Phyre^2

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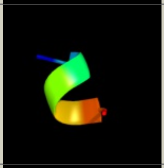
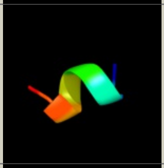
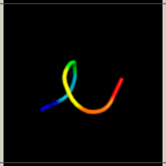
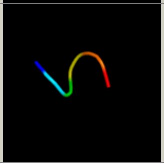
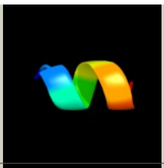
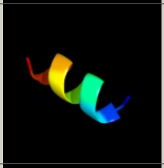
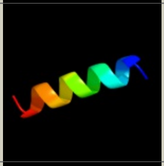
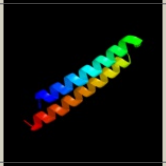
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fqjC_	Alignment		30.4	30	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**retinal rod rhodopsin-sensitive cgmp 3',5'- **PDBTitle:** crystal structure of the heterotrimeric complex of the rgs2 domain of rgs9, the gamma subunit of phosphodiesterase and3 the gt/i1 chimera alpha subunit [(rgs9)-(pdegamma)-4 (gt/i1alpha)-(gdp)-(alf4-)-(mg2+)]
2	c1u3fA_	Alignment		25.4	57	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydrofolate synthetase; **PDBTitle:** structural and functional characterization of a 5,10-2 methenyltetrahydrofolate synthetase from mycoplasma3 pneumoniae (gi: 13508087)
3	d1sbqa_	Alignment		25.4	57	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
4	c2jziB_	Alignment		23.6	75	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase 2b **PDBTitle:** structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
5	c2jcbA_	Alignment		20.0	57	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase family protein; **PDBTitle:** the crystal structure of 5-formyl-tetrahydrofolate2 cycloligase from bacillus anthracis (ba4489)
6	c3hy4A_	Alignment		19.8	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formyltetrahydrofolate cyclo-ligase; **PDBTitle:** structure of human mthfs with n5-iminium phosphate
7	d2hzab1	Alignment		18.2	55	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
8	c2r2vB_	Alignment		18.0	36	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
9	d2hzaa1	Alignment		17.3	44	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
10	d1wkca_	Alignment		16.5	100	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
11	c1ydmC_	Alignment		13.7	67	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein yqgn; **PDBTitle:** x-ray structure of northeast structural genomics target sr44

12	c2r28D_	Alignment		12.5	75	**PDB header:**metal binding protein/hydrolase **Chain:** D: **PDB Molecule:**serine/threonine-protein phosphatase 2b **PDBTitle:** the complex structure of calmodulin bound to a calcineurin2 peptide
13	c2kzuA_	Alignment		11.6	50	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death-associated protein 6; **PDBTitle:** daxx helical bundle (dhb) domain / rassf1c complex
14	d2bj7a1	Alignment		9.8	45	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
15	d1soua_	Alignment		9.6	67	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
16	d2i8da1	Alignment		9.4	6	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
17	d1wf3a2	Alignment		9.1	33	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
18	c3rkoK_	Alignment		8.4	19	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
19	c2ovmB_	Alignment		8.1	42	**PDB header:**transcription **Chain:** B: **PDB Molecule:**ncor; **PDBTitle:** progesterone receptor with bound asoprisnil and a peptide2 from the co-repressor ncor
20	d1egaa2	Alignment		7.7	36	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
21	d1aoya_	Alignment	not modelled	7.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
22	c2ksdA_	Alignment	not modelled	7.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aerobic respiration control sensor protein arcb; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor arcb, center for structures of3 membrane proteins (csmp) target 4310c
23	d1qlec_	Alignment	not modelled	6.6	20	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
24	c2yggA_	Alignment	not modelled	6.4	44	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** complex of cambr and cam
25	d1vp6a_	Alignment	not modelled	6.1	6	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
26	c2voiB_	Alignment	not modelled	6.1	75	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bh3-interacting domain death agonist p13; **PDBTitle:** structure of mouse a1 bound to the bid bh3-domain
27	c2kjrA_	Alignment	not modelled	5.9	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cg11242; **PDBTitle:** solution nmr structure of the n-terminal ubiquitin-like2 domain from tubulin-binding cofactor b, cg11242, from3 drosophila melanogaster. northeast structural genomics4 consortium target fr629a (residues 8-92)
						PDB header:signaling protein

28	c1usdA_	Alignment	not modelled	5.3	37	**Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
29	c1lt1G_	Alignment	not modelled	5.2	20	**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
30	c1q5vB_	Alignment	not modelled	5.1	55	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr