Phyre^2

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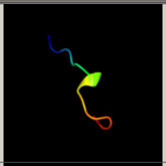
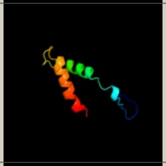
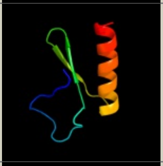
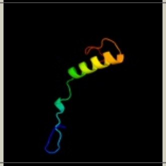
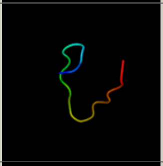
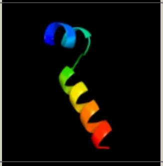
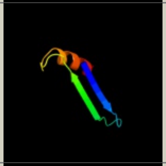
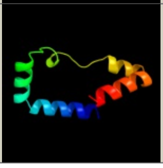
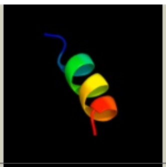
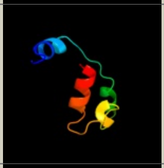
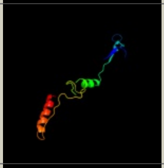
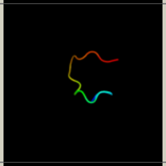
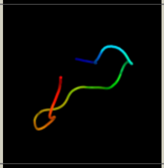
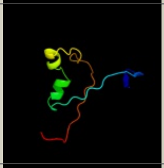
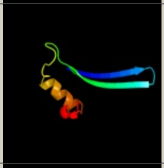
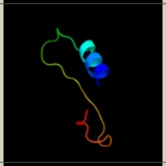
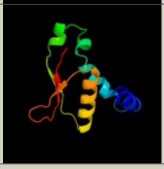
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fggA_	Alignment		32.7	46	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bce2196; **PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
2	c1nw1A_	Alignment		22.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline kinase (49.2 kd); **PDBTitle:** crystal structure of choline kinase
3	d1nw1a_	Alignment		22.4	23	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Choline kinase
4	d1v5ma_	Alignment		21.7	26	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
5	c3mesB_	Alignment		17.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
6	d1bbpa_	Alignment		14.0	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
7	c2hzqA_	Alignment		13.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**apolipoprotein d; **PDBTitle:** crystal structure of human apolipoprotein d (apod) in2 complex with progesterone
8	d2ox7a1	Alignment		13.7	33	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
9	c3ha4C_	Alignment		13.4	24	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**mix1; **PDBTitle:** crystal structure of the type one membrane protein mix1 from2 leishmania
10	d1gkab_	Alignment		12.7	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
11	d1axia_	Alignment		12.3	27	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines

12	d2b7ea1	Alignment		11.2	43	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
13	c1zxjB_	Alignment		10.7	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein mg377 homolog; **PDBTitle:** crystal structure of the hypthetical mycoplasma protein,2 mpn555
14	c1h4tD_	Alignment		10.4	25	**PDB header:**aminoacyl-trna synthetase **Chain:** D: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
15	d2p84a1	Alignment		10.0	31	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
16	c2qyzA_	Alignment		9.9	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the uncharacterized protein ctc02137 from2 clostridium tetani e88
17	d1osce_	Alignment		9.0	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
18	d1pm1x_	Alignment		8.8	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
19	c3c8uA_	Alignment		8.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
20	d1whra_	Alignment		8.0	14	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
21	c1wqdA_	Alignment	not modelled	7.9	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omtx2; **PDBTitle:** an unusual fold for potassium channel blockers: nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
22	c3fwlA_	Alignment	not modelled	7.9	21	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
23	c3lx6B_	Alignment	not modelled	7.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** structure of probable cytosine-specific methyltransferase from2 shigella flexneri
24	d1hgua_	Alignment	not modelled	7.4	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
25	c1wqcA_	Alignment	not modelled	7.3	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omtx1; **PDBTitle:** an unusual fold for potassium channel blockers : nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
26	d1v65a_	Alignment	not modelled	7.2	25	**Fold:**KRAB domain (Kruppel-associated box) **Superfamily:**KRAB domain (Kruppel-associated box) **Family:**KRAB domain (Kruppel-associated box)
27	d1mg4a_	Alignment	not modelled	7.2	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
28	c2l23A_	Alignment	not modelled	7.0	58	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25;

						PDBTitle: nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
29	c3rfrI_	Alignment	not modelled	6.9	13	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
30	d1m8na_	Alignment	not modelled	6.6	46	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**An insect antifreeze protein **Family:**An insect antifreeze protein
31	d1clvi_	Alignment	not modelled	6.5	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
32	c3rgbA_	Alignment	not modelled	6.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
33	c1yewI_	Alignment	not modelled	6.3	19	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
34	c2qrvA_	Alignment	not modelled	6.3	22	**PDB header:**transferase/transferase regulator **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a; **PDBTitle:** structure of dnmt3a-dnmt3l c-terminal domain complex
35	c3dwlF_	Alignment	not modelled	6.3	20	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**actin-related protein 2/3 complex subunit 4; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
36	d1ewna_	Alignment	not modelled	6.2	27	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**3-methyladenine DNA glycosylase (AAG, ANPG, MPG)
37	c3chxE_	Alignment	not modelled	6.0	12	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
38	c2qrvC_	Alignment	not modelled	5.9	20	**PDB header:**transferase/transferase regulator **Chain:** C: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3-like; **PDBTitle:** structure of dnmt3a-dnmt3l c-terminal domain complex
39	d1wjpa2	Alignment	not modelled	5.9	46	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
40	d1v7wa2	Alignment	not modelled	5.8	13	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
41	d1n0sa_	Alignment	not modelled	5.8	20	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
42	d1mjda_	Alignment	not modelled	5.8	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
43	d2axla1	Alignment	not modelled	5.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
44	d1e6ya1	Alignment	not modelled	5.2	46	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
45	c3c5iD_	Alignment	not modelled	5.2	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**choline kinase; **PDBTitle:** crystal structure of plasmodium knowlesi choline kinase, pkh_134520
46	c1ydiB_	Alignment	not modelled	5.1	37	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**alpha-actinin 4; **PDBTitle:** human vinculin head domain (vh1, 1-258) in complex with2 human alpha-actinin's vinculin-binding site (residues 731-3 760)
47	c1zx3A_	Alignment	not modelled	5.1	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ne0241; **PDBTitle:** structure of ne0241 protein of unknown function from nitrosomonas2 europaea