Phyre^2

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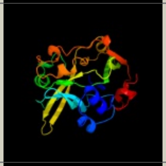
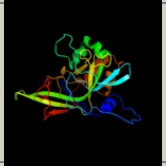
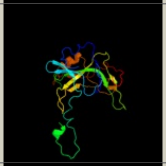
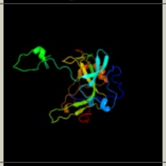
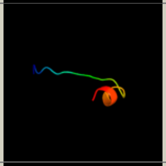
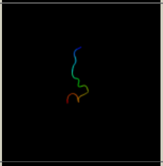
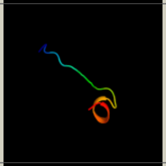
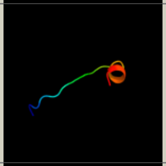
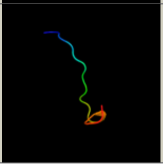
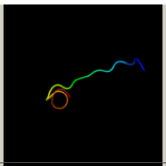
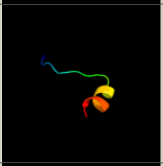
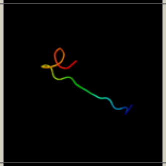
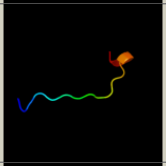
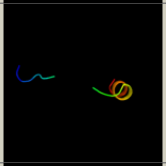
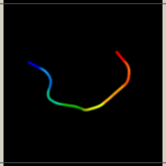
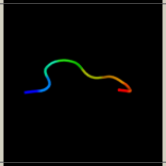
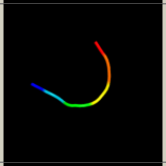
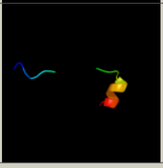
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2icuB_	Alignment		100.0	98	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein yedk; **PDBTitle:** crystal structure of hypothetical protein yedk from escherichia coli
2	d2f20a1	Alignment		100.0	20	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
3	d2bdva1	Alignment		100.0	38	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
4	d1zn6a1	Alignment		100.0	20	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
5	c2aegA_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein agr_pat_140; **PDBTitle:** x-ray crystal structure of protein atu5096 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr63.
6	d2aega1	Alignment		100.0	15	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
7	c3uksB_	Alignment		36.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sedoheptulose-1,7 bisphosphatase, putative; **PDBTitle:** 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
8	d1d9qa_	Alignment		34.1	41	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
9	d1bk4a_	Alignment		34.0	44	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
10	d1nuwa_	Alignment		33.2	50	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	c2gq1A_	Alignment		32.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphatase; **PDBTitle:** crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions

12	d1ftaa_	Alignment		32.0	44	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
13	d1spia_	Alignment		30.4	37	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
14	c2fhyL_	Alignment		27.9	44	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**fructose-1,6-bisphosphatase 1; **PDBTitle:** structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
15	c1v55B_	Alignment		22.0	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
16	d3dtub1	Alignment		17.3	41	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
17	d2hewf1	Alignment		17.0	25	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
18	c2hewF_	Alignment		17.0	25	**PDB header:**cytokine **Chain:** F: **PDB Molecule:**tumor necrosis factor ligand superfamily member 4; **PDBTitle:** the x-ray crystal structure of murine ox40l
19	c2yqpA_	Alignment		16.9	50	**PDB header:**gene regulation, hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx59; **PDBTitle:** solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
20	d3ehbb1	Alignment		15.9	29	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
21	d2hevf1	Alignment	not modelled	14.6	38	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
22	c2dhiA_	Alignment	not modelled	14.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pleckstrin homology domain-containing family b **PDBTitle:** solution structure of the ph domain of evectin-2 from mouse
23	c1m57H_	Alignment	not modelled	14.2	35	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
24	c1ar1B_	Alignment	not modelled	13.7	29	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
25	c1uijA_	Alignment	not modelled	12.8	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
26	d1v54b1	Alignment	not modelled	11.5	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
27	c3c3vA_	Alignment	not modelled	10.9	10	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
28	c1fftG_	Alignment	not modelled	9.4	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli

29	c2b3gB_	Alignment	not modelled	9.0	42	**PDB header:**replication **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53n (fragment 33-60) bound to rpa70n
30	d2k49a2	Alignment	not modelled	8.7	20	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
31	c3kscD_	Alignment	not modelled	8.1	8	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
32	d2k8ea1	Alignment	not modelled	8.1	26	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
33	c1jsuC_	Alignment	not modelled	8.0	27	**PDB header:**complex (transferase/cyclin/inhibitor) **Chain:** C: **PDB Molecule:**p27; **PDBTitle:** p27(kip1)/cyclin a/cdk2 complex
34	d2gysa1	Alignment	not modelled	7.8	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
35	c2l14B_	Alignment	not modelled	7.6	26	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** structure of cbp nuclear coactivator binding domain in complex with2 p53 tad
36	c2k8eA_	Alignment	not modelled	7.5	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
37	c1t3bA_	Alignment	not modelled	7.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
38	c2gs0B_	Alignment	not modelled	7.3	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** nmr structure of the complex between the ph domain of the2 tfb1 subunit from tfiih and the activation domain of p53
39	c3rbbA_	Alignment	not modelled	6.9	44	**PDB header:**viral protein, protein binding **Chain:** A: **PDB Molecule:**protein nef; **PDBTitle:** hiv-1 nef protein in complex with engineered hck sh3 domain
40	d1cyxa_	Alignment	not modelled	6.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
41	c1cyxA_	Alignment	not modelled	6.6	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cyoa; **PDBTitle:** quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
42	c3qacA_	Alignment	not modelled	5.6	10	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin seed storage protein; **PDBTitle:** structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
43	d1kr4a_	Alignment	not modelled	5.6	23	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
44	d2k57a1	Alignment	not modelled	5.5	29	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**YgdI/YgdR-like
45	c2b7fD_	Alignment	not modelled	5.4	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design
46	d1f0ya1	Alignment	not modelled	5.4	29	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
47	d1p1la_	Alignment	not modelled	5.3	23	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)