Phyre^2

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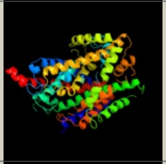
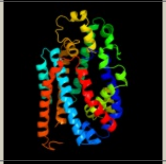
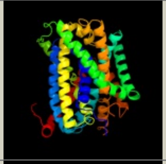
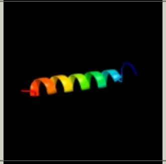
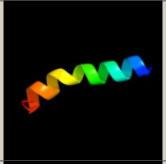
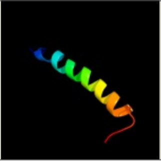
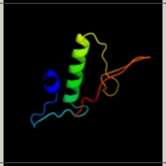
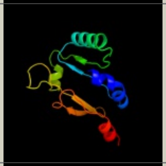
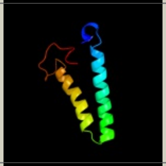
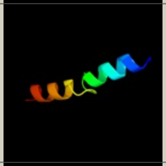
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hfxA_	Alignment		100.0	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
2	c2w8aC_	Alignment		100.0	34	**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
3	c2xq2A_	Alignment		98.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
4	c3dh4A_	Alignment		97.9	13	**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	d2a65a1	Alignment		97.7	12	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
6	c2jlnA_	Alignment		97.5	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
7	c3giaA_	Alignment		96.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
8	c3lrcC_	Alignment		94.1	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
9	c1u7mB_	Alignment		50.3	25	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**four-helix bundle model; **PDBTitle:** solution structure of a diiron protein model: due ferri(ii)2 turn mutant
10	d1ylxa1	Alignment		36.8	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
11	c2hz8A_	Alignment		36.3	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed diiron protein; **PDBTitle:** qm/mm structure refined from nmr-structure of a single2 chain diiron protein

12	c1lt1G_	Alignment		32.4	33	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**l13g-df1; **PDBTitle:** sliding helix induced change of coordination geometry in a2 model di-mn(ii) protein
13	d1z2la1	Alignment		25.1	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
14	d2cv4a1	Alignment		25.0	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
15	c3gztF_	Alignment		22.4	30	**PDB header:**virus **Chain:** F: **PDB Molecule:**outer capsid glycoprotein vp7; **PDBTitle:** vp7 recoated rotavirus dlp
16	c3s0xB_	Alignment		22.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase a24b, flak domain protein; **PDBTitle:** the crystal structure of gxgd membrane protease flak
17	c2kvlA_	Alignment		20.6	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major outer capsid protein vp7; **PDBTitle:** nmr structure of the c-terminal domain of vp7
18	d2axtm1	Alignment		19.8	31	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein M, PsbM **Family:**PsbM-like
19	d1j5ya2	Alignment		19.0	12	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
20	d2guka1	Alignment		17.6	45	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
21	c3g40A_	Alignment	not modelled	16.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**na-k-cl cotransporter; **PDBTitle:** crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
22	d1kf6d_	Alignment	not modelled	15.6	18	**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)
23	c1x59A_	Alignment	not modelled	15.2	60	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** solution structures of the whep-trs domain of human2 histidyl-trna synthetase
24	c3l09B_	Alignment	not modelled	14.8	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
25	c1bmlD_	Alignment	not modelled	14.8	16	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**streptokinase; **PDBTitle:** complex of the catalytic domain of human plasmin and streptokinase
26	d1c4pc_	Alignment	not modelled	13.7	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
27	c2qksA_	Alignment	not modelled	13.5	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
28	c3g36D_	Alignment	not modelled	13.4	13	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal

						domain
29	c3u4gA_	Alignment	not modelled	13.3	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
30	d1a7ja_	Alignment	not modelled	13.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
31	d2f2ha1	Alignment	not modelled	12.8	25	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
32	d2p6va1	Alignment	not modelled	12.7	24	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
33	d2vo9a1	Alignment	not modelled	11.7	12	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanY-like
34	c2z9oB_	Alignment	not modelled	10.6	6	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**replication initiation protein; **PDBTitle:** crystal structure of the dimeric form of repe in complex with the repe2 operator dna
35	c1z0zC_	Alignment	not modelled	10.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
36	d1s0yb_	Alignment	not modelled	10.0	36	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
37	d2g3qa1	Alignment	not modelled	9.7	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
38	c3ej9D_	Alignment	not modelled	9.7	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-subunit of trans-3-chloroacrylic acid dehalogenase; **PDBTitle:** structural and mechanistic analysis of trans-3-chloroacrylic acid2 dehalogenase activity
39	c2ksnA_	Alignment	not modelled	9.5	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
40	c3eofB_	Alignment	not modelled	9.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
41	d1z0sa1	Alignment	not modelled	9.0	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
42	c3kl9F_	Alignment	not modelled	8.9	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
43	c2dn9A_	Alignment	not modelled	8.9	9	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
44	c3zqsB_	Alignment	not modelled	8.9	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase fancl; **PDBTitle:** human fancl central domain
45	c3by7E_	Alignment	not modelled	8.8	50	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein structurally similar to sm/lsm-like2 rna-binding proteins (jcvi_pep_1096686650277) from uncultured marine3 organism at 2.60 a resolution
46	d1gxma_	Alignment	not modelled	8.7	28	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
47	d1f9fa_	Alignment	not modelled	8.6	16	**Fold:**Ferredoxin-like **Superfamily:**Viral DNA-binding domain **Family:**Viral DNA-binding domain
48	c2la3A_	Alignment	not modelled	8.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
49	d1repc2	Alignment	not modelled	8.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
50	c3lklB_	Alignment	not modelled	8.2	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
51	c2vo9C_	Alignment	not modelled	8.1	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase; **PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
52	c1pk1B_	Alignment	not modelled	8.1	10	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
53	d2a7sa1	Alignment	not modelled	8.1	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
54	d3b45a1	Alignment	not modelled	8.0	20	**Fold:**Rhomboid-like **Superfamily:**Rhomboid-like

						Family: Rhomboid-like
55	c2jnvA_	Alignment	not modelled	7.9	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
56	c3rzaA_	Alignment	not modelled	7.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
57	d1y0ua_	Alignment	not modelled	7.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
58	d1o5wa2	Alignment	not modelled	7.8	9	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
59	c2l69A_	Alignment	not modelled	7.8	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
60	c3jycA_	Alignment	not modelled	7.7	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**inward-rectifier k+ channel kir2.2; **PDBTitle:** crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
61	d1r76a_	Alignment	not modelled	7.7	18	**Fold:**alpha/alpha toroid **Superfamily:**Family 10 polysaccharide lyase **Family:**Family 10 polysaccharide lyase
62	d1vrga1	Alignment	not modelled	7.7	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
63	c3ps5A_	Alignment	not modelled	7.7	10	**PDB header:**hydrolase, signaling protein **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 6; **PDBTitle:** crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
64	d1z3xa1	Alignment	not modelled	7.6	20	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
65	c3gycB_	Alignment	not modelled	7.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
66	c3c4rC_	Alignment	not modelled	7.4	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein encoded by2 cryptic prophage
67	d1qqra_	Alignment	not modelled	7.4	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
68	d2j8cl1	Alignment	not modelled	7.3	14	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
69	c2k10A_	Alignment	not modelled	7.3	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**ranatuerin-2csa; **PDBTitle:** confirmational analysis of the broad-spectrum antibacterial2 peptide, rantuerin-2csa: identification of a full length3 helix-turn-helix motif
70	c3kv1A_	Alignment	not modelled	7.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
71	d1pixa2	Alignment	not modelled	7.2	11	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
72	d1egwa_	Alignment	not modelled	7.1	10	**Fold:**SRF-like **Superfamily:**SRF-like **Family:**SRF-like
73	c2bj3D_	Alignment	not modelled	7.1	20	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
74	c3au5B_	Alignment	not modelled	7.0	18	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**myosin-x; **PDBTitle:** structure of the human myosin-x myth4-ferm cassette
75	d1nj1a1	Alignment	not modelled	7.0	12	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
76	d1rh5a_	Alignment	not modelled	7.0	13	**Fold:**Preprotein translocase SecY subunit **Superfamily:**Preprotein translocase SecY subunit **Family:**Preprotein translocase SecY subunit
77	c1v85A_	Alignment	not modelled	7.0	10	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
78	d1pk3a1	Alignment	not modelled	7.0	10	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
79	d1udxa3	Alignment	not modelled	7.0	17	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
						Fold: Ribbon-helix-helix

80	d2hzaa1	Alignment	not modelled	7.0	27	**Superfamily:**Ribbon-helix-helix **Family:**CopG-like
81	c3kpaB_	Alignment	not modelled	7.0	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**probable ubiquitin fold modifier conjugating enzyme; **PDBTitle:** ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
82	d2p41a1	Alignment	not modelled	6.9	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
83	c2o9xA_	Alignment	not modelled	6.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**reductase, assembly protein; **PDBTitle:** crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
84	c1q5vB_	Alignment	not modelled	6.9	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
85	c1usdA_	Alignment	not modelled	6.8	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
86	c3bm2B_	Alignment	not modelled	6.8	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein ydja; **PDBTitle:** crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
87	c3eyyA_	Alignment	not modelled	6.8	16	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
88	c3k7cC_	Alignment	not modelled	6.8	10	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase; **PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
89	c3qyfA_	Alignment	not modelled	6.8	15	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of the crispr-associated protein sso1393 from2 sulfolobus solfataricus
90	c3komB_	Alignment	not modelled	6.8	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of apo transketolase from francisella tularensis
91	d1ej5a_	Alignment	not modelled	6.7	25	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
92	c3o5cA_	Alignment	not modelled	6.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
93	d1y5ic1	Alignment	not modelled	6.7	9	**Fold:**Heme-binding four-helical bundle **Superfamily:**Respiratory nitrate reductase 1 gamma chain **Family:**Respiratory nitrate reductase 1 gamma chain
94	d2otaa1	Alignment	not modelled	6.7	36	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
95	c3lloA_	Alignment	not modelled	6.7	22	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**prestin; **PDBTitle:** crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
96	c3ng0A_	Alignment	not modelled	6.7	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
97	d2hzab1	Alignment	not modelled	6.6	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
98	d1ji5a_	Alignment	not modelled	6.6	17	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
99	c2ca9B_	Alignment	not modelled	6.6	20	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation