Phyre2

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Description	P0A993
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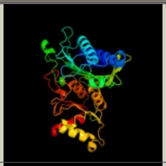
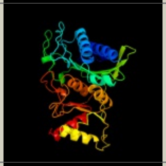
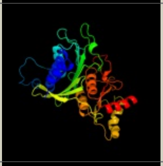
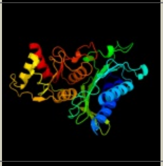
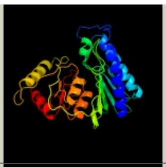
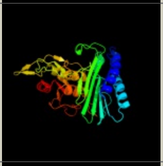
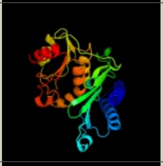
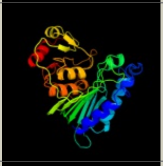
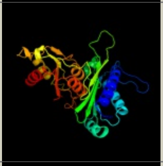
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nuwa_	Alignment		100.0	42	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
2	c2gq1A_	Alignment		100.0	97	**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
3	c2fhyL_	Alignment		100.0	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
4	d1ftaa_	Alignment		100.0	44	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
5	d1spia_	Alignment		100.0	47	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
6	d1bk4a_	Alignment		100.0	45	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
7	d1d9qa_	Alignment		100.0	46	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
8	c3uksB_	Alignment		100.0	28	**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
9	d1lbva_	Alignment		99.9	21	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
10	d1g0ha_	Alignment		99.9	17	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	d2hhma_	Alignment		99.8	16	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like

12	c2qflA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
13	c2p3nB_	Alignment		99.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** thermotoga maritima impase tm1415
14	c3luzA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extragenic suppressor protein suhb; **PDBTitle:** crystal structure of extragenic suppressor protein suhb from2 bartonella henselae, via combined iodide sad molecular replacement
15	d1vdwa_	Alignment		99.8	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
16	c2q74B_	Alignment		99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** mycobacterium tuberculosis suhb
17	c2czhB_	Alignment		99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
18	c2fvzB_	Alignment		99.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** human inositol monophosphatase 2
19	d1xi6a_	Alignment		99.8	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
20	c2pcrA_	Alignment		99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
21	d1jp4a_	Alignment	not modelled	99.7	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	d1ka1a_	Alignment	not modelled	99.7	15	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
23	c3b8bA_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysq, sulfite synthesis pathway protein; **PDBTitle:** crystal structure of cysq from bacteroides thetaiotaomicron, a2 bacterial member of the inositol monophosphatase family
24	d1inpa_	Alignment	not modelled	99.3	14	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	d1o12a1	Alignment	not modelled	66.2	28	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
26	d1ni9a_	Alignment	not modelled	53.9	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
27	c2icuB_	Alignment	not modelled	35.5	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein yedk; **PDBTitle:** crystal structure of hypothetical protein yedk from escherichia coli
28	d1hi9a_	Alignment	not modelled	33.8	20	**Fold:**Dipeptide transport protein **Superfamily:**Dipeptide transport protein **Family:**Dipeptide transport protein
						Fold: YrdC/RibB

29	d1k7ja_	Alignment	not modelled	32.0	25	**Superfamily:**YrdC/RibB **Family:**YrdC-like
30	d1r89a1	Alignment	not modelled	25.7	33	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
31	d2bdva1	Alignment	not modelled	23.1	15	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
32	d3pmga4	Alignment	not modelled	18.9	83	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
33	d1kfia4	Alignment	not modelled	18.3	67	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
34	c3f56F_	Alignment	not modelled	17.5	20	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
35	d2dlxa1	Alignment	not modelled	17.2	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
36	c1avoA_	Alignment	not modelled	14.6	35	**PDB header:**proteasome activator **Chain:** A: **PDB Molecule:**11s regulator; **PDBTitle:** proteasome activator reg(alpha)
37	d1uxya2	Alignment	not modelled	13.8	17	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
38	d1x87a_	Alignment	not modelled	13.0	23	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
39	c1svfB_	Alignment	not modelled	11.2	40	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein (fusion glycoprotein); **PDBTitle:** paramyxovirus sv5 fusion protein core
40	c2h31A_	Alignment	not modelled	10.9	10	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
41	c1sz1A_	Alignment	not modelled	10.3	33	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
42	d2guka1	Alignment	not modelled	10.0	19	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
43	d1f7da_	Alignment	not modelled	9.5	16	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
44	d1ufga_	Alignment	not modelled	9.3	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
45	d3orca_	Alignment	not modelled	8.5	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
46	c3c1zA_	Alignment	not modelled	8.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna integrity scanning protein disa; **PDBTitle:** structure of the ligand-free form of a bacterial dna damage2 sensor protein
47	d1lj8a4	Alignment	not modelled	7.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
48	d1ak0a_	Alignment	not modelled	7.9	14	**Fold:**Phospholipase C/P1 nuclease **Superfamily:**Phospholipase C/P1 nuclease **Family:**P1 nuclease
49	d2aega1	Alignment	not modelled	7.8	14	**Fold:**BB1717-like **Superfamily:**BB1717-like **Family:**BB1717-like
50	c2aegA_	Alignment	not modelled	7.8	14	**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.
51	c2k2wA_	Alignment	not modelled	7.4	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**recombination and dna repair protein; **PDBTitle:** second brct domain of nbs1
52	c1m2wA_	Alignment	not modelled	7.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol dehydrogenase; **PDBTitle:** pseudomonas fluorescens mannitol 2-dehydrogenase ternary complex with2 nad and d-mannitol
53	d1icfi_	Alignment	not modelled	7.2	16	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
54	d2bbga_	Alignment	not modelled	7.0	36	**Fold:**Amb V allergen **Superfamily:**Amb V allergen **Family:**Amb V allergen
55	d2i9wa3	Alignment	not modelled	6.7	15	**Fold:**Sec-C motif **Superfamily:**Sec-C motif

						Family: Sec-C motif
56	d1zsqa1	Alignment	not modelled	6.6	14	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**GRAM domain
57	c2oszA_	Alignment	not modelled	6.6	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
58	d1m1la_	Alignment	not modelled	6.5	50	**Fold:**Suppressor of Fused, N-terminal domain **Superfamily:**Suppressor of Fused, N-terminal domain **Family:**Suppressor of Fused, N-terminal domain
59	d2qw7a1	Alignment	not modelled	6.4	20	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
60	d1yira1	Alignment	not modelled	6.3	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase C-terminal domain
61	d1nkga3	Alignment	not modelled	6.2	23	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
62	d1tk9a_	Alignment	not modelled	6.0	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
63	c1ikqA_	Alignment	not modelled	6.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type
64	c3nohA_	Alignment	not modelled	5.9	33	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative peptide binding protein; **PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
65	c3jxoB_	Alignment	not modelled	5.8	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
66	d1f15b_	Alignment	not modelled	5.7	25	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
67	c1f15C_	Alignment	not modelled	5.7	25	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** cucumber mosaic virus (strain fny)
68	d1z9ha1	Alignment	not modelled	5.6	11	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
69	d1ydua1	Alignment	not modelled	5.4	6	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
70	d1f74a_	Alignment	not modelled	5.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
71	d1tu2b1	Alignment	not modelled	5.3	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
72	d2cqqa1	Alignment	not modelled	5.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
73	d1olma2	Alignment	not modelled	5.3	18	**Fold:**Supernatant protein factor (SPF), C-terminal domain **Superfamily:**Supernatant protein factor (SPF), C-terminal domain **Family:**Supernatant protein factor (SPF), C-terminal domain
74	d2hd3a1	Alignment	not modelled	5.3	20	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
75	c2zv4O_	Alignment	not modelled	5.3	23	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
76	d2fb5a1	Alignment	not modelled	5.2	13	**Fold:**YojJ-like **Superfamily:**YojJ-like **Family:**YojJ-like
77	d1ukfa_	Alignment	not modelled	5.1	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3