Phyre2

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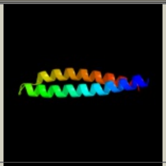
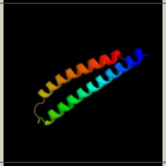
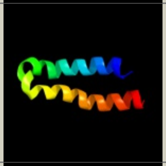
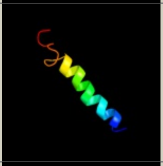
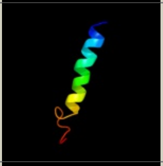
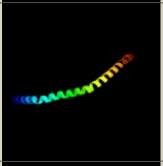
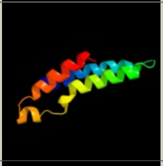
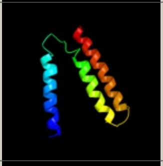
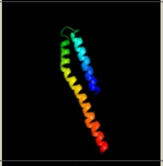
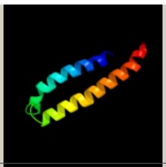
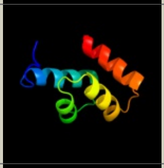
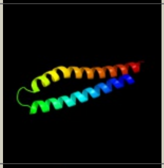
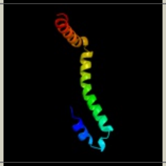
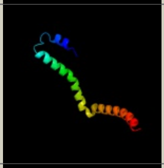
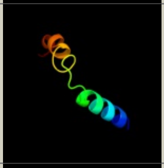
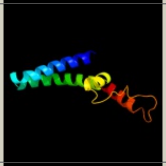
Description	P64581
Date	Thu Jan 5 12:09:38 GMT 2012
Unique Job ID	4f469329aba5c50a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nfoA_	Alignment		91.4	15	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein e2; **PDBTitle:** apolipoprotein e2 (apoe2, d154a mutation)
2	d1gs9a_	Alignment		88.3	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Apolipoprotein **Family:**Apolipoprotein
3	c2x43S_	Alignment		80.0	8	**PDB header:**membrane protein **Chain:** S: **PDB Molecule:**sherp; **PDBTitle:** structural basis of molecular recognition by sherp at membrane2 surfaces
4	c3kdpG_	Alignment		72.3	31	**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		72.3	31	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
6	c3r2pA_	Alignment		60.9	13	**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.
7	c1av1B_	Alignment		58.8	12	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**apolipoprotein a-i; **PDBTitle:** crystal structure of human apolipoprotein a-i
8	d1eq1a_	Alignment		41.8	19	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
9	c2a01B_	Alignment		39.4	21	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**apolipoprotein a-i; **PDBTitle:** crystal structure of lipid-free human apolipoprotein a-i
10	c3gvmA_	Alignment		35.3	7	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
11	c2jwaA_	Alignment		31.4	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure

12	d1wa8b1	Alignment		25.6	11	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
13	d1ryka_	Alignment		24.7	5	**Fold:**SAM domain-like **Superfamily:**Hypothetical protein YjbJ **Family:**Hypothetical protein YjbJ
14	c2vs0B_	Alignment		23.6	11	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
15	d1i6la_	Alignment		23.4	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
16	c3prhB_	Alignment		22.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
17	d2ooca1	Alignment		21.5	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**SphA-like
18	c1p58F_	Alignment		21.4	15	**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
19	c3e0sA_	Alignment		21.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 chlorobium tepidum
20	c3lw5K_	Alignment		20.1	44	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem i reaction center subunit x psak; **PDBTitle:** improved model of plant photosystem i
21	c2l5bA_	Alignment	not modelled	19.4	29	**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
22	d2gtsa1	Alignment	not modelled	17.1	16	**Fold:**Ferritin-like **Superfamily:**HP0062-like **Family:**HP0062-like
23	d1wa8a1	Alignment	not modelled	16.7	12	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
24	d1nekd_	Alignment	not modelled	16.5	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)
25	c3onjA_	Alignment	not modelled	12.0	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
26	d1vcsa1	Alignment	not modelled	11.8	11	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
27	d1s35a1	Alignment	not modelled	11.7	12	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
28	d1c99a_	Alignment	not modelled	10.0	28	**Fold:**Transmembrane helix hairpin **Superfamily:**F1F0 ATP synthase subunit C **Family:**F1F0 ATP synthase subunit C
						PDB header:cell adhesion

29	c2kncB_	Alignment	not modelled	9.7	5	**Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
30	d1eiya1	Alignment	not modelled	9.5	23	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Phenylalanyl-tRNA synthetase (PheRS)
31	d1k75a_	Alignment	not modelled	9.3	10	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
32	d1f16a_	Alignment	not modelled	8.9	21	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
33	c2g36A_	Alignment	not modelled	8.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution
34	c3py7A_	Alignment	not modelled	7.9	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
35	c1n54A_	Alignment	not modelled	7.8	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**80 kda nuclear cap binding protein; **PDBTitle:** cap binding complex m7gpppg free
36	c2kbvA_	Alignment	not modelled	7.8	30	**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
37	c2j5dA_	Alignment	not modelled	7.6	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
38	d1q2ha_	Alignment	not modelled	7.6	20	**Fold:**Dimerisation interlock **Superfamily:**Phenylalanine zipper **Family:**Adapter protein APS, dimerisation domain
39	c2v8sV_	Alignment	not modelled	7.2	15	**PDB header:**protein transport **Chain:** V: **PDB Molecule:**vesicle transport through interaction with **PDBTitle:** vti1b habc domain - epsinr enth domain complex
40	c2ww9B_	Alignment	not modelled	7.1	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
41	c1yi8C_	Alignment	not modelled	7.1	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl trrna synthetase ii from deinococcus2 radiodurans in complex with l-trp
42	c1q90L_	Alignment	not modelled	7.1	27	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
43	d1q90l_	Alignment	not modelled	7.1	27	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
44	c1ywwA_	Alignment	not modelled	6.9	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa4738; **PDBTitle:** nmr structure of p. aeruginosa protein pa4738: northeast2 structural genomics consortium target pap2
45	c1xq8A_	Alignment	not modelled	6.8	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**alpha-synuclein; **PDBTitle:** human micelle-bound alpha-synuclein
46	c3hd7A_	Alignment	not modelled	6.7	14	**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
47	c2p2uA_	Alignment	not modelled	6.6	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**host-nuclease inhibitor protein gam, putative; **PDBTitle:** crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris
48	d1l2pa_	Alignment	not modelled	6.5	13	**Fold:**Single transmembrane helix **Superfamily:**F1F0 ATP synthase subunit B, membrane domain **Family:**F1F0 ATP synthase subunit B, membrane domain
49	c3m5wB_	Alignment	not modelled	6.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
50	c3b9yA_	Alignment	not modelled	6.3	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
51	d1szia_	Alignment	not modelled	6.1	22	**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
52	d1tqga_	Alignment	not modelled	6.0	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Chemotaxis protein CheA P1 domain
53	c3kb8A_	Alignment	not modelled	5.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp

54	d2o97b1	Alignment	not modelled	5.6	16	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
55	c2ka2A_	Alignment	not modelled	5.6	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
56	c2ka1B_	Alignment	not modelled	5.6	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
57	c2ks1B_	Alignment	not modelled	5.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
58	c2k1lB_	Alignment	not modelled	5.5	31	**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
59	c2k1lA_	Alignment	not modelled	5.5	31	**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
60	c2k1kA_	Alignment	not modelled	5.5	31	**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
61	c2k1kB_	Alignment	not modelled	5.5	31	**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
62	d1dqna_	Alignment	not modelled	5.5	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
63	d1g9sa_	Alignment	not modelled	5.5	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	c2el7A_	Alignment	not modelled	5.3	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
65	c2hroA_	Alignment	not modelled	5.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
66	c2ka2B_	Alignment	not modelled	5.2	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
67	c2ka1A_	Alignment	not modelled	5.2	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles