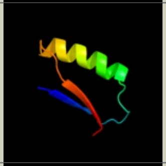
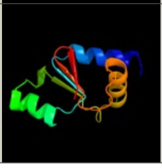
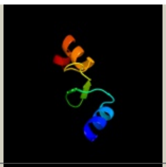
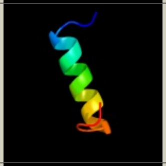
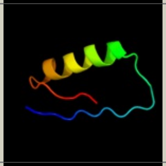
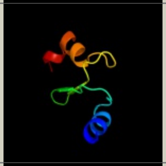
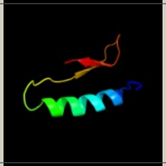
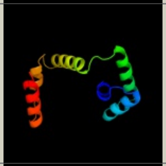
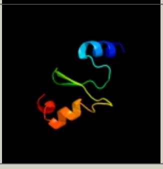
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wssS_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** S: **PDB Molecule:**atp synthase subunit o, mitochondrial; **PDBTitle:** the structure of the membrane extrinsic region of bovine2 atp synthase
2	d1abva_	Alignment		99.9	100	**Fold:**ATPD N-terminal domain-like **Superfamily:**N-terminal domain of the delta subunit of the F1F0-ATP synthase **Family:**N-terminal domain of the delta subunit of the F1F0-ATP synthase
3	c2a7uB_	Alignment		99.9	100	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase delta chain; **PDBTitle:** nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
4	c2jmxA_	Alignment		99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase o subunit, mitochondrial; **PDBTitle:** oscp-nt (1-120) in complex with n-terminal (1-25) alpha2 subunit from f1-atpase
5	c2dm9B_	Alignment		93.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of ph1978 from pyrococcus horikoshii ot3
6	d2dm9a1	Alignment		93.7	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**V-type ATPase subunit E-like **Family:**V-type ATPase subunit E
7	c3lg8B_	Alignment		85.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**a-type atp synthase subunit e; **PDBTitle:** crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
8	c3k5bE_	Alignment		78.6	25	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
9	c3ipzA_	Alignment		46.1	10	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
10	c2ayaA_	Alignment		29.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit tau; **PDBTitle:** solution structure of the c-terminal 14 kda domain of the2 tau subunit from escherichia coli dna polymerase iii
11	c2jacA_	Alignment		24.0	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast

12	c3gx8A_	Alignment		22.5	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-5, mitochondrial; **PDBTitle:** structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
13	d1sqwa2	Alignment		20.9	14	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Nip7p homolog, N-terminal domain
14	c3c1sA_	Alignment		19.9	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
15	d2uubc1	Alignment		19.5	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
16	c3d5jB_	Alignment		15.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
17	d2hc5a1	Alignment		12.9	20	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
18	c2klxA_	Alignment		12.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
19	d1okra_	Alignment		10.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
20	c3h8qB_	Alignment		9.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
21	d1ktea_	Alignment	not modelled	9.5	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
22	c2rrnA_	Alignment	not modelled	9.3	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** solution structure of secdf periplasmic domain p4
23	c2hzfA_	Alignment	not modelled	9.0	14	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
24	d1ts9a_	Alignment	not modelled	8.8	14	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
25	d1w5fa2	Alignment	not modelled	7.9	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
26	c1sqwA_	Alignment	not modelled	7.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**saccharomyces cerevisiae nip7p homolog; **PDBTitle:** crystal structure of kd93, a novel protein expressed in the2 human pro
27	c2q2gA_	Alignment	not modelled	7.1	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock 40 kda protein, putative (fragment); **PDBTitle:** crystal structure of dimerization domain of hsp40 from2 cryptosporidium parvum, cgd2_1800
28	c2ht9A_	Alignment	not modelled	6.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2;

						PDBTitle: the structure of dimeric human glutaredoxin 2
29	c3ic4A_	Alignment	not modelled	6.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
30	c2nn6E_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase/transferase **Chain:** E: **PDB Molecule:**exosome complex exonuclease rrp42; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
31	c2kwaA_	Alignment	not modelled	6.5	26	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
32	c2d4gA_	Alignment	not modelled	6.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu11850; **PDBTitle:** structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
33	c3fzaA_	Alignment	not modelled	6.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
34	c3qmxA_	Alignment	not modelled	6.1	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin a; **PDBTitle:** x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
35	d1jhba_	Alignment	not modelled	6.0	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
36	c2e7pC_	Alignment	not modelled	5.7	17	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
37	c2zdiA_	Alignment	not modelled	5.7	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**prefoldin subunit beta; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
38	d1h72c1	Alignment	not modelled	5.7	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
39	d1iqca2	Alignment	not modelled	5.5	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
40	c3pp5A_	Alignment	not modelled	5.3	31	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
41	d1l8na1	Alignment	not modelled	5.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
42	d2ff4a1	Alignment	not modelled	5.3	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
43	c2ve7C_	Alignment	not modelled	5.2	13	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**kinetochore protein nuf2, kinetochore protein spc24; **PDBTitle:** crystal structure of a bonsai version of the human ndc802 complex
44	c2vhdB_	Alignment	not modelled	5.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form