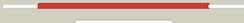
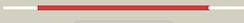
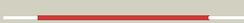
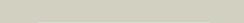


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AAW1
Date	Thu Jan 5 11:13:59 GMT 2012
Unique Job ID	6c17ba53899727f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tebA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease/exonuclease/phosphatase; PDBTitle: endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
2	c3ngoA_	 Alignment		100.0	16	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
3	c3g6sA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative endonuclease/exonuclease/phosphatase PDBTitle: crystal structure of the2 endonuclease/exonuclease/phosphatase (bvu_0621) from3 bacteroides vulgatus. northeast structural genomics4 consortium target bvr56d
4	c3mprB_	 Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: putative endonuclease/exonuclease/phosphatase family PDBTitle: crystal structure of endonuclease/exonuclease/phosphatase family2 protein from bacteroides thetaiotaomicron, northeast structural3 genomics consortium target btr318a
5	c2j63B_	 Alignment		100.0	20	PDB header: lyase Chain: B: PDB Molecule: ap-endonuclease; PDBTitle: crystal structure of ap endonuclease lmap from leishmania2 major
6	c3l1wE_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown conserved2 protein from enterococcus faecalis v583
7	d2ddra1	 Alignment		100.0	19	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
8	c1e9nB_	 Alignment		100.0	21	PDB header: dna repair Chain: B: PDB Molecule: dna-(apurinic or apyrimidinic site) lyase; PDBTitle: a second divalent metal ion in the active site of a new2 crystal form of human apurinic/apyrimidinic endonuclease,3 ape1, and its implications for the catalytic mechanism
9	d1sr4b_	 Alignment		100.0	17	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
10	d1zwxal	 Alignment		100.0	19	Fold: DNase I-like Superfamily: DNase I-like Family: Sphingomyelin phosphodiesterase-like
11	d1akoa_	 Alignment		100.0	21	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like

12	c2jc5A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease; PDBTitle: apurinic apyrimidinic (ap) endonuclease (nape) from2 neisseria meningitidis
13	c3i46B_	Alignment		100.0	16	PDB header: toxin Chain: B: PDB Molecule: beta-hemolysin; PDBTitle: crystal structure of beta toxin from staphylococcus aureus f277a,2 p278a mutant with bound calcium ions
14	c2voaB_	Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: exodeoxyribonuclease iii; PDBTitle: structure of an ap endonuclease from archaeoglobus fulgidus
15	c3g0rA_	Alignment		100.0	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease; PDBTitle: complex of mth0212 and an 8bp dsdna with distorted ends
16	d1vyba_	Alignment		99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
17	d2f1na1	Alignment		99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
18	d1hd7a_	Alignment		99.9	19	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
19	c2jc4A_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease iii; PDBTitle: 3'-5' exonuclease (nexo) from neisseria meningitidis
20	d2a40b1	Alignment		99.9	15	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
21	d1wdua_	Alignment	not modelled	99.9	13	Fold: DNase I-like Superfamily: DNase I-like Family: DNase I-like
22	d2imqx1	Alignment	not modelled	99.9	16	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
23	c2ei9A_	Alignment	not modelled	99.9	15	PDB header: gene regulation Chain: A: PDB Molecule: non-ltr retrotransposon r1bmks orf2 protein; PDBTitle: crystal structure of r1bm endonuclease domain
24	c3mtcA_	Alignment	not modelled	99.9	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: type ii inositol-1,4,5-trisphosphate 5-phosphatase; PDBTitle: crystal structure of inpp5b in complex with phosphatidylinositol 4-2 phosphate
25	c3nr8A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; PDBTitle: crystal structure of human ship2
26	c2xswB_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: 72 kda inositol polyphosphate 5-phosphatase; PDBTitle: crystal structure of human inpp5e
27	d1i9za_	Alignment	not modelled	99.6	14	Fold: DNase I-like Superfamily: DNase I-like Family: Inositol polyphosphate 5-phosphatase (IPP5)
28	d1emsa2	Alignment	not modelled	83.9	7	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase

29	c2w1vA	Alignment	not modelled	61.9	19	PDB header: hydrolase Chain: A: PDB Molecule: nitrilase homolog 2; PDBTitle: crystal structure of mouse nitrilase-2 at 1.4a resolution
30	c2vhiG	Alignment	not modelled	61.7	20	PDB header: hydrolase Chain: G: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from <i>Drosophila melanogaster</i>
31	d1f89a	Alignment	not modelled	60.7	14	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Nitrilase
32	c3hkxA	Alignment	not modelled	53.4	14	PDB header: hydrolase Chain: A: PDB Molecule: amidase; PDBTitle: crystal structure analysis of an amidase from <i>Nesterenkonia</i> sp.
33	c2plqA	Alignment	not modelled	47.0	15	PDB header: hydrolase Chain: A: PDB Molecule: aliphatic amidase; PDBTitle: crystal structure of the amidase from <i>Geobacillus pallidus</i> rapc8
34	c1emsB	Alignment	not modelled	45.2	7	PDB header: antitumor protein Chain: B: PDB Molecule: nit-fragile histidine triad fusion protein; PDBTitle: crystal structure of the <i>C. elegans</i> nitfhit protein
35	c3ilvA	Alignment	not modelled	31.7	17	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from <i>Cytophaga hutchinsonii</i>
36	c2e2kC	Alignment	not modelled	29.2	5	PDB header: hydrolase Chain: C: PDB Molecule: formamidase; PDBTitle: <i>Helicobacter pylori</i> formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
37	c3n05B	Alignment	not modelled	26.6	18	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from <i>Streptomyces2 avermitilis</i>
38	d1uf5a	Alignment	not modelled	22.8	14	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamylase
39	d3bula2	Alignment	not modelled	20.4	21	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
40	c2e11B	Alignment	not modelled	16.1	10	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from <i>Xanthomonas campestris</i> : a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
41	d1xrsb1	Alignment	not modelled	14.3	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
42	c1chmA	Alignment	not modelled	13.6	12	PDB header: creatinase Chain: A: PDB Molecule: creatin amidinohydrolase; PDBTitle: enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
43	c1y80A	Alignment	not modelled	12.9	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from <i>Moraxella thermoacetica</i>
44	c1xrsB	Alignment	not modelled	12.3	11	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
45	c3tliC	Alignment	not modelled	10.4	17	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
46	c3jvvA	Alignment	not modelled	10.4	11	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of <i>P. aeruginosa</i> pilt with bound amp-ppp
47	d7reqa2	Alignment	not modelled	10.1	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
48	d1edqa1	Alignment	not modelled	9.8	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
49	d1ccwa	Alignment	not modelled	9.3	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
50	d1j31a	Alignment	not modelled	9.2	18	Fold: Carbon-nitrogen hydrolase Superfamily: Carbon-nitrogen hydrolase Family: Carbamylase
51	c1bmtB	Alignment	not modelled	8.5	21	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
52	c2yxbA	Alignment	not modelled	8.4	11	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from <i>Aeropyrum pernix</i>
53	c3nrBd	Alignment	not modelled	8.2	24	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from <i>Pseudomonas putida</i> kt2440 at 2.05 a resolution
54	c1k98A	Alignment	not modelled	8.2	21	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment

55	c3menC_	Alignment	not modelled	8.1	14	PDB header: hydrolase Chain: C: PDB Molecule: acetyl polyamine aminohydrolase; PDBTitle: crystal structure of acetyl polyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
56	c2eyuA_	Alignment	not modelled	7.3	11	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilT; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilT
57	c3n0vD_	Alignment	not modelled	7.1	18	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
58	c2qlvB_	Alignment	not modelled	7.0	39	PDB header: transferase/protein binding Chain: B: PDB Molecule: protein sip2; PDBTitle: crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
59	c3ezxA_	Alignment	not modelled	6.8	11	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
60	c3obiC_	Alignment	not modelled	6.6	18	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
61	c3o1lB_	Alignment	not modelled	6.6	35	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
62	d3bzka5	Alignment	not modelled	6.5	6	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
63	c3louB_	Alignment	not modelled	6.5	29	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
64	d2qlvb1	Alignment	not modelled	6.5	39	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
65	d1g6oa_	Alignment	not modelled	6.5	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
66	c3p9xB_	Alignment	not modelled	6.4	13	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
67	c2i2xD_	Alignment	not modelled	6.3	17	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
68	d1p9ra_	Alignment	not modelled	6.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	d2eg6a1	Alignment	not modelled	5.6	50	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Dihydroorotase
70	d1fmfa_	Alignment	not modelled	5.5	22	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
71	c3pn9C_	Alignment	not modelled	5.4	10	PDB header: hydrolase Chain: C: PDB Molecule: proline dipeptidase; PDBTitle: crystal structure of a proline dipeptidase from streptococcus2 pneumoniae tigr4
72	d1hjra_	Alignment	not modelled	5.2	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
73	c3o5vA_	Alignment	not modelled	5.2	14	PDB header: hydrolase Chain: A: PDB Molecule: x-pro dipeptidase; PDBTitle: the crystal structure of the creatinase/prolidase n-terminal domain of2 an x-pro dipeptidase from streptococcus pyogenes to 1.85a
74	d1z0na1	Alignment	not modelled	5.2	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
75	d1q8ia1	Alignment	not modelled	5.1	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
76	c3i7mA_	Alignment	not modelled	5.1	15	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.