Phyre2

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Description	P0ADG4
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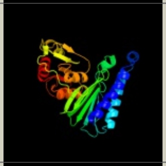
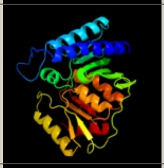
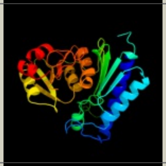
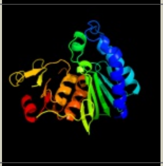
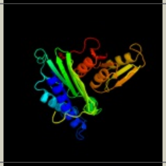
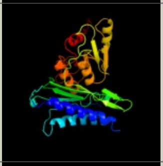
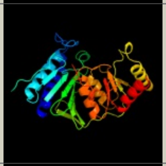
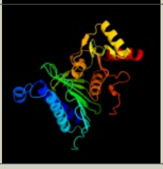
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qflA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
2	c2p3nB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** thermotoga maritima impase tm1415
3	c3luzA_	Alignment		100.0	44	**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
4	d2hhma_	Alignment		100.0	32	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
5	c2czhB_	Alignment		100.0	33	**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)
6	c2fvzB_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** human inositol monophosphosphatase 2
7	c2pcrA_	Alignment		100.0	35	**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
8	d1g0ha_	Alignment		100.0	25	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
9	c2q74B_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** mycobacterium tuberculosis suhb
10	d1jp4a_	Alignment		100.0	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	d1ka1a_	Alignment		100.0	28	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like

12	d1vdwa_	Alignment		100.0	31	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
13	d1xi6a_	Alignment		100.0	29	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
14	d1lbva_	Alignment		100.0	31	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	c3b8bA_	Alignment		100.0	25	**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
16	d1inpa_	Alignment		100.0	24	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	c3uksB_	Alignment		99.9	18	**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
18	d1d9qa_	Alignment		99.9	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
19	d1nuwa_	Alignment		99.6	16	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
20	c2fhyL_	Alignment		99.6	12	**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
21	d1ftaa_	Alignment	not modelled	99.5	15	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	d1bk4a_	Alignment	not modelled	99.4	15	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
23	c2gq1A_	Alignment	not modelled	99.3	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
24	d1spia_	Alignment	not modelled	99.1	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	d1ni9a_	Alignment	not modelled	93.5	22	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
26	d1o12a1	Alignment	not modelled	58.1	36	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
27	c3fhkF_	Alignment	not modelled	49.2	8	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**upf0403 protein yphp; **PDBTitle:** crystal structure of apc1446, b.subtilis yphp disulfide2 isomerase
28	d1mdah_	Alignment	not modelled	32.2	20	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
29	d1r89a1	Alignment	not modelled	17.0	33	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain

29		Alignment	not modelled			**Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
30	c3mx7A_	Alignment	not modelled	16.2	20	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
31	c1ikqA_	Alignment	not modelled	14.3	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type
32	d2ns0a1	Alignment	not modelled	14.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
33	d3pmga4	Alignment	not modelled	12.6	13	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
34	c2o7jA_	Alignment	not modelled	11.5	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
35	d2dsqg1	Alignment	not modelled	11.2	20	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
36	c2pncB_	Alignment	not modelled	9.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase, liver isozyme; **PDBTitle:** crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
37	d2j9ga2	Alignment	not modelled	9.7	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
38	c3g5uB_	Alignment	not modelled	9.3	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
39	d1icfi_	Alignment	not modelled	8.9	23	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
40	d2g5gx1	Alignment	not modelled	8.7	18	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**ChaN-like
41	d1w96a2	Alignment	not modelled	7.9	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
42	c3b5xB_	Alignment	not modelled	7.5	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
43	c3equB_	Alignment	not modelled	7.5	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
44	d1kfia4	Alignment	not modelled	7.4	38	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
45	c2hydB_	Alignment	not modelled	7.3	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
46	c1sz1A_	Alignment	not modelled	6.9	27	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
47	d1l0wa2	Alignment	not modelled	6.8	32	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
48	d1g4ma1	Alignment	not modelled	6.5	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
49	c2h7tA_	Alignment	not modelled	6.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**insulin-like growth factor-binding protein 2; **PDBTitle:** solution structure of the c-terminal domain of insulin-like2 growth factor binding protein 2 (igfbp-2)