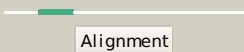

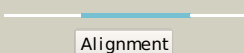
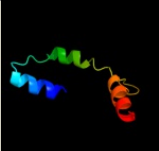
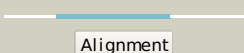

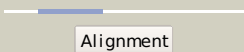

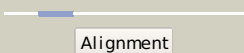
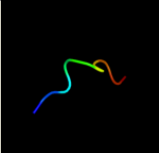
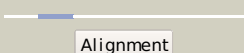
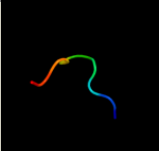
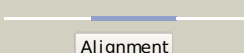
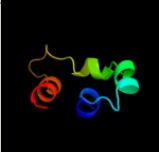
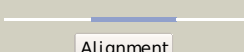

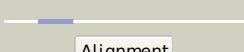

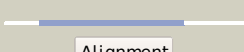
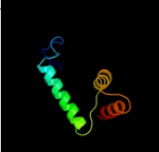
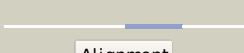












Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ADN2
Date	Thu Jan 5 11:21:25 GMT 2012
Unique Job ID	3d423dd00147618d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b74a1	 Alignment		41.0	30	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
2	c2z7bA	 Alignment		39.1	15	PDB header: lyase Chain: A: PDB Molecule: mlr6791 protein; PDBTitle: crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
3	c3e0dA	 Alignment		30.7	28	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase iii subunit alpha; PDBTitle: insights into the replisome from the crystal structure of the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
4	d2efva1	 Alignment		28.8	22	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: MJ0366-like
5	c2jfnA	 Alignment		25.8	50	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
6	c2ohoA	 Alignment		23.4	30	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
7	d1or7c	 Alignment		23.4	19	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
8	c1or7C	 Alignment		23.4	19	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
9	c2jfoB	 Alignment		22.7	30	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
10	c3pt8B	 Alignment		21.1	9	PDB header: oxygen transport Chain: B: PDB Molecule: hemoglobin iii; PDBTitle: structure of hbii-iii-cn from lucina pectinata at ph 5.0
11	c2qdiA	 Alignment		20.1	32	PDB header: antitumor protein Chain: A: PDB Molecule: retinoblastoma-associated protein; PDBTitle: crystal structure of the retinoblastoma protein n-domain2 provides insight into tumor suppression, ligand3 interaction and holoprotein architecture

12	c3outC_	Alignment		19.8	30	PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
13	c2jfbB_	Alignment		19.7	40	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
14	c3hfrA_	Alignment		17.4	30	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
15	c2jfqA_	Alignment		17.2	30	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
16	c2dwuA_	Alignment		16.9	40	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
17	c2gzmB_	Alignment		16.7	30	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus2 anthracis
18	c1b74A_	Alignment		16.7	30	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
19	d1pl8a2	Alignment		16.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
20	c1zuwA_	Alignment		15.5	40	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
21	d1uwya2	Alignment	not modelled	14.5	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases
22	c2qfiB_	Alignment	not modelled	14.4	9	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump yieF; PDBTitle: structure of the zinc transporter yiiP
23	d1skza1	Alignment	not modelled	14.0	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Huristasin-like
24	d2qfia2	Alignment	not modelled	13.7	9	Fold: Cation efflux protein transmembrane domain-like Superfamily: Cation efflux protein transmembrane domain-like Family: Cation efflux protein transmembrane domain-like
25	c3ajfA_	Alignment	not modelled	11.4	19	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: structural insights into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
26	d1ckma1	Alignment	not modelled	11.3	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
27	c2kvsA_	Alignment	not modelled	11.3	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mw0776; PDBTitle: nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target3 zr215
28	c3r6uA_	Alignment	not modelled	10.9	7	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opubc from bacillus2 subtilis

29	d2ea9a1	Alignment	not modelled	9.6	31	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
30	c3d9oB	Alignment	not modelled	9.6	8	PDB header: transcription Chain: B: PDB Molecule: rna-binding protein 16; PDBTitle: snapshots of the rna processing factor scaf8 bound to different2 phosphorylated forms of the carboxy-terminal domain of rna-polymerase3 ii
31	c2bnlE	Alignment	not modelled	9.5	12	PDB header: stress-response Chain: E: PDB Molecule: modulator protein rsbr; PDBTitle: the structure of the n-terminal domain of rsbr
32	c3fp5A	Alignment	not modelled	9.4	9	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl-coa binding protein; PDBTitle: crystal structure of acbp from moniliophthora perniciosa
33	c1vjgB	Alignment	not modelled	9.3	25	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
34	d2h28a1	Alignment	not modelled	9.2	28	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
35	c3dofB	Alignment	not modelled	8.8	5	PDB header: signaling protein/hydrolase Chain: B: PDB Molecule: adp-ribosylation factor-like protein 2-binding PDBTitle: complex of arl2 and bart, crystal form 2
36	c2hnhA	Alignment	not modelled	8.8	17	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
37	c2jzfA	Alignment	not modelled	8.7	50	PDB header: viral protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
38	c2kqvA	Alignment	not modelled	8.4	13	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: sars coronavirus-unique domain (sud): three-domain molecular2 architecture in solution and rna binding. i: structure of the sud-m3 domain of sud-mc
39	d2ixoa1	Alignment	not modelled	8.4	27	Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
40	d2fmma1	Alignment	not modelled	8.2	71	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
41	c2i6oA	Alignment	not modelled	7.9	26	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
42	d1e3ja2	Alignment	not modelled	7.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
43	d1nb5i	Alignment	not modelled	7.4	20	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cystatins
44	c2k0sA	Alignment	not modelled	7.0	5	PDB header: structural protein Chain: A: PDB Molecule: adp-ribosylation factor-like protein 2-binding PDBTitle: solution nmr structure of protein bc066483
45	d2inwa1	Alignment	not modelled	7.0	28	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
46	d1nxza2	Alignment	not modelled	6.8	27	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
47	c3sb1B	Alignment	not modelled	6.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hydrogenase expression protein; PDBTitle: hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
48	c3s4oB	Alignment	not modelled	6.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
49	d1hvxa1	Alignment	not modelled	6.4	28	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
50	d2di0a1	Alignment	not modelled	6.3	18	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
51	c2wsc1	Alignment	not modelled	6.3	26	PDB header: photosynthesis Chain: 1: PDB Molecule: at3g54890; PDBTitle: improved model of plant photosystem i
52	d1eg3a2	Alignment	not modelled	6.2	29	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
53	d1dwka2	Alignment	not modelled	6.2	23	Fold: Cyanase C-terminal domain Superfamily: Cyanase C-terminal domain Family: Cyanase C-terminal domain
54	c1uwyA	Alignment	not modelled	6.1	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase m; PDBTitle: crystal structure of human carboxypeptidase m

55	d1p16a1	Alignment	not modelled	6.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
56	d1k18a_	Alignment	not modelled	6.0	60	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
57	c1hn3A_	Alignment	not modelled	5.8	26	PDB header: antitumor protein Chain: A: PDB Molecule: p19 arf protein; PDBTitle: solution structure of the n-terminal 37 amino acids of the2 mouse arf tumor suppressor protein
58	c1ztoA_	Alignment	not modelled	5.7	23	PDB header: potassium channel Chain: A: PDB Molecule: potassium channel protein rck4; PDBTitle: inactivation gate of potassium channel rck4, nmr, 82 structures
59	c3kw2A_	Alignment	not modelled	5.7	33	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
60	c1t8jA_	Alignment	not modelled	5.6	50	PDB header: de novo protein Chain: A: PDB Molecule: bba5; PDBTitle: nmr structure of bba5, a compact, independently folded bba2 motif
61	d2fmla1	Alignment	not modelled	5.5	75	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Nudix-associated domain
62	c1y32A_	Alignment	not modelled	5.5	100	PDB header: unknown function Chain: A: PDB Molecule: humanin; PDBTitle: nmr structure of humanin in 30% tfe solution
63	c2z0vA_	Alignment	not modelled	5.4	15	PDB header: endocytosis Chain: A: PDB Molecule: sh3-containing grb2-like protein 3; PDBTitle: crystal structure of bar domain of endophilin-iii
64	d1r9ja3	Alignment	not modelled	5.4	19	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
65	c1cpbB_	Alignment	not modelled	5.4	20	PDB header: hydrolase (c-terminal peptidase) Chain: B: PDB Molecule: carboxypeptidase b; PDBTitle: structure of carboxypeptidase b at 2.8 angstroms resolution
66	c3entB_	Alignment	not modelled	5.4	38	PDB header: structural protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of nitroliin, a betagamma-crystallin from2 nitrosospira multiformis-in alternate space group (p65)
67	d2j7ja3	Alignment	not modelled	5.4	20	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
68	c2egwB_	Alignment	not modelled	5.3	40	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rna methyltransferase with sah ligand
69	c2bn8A_	Alignment	not modelled	5.3	42	PDB header: cell cycle protein Chain: A: PDB Molecule: cell division activator ceda; PDBTitle: solution structure and interactions of the e.coli cellI2 division activator protein ceda
70	c3ulxA_	Alignment	not modelled	5.3	32	PDB header: dna binding protein Chain: A: PDB Molecule: stress-induced transcription factor nac1; PDBTitle: crystal structural of the conserved domain of rice stress-responsive2 nac1
71	d2ptfa1	Alignment	not modelled	5.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
72	c3aqoD_	Alignment	not modelled	5.2	21	PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
73	d1ut7a_	Alignment	not modelled	5.1	29	Fold: NAC domain Superfamily: NAC domain Family: NAC domain
74	c2boaB_	Alignment	not modelled	5.1	20	PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase a4; PDBTitle: human procarboxypeptidase a4.