Phyre^2

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Description	P77307
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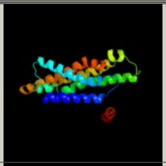
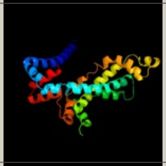
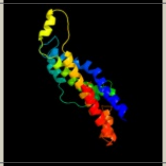
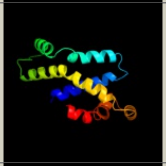
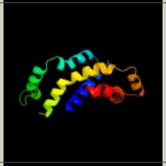
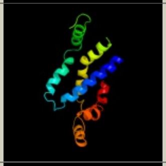
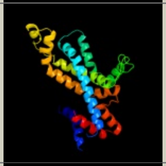
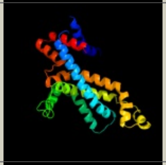
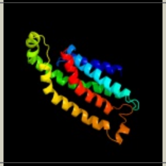
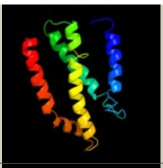
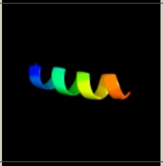
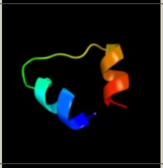
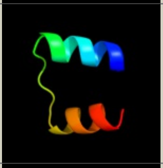
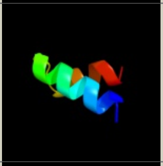
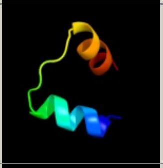
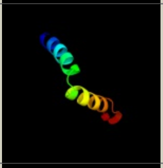
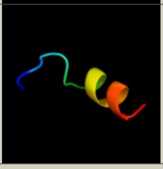
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k07A_	Alignment		95.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
2	d3d31c1	Alignment		93.7	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	c3d31D_	Alignment		93.7	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
4	d3dhwa1	Alignment		92.9	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
5	c2r6gF_	Alignment		88.0	13	**PDB header:**hydrolase/transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** the crystal structure of the e. coli maltose transporter
6	d2r6gf2	Alignment		83.2	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
7	c3fh6F_	Alignment		80.5	12	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
8	c2onkC_	Alignment		69.7	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**molybdate/tungstate abc transporter, permease **PDBTitle:** abc transporter modbc in complex with its binding protein2 moda
9	d2onkc1	Alignment		69.7	12	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
10	c3aqpB_	Alignment		65.8	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
11	d2r6gg1	Alignment		59.3	11	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like

12	d1iwga8	Alignment		39.5	19	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
13	c2jobA_	Alignment		35.0	18	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
14	d2gy9p1	Alignment		34.5	28	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
15	d2uubp1	Alignment		32.7	27	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
16	d1cuka1	Alignment		31.5	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
17	d3bn0a1	Alignment		27.1	8	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
18	c2akcC_	Alignment		24.2	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**class a nonspecific acid phosphatase phon; **PDBTitle:** crystal structure of tungstate complex of the phon protein2 from s. typhimurium
19	c3i5dC_	Alignment		22.1	21	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**p2x purinoceptor; **PDBTitle:** crystal structure of the atp-gated p2x4 ion channel in the closed, apo2 state at 3.5 angstroms (r3)
20	c2amwA_	Alignment		21.5	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ne2163; **PDBTitle:** solution nmr structure of protein ne2163 from nitrosomonas europaea.2 northeast structural genomics consortium target net1.
21	c3idwA_	Alignment	not modelled	19.7	21	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
22	c2lkiA_	Alignment	not modelled	19.5	31	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
23	c3h4cA_	Alignment	not modelled	19.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor tfiib-like; **PDBTitle:** structure of the c-terminal domain of transcription factor iib from2 trypanosoma brucei
24	d1njra_	Alignment	not modelled	15.4	16	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
25	d1pn2a1	Alignment	not modelled	10.7	39	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
26	d1iwga7	Alignment	not modelled	8.6	23	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
27	c3mlgB_	Alignment	not modelled	7.5	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein, linker, putative **PDBTitle:** 2ouf-2x, a designed knotted protein
28	c3beyC_	Alignment	not modelled	7.5	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural

						genomics consortium target3 tt217
29	d1u14a_	Alignment	not modelled	7.5	17	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
30	d1oqya2	Alignment	not modelled	6.8	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
31	d1ijwc_	Alignment	not modelled	6.6	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
32	c2k29A_	Alignment	not modelled	6.1	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
33	c3rxyA_	Alignment	not modelled	5.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nif3 protein; **PDBTitle:** crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
34	d1hcra_	Alignment	not modelled	5.8	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
35	d2c4va1	Alignment	not modelled	5.7	7	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
36	d1oqya1	Alignment	not modelled	5.3	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
37	c1pn2D_	Alignment	not modelled	5.3	39	**PDB header:**lyase **Chain:** D: **PDB Molecule:**peroxisomal hydratase-dehydrogenase-epimerase; **PDBTitle:** crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2