Phyre^2

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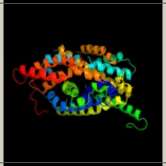
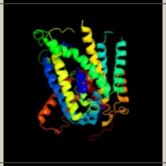
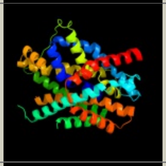
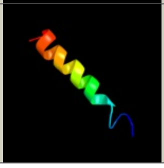
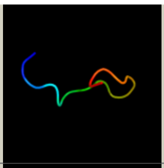
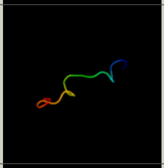
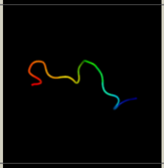
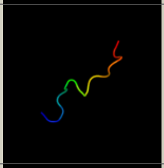
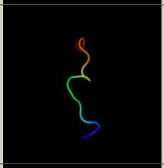
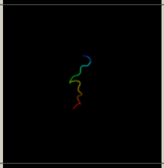
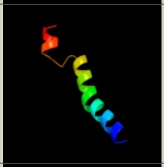
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jlnA_	Alignment		100.0	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
2	c2xq2A_	Alignment		99.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
3	c3giaA_	Alignment		99.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
4	c3dh4A_	Alignment		99.2	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
5	c3lrcC_	Alignment		98.8	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
6	c3hfxA_	Alignment		92.9	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
7	d2a65a1	Alignment		89.4	14	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
8	c3qnqD_	Alignment		70.0	14	**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
9	c2w8aC_	Alignment		53.0	16	**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
10	d2oara1	Alignment		24.2	11	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
11	c1bh0A_	Alignment		24.0	23	**PDB header:**synthetic hormone **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** structure of a glucagon analog

12	c2ke4A_	Alignment		19.8	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
13	c1nauA_	Alignment		18.8	10	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
14	c3o2tA_	Alignment		18.5	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the n-terminal domain of human symplekin
15	c3o2qD_	Alignment		17.8	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
16	c3odrA_	Alignment		17.8	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the n-terminal domain of human symplekin
17	c3odsA_	Alignment		15.3	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the k185a mutant of the n-terminal domain of2 human symplekin
18	c3gs3A_	Alignment		14.7	31	**PDB header:**transcription, protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** structure of the n-terminal heat domain of symplekin from d.2 melanogaster
19	c2oarA_	Alignment		13.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
20	d1t98a1	Alignment		11.2	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MukF N-terminal domain-like
21	c1d0rA_	Alignment	not modelled	10.7	18	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
22	c2wj8N_	Alignment	not modelled	10.7	15	**PDB header:**rna binding protein/rna **Chain:** N: **PDB Molecule:**nucleoprotein; **PDBTitle:** respiratory syncitial virus ribonucleoprotein
23	c2ntxB_	Alignment	not modelled	10.7	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
24	d1mpga2	Alignment	not modelled	10.5	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**DNA repair glycosylase, N-terminal domain
25	d1iyjb5	Alignment	not modelled	9.7	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
26	c3mtvA_	Alignment	not modelled	9.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**papain-like cysteine protease; **PDBTitle:** the crystal structure of the prrsv nonstructural protein nsp1
27	d1xrsb2	Alignment	not modelled	9.6	29	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
28	c2kmgA_	Alignment	not modelled	9.2	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro

29	c2bbjB_	Alignment	not modelled	8.9	14	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
30	d2dnta1	Alignment	not modelled	8.5	8	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo domain
31	d1ci4a_	Alignment	not modelled	7.8	14	**Fold:**SAM domain-like **Superfamily:**Barrier-to-autointegration factor, BAF **Family:**Barrier-to-autointegration factor, BAF
32	c3dvkB_	Alignment	not modelled	7.5	30	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-dependent r-type calcium channel subunit alpha-1e; **PDBTitle:** crystal structure of ca2+/cam-cav2.3 iq domain complex
33	d3cx5e2	Alignment	not modelled	7.3	18	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
34	d1miua5	Alignment	not modelled	7.3	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
35	c1jrjA_	Alignment	not modelled	7.0	14	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
36	c2czsB_	Alignment	not modelled	6.9	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c, putative; **PDBTitle:** crystal structure analysis of the diheme c-type cytochrome dhc2
37	c3c66B_	Alignment	not modelled	6.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
38	c2lf6A_	Alignment	not modelled	6.7	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab1; **PDBTitle:** solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a
39	d1lgha_	Alignment	not modelled	6.6	40	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
40	d1fcda2	Alignment	not modelled	6.5	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
41	c3siqF_	Alignment	not modelled	6.4	20	**PDB header:**ligase **Chain:** F: **PDB Molecule:**apoptosis 1 inhibitor; **PDBTitle:** crystal structure of autoinhibited diap1-bir1 domain
42	d1jj2y_	Alignment	not modelled	6.4	33	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
43	c3g36D_	Alignment	not modelled	6.3	21	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
44	d1qi9a_	Alignment	not modelled	6.2	25	**Fold:**Acid phosphatase/Vanadium-dependent haloperoxidase **Superfamily:**Acid phosphatase/Vanadium-dependent haloperoxidase **Family:**Haloperoxidase (bromoperoxidase)
45	c3ilaG_	Alignment	not modelled	6.2	29	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
46	c1yshD_	Alignment	not modelled	6.2	33	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
47	d1v4sa1	Alignment	not modelled	6.1	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
48	c4a17Y_	Alignment	not modelled	6.1	17	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
49	c2kvlA_	Alignment	not modelled	6.1	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
50	d1bcce2	Alignment	not modelled	6.1	13	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
51	c2ht2B_	Alignment	not modelled	6.0	14	**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
52	c2lf3A_	Alignment	not modelled	5.9	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab3; **PDBTitle:** solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
53	c3bxlB_	Alignment	not modelled	5.9	21	**PDB header:**membrane protein, signaling protein **Chain:** B: **PDB Molecule:**voltage-dependent r-type calcium channel subunit **PDBTitle:** crystal structure of the r-type calcium channel (cav2.3) iq2 domain and ca2+calmodulin complex

54	d1rg6a_	Alignment	not modelled	5.9	10	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
55	c1ciiA_	Alignment	not modelled	5.9	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
56	c3cc4Z_	Alignment	not modelled	5.8	50	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
57	d2q66a1	Alignment	not modelled	5.8	14	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Poly(A) polymerase, PAP, middle domain
58	c2qa4Z_	Alignment	not modelled	5.8	44	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
59	d1vqoz1	Alignment	not modelled	5.8	44	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
60	d1ppje2	Alignment	not modelled	5.8	27	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
61	d2o8pa1	Alignment	not modelled	5.7	33	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
62	d1bg3a3	Alignment	not modelled	5.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
63	d3bbda1	Alignment	not modelled	5.6	8	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
64	d1wgma_	Alignment	not modelled	5.5	7	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
65	d1bdga1	Alignment	not modelled	5.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
66	d1a7ja_	Alignment	not modelled	5.5	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
67	d1j72a1	Alignment	not modelled	5.5	25	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
68	c2v6zM_	Alignment	not modelled	5.5	7	**PDB header:**transferase **Chain:** M: **PDB Molecule:**dna polymerase epsilon subunit 2; **PDBTitle:** solution structure of amino terminal domain of human dna2 polymerase epsilon subunit b
69	d3efza1	Alignment	not modelled	5.4	33	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
70	c3efzA_	Alignment	not modelled	5.4	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**14-3-3 protein; **PDBTitle:** crystal structure of a 14-3-3 protein from cryptosporidium parvum2 (cgd1_2980)
71	c2kncA_	Alignment	not modelled	5.4	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
72	d1ffkw_	Alignment	not modelled	5.4	40	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
73	c3o7bA_	Alignment	not modelled	5.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosome biogenesis nep1 rna methyltransferase; **PDBTitle:** crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
74	c1afoB_	Alignment	not modelled	5.4	17	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
75	c2voyB_	Alignment	not modelled	5.3	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
76	c2w9jB_	Alignment	not modelled	5.2	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle subunit srp14; **PDBTitle:** the crystal structure of srp14 from the schizosaccharomyces2 pombe signal recognition particle
77	c2rowA_	Alignment	not modelled	5.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rho-associated protein kinase 2; **PDBTitle:** the c1 domain of rock ii
78	c2kb1A_	Alignment	not modelled	5.2	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
79	d1otsa_	Alignment	not modelled	5.2	14	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
						PDB header:unknown function

80	c1z65A_	Alignment	not modelled	5.1	15	**Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
81	c3jyw9_	Alignment	not modelled	5.1	38	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
82	d2iuba2	Alignment	not modelled	5.0	5	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
83	c3dvmB_	Alignment	not modelled	5.0	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-dependent p/q-type calcium channel subunit alpha- **PDBTitle:** crystal structure of ca2+/cam-cav2.1 iq domain complex
84	d2jn4a1	Alignment	not modelled	5.0	0	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU