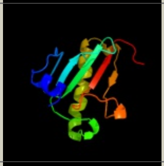
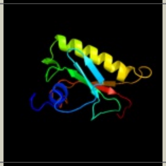
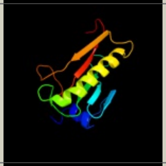
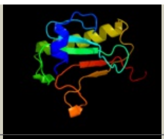
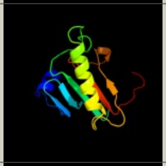
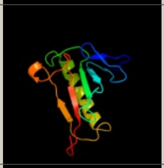
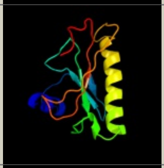
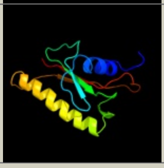
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ACE7
Date	Thu Jan 5 11:18:01 GMT 2012
Unique Job ID	b028095673a9a3df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n1tE_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**hit-like protein hint; **PDBTitle:** crystal structure of the h101a mutant echint gmp complex
2	d1xqua_	Alignment		100.0	48	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
3	c1xquA_	Alignment		100.0	48	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family hydrolase; **PDBTitle:** hit family hydrolase from clostridium thermocellum cth-393
4	d1kpfa_	Alignment		100.0	47	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
5	c3l7xA_	Alignment		100.0	29	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
6	c3ksvA_	Alignment		100.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major
7	d1rzya_	Alignment		100.0	46	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
8	c3o0mB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
9	c3imiB_	Alignment		100.0	29	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
10	c3lb5B_	Alignment		100.0	35	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**hit-like protein involved in cell-cycle regulation; **PDBTitle:** crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
11	c2eo4A_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**150aa long hypothetical histidine triad nucleotide-binding **PDBTitle:** crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7

12	c3anoA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
13	c3oj7A_	Alignment		100.0	44	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative histidine triad family protein; **PDBTitle:** crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
14	d1y23a_	Alignment		100.0	34	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
15	c1emsB_	Alignment		99.9	25	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
16	d1emsa1	Alignment		99.9	22	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
17	c3p0tB_	Alignment		99.9	31	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
18	d2oika1	Alignment		99.9	15	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
19	c3r6fA_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
20	d1guqa2	Alignment		99.9	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
21	d1z84a2	Alignment	not modelled	99.9	10	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
22	d1fita_	Alignment	not modelled	99.9	19	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	c1gupC_	Alignment	not modelled	99.9	13	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** structure of nucleotidyltransferase complexed with udp-2 galactose
24	c1zwjA_	Alignment	not modelled	99.9	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative galactose-1-phosphate uridyl transferase; **PDBTitle:** x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
25	c3i24B_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
26	c3i4sB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
27	c3nrdB_	Alignment	not modelled	99.8	15	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
28	c3oheA_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad protein (maqu_1709)

						from2 marinobacter aquaeolei vt8 at 1.20 a resolution
29	d1z84a1	Alignment	not modelled	99.4	10	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
30	d3bl9a1	Alignment	not modelled	99.4	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
31	c3bl9B_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493
32	d1vlra1	Alignment	not modelled	99.2	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
33	c1xmlA_	Alignment	not modelled	99.0	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock-like protein 1; **PDBTitle:** structure of human dcps
34	d1guqa1	Alignment	not modelled	98.1	10	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
35	d2pofa1	Alignment	not modelled	95.9	17	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**CDH-like
36	c3csqC_	Alignment	not modelled	40.3	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
37	c3hfnA_	Alignment	not modelled	33.4	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**asl2047 protein; **PDBTitle:** crystal structure of an hfq protein from anabaena sp.
38	c1qyuA_	Alignment	not modelled	18.8	41	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
39	d1v9ka_	Alignment	not modelled	17.1	33	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
40	d2cs7a1	Alignment	not modelled	15.4	25	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
41	c2i82D_	Alignment	not modelled	15.1	33	**PDB header:**lyase/rna **Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
42	d2at2a1	Alignment	not modelled	14.4	9	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
43	d1v9fa_	Alignment	not modelled	14.1	41	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
44	c1v9fA_	Alignment	not modelled	14.1	41	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
45	c3hfoC_	Alignment	not modelled	13.5	19	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**ssr3341 protein; **PDBTitle:** crystal structure of an hfq protein from synechocystis sp.
46	c3sdsA_	Alignment	not modelled	12.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
47	d2hnga1	Alignment	not modelled	12.6	12	**Fold:**SecB-like **Superfamily:**SecB-like **Family:**SP1558-like
48	d1ryba_	Alignment	not modelled	12.3	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
49	c1t3bA_	Alignment	not modelled	12.2	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
50	c2qwwB_	Alignment	not modelled	12.1	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
51	c2ef0A_	Alignment	not modelled	11.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
52	d1tuga1	Alignment	not modelled	11.1	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
53	d1vlva1	Alignment	not modelled	10.9	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
54	d1ekxa1	Alignment	not modelled	10.6	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
55	c3gd5D_	Alignment	not modelled	10.5	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
56	d1pg5a1	Alignment	not modelled	10.3	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
57	d1pvva1	Alignment	not modelled	9.6	9	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
58	c3lxmC_	Alignment	not modelled	9.4	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
59	c3l6tB_	Alignment	not modelled	9.4	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobilization protein trai; **PDBTitle:** crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
60	d1otha1	Alignment	not modelled	9.4	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
61	d1dxha1	Alignment	not modelled	9.3	6	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
62	c2qgpA_	Alignment	not modelled	8.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
63	c3vg8F_	Alignment	not modelled	8.4	22	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**hypothetical protein tthb210; **PDBTitle:** crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8
64	d1ex4a1	Alignment	not modelled	8.3	19	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
65	d1ml4a1	Alignment	not modelled	8.1	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
66	c3py7A_	Alignment	not modelled	8.0	7	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,paxillin ld1,protein e6 **PDBTitle:** crystal structure of full-length bovine papillomavirus oncoprotein e62 in complex with ld1 motif of paxillin at 2.3a resolution
67	c2elpA_	Alignment	not modelled	7.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
68	d2jz6a1	Alignment	not modelled	7.9	25	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
69	d2d8ya1	Alignment	not modelled	7.4	11	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
70	c1jzdA_	Alignment	not modelled	7.1	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
71	d1j0ga_	Alignment	not modelled	6.9	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**BM-002-like
72	c1fvoB_	Alignment	not modelled	6.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
73	c3fmbA_	Alignment	not modelled	6.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dimeric protein of unknown function and ferredoxin-like **PDBTitle:** crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
74	c2dnfA_	Alignment	not modelled	6.3	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**doublecortin domain-containing protein 2; **PDBTitle:** solution structure of rsgi ruh-062, a dcx domain from human
75	c3d6nB_	Alignment	not modelled	6.2	8	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
76	c2at2B_	Alignment	not modelled	6.2	9	**PDB header:** **PDB COMPND:**
77	c2rgwD_	Alignment	not modelled	6.1	6	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
78	d1u2ma_	Alignment	not modelled	6.1	11	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
79	c2k6pA_	Alignment	not modelled	6.1	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423;

						PDBTitle: solution structure of hypothetical protein, hp1423
80	d1p4da_	Alignment	not modelled	6.1	8	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
81	c2zaeC_	Alignment	not modelled	6.0	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease p protein component 1; **PDBTitle:** crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
82	d1duvg1	Alignment	not modelled	5.8	6	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
83	c1zq2A_	Alignment	not modelled	5.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
84	d1wira_	Alignment	not modelled	5.4	20	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**variant C2H2 finger
85	d1ihwa_	Alignment	not modelled	5.2	19	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
86	d1abaa_	Alignment	not modelled	5.2	0	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	c1vlvA_	Alignment	not modelled	5.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
88	d1oqka_	Alignment	not modelled	5.2	10	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
89	d1uf0a_	Alignment	not modelled	5.2	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
90	d1wiia_	Alignment	not modelled	5.2	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
91	c3tpfF_	Alignment	not modelled	5.1	23	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
92	d2bo9b2	Alignment	not modelled	5.1	23	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
93	c2p2gD_	Alignment	not modelled	5.1	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form