Phyre2

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Description	P51024
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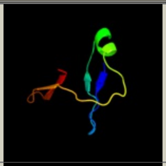
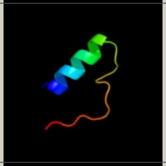
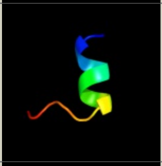
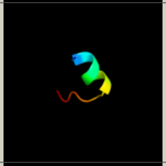
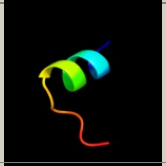
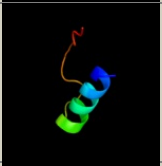
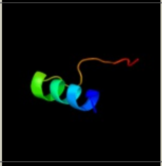
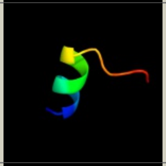
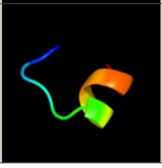
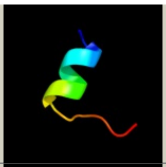
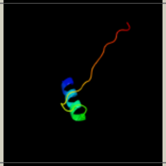
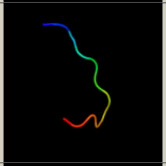
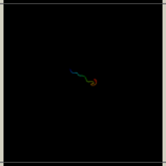
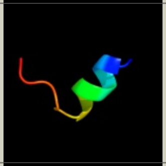
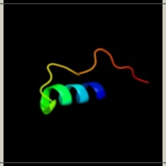
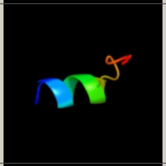
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l0cA_	Alignment		28.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
2	c3ep1B_	Alignment		20.9	23	**PDB header:**immune system **Chain:** B: **PDB Molecule:**pgrp-hd - peptidoglycan recognition protein **PDBTitle:** structure of the pgrp-hd from alvinella pompejana
3	c3ky8B_	Alignment		18.0	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**putative riboflavin biosynthesis protein; **PDBTitle:** crystal structure of putative riboflavin biosynthesis protein2 (yp_001092907.1) from shewanella sp. pv-4 at 2.12 a resolution
4	c3jtwB_	Alignment		17.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution
5	c2gd9A_	Alignment		15.9	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein yyap; **PDBTitle:** crystal structure of a putative dihydrofolate reductase (bsu40760,2 yyap) from bacillus subtilis at 2.30 a resolution
6	c3kgyA_	Alignment		15.1	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bifunctional deaminase-reductase domain protein; **PDBTitle:** crystal structure of putative dihydrofolate reductase (yp_001636057.1)2 from chloroflexus aurantiacus j-10-fl at 1.50 a resolution
7	c2xw7A_	Alignment		14.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** structure of mycobacterium smegmatis putative reductase ms0308
8	c2xz8A_	Alignment		13.4	22	**PDB header:**immune system **Chain:** A: **PDB Molecule:**peptidoglycan-recognition protein lf; **PDBTitle:** crystal structure of the lfw ectodomain of the2 peptidoglycan recognition protein lf
9	d1sxra_	Alignment		10.3	22	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
10	d1d1ga_	Alignment		10.1	29	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
11	c3hlsE_	Alignment		9.9	42	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** crystal structure of the signaling helix coiled-coil doimain2 of the beta-1 subunit of the soluble guanylyl cyclase

12	d2b3za1	Alignment		9.5	14	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**RibD C-terminal domain-like
13	d2d28c1	Alignment		9.3	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
14	c2v5iA_	Alignment		9.0	58	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**salmonella typhimurium db7155 bacteriophage det7 **PDBTitle:** structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
15	c3iyjE_	Alignment		8.9	40	**PDB header:**virus **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** bovine papillomavirus type 1 outer capsid
16	d2azna1	Alignment		8.7	43	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**RibD C-terminal domain-like
17	c1s2jA_	Alignment		8.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan recognition protein sa cg11709-pa; **PDBTitle:** crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
18	c3op0B_	Alignment		8.2	25	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
19	c2p4gA_	Alignment		8.2	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
20	d1hk9a_	Alignment		8.0	44	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
21	c2o7pA_	Alignment	not modelled	8.0	57	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
22	d1vr0a1	Alignment	not modelled	7.8	17	**Fold:**ComB-like **Superfamily:**ComB-like **Family:**ComB-like
23	c2zxeG_	Alignment	not modelled	7.8	33	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
24	c2zy3A_	Alignment	not modelled	7.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
25	d2p4pa1	Alignment	not modelled	7.1	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
26	c3ol0C_	Alignment	not modelled	7.1	18	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
27	d1zhva1	Alignment	not modelled	6.9	48	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
28	c2d5nB_	Alignment	not modelled	6.1	14	**PDB header:**hydrolase, oxidoreductase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** crystal structure of a bifunctional deaminase and

						reductase2 involved in riboflavin biosynthesis
29	d1z7ga1	Alignment	not modelled	5.7	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
30	d1u1sa1	Alignment	not modelled	5.5	33	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
31	d1dzla_	Alignment	not modelled	5.4	13	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
32	c1dzlA_	Alignment	not modelled	5.4	13	**PDB header:**virus **Chain:** A: **PDB Molecule:**late major capsid protein l1; **PDBTitle:** l1 protein of human papillomavirus 16
33	d1tzpa_	Alignment	not modelled	5.2	25	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**MepA-like
34	c3dsoA_	Alignment	not modelled	5.2	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein copk; **PDBTitle:** crystal structure of cu(i) bound copper resistance protein copk