Phyre2

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Description	P0ADQ7
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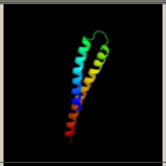
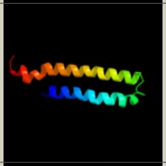
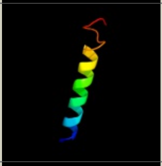
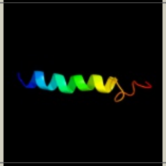
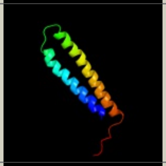
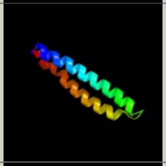
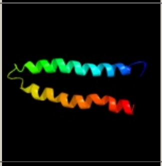
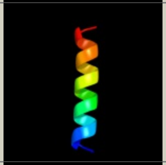
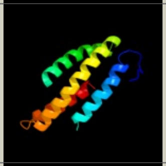
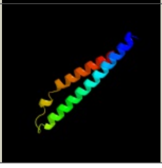
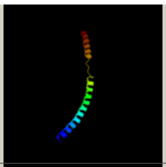
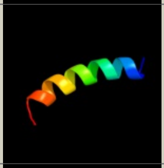
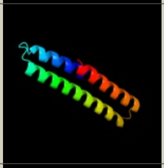
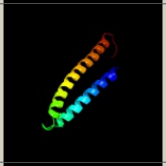
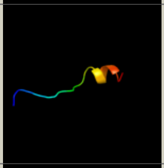
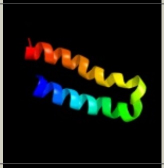
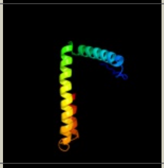
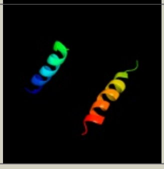
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vs0B_	Alignment		88.0	14	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
2	c3gvmA_	Alignment		85.8	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
3	d1wa8b1	Alignment		81.4	17	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
4	c3kdpG_	Alignment		69.7	38	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
5	c3kdpH_	Alignment		69.7	38	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
6	d1wa8a1	Alignment		69.6	16	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
7	c1nfoA_	Alignment		63.1	13	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein e2; **PDBTitle:** apolipoprotein e2 (apoe2, d154a mutation)
8	d1eq1a_	Alignment		49.5	9	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
9	c2jwaA_	Alignment		35.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
10	c2kbbA_	Alignment		32.0	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin rod domain, 1655-1822
11	d1gs9a_	Alignment		30.2	6	**Fold:**Four-helical up-and-down bundle **Superfamily:**Apolipoprotein **Family:**Apolipoprotein

12	c3hd7A_	Alignment		28.6	12	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
13	c2l5bA_	Alignment		26.5	33	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**activator of apoptosis harakiri; **PDBTitle:** solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
14	c3lf9A_	Alignment		23.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**4e10_d0_1is1a_001_c (t161); **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
15	d1v9da_	Alignment		22.8	11	**Fold:**Formin homology 2 domain (FH2 domain) **Superfamily:**Formin homology 2 domain (FH2 domain) **Family:**Formin homology 2 domain (FH2 domain)
16	c1iijA_	Alignment		21.6	41	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
17	c2x43S_	Alignment		21.2	10	**PDB header:**membrane protein **Chain:** S: **PDB Molecule:**sherp; **PDBTitle:** structural basis of molecular recognition by sherp at membrane2 surfaces
18	c3o3nB_	Alignment		20.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
19	c2dbiA_	Alignment		20.3	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
20	d1f16a_	Alignment		20.0	26	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
21	c1av1B_	Alignment	not modelled	19.9	16	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**apolipoprotein a-i; **PDBTitle:** crystal structure of human apolipoprotein a-i
22	c3o4xF_	Alignment	not modelled	19.5	9	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
23	c3o4xE_	Alignment	not modelled	19.5	9	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
24	c2k14A_	Alignment	not modelled	18.8	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**yuaf protein; **PDBTitle:** solution structure of the soluble domain of the nfed2 protein yuaf from bacillus subtilis
25	c3lw5K_	Alignment	not modelled	17.8	31	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak; **PDBTitle:** improved model of plant photosystem i
26	c3r2pA_	Alignment	not modelled	15.5	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein a-i; **PDBTitle:** 2.2 angstrom crystal structure of c terminal truncated human2 apolipoprotein a-i reveals the assembly of hdl by dimerization.
27	c2y44A_	Alignment	not modelled	15.3	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamic acid/alanine-rich protein; **PDBTitle:** crystal structure of garp from trypanosoma congolense
28	c2k9yB_	Alignment	not modelled	15.2	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0

29	c2z6eC_	Alignment	not modelled	14.6	11	**PDB header:**protein fibril regulator **Chain:** C: **PDB Molecule:**disheveled-associated activator of morphogenesis **PDBTitle:** crystal structure of human daam1 fh2
30	d1nekd_	Alignment	not modelled	14.4	7	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
31	c2k9yA_	Alignment	not modelled	13.8	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
32	d1i6la_	Alignment	not modelled	13.6	1	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
33	d2csga1	Alignment	not modelled	13.3	8	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
34	c3e0sA_	Alignment	not modelled	13.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 chlorobium tepidum
35	c1p58F_	Alignment	not modelled	12.4	18	**PDB header:**virus **Chain:** F: **PDB Molecule:**envelope protein m; **PDBTitle:** complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
36	c3peuB_	Alignment	not modelled	11.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoporin gle1; **PDBTitle:** s. cerevisiae dbp5 l327v c-terminal domain bound to gle1 h337r and ip6
37	d1vcsa1	Alignment	not modelled	10.7	15	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
38	c2j1dG_	Alignment	not modelled	9.9	11	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**disheveled-associated activator of morphogenesis 1; **PDBTitle:** crystallization of hdaam1 c-terminal fragment
39	c3sz3A_	Alignment	not modelled	9.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
40	d1lvfa_	Alignment	not modelled	8.6	15	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
41	c2kncB_	Alignment	not modelled	8.5	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
42	c3prhB_	Alignment	not modelled	8.3	3	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
43	d1szia_	Alignment	not modelled	8.2	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain **Family:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
44	d1ef1c_	Alignment	not modelled	7.7	18	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Moesin tail domain **Family:**Moesin tail domain
45	d1ykhb1	Alignment	not modelled	7.3	13	**Fold:**Mediator hinge subcomplex-like **Superfamily:**Mediator hinge subcomplex-like **Family:**CSE2-like
46	c2pnvA_	Alignment	not modelled	7.2	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
47	c2k1lA_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
48	c2k1lB_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
49	c2k1kA_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
50	c2k1kB_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
51	c3onjA_	Alignment	not modelled	6.9	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
52	c2f42A_	Alignment	not modelled	6.2	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stip1 homology and u-box containing protein 1; **PDBTitle:** dimerization and u-box domains of zebrafish c-terminal of hsp702 interacting protein
53	c1nohB_	Alignment	not modelled	6.2	11	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly

54	d1ryka_	Alignment	not modelled	5.6	6	**Fold:**SAM domain-like **Superfamily:**Hypothetical protein YjbJ **Family:**Hypothetical protein YjbJ
55	d1q90l_	Alignment	not modelled	5.5	40	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
56	c1q90L_	Alignment	not modelled	5.5	40	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
57	c3zrwB_	Alignment	not modelled	5.5	7	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz; **PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant
58	c3n9iA_	Alignment	not modelled	5.4	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
59	d2ooca1	Alignment	not modelled	5.3	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**SphA-like
60	c1urqA_	Alignment	not modelled	5.2	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m-tomosyn isoform; **PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
61	c2wukD_	Alignment	not modelled	5.1	6	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
62	d1slqa_	Alignment	not modelled	5.1	15	**Fold:**VP4 membrane interaction domain **Superfamily:**VP4 membrane interaction domain **Family:**VP4 membrane interaction domain
63	c2kbvA_	Alignment	not modelled	5.1	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
64	c3a0hX_	Alignment	not modelled	5.1	56	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
65	c3a0bX_	Alignment	not modelled	5.1	56	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
66	c3a0bx_	Alignment	not modelled	5.1	56	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of br-substituted photosystem ii complex