Phyre^2

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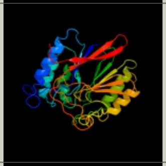
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ib7A_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
2	d3d03a1	Alignment		100.0	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
3	c2hy1A_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
4	d2hy1a1	Alignment		100.0	31	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
5	d2nxfa1	Alignment		100.0	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
6	c2xmoB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
7	c3av0A_	Alignment		100.0	13	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
8	c3auzA_	Alignment		100.0	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
9	c3t1iC_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
10	c2q8uA_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
11	c3qg5D_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair

12	d1ii7a_	Alignment		99.9	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
13	d1utea_	Alignment		99.9	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
14	d2yvta1	Alignment		99.9	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
15	c3qfnA_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
16	d1uf3a_	Alignment		99.9	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
17	c1qhwA_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (purple acid phosphatase); **PDBTitle:** purple acid phosphatase from rat bone
18	d1qhwa_	Alignment		99.9	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
19	d1xzwa2	Alignment		99.9	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
20	d2qfra2	Alignment		99.9	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
21	c3rl4A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
22	c1kbpB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
23	d1s3la_	Alignment	not modelled	99.9	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
24	c1s3mA_	Alignment	not modelled	99.9	16	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
25	c1xzwB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
26	d2a22a1	Alignment	not modelled	99.9	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
27	d1z2wa1	Alignment	not modelled	99.9	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
28	d1nnwa_	Alignment	not modelled	99.8	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Phosphoesterase-related
29	c1su1A_	Alignment	not modelled	99.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce;

29	c1su1A_	Alignment	not modelled	99.8	20	**PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
30	d1su1a_	Alignment	not modelled	99.8	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
31	c3rqzC_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
32	d3ck2a1	Alignment	not modelled	99.8	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
33	c2kknA_	Alignment	not modelled	99.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
34	d1xm7a_	Alignment	not modelled	99.6	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
35	d1usha2	Alignment	not modelled	99.6	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
36	c1oidA_	Alignment	not modelled	99.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
37	d2z1aa2	Alignment	not modelled	99.4	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
38	c3qfkA_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
39	c2z1aA_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
40	c3ivdA_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotidase; **PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
41	d1g5ba_	Alignment	not modelled	99.2	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
42	c2wdfA_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
43	d1t71a_	Alignment	not modelled	99.1	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
44	c3gveB_	Alignment	not modelled	99.1	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
45	c3zu0A_	Alignment	not modelled	99.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
46	d3c9fa2	Alignment	not modelled	99.0	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
47	c3jyfB_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
48	d2z06a1	Alignment	not modelled	98.7	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
49	c3c9fB_	Alignment	not modelled	98.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
50	d1t70a_	Alignment	not modelled	98.3	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
51	c2qjcA_	Alignment	not modelled	98.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
52	c2dfjA_	Alignment	not modelled	97.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
53	c3e0jG_	Alignment	not modelled	97.2	20	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
54	c2zbmA_	Alignment	not modelled	97.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2

						tyrosine phosphatase
55	d1jk7a_	Alignment	not modelled	96.9	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
56	d3c5wc1	Alignment	not modelled	96.8	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
57	d1s70a_	Alignment	not modelled	96.6	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
58	c2jogA_	Alignment	not modelled	96.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
59	d1s95a_	Alignment	not modelled	96.3	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
60	c3icfB_	Alignment	not modelled	96.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t; **PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
61	c1auiA_	Alignment	not modelled	95.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
62	d1auia_	Alignment	not modelled	95.8	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
63	c2p6bC_	Alignment	not modelled	95.6	14	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
64	d2p6ba1	Alignment	not modelled	95.6	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
65	c1wao4_	Alignment	not modelled	94.6	14	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
66	c3floG_	Alignment	not modelled	91.5	9	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase alpha subunit b; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
67	c3lmaC_	Alignment	not modelled	41.3	20	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**stage v sporulation protein ad (spovad); **PDBTitle:** crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
68	d1zhxa1	Alignment	not modelled	27.6	16	**Fold:**Oxysterol-binding protein-like **Superfamily:**Oxysterol-binding protein-like **Family:**Oxysterol-binding protein
69	d1gg4a1	Alignment	not modelled	20.4	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
70	d1s1da_	Alignment	not modelled	17.8	40	**Fold:**5-bladed beta-propeller **Superfamily:**Apyrase **Family:**Apyrase
71	c3menC_	Alignment	not modelled	14.7	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**acetylpolyamine aminohydrolase; **PDBTitle:** crystal structure of acetylpolyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
72	c3q9cF_	Alignment	not modelled	8.6	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetylpolyamine amidohydrolase; **PDBTitle:** crystal structure of h159a apah complexed with n8-acetylspermidine
73	c2gx8B_	Alignment	not modelled	8.4	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
74	c3ew8A_	Alignment	not modelled	7.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
75	d1heya_	Alignment	not modelled	7.7	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c3ngoA_	Alignment	not modelled	7.7	11	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ccr4-not transcription complex subunit 6-like; **PDBTitle:** crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
77	d2gx8a1	Alignment	not modelled	7.1	12	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
78	c2y1hA_	Alignment	not modelled	7.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3; **PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3)
79	c3o0dF_	Alignment	not modelled	7.0	30	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
80	d1dz3a_	Alignment	not modelled	6.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like

						Family: CheY-related
81	c3h02F_	Alignment	not modelled	5.9	11	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
82	c2nydB_	Alignment	not modelled	5.6	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
83	c3g7nA_	Alignment	not modelled	5.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
84	d1tiaa_	Alignment	not modelled	5.2	35	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
85	d3tgla_	Alignment	not modelled	5.1	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
86	c3rsiA_	Alignment	not modelled	5.1	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196