Phyre^2

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Description	Q9QXE4
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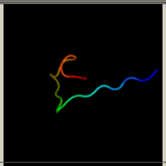
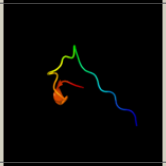
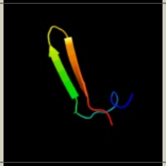
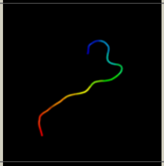
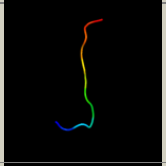
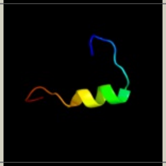
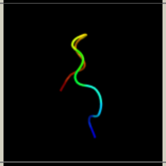
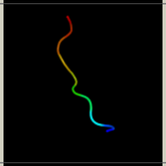
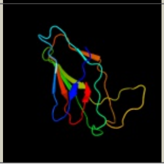
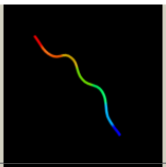
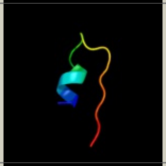
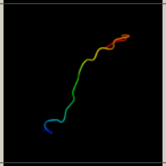
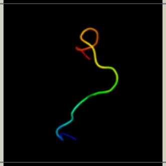
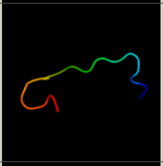
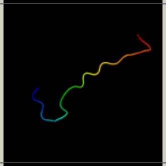
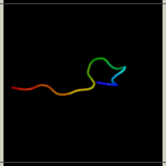
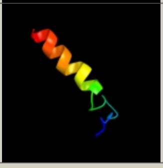
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3absD_	Alignment		19.8	35	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
2	c3anyB_	Alignment		19.8	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
3	c3hxrA_	Alignment		19.5	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin nup120; **PDBTitle:** nucleoporin nup120 from s.cerevisiae (aa 1-757)
4	c3upsA_	Alignment		18.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
5	d2o5aa1	Alignment		17.7	42	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
6	c3s63B_	Alignment		16.2	32	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**saposin-like protein; **PDBTitle:** saposin-like protein na-slp-1
7	d2id1a1	Alignment		14.7	58	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
8	d1oa8a_	Alignment		12.6	32	**Fold:**AXH domain **Superfamily:**AXH domain **Family:**AXH domain
9	d1sr4a_	Alignment		10.8	30	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
10	c1sr4A_	Alignment		10.8	30	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cytolethal distending toxin subunit a; **PDBTitle:** crystal structure of the haemophilus ducreyi cytolethal2 distending toxin
11	d1nlqa_	Alignment		10.7	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Nucleoplasmin-like core domain **Family:**Nucleoplasmin-like core domain

12	d3proc2	Alignment		9.1	43	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
13	c3ce8A_	Alignment		8.6	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
14	c3npeA_	Alignment		8.5	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; **PDBTitle:** structure of vp14 in complex with oxygen
15	d1v5xa_	Alignment		8.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
16	d1piia1	Alignment		7.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
17	c2biwC_	Alignment		7.4	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**apocarotenoid-cleaving oxygenase; **PDBTitle:** crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
18	c3fsnA_	Alignment		7.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**retinal pigment epithelium-specific 65 kda protein; **PDBTitle:** crystal structure of rpe65 at 2.14 angstrom resolution
19	d1gl5a_	Alignment		6.9	22	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
20	d1a4ia1	Alignment		6.8	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
21	c2ab9A_	Alignment	not modelled	6.6	50	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**pro-sfti-1; **PDBTitle:** discovery, structural determination and processing of the2 precursor protein that produces the cyclic trypsin3 inhibitor sfti-1
22	d1aisb1	Alignment	not modelled	6.5	43	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
23	c2jeuA_	Alignment	not modelled	6.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein e2; **PDBTitle:** transcription activator structure reveals redox control of2 a replication initiation reaction
24	c4esrB_	Alignment	not modelled	6.0	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**jouberin; **PDBTitle:** molecular and structural characterization of the sh3 domain of ahi-12 in regulation of cellular resistance of bcr-abl+ chronic myeloid3 leukemia cells to tyrosine kinase inhibitors
25	c1s1nA_	Alignment	not modelled	5.9	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**nephrocystin 1; **PDBTitle:** sh3 domain of human nephrocystin
26	d1sgva2	Alignment	not modelled	5.8	8	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
27	c2kqrA_	Alignment	not modelled	5.8	57	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the n-terminal domain (residues 1-111) of brugia2 malayi asparaginyl-trna synthetase
28	c2eiuE_	Alignment	not modelled	5.8	52	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein aq_1627; **PDBTitle:** crystal structure of a putative protein (aq1627) from

						aquifex aeolicus
29	c2x3wD_	Alignment	not modelled	5.7	13	**PDB header:**endocytosis **Chain:** D: **PDB Molecule:**protein kinase c and casein kinase substrate in neurons **PDBTitle:** structure of mouse syndapin i (crystal form 2)
30	c2eouA_	Alignment	not modelled	5.5	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 370-2 400) of human zinc finger protein 473
31	d1wfwa_	Alignment	not modelled	5.4	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
32	c1plpA_	Alignment	not modelled	5.4	45	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**phospholamban; **PDBTitle:** solution structure of the cytoplasmic domain of2 phospholamban
33	c3cs5B_	Alignment	not modelled	5.4	57	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
34	d1ckaa_	Alignment	not modelled	5.4	9	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
35	d1usra_	Alignment	not modelled	5.3	29	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
36	c2jnrA_	Alignment	not modelled	5.2	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vir165; **PDBTitle:** discovery and optimization of a natural hiv-1 entry2 inhibitor targeting the gp41 fusion peptide
37	d2gova1	Alignment	not modelled	5.1	13	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
38	c2c2xB_	Alignment	not modelled	5.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
39	c3cs5C_	Alignment	not modelled	5.1	57	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942