










Phyre2

Email	mdejesus@rockefeller.edu
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zonA_	Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: histidinol phosphate phosphatase from mycobacterium tuberculosis
2	c2qfiA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of subh: inositol monophosphatase and extragenic2 suppressor from e. coli
3	c4n81A_	Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis
4	c2p3nB_	Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
5	d2hhma_	Alignment		100.0	27	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
6	c3rydA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal strucutre of ca bound impase family protein from2 staphylococcus aureus
7	c4gdgA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase1 from entamoeba histolytica
8	c3t0jB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of inositol monophosphatase - ii from staphylococcus2 aureus mssa476
9	c5eq9A_	Alignment		100.0	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: crystal structure of medicago truncatula histidinol-phosphate2 phosphatase (mthpp) in complex with l-histidinol phosphate and mg2+
10	c3luzA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: extragenic suppressor protein subh; PDBTitle: crystal structure of extragenic suppressor protein subh from2 bartonella henselae, via combined iodide sad molecular replacement
11	c3qmfA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of an inositol monophosphatase family protein2 (sas2203) from staphylococcus aureus mssa476

12	c2czhB_	Alignment		100.0	30	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)
13	d1ka1a_	Alignment		100.0	31	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
14	c2fvzB_	Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: human inositol monophosphatase 2
15	d1g0ha_	Alignment		100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
16	c5esyA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: sal1 phosphatase; PDBTitle: arabidopsis thaliana sal1
17	c5zhbB_	Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
18	c2q74B_	Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis suhb
19	c5djjA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: 3'-phosphoadenosine 5'-phosphate phosphatase; PDBTitle: structure of m. tuberculosis cysq, a pap phosphatase with po4 and 2mg2 bound
20	c2pcrA_	Alignment		100.0	30	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	100.0	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	c4j13B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase2 from entamoeba histolytica
23	d1vdwa_	Alignment	not modelled	100.0	25	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
24	c3b8bA_	Alignment	not modelled	100.0	22	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
25	d1xi6a_	Alignment	not modelled	100.0	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
26	d1lbva_	Alignment	not modelled	100.0	27	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
27	d1inpa_	Alignment	not modelled	100.0	27	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
28	c5iz3B_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: predicted protein; PDBTitle: p. patens sedoheptulose-1,7-bisphosphatase
						PDB header: hydrolase Chain: B: PDB Molecule: sedoheptulose-1,7 bisphosphatase.

29	c3uksB_	Alignment	not modelled	99.9	13	putative; PDBTitle: 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
30	d1d9qa_	Alignment	not modelled	99.9	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	d1nuwa_	Alignment	not modelled	99.5	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
32	d1ftaa_	Alignment	not modelled	99.4	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
33	c2fhyL_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: L: PDB Molecule: fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel benzoxazole as2 allosteric inhibitor
34	d1bk4a_	Alignment	not modelled	99.2	14	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
35	c2gq1A_	Alignment	not modelled	99.2	14	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
36	c5oezA_	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: A: PDB Molecule: fbp protein; PDBTitle: crystal structure of leishmania major fructose-1,6-bisphosphatase in2 apo form.
37	d1spia_	Alignment	not modelled	99.0	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
38	c3rojD_	Alignment	not modelled	96.9	25	PDB header: hydrolase Chain: D: PDB Molecule: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7- PDBTitle: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase2 of synechocystis sp. pcc 6803
39	c6aayB_	Alignment	not modelled	96.8	23	PDB header: hydrolase Chain: B: PDB Molecule: fructose-1,6-bisphosphatase class 2; PDBTitle: crystal structure of apo fructose-1,6-bisphosphatase from2 mycobacterium tuberculosis
40	d1ni9a_	Alignment	not modelled	96.0	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Glpx-like bacterial fructose-1,6-bisphosphatase
41	c3fhkF_	Alignment	not modelled	58.0	17	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
42	d1o12a1	Alignment	not modelled	55.7	64	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
43	d1r89a1	Alignment	not modelled	27.2	33	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
44	d1mdah_	Alignment	not modelled	15.6	14	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
45	c4xwzA_	Alignment	not modelled	15.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
46	c3equB_	Alignment	not modelled	14.6	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: penicillin-binding protein 2; PDBTitle: crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
47	c2pncB_	Alignment	not modelled	14.6	31	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
48	c1ikqA_	Alignment	not modelled	14.4	42	PDB header: transferase Chain: A: PDB Molecule: exotoxin a; PDBTitle: pseudomonas aeruginosa exotoxin a, wild type
49	d2dsqg1	Alignment	not modelled	14.3	40	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
50	d1icfi_	Alignment	not modelled	13.3	38	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
51	d1g4ma1	Alignment	not modelled	12.9	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
52	c1sz1A_	Alignment	not modelled	12.0	25	PDB header: transferase/rna Chain: A: PDB Molecule: trna nucleotidyltransferase; PDBTitle: mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
53	c6bmcA_	Alignment	not modelled	11.9	36	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
54	c2h7tA_	Alignment	not modelled	11.5	31	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)

55	c4xq7A	Alignment	not modelled	11.2	40	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthase-like protein; PDBTitle: the crystal structure of the oas-like domain (old) of human oasl
56	d2dsrg1	Alignment	not modelled	11.1	33	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
57	c2a8vA	Alignment	not modelled	10.7	10	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
58	c5hudA	Alignment	not modelled	10.3	31	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
59	d2b7oa1	Alignment	not modelled	9.9	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
60	c2ykyB	Alignment	not modelled	9.5	28	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: structural determinants of the beta-selectivity of a bacterial2 aminotransferase
61	c3hn0A	Alignment	not modelled	9.5	12	PDB header: transport protein Chain: A: PDB Molecule: nitrate transport protein; PDBTitle: crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
62	c4m4xA	Alignment	not modelled	9.4	18	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
63	c5uxmA	Alignment	not modelled	9.3	31	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
64	c4a0aA	Alignment	not modelled	9.2	22	PDB header: transferase Chain: A: PDB Molecule: beta-phenylalanine aminotransferase; PDBTitle: biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
65	d1cf1a1	Alignment	not modelled	9.1	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
66	c4ppmB	Alignment	not modelled	9.0	17	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of pige: a transaminase involved in the biosynthesis2 of 2-methyl-3-n-amylyl-pyrrole (map) from serratia sp. fs14
67	d2g5gx1	Alignment	not modelled	8.9	6	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: ChaN-like
68	c6ei9A	Alignment	not modelled	8.9	17	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
69	c4mfkA	Alignment	not modelled	8.7	23	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein tcp24; PDBTitle: the crystal structure of acyltransferase in complex with decanoyl-coa
70	c3ue3A	Alignment	not modelled	8.6	11	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbp3
71	d1w7ca1	Alignment	not modelled	8.3	46	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
72	c1px5A	Alignment	not modelled	8.0	50	PDB header: transferase Chain: A: PDB Molecule: 2'-5'-oligoadenylate synthetase 1; PDBTitle: crystal structure of the 2'-specific and double-stranded2 rna-activated interferon-induced antiviral protein 2'-5'-3 oligoadenylate synthetase
73	c4bgaB	Alignment	not modelled	7.6	23	PDB header: transferase Chain: B: PDB Molecule: predicted molecular chaperone distantly related to PDBTitle: nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
74	d1rmja	Alignment	not modelled	7.6	36	Fold: Thyroglobulin type-1 domain Superfamily: Thyroglobulin type-1 domain Family: Thyroglobulin type-1 domain
75	c4uoxB	Alignment	not modelled	7.1	15	PDB header: transferase Chain: B: PDB Molecule: putrescine aminotransferase; PDBTitle: crystal structure of ygig in complex with pyridoxal-5'-phosphate2 and putrescine
76	d3pmga4	Alignment	not modelled	7.0	16	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
77	d1kfia4	Alignment	not modelled	6.9	57	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
78	c1ayrA	Alignment	not modelled	6.9	23	PDB header: sensory transduction Chain: A: PDB Molecule: arrestin; PDBTitle: arrestin from bovine rod outer segments
79	c3b0vD	Alignment	not modelled	6.7	15	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna

80	d1w6ga1	Alignment	not modelled	6.7	38	Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
81	d1g3pa2	Alignment	not modelled	6.5	57	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
82	d2j9ga2	Alignment	not modelled	6.2	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
83	c3dgsA_	Alignment	not modelled	6.1	33	PDB header: viral protein Chain: A; PDB Molecule: coat protein a; PDBTitle: changing the determinants of protein stability from covalent to non-2 covalent interactions by in-vitro evolution: a structural and3 energetic analysis
84	c1w7cA_	Alignment	not modelled	5.9	46	PDB header: oxidoreductase Chain: A; PDB Molecule: lysyl oxidase; PDBTitle: pplo at 1.23 angstroms
85	c5v6iA_	Alignment	not modelled	5.8	28	PDB header: sugar binding protein Chain: A; PDB Molecule: trmv resistance protein y3; PDBTitle: glycan binding protein y3 from mushroom coprinus comatus possesses2 anti-leukemic activity - pt derivative
86	c5ykrB_	Alignment	not modelled	5.5	22	PDB header: transferase Chain: B; PDB Molecule: probable aminotransferase; PDBTitle: crystal structure of a glutamate-1-semialdehyde-aminomutase from2 pseudomonas aeruginosa pao1
87	c3djeA_	Alignment	not modelled	5.5	15	PDB header: oxidoreductase Chain: A; PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
88	d3duea1	Alignment	not modelled	5.4	11	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like
89	c1gn4B_	Alignment	not modelled	5.1	5	PDB header: oxidoreductase Chain: B; PDB Molecule: superoxide dismutase; PDBTitle: h145e mutant of mycobacterium tuberculosis iron-superoxide dismutase.