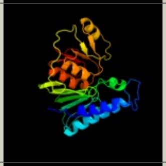
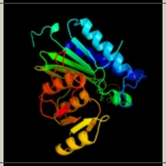
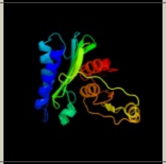
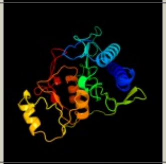
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P22255
Date	Thu Jan 5 11:38:47 GMT 2012
Unique Job ID	88104b0d91495aa5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hhma_	Alignment		100.0	24	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
2	c2qflA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
3	c2p3nB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** thermotoga maritima impase tm1415
4	d1jp4a_	Alignment		100.0	23	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
5	c3b8bA_	Alignment		100.0	47	**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
6	c3luzA_	Alignment		100.0	25	**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
7	c2czhB_	Alignment		100.0	26	**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)
8	d1g0ha_	Alignment		100.0	17	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
9	c2fvzB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** human inositol monophosphatase 2
10	d1ka1a_	Alignment		100.0	29	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	c2q74B_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** mycobacterium tuberculosis suhb

12	d1xi6a_	Alignment		100.0	21	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
13	d1vdwa_	Alignment		100.0	22	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
14	c2pcrA_	Alignment		100.0	24	**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
15	d1lbva_	Alignment		100.0	20	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
16	d1inpa_	Alignment		100.0	25	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	c3uksB_	Alignment		99.8	16	**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		99.8	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
19	d1nuwa_	Alignment		99.4	16	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
20	c2fhyL_	Alignment		99.4	17	**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	99.3	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
22	c2gq1A_	Alignment	not modelled	99.1	17	**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
23	d1bk4a_	Alignment	not modelled	99.1	15	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
24	d1spia_	Alignment	not modelled	98.9	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	d1ni9a_	Alignment	not modelled	96.5	17	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
26	d1o12a1	Alignment	not modelled	60.8	45	**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	42.9	13	**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	42.5	16	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
29	d2dsqg1	Alignment	not modelled	29.4	27	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain

						Family: Thyroglobulin type-1 domain
30	d1icfi_	Alignment	not modelled	28.4	31	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
31	d1g4ma1	Alignment	not modelled	25.3	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
32	c2h7tA_	Alignment	not modelled	23.9	25	**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)
33	d1rmja_	Alignment	not modelled	21.2	31	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
34	d1cf1a1	Alignment	not modelled	21.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
35	c1cf1B_	Alignment	not modelled	20.2	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**protein (arrestin); **PDBTitle:** arrestin from bovine rod outer segments
36	d2dsrg1	Alignment	not modelled	20.2	27	**Fold:**Thyroglobulin type-1 domain **Superfamily:**Thyroglobulin type-1 domain **Family:**Thyroglobulin type-1 domain
37	c1ikqA_	Alignment	not modelled	19.9	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type
38	c2pncB_	Alignment	not modelled	18.8	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
39	d1x4ka1	Alignment	not modelled	18.6	63	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
40	c3equB_	Alignment	not modelled	18.0	16	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
41	d1r89a1	Alignment	not modelled	17.5	27	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**Archaeal tRNA CCA-adding enzyme substrate-binding domain
42	c3g5uB_	Alignment	not modelled	16.1	12	**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
43	c3b5xB_	Alignment	not modelled	15.0	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
44	c2hydB_	Alignment	not modelled	12.6	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
45	d1w7ca1	Alignment	not modelled	12.2	38	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
46	d2g5gx1	Alignment	not modelled	11.9	6	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**ChaN-like
47	c1ayrA_	Alignment	not modelled	11.6	19	**PDB header:**sensory transduction **Chain:** A: **PDB Molecule:**arrestin; **PDBTitle:** arrestin from bovine rod outer segments
48	c3ue3A_	Alignment	not modelled	11.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
49	d3pmga4	Alignment	not modelled	9.7	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
50	d1kfia4	Alignment	not modelled	8.9	50	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
51	c1sz1A_	Alignment	not modelled	8.7	20	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna nucleotidyltransferase; **PDBTitle:** mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
52	c3b5wE_	Alignment	not modelled	8.5	18	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
53	c3djeA_	Alignment	not modelled	8.1	14	**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
54	c1w7cA_	Alignment	not modelled	8.1	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** pplo at 1.23 angstroms
55	d1p7ga2	Alignment	not modelled	7.8	20	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain

56	d1dfma_	Alignment	not modelled	7.7	50	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglII
57	d2b7oa1	Alignment	not modelled	7.7	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
58	c1gn4B_	Alignment	not modelled	7.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**superoxide dismutase; **PDBTitle:** h145e mutant of mycobacterium tuberculosis iron-superoxide2 dismutase.
59	d2j9ga2	Alignment	not modelled	7.3	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
60	d1d6za1	Alignment	not modelled	7.2	23	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
61	c1pmdA_	Alignment	not modelled	7.1	15	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**peptidoglycan synthesis multifunctional enzyme; **PDBTitle:** penicillin-binding protein 2x (pbp-2x)
62	c1jsyA_	Alignment	not modelled	6.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bovine arrestin-2 (full length); **PDBTitle:** crystal structure of bovine arrestin-2
63	c3higB_	Alignment	not modelled	6.7	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amiloride-sensitive amine oxidase; **PDBTitle:** crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
64	d1w2za1	Alignment	not modelled	6.7	31	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
65	d1idsa2	Alignment	not modelled	6.4	10	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
66	d1f46a_	Alignment	not modelled	6.4	21	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain
67	d1tuea_	Alignment	not modelled	6.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	d1g3pa2	Alignment	not modelled	6.0	71	**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
69	c1px5A_	Alignment	not modelled	5.9	29	**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
70	d1m1la_	Alignment	not modelled	5.9	23	**Fold:**Suppressor of Fused, N-terminal domain **Superfamily:**Suppressor of Fused, N-terminal domain **Family:**Suppressor of Fused, N-terminal domain
71	c2cw3A_	Alignment	not modelled	5.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron superoxide dismutase; **PDBTitle:** x-ray structure of pmsod2, superoxide dismutase from2 perkinsus marinus
72	d1wdjb_	Alignment	not modelled	5.6	33	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
73	c3dgsA_	Alignment	not modelled	5.5	60	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**coat protein a; **PDBTitle:** changing the determinants of protein stability from2 covalent to non-covalent interactions by in-vitro3 evolution: a structural and energetic analysis
74	c1jibA_	Alignment	not modelled	5.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neopullulanase; **PDBTitle:** complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
75	c1ma1E_	Alignment	not modelled	5.4	5	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**superoxide dismutase; **PDBTitle:** structure and properties of the atypical iron superoxide2 dismutase from methanobacterium thermoautotrophicum
76	c1kkcB_	Alignment	not modelled	5.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** crystal structure of aspergillus fumigatus mnsod
77	c1svfB_	Alignment	not modelled	5.3	36	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**protein (fusion glycoprotein); **PDBTitle:** paramyxovirus sv5 fusion protein core
78	c3ot2B_	Alignment	not modelled	5.3	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
79	c3ot2A_	Alignment	not modelled	5.3	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution