Phyre2

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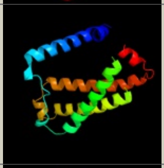
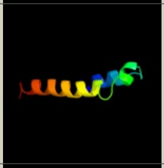
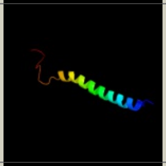
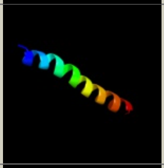
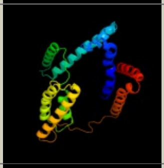
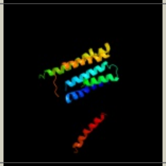
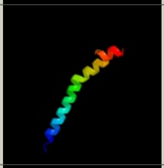
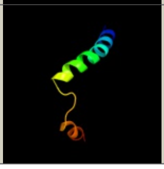
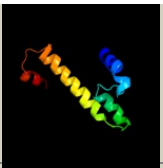
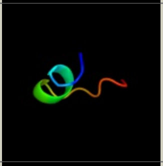
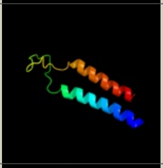
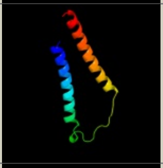
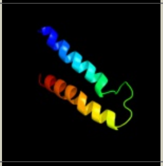
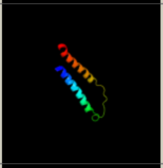
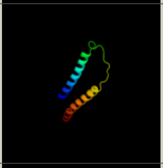
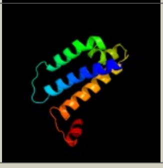
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qnqD_	Alignment		51.8	7	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
2	d1y5ic1	Alignment		30.0	11	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
3	d1fftb2	Alignment		18.7	10	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
4	c2w8aC_	Alignment		17.8	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
5	c2bbjB_	Alignment		17.4	8	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
6	c2kncA_	Alignment		14.0	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	c2rddB_	Alignment		13.4	7	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
8	c2xq2A_	Alignment		13.2	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
9	c2xutC_	Alignment		13.0	4	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
10	d2oara1	Alignment		12.6	11	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
11	c2jlnA_	Alignment		12.2	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter

12	d1j4na_	Alignment		12.1	7	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
13	d1u5ta1	Alignment		12.1	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
14	c3mk7F_	Alignment		11.8	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
15	d3ehbb2	Alignment		10.8	13	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
16	c1vryA_	Alignment		10.4	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycine receptor alpha-1 chain; **PDBTitle:** second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
17	c1m57H_	Alignment		9.9	12	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
18	d3dtub2	Alignment		9.6	11	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
19	c1ymgA_	Alignment		9.0	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
20	d1ymga1	Alignment		9.0	9	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
21	c1fftG_	Alignment	not modelled	8.9	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
22	c2kncB_	Alignment	not modelled	8.8	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
23	d1bg6a1	Alignment	not modelled	8.8	21	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
24	d1o82a_	Alignment	not modelled	8.7	22	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48
25	c1qleB_	Alignment	not modelled	8.5	13	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
26	c1ar1B_	Alignment	not modelled	8.5	13	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
27	c3cuqA_	Alignment	not modelled	8.5	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
28	c1u5tA_	Alignment	not modelled	8.3	36	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7;

						PDBTitle: structure of the escrt-ii endosomal trafficking complex
29	c2zmeA_	Alignment	not modelled	8.1	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
30	c3si5X_	Alignment	not modelled	8.1	30	**PDB header:**cell cycle **Chain:** X: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
31	c3si5Y_	Alignment	not modelled	7.9	30	**PDB header:**cell cycle **Chain:** Y: **PDB Molecule:**protein casc5; **PDBTitle:** kinetochore-bubr1 kinase complex
32	d1mmsa2	Alignment	not modelled	7.8	19	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
33	d2d6fc1	Alignment	not modelled	7.7	33	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
34	d3cjsb1	Alignment	not modelled	7.6	24	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
35	d1rc2a_	Alignment	not modelled	7.5	10	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
36	c2oarA_	Alignment	not modelled	7.4	4	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
37	c2ksfA_	Alignment	not modelled	7.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c
38	d2iuba2	Alignment	not modelled	7.2	4	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
39	d1eysh2	Alignment	not modelled	7.1	20	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
40	c3rkoM_	Alignment	not modelled	7.0	8	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
41	c3cjtP_	Alignment	not modelled	6.9	24	**PDB header:**transferase/ribosomal protein **Chain:** P: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
42	c2l2tA_	Alignment	not modelled	6.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
43	c3ke2A_	Alignment	not modelled	6.8	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
44	d2a65a1	Alignment	not modelled	6.7	9	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
45	d1tm9a_	Alignment	not modelled	6.6	14	**Fold:**Hypothetical protein MG354 **Superfamily:**Hypothetical protein MG354 **Family:**Hypothetical protein MG354
46	c1c9bI_	Alignment	not modelled	6.4	22	**PDB header:**transcription/dna **Chain:** I: **PDB Molecule:**general transcription factor iib; **PDBTitle:** crystal structure of a human tbp core domain-human tfiib2 core domain complex bound to an extended, modified3 adenoviral major late promoter (admlp)
47	c1s5rA_	Alignment	not modelled	6.3	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group box transcription factor 1; **PDBTitle:** solution structure of hbp1 sid-msin3a pah2 complex
48	d2vv5a3	Alignment	not modelled	6.2	5	**Fold:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Superfamily:**Mechanosensitive channel protein MscS (YggB), transmembrane region **Family:**Mechanosensitive channel protein MscS (YggB), transmembrane region
49	d2csba3	Alignment	not modelled	6.2	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
50	c3gdzA_	Alignment	not modelled	6.1	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
51	c3kl4B_	Alignment	not modelled	6.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**signal peptide of yeast dipeptidyl aminopeptidase b; **PDBTitle:** recognition of a signal peptide by the signal recognition particle
52	c1ponB_	Alignment	not modelled	6.0	18	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
53	c3rfrI_	Alignment	not modelled	5.9	3	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob;

		Alignment	not modelled	5.9	5	**PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
54	c2kluA_	Alignment	not modelled	5.8	9	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
55	d2h8aa1	Alignment	not modelled	5.7	14	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
56	c2k6oA_	Alignment	not modelled	5.6	27	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cathelicidin antimicrobial peptide; **PDBTitle:** human ll-37 structure
57	d2pp6a1	Alignment	not modelled	5.6	24	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
58	c1tr8A_	Alignment	not modelled	5.6	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
59	d1nera_	Alignment	not modelled	5.5	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
60	d1vola2	Alignment	not modelled	5.5	22	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
61	d2bnma1	Alignment	not modelled	5.4	41	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
62	d1rzsa_	Alignment	not modelled	5.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
63	c1s6cB_	Alignment	not modelled	5.4	0	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily d member 2; **PDBTitle:** crystal structure of the complex between kchip1 and kv4.2 n1-30
64	c1yewC_	Alignment	not modelled	5.4	10	**PDB header:**oxidoreductase, membrane protein **Chain:** C: **PDB Molecule:**particulate methane monooxygenase subunit c2; **PDBTitle:** crystal structure of particulate methane monooxygenase
65	c2dalA_	Alignment	not modelled	5.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein kiaa0794; **PDBTitle:** solution structure of the novel identified uba-like domain2 in the n-terminal of human fas associated factor 1 protein
66	d1gyxa_	Alignment	not modelled	5.3	17	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
67	c2op8A_	Alignment	not modelled	5.3	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
68	d1v92a_	Alignment	not modelled	5.2	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
69	d1khia2	Alignment	not modelled	5.2	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
70	d1xmta_	Alignment	not modelled	5.2	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
71	c3rgbA_	Alignment	not modelled	5.2	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
72	d1dwka1	Alignment	not modelled	5.2	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
73	c2vv5D_	Alignment	not modelled	5.1	8	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
74	d1qd1a2	Alignment	not modelled	5.1	17	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
75	c2jp3A_	Alignment	not modelled	5.1	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
76	c1kftA_	Alignment	not modelled	5.1	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
77	d1kfta_	Alignment	not modelled	5.1	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
78	c2g9pA_	Alignment	not modelled	5.1	25	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
						PDB header:ion channel/receptor **Chain:** C: **PDB Molecule:**acetylcholine receptor protein, delta

79	c2bg9C_	Alignment	not modelled	5.1	13	chain; **PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
80	c1bvyF_	Alignment	not modelled	5.0	10	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)