Phyre^2

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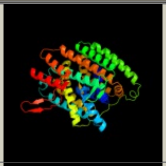
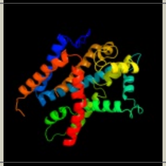
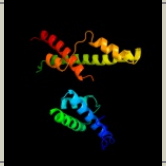
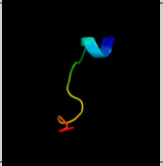
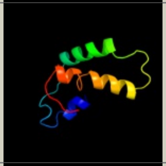
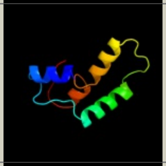
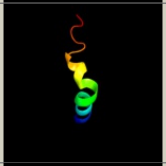
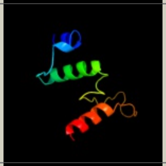
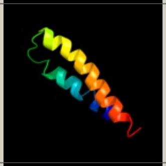
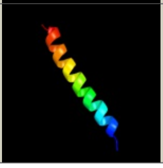
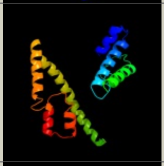
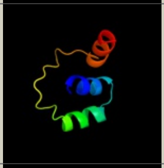
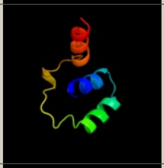
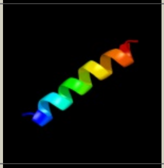
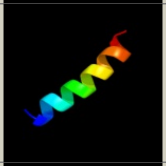
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qe7A_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uracil permease; **PDBTitle:** crystal structure of uracil transporter--uraa
2	d2a65a1	Alignment		29.6	7	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
3	c3orgB_	Alignment		23.7	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
4	c3lpzA_	Alignment		22.4	0	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
5	c1unhD_	Alignment		17.1	23	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
6	d1unld_	Alignment		16.4	23	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
7	c3nd0A_	Alignment		15.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
8	c1bzkA_	Alignment		11.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein (band 3 anion transport protein); **PDBTitle:** structural studies on the effects of the deletion in the2 red cell anion exchanger (band3, ae1) associated with3 south east asian ovalocytosis.
9	c2d4vD_	Alignment		11.1	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
10	c2bbjB_	Alignment		10.4	4	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
11	c2kpeA_	Alignment		9.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles

12	c2kpeB_	Alignment		9.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
13	c2ht2B_	Alignment		9.7	9	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
14	c2xteH_	Alignment		9.1	24	**PDB header:**transcription **Chain:** H: **PDB Molecule:**f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
15	c3fgxA_	Alignment		8.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rbstp2171; **PDBTitle:** structure of uncharacterised protein rbstp2171 from bacillus2 stearothermophilus
16	c2xtdB_	Alignment		8.5	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tbl1 f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
17	c1bttA_	Alignment		8.1	18	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
18	c1btsA_	Alignment		8.1	18	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
19	d1v53a1	Alignment		7.9	7	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
20	d1g2ua_	Alignment		7.8	7	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
21	c2e0cA_	Alignment	not modelled	7.4	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**409aa long hypothetical nadp-dependent isocitrate **PDBTitle:** crystal structure of isocitrate dehydrogenase from sulfolobus tokodaii2 strain7 at 2.0 a resolution
22	d1rutx4	Alignment	not modelled	7.3	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
23	c1x0lB_	Alignment	not modelled	7.2	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
24	c3u1hA_	Alignment	not modelled	7.2	2	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydrogenase; **PDBTitle:** crystal structure of ipmdh from the last common ancestor of bacillus
25	d1xaca_	Alignment	not modelled	7.1	7	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
26	d1cnza_	Alignment	not modelled	7.1	5	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
27	c3a0bt_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
28	d2axtt1	Alignment	not modelled	6.3	21	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein T, PsbT **Family:**PsbT-like

29	c2axtt_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center t protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
30	c3a0ht_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
31	c3a0hT_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
32	c3kziT_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
33	c2axtT_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center t protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
34	c3arcT_	Alignment	not modelled	6.3	21	**PDB header:**electron transport, photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
35	c1svfB_	Alignment	not modelled	6.3	31	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein (fusion glycoprotein); **PDBTitle:** paramyxovirus sv5 fusion protein core
36	c1s5lT_	Alignment	not modelled	6.3	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii psbt protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
37	c1s5lt_	Alignment	not modelled	6.3	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii psbt protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
38	d1mswd_	Alignment	not modelled	6.3	44	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**T7 RNA polymerase
39	c3prrT_	Alignment	not modelled	6.3	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
40	c3bz1T_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
41	c3prqT_	Alignment	not modelled	6.3	21	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
42	c3bz2T_	Alignment	not modelled	6.3	21	**PDB header:**electron transport **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
43	c2qeuA_	Alignment	not modelled	6.2	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
44	c1wazA_	Alignment	not modelled	6.2	5	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
45	d1cm7a_	Alignment	not modelled	6.2	5	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
46	c2pjvA_	Alignment	not modelled	6.0	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** solution structure of hiv-1 gp41 fusion domain bound to dpc2 micelle
47	d1vlca_	Alignment	not modelled	6.0	2	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
48	d1wpwa_	Alignment	not modelled	5.9	2	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
49	d2pnga1	Alignment	not modelled	5.9	10	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
50	c3s0xB_	Alignment	not modelled	5.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
51	c1erfA_	Alignment	not modelled	5.8	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane glycoprotein; **PDBTitle:** conformational mapping of the n-terminal fusion peptide of2 hiv-1 gp41 using 13c-enhanced fourier transform infrared3 spectroscopy (ftir)
52	d1hqsa_	Alignment	not modelled	5.7	5	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
53	c2gfpA_	Alignment	not modelled	5.7	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2,

54	c3r8wC_	Alignment	not modelled	5.6	7	chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
55	d1w0da_	Alignment	not modelled	5.6	10	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
56	c1mxeE_	Alignment	not modelled	5.5	57	**PDB header:**metal binding protein **Chain:** E: **PDB Molecule:**target sequence of rat calmodulin-dependent **PDBTitle:** structure of the complex of calmodulin with the target2 sequence of camki
57	c1mxeF_	Alignment	not modelled	5.5	57	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**target sequence of rat calmodulin-dependent **PDBTitle:** structure of the complex of calmodulin with the target2 sequence of camki
58	c3spaA_	Alignment	not modelled	5.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial rna polymerase
59	c2jd3B_	Alignment	not modelled	5.4	7	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
60	d1gr0a1	Alignment	not modelled	5.4	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	c1afoB_	Alignment	not modelled	5.4	23	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
62	d1a05a_	Alignment	not modelled	5.4	5	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
63	d2vzsa2	Alignment	not modelled	5.4	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
64	d1pb1a_	Alignment	not modelled	5.4	5	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
65	c3neyC_	Alignment	not modelled	5.3	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** crystal structure of the kinase domain of mpp1/p55
66	c2qfyE_	Alignment	not modelled	5.3	2	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**isocitrate dehydrogenase [nadp]; **PDBTitle:** crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
67	d3e46a1	Alignment	not modelled	5.3	40	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
68	d1q90r_	Alignment	not modelled	5.3	26	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
69	c1q90R_	Alignment	not modelled	5.3	26	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
70	c2kncA_	Alignment	not modelled	5.2	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
71	c2d1cB_	Alignment	not modelled	5.2	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** crystal structure of tt0538 protein from thermus thermophilus hb8
72	c2kjfA_	Alignment	not modelled	5.2	23	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**carnocyclin-a; **PDBTitle:** the solution structure of the circular bacteriocin2 carnocyclin a (ccla)
73	c2l9xA_	Alignment	not modelled	5.2	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** trn- peptide of the two-component bacteriocin thuricin cd
74	c1b9uA_	Alignment	not modelled	5.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
75	c1btrA_	Alignment	not modelled	5.2	16	**PDB header:**anion transport **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
76	c1btqA_	Alignment	not modelled	5.2	16	**PDB header:**anion transport **Chain:** A: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** the solution structures of the first and second2 transmembrane-spanning segments of band 3
77	c3p5nA_	Alignment	not modelled	5.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**riboflavin uptake protein; **PDBTitle:** structure and mechanism of the s component of a bacterial ecf2 transporter