

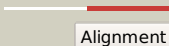



















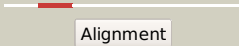
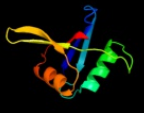




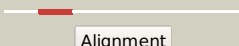

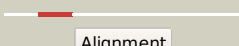
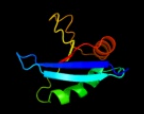
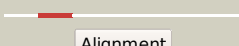

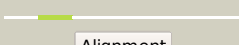
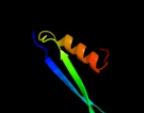

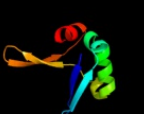


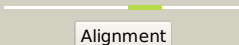
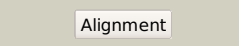




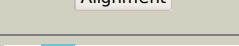
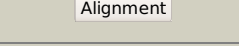


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A1A5B6
Date	Wed Jul 10 14:22:24 BST 2013
Unique Job ID	90d745b2bd215cf8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g77A_	 Alignment		100.0	20	PDB header: hydrolase activator/protein transport Chain: A; PDB Molecule: gtpase-activating protein gyp1; PDBTitle: crystal structure of gyp1 tbc domain in complex with rab332 gtpase bound to gdp and alf3
2	c2qfzB_	 Alignment		100.0	21	PDB header: hydrolase activator Chain: B; PDB Molecule: tbc1 domain family member 22a; PDBTitle: crystal structure of human tbc1 domain family member 22a
3	c4hlqE_	 Alignment		100.0	27	PDB header: hydrolase activator/protein transport Chain: E; PDB Molecule: tbc1 domain family member 20; PDBTitle: crystal structure of human rab1b bound to gdp and bef3 in complex with2 the gap domain of tbc1d20 from homo sapiens
4	c2qq8A_	 Alignment		100.0	25	PDB header: hydrolase activator Chain: A; PDB Molecule: tbc1 domain family member 14; PDBTitle: crystal structure of the putative rabgap domain of human2 tbc1 domain family member 14
5	c3qyeA_	 Alignment		100.0	22	PDB header: hydrolase activator Chain: A; PDB Molecule: tbc1 domain family member 1; PDBTitle: crystal structure of human tbc1d1 rabgap domain
6	c3qybA_	 Alignment		100.0	23	PDB header: hydrolase activator Chain: A; PDB Molecule: tbc1 domain family member 4; PDBTitle: x-ray crystal structure of human tbc1d4 (as160) rabgap domain
7	d1fkma1	 Alignment		100.0	23	Fold: Left-handed superhelix Superfamily: Ypt/Rab-GAP domain of gyp1p Family: Ypt/Rab-GAP domain of gyp1p
8	c3qwlA_	 Alignment		100.0	12	PDB header: hydrolase activator Chain: A; PDB Molecule: tbc1 domain family member 7; PDBTitle: crystal structure of human tbc1 domain family member 7
9	c3dzxA_	 Alignment		100.0	18	PDB header: hydrolase activator Chain: A; PDB Molecule: tbc1 domain family member 22b; PDBTitle: crystal structure of the rabgap domain of human tbc1d22b
10	c3hziB_	 Alignment		100.0	24	PDB header: hydrolase activator Chain: B; PDB Molecule: rab gtpase-activating protein 1-like; PDBTitle: crystal structure of the rabgap domain of the rabgap112 protein
11	d1fkma2	 Alignment		99.6	17	Fold: Left-handed superhelix Superfamily: Ypt/Rab-GAP domain of gyp1p Family: Ypt/Rab-GAP domain of gyp1p

12	d1wmha_	 Alignment		97.9	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
13	c2ktrA_	 Alignment		97.6	15	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
14	d2bkfa1	 Alignment		97.4	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
15	d1wj6a_	 Alignment		97.3	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
16	d1ip9a_	 Alignment		96.6	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
17	d1wmhb_	 Alignment		93.5	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
18	d2i1sa1	 Alignment		63.1	14	Fold: MM3350-like Superfamily: MM3350-like Family: MM3350-like
19	c2c60A_	 Alignment		62.9	22	PDB header: transferase Chain: A: PDB Molecule: human mitogen-activated protein kinase kinase PDBTitle: crystal structure of human mitogen-activated protein kinase2 kinase kinase 3 isoform 2 phox domain at 1.25 a resolution
20	d2c60a1	 Alignment		62.6	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
21	c4gaoA_	 Alignment	not modelled	61.4	9	PDB header: ligase/peptide Chain: A: PDB Molecule: dcn1-like protein 2; PDBTitle: dcnl complex with n-terminally acetylated nedd8 e2 peptide
22	d1jhda2	 Alignment	not modelled	55.0	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
23	d2nptb1	 Alignment	not modelled	54.1	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
24	d1x6va2	 Alignment	not modelled	47.7	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
25	c2qjfb_	 Alignment	not modelled	41.8	19	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'- PDBTitle: crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
26	c1jhdA_	 Alignment	not modelled	41.1	23	PDB header: transferase Chain: A: PDB Molecule: sulfate adenyltransferase; PDBTitle: crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
27	c2wo3B_	 Alignment	not modelled	38.3	24	PDB header: transferase/signaling protein Chain: B: PDB Molecule: ephrin-a2; PDBTitle: crystal structure of the epha4-ephrina2 complex
28	c3kevA_	 Alignment	not modelled	33.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galieria sulfuraria dcn1 domain-containing protein; PDBTitle: x-ray crystal structure of a dcn1 domain-containing protein from2 galdieria sulfuraria

29	c1xjqA	Alignment	not modelled	30.0	19	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
30	c2v6zM	Alignment	not modelled	28.7	26	PDB header: transferase Chain: M: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: solution structure of amino terminal domain of human dna2 polymerase epsilon subunit b
31	c3riuC	Alignment	not modelled	27.5	12	PDB header: hydrolase Chain: C: PDB Molecule: translin associated factor x, isoform b; PDBTitle: crystal structure of drosophila hexameric c3po formed by truncated2 translin and trax
32	d1u5ta1	Alignment	not modelled	26.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
33	c1xnjB	Alignment	not modelled	26.7	19	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
34	c2is9A	Alignment	not modelled	26.3	7	PDB header: transcription Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: structure of yeast dcn-1
35	c2js3B	Alignment	not modelled	25.7	60	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
36	d1wgra	Alignment	not modelled	25.3	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
37	d1x87a	Alignment	not modelled	25.2	24	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
38	d1erda	Alignment	not modelled	24.3	42	Fold: Protozoan pheromone-like Superfamily: Protozoan pheromone proteins Family: Protozoan pheromone proteins
39	c1erdA	Alignment	not modelled	24.3	42	PDB header: pheromone Chain: A: PDB Molecule: pheromone er-2; PDBTitle: the nmr solution structure of the pheromone er-2 from the2 ciliated protozoan euplotes raikovi
40	d1pqsa	Alignment	not modelled	24.2	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
41	c2kc1A	Alignment	not modelled	23.3	12	PDB header: structural protein Chain: A: PDB Molecule: mkiaa1027 protein; PDBTitle: nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
42	d1gtea5	Alignment	not modelled	21.8	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
43	d2cu1a1	Alignment	not modelled	21.7	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
44	c4gbaA	Alignment	not modelled	20.8	10	PDB header: ligase/peptide Chain: A: PDB Molecule: dcn1-like protein 3; PDBTitle: dcn1 complex with n-terminally acetylated nedd8 e2 peptide
45	c3bq3A	Alignment	not modelled	20.1	8	PDB header: cell cycle, ligase Chain: A: PDB Molecule: defective in cullin neddylation protein 1; PDBTitle: crystal structure of s. cerevisiae dcn1
46	d1cexa	Alignment	not modelled	19.5	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
47	d1g8fa2	Alignment	not modelled	18.6	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
48	d1iyb1	Alignment	not modelled	18.6	30	Fold: BRCA2 helical domain Superfamily: BRCA2 helical domain Family: BRCA2 helical domain
49	d1uwka	Alignment	not modelled	18.2	14	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
50	d1zkda1	Alignment	not modelled	17.8	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: RPA4359-like
51	c2rdcA	Alignment	not modelled	17.6	24	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
52	d1m8pa2	Alignment	not modelled	17.6	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: ATP sulfurylase catalytic domain
53	c2r83B	Alignment	not modelled	17.4	19	PDB header: endocytosis, exocytosis Chain: B: PDB Molecule: synaptotagmin-1; PDBTitle: crystal structure analysis of human synaptotagmin 1 c2a-c2b
54	c4f3nA	Alignment	not modelled	17.0	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized acr, cog1565 superfamily; PDBTitle: high resolution native crystal structure of an uncharacterized acr,2 cog1565 superfamily protein from burkholderia thailandensis, solved3 by iodide ion sad
						Fold: OB-fold

55	d1k28a1	Alignment	not modelled	16.7	41	Superfamily: gp5 N-terminal domain-like Family: gp4 N-terminal domain-like
56	c2fknC	Alignment	not modelled	15.8	17	PDB header: lyase Chain: C: PDB Molecule: urocanate hydratase; PDBTitle: crystal structure of urocanase from bacillus subtilis
57	d1xsva	Alignment	not modelled	15.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
58	d1v92a	Alignment	not modelled	15.4	44	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TAP-C domain-like
59	c2datA	Alignment	not modelled	15.4	15	PDB header: transcription Chain: A: PDB Molecule: possible global transcription activator snf212; PDBTitle: solution structure of the bromodomain of human swi/snf2 related matrix associated actin dependent regulator of3 cromatin subfamily a member 2
60	c1sghA	Alignment	not modelled	15.4	30	PDB header: structural protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin ferm domain bound to ebp50 c-terminal peptide
61	c2h89B	Alignment	not modelled	15.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
62	c2I92A	Alignment	not modelled	14.6	54	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f
63	c3rjoA	Alignment	not modelled	14.3	10	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of erap1 peptide binding domain
64	c2I1jA	Alignment	not modelled	14.3	25	PDB header: cell adhesion, membrane protein Chain: A: PDB Molecule: moesin; PDBTitle: moesin from spodoptera frugiperda at 2.1 angstroms resolution
65	d1wt8a1	Alignment	not modelled	13.9	80	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
66	c3mzyA	Alignment	not modelled	13.4	11	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
67	d1n0ea	Alignment	not modelled	13.3	13	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
68	c2g0bG	Alignment	not modelled	13.2	8	PDB header: transferase Chain: G: PDB Molecule: feem; PDBTitle: the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
69	c1n0fF	Alignment	not modelled	13.2	13	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mraz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
70	c3hugA	Alignment	not modelled	12.9	16	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
71	c3vpbF	Alignment	not modelled	12.9	43	PDB header: ligase Chain: F: PDB Molecule: alpha-aminoadipate carrier protein lysw; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
72	c3axjB	Alignment	not modelled	11.9	17	PDB header: dna binding protein Chain: B: PDB Molecule: translin associated factor x, isoform b; PDBTitle: high resolution crystal structure of c3po
73	d3d7ca1	Alignment	not modelled	11.7	13	Fold: Bromodomain-like Superfamily: Bromodomain Family: Bromodomain
74	c2j89A	Alignment	not modelled	11.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine sulfoxide reductase a; PDBTitle: functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
75	c2damA	Alignment	not modelled	11.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: etea protein; PDBTitle: solution structure of the novel identified uba-like domain2 in the n-terminal of human etea protein
76	c3vepA	Alignment	not modelled	11.3	19	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
77	c3se6A	Alignment	not modelled	11.1	14	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 2; PDBTitle: crystal structure of the human endoplasmic reticulum aminopeptidase 2
78	c4f5cA	Alignment	not modelled	11.0	11	PDB header: hydrolase/viral protein Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of the spike receptor binding domain of a porcine2 respiratory coronavirus in complex with the pig aminopeptidase n3 ectodomain
79	c1a6cA	Alignment	not modelled	10.9	19	PDB header: virus Chain: A: PDB Molecule: tobacco ringspot virus capsid protein; PDBTitle: structure of tobacco ringspot virus
						Fold: DNA/RNA-binding 3-helical bundle

80	d1s7oa_	Alignment	not modelled	10.8	17	Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
81	c1kilE_	Alignment	not modelled	10.8	57	PDB header: membrane protein Chain: E; PDB Molecule: complexin i snare-complex binding region; PDBTitle: three-dimensional structure of the complexin/snare complex
82	d2hzaa1	Alignment	not modelled	10.7	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
83	c3qztA_	Alignment	not modelled	10.6	13	PDB header: transcription/nuclear protein Chain: A; PDB Molecule: nucleosome-remodeling factor subunit bptf; PDBTitle: crystal structure of bptf bromo in complex with histone h4k16ac - form2 ii
84	c1p0oA_	Alignment	not modelled	10.5	21	PDB header: ribosome Chain: A; PDB Molecule: 19-mer peptide from 50s ribosomal protein l1; PDBTitle: hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
85	c3hzuA_	Alignment	not modelled	10.5	22	PDB header: transferase Chain: A; PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
86	c3piiA_	Alignment	not modelled	10.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
87	d1shxa1	Alignment	not modelled	9.7	27	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Ephrin ectodomain
88	c2x11B_	Alignment	not modelled	9.7	27	PDB header: receptor/signaling protein Chain: B; PDB Molecule: ephrin-a5; PDBTitle: crystal structure of the complete epha2 ectodomain in2 complex with ephrin a5 receptor binding domain
89	c2emtB_	Alignment	not modelled	9.5	30	PDB header: cell adhesion Chain: B; PDB Molecule: radixin; PDBTitle: crystal structure analysis of the radixin ferm domain2 complexed with adhesion molecule psgl-1
90	c3fmxX_	Alignment	not modelled	9.5	36	PDB header: oxidoreductase Chain: X; PDB Molecule: tartrate dehydrogenase/decarboxylase; PDBTitle: crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
91	d1pugb_	Alignment	not modelled	9.1	22	Fold: YbaB-like Superfamily: YbaB-like Family: YbaB-like
92	c1gg3A_	Alignment	not modelled	9.1	16	PDB header: membrane protein Chain: A; PDB Molecule: erythroid membrane protein 4.1r; PDBTitle: crystal structure of the protein 4.1r membrane binding2 domain
93	d1q1oa_	Alignment	not modelled	8.9	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
94	d1miva1	Alignment	not modelled	8.9	31	Fold: BRCA2 helical domain Superfamily: BRCA2 helical domain Family: BRCA2 helical domain
95	d2f1ka1	Alignment	not modelled	8.5	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
96	c3zc1E_	Alignment	not modelled	8.4	13	PDB header: hydrolase Chain: E; PDB Molecule: aftrx; PDBTitle: crystal structure of afc3po
97	c3nxbB_	Alignment	not modelled	8.3	11	PDB header: transcription Chain: B; PDB Molecule: cat eye syndrome critical region protein 2; PDBTitle: crystal structure of the bromodomain of human cecr2
98	d1c20a_	Alignment	not modelled	8.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
99	d2c5lc1	Alignment	not modelled	8.1	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD