Phyre^2

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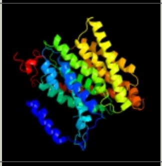
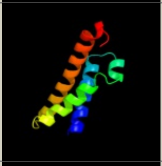
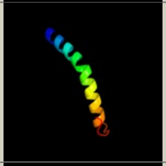
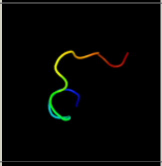
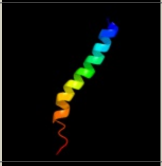
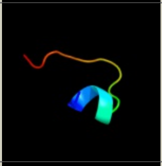
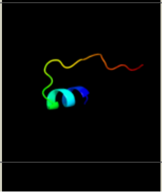
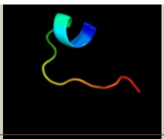
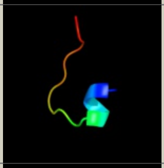
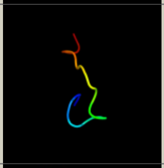
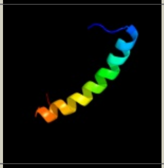
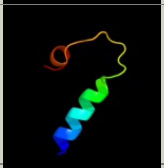
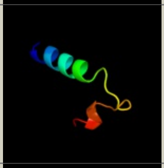
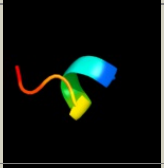
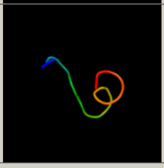
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b2hA_	Alignment		100.0	39	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
2	d1u7ga_	Alignment		100.0	96	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter
3	c3c1iA_	Alignment		100.0	99	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonia channel; **PDBTitle:** substrate binding, deprotonation and selectivity at the2 periplasmic entrance of the e. coli ammonia channel amtb
4	c3hd6A_	Alignment		100.0	21	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
5	c3b9yA_	Alignment		100.0	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
6	c3k3gA_	Alignment		30.4	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
7	c3qnqD_	Alignment		13.1	14	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
8	d1u1ha2	Alignment		13.0	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
9	c2kncA_	Alignment		12.1	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c2nq5A_	Alignment		11.8	53	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of methyltransferase from streptococcus2 mutans
11	d1u1ha1	Alignment		11.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase

12	c3l7sA_	Alignment		10.8	53	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate--homocysteine **PDBTitle:** crystal structure of mete coordinated with zinc from streptococcus2 mutans
13	c1t7lA_	Alignment		10.7	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of cobalamin-independent methionine2 synthase from t. maritima
14	c1u22A_	Alignment		10.3	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
15	c3lr4A_	Alignment		8.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
16	d1z9ha1	Alignment		8.6	19	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
17	d1vk5a_	Alignment		8.5	21	**Fold:**Hypothetical protein At3g22680 **Superfamily:**Hypothetical protein At3g22680 **Family:**Hypothetical protein At3g22680
18	c1vk5A_	Alignment		8.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**expressed protein; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana at3g22680
19	c3da4B_	Alignment		8.4	56	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
20	c2dp3A_	Alignment		6.3	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
21	d1fftb2	Alignment	not modelled	6.2	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
22	d1ttja_	Alignment	not modelled	6.0	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
23	d1ezfa_	Alignment	not modelled	6.0	28	**Fold:**Terpenoid synthases **Superfamily:**Terpenoid synthases **Family:**Squalene synthase
24	c1ru7B_	Alignment	not modelled	5.6	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** 1934 human h1 hemagglutinin
25	d1kv5a_	Alignment	not modelled	5.6	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
26	c2l9uA_	Alignment	not modelled	5.2	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
27	c1mqlB_	Alignment	not modelled	5.1	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin ha2 chain; **PDBTitle:** bha of ukr/63