Phyre^2

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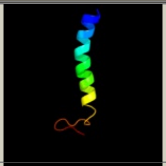
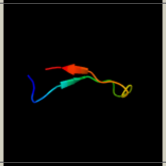
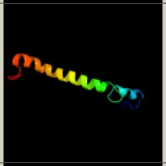
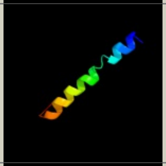
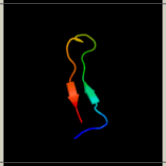
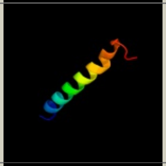
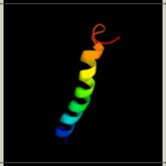
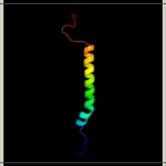
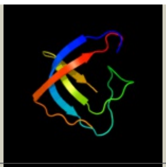
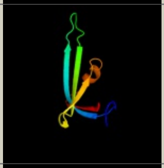
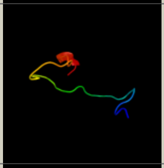
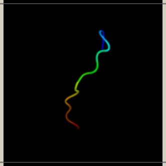
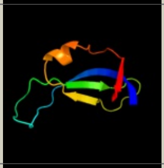
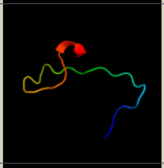
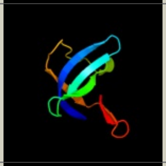
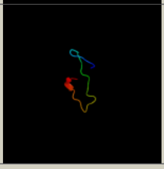
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kluA_	Alignment		87.9	20	**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
2	c3db3A_	Alignment		86.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
3	d1bcoa1	Alignment		79.3	19	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
4	c2jp3A_	Alignment		76.4	14	**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
5	c2l2tA_	Alignment		50.6	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
6	c1bcoA_	Alignment		50.2	19	**PDB header:**transposase **Chain:** A: **PDB Molecule:**bacteriophage mu transposase; **PDBTitle:** bacteriophage mu transposase core domain
7	c2jqoA_	Alignment		32.2	19	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yoba; **PDBTitle:** nmr solution structure of bacillus subtilis yoba 21-120:2 northeast structural genomics consortium target sr547
8	c1afoB_	Alignment		31.9	18	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
9	c2jo1A_	Alignment		29.2	17	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
10	c1kqfB_	Alignment		25.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
11	c2k52A_	Alignment		22.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b

12	d1v43a2	Alignment		21.8	13	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
13	c3f1zF_	Alignment		20.6	31	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**putative nucleic acid-binding lipoprotein; **PDBTitle:** crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
14	d1ugpb_	Alignment		19.5	18	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
15	c3dwqD_	Alignment		16.5	43	**PDB header:**toxin **Chain:** D: **PDB Molecule:**subtilase cytotoxin, subunit b; **PDBTitle:** crystal structure of the a-subunit of the ab5 toxin from e.2 coli with neu5gc-2,3gal-1,3glcnac
16	c2l0cA_	Alignment		16.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
17	d1y5ic1	Alignment		15.7	18	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
18	c3qz9D_	Alignment		15.6	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
19	d2ahob2	Alignment		14.8	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
20	c2dxcG_	Alignment		14.3	11	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
21	c3kdpH_	Alignment	not modelled	14.1	26	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
22	c3kdpG_	Alignment	not modelled	14.1	26	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
23	d1v29b_	Alignment	not modelled	13.5	7	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
24	c2ky9A_	Alignment	not modelled	13.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydhk; **PDBTitle:** solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
25	d2qdyb1	Alignment	not modelled	12.6	15	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
26	d1vqoq1	Alignment	not modelled	12.2	31	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
27	d2e74f1	Alignment	not modelled	11.9	20	**Fold:**Single transmembrane helix **Superfamily:**PetM subunit of the cytochrome b6f complex **Family:**PetM subunit of the cytochrome b6f complex
28	c2kpeB_	Alignment	not modelled	11.0	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles

29	c2kpeA_	Alignment	not modelled	11.0	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
30	c1s1iQ_	Alignment	not modelled	10.9	14	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
31	c3i4oA_	Alignment	not modelled	10.3	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
32	d1wjsa_	Alignment	not modelled	10.3	19	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
33	c2qtsA_	Alignment	not modelled	10.3	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acid-sensing ion channel; **PDBTitle:** structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
34	d3d31a1	Alignment	not modelled	10.3	9	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
35	c2zkrq_	Alignment	not modelled	9.3	20	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
36	d1hr0w_	Alignment	not modelled	9.2	37	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
37	c2kncA_	Alignment	not modelled	9.0	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
38	c3cm1C_	Alignment	not modelled	8.4	19	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**ssga-like sporulation-specific cell division protein; **PDBTitle:** crystal structure of ssga-like sporulation-specific cell division2 protein (yp_290167.1) from thermobifida fusca yx-er1 at 2.60 a3 resolution
39	d2k5qa1	Alignment	not modelled	8.3	9	**Fold:**OB-fold **Superfamily:**BC4932-like **Family:**BC4932-like
40	d1fvia1	Alignment	not modelled	8.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
41	d1fftb2	Alignment	not modelled	7.6	11	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
42	c2ahoB_	Alignment	not modelled	7.6	11	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** structure of the archaeal initiation factor eif2 alpha-2 gamma heterodimer from sulfolobus solfataricus complexed3 with gdpnp
43	c2k1aA_	Alignment	not modelled	7.6	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
44	d1h9ra2	Alignment	not modelled	7.5	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
45	c2jwaA_	Alignment	not modelled	7.5	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
46	c3j0cH_	Alignment	not modelled	7.5	11	**PDB header:**virus **Chain:** H: **PDB Molecule:**e2 envelope glycoprotein; **PDBTitle:** models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
47	d1qcsa1	Alignment	not modelled	7.3	32	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
48	d1f20a1	Alignment	not modelled	7.1	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
49	c2zxeG_	Alignment	not modelled	6.7	17	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
50	c2e6zA_	Alignment	not modelled	6.7	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
51	c2xzn2_	Alignment	not modelled	6.5	27	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**40s ribosomal protein s8; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
52	d1y14b1	Alignment	not modelled	6.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

53	c2zklA_	Alignment	not modelled	6.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
54	d1h9ma2	Alignment	not modelled	6.3	6	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
55	c2ks1B_	Alignment	not modelled	6.2	11	**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
56	d1h6la_	Alignment	not modelled	6.2	18	**Fold:**6-bladed beta-propeller **Superfamily:**Thermostable phytase (3-phytase) **Family:**Thermostable phytase (3-phytase)
57	c3u5cl_	Alignment	not modelled	6.0	36	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**40s ribosomal protein s8-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
58	c4a1aP_	Alignment	not modelled	6.0	14	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **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 3.
59	c3iz5U_	Alignment	not modelled	6.0	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
60	c1vf5G_	Alignment	not modelled	5.8	21	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**protein pet g; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
61	d1vf5g_	Alignment	not modelled	5.8	21	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
62	c1ddiA_	Alignment	not modelled	5.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha- **PDBTitle:** crystal structure of sir-fp60
63	c2k21A_	Alignment	not modelled	5.6	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
64	d3bn0a1	Alignment	not modelled	5.5	15	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
65	c2kcyA_	Alignment	not modelled	5.5	25	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s8e; **PDBTitle:** solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nesg) target tr71d
66	c2kcoA_	Alignment	not modelled	5.5	18	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s8e; **PDBTitle:** solution nmr structure of ribosomal protein sso0164 from2 sulfolobus solfataricus. northeast structural genomics3 consortium (nesg) target sst4.
67	c1fftG_	Alignment	not modelled	5.4	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
68	c3izcU_	Alignment	not modelled	5.3	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
69	d1q46a2	Alignment	not modelled	5.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
70	d1oi1a2	Alignment	not modelled	5.3	12	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
71	d1g2914	Alignment	not modelled	5.2	16	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
72	c2khjA_	Alignment	not modelled	5.2	21	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
73	d2e74g1	Alignment	not modelled	5.2	19	**Fold:**Single transmembrane helix **Superfamily:**PetG subunit of the cytochrome b6f complex **Family:**PetG subunit of the cytochrome b6f complex
74	c2khiA_	Alignment	not modelled	5.1	29	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1