



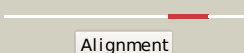

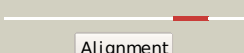



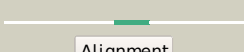

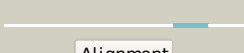

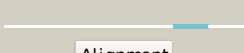


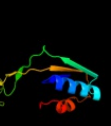



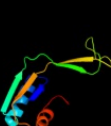

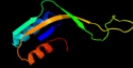




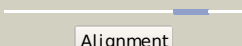

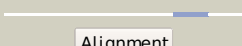

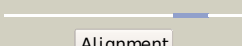

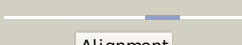




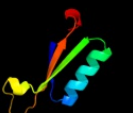

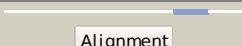
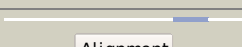
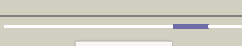

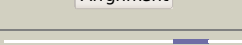
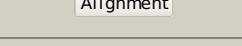
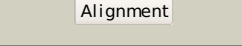



Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P15032
Date	Thu Jan 5 11:34:17 GMT 2012
Unique Job ID	dfc42f2183d2aba1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h4rA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
2	c3l0aA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
3	c1w36E_	 Alignment		97.6	21	PDB header: recombination Chain: E: PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
4	d1w36b3	 Alignment		96.7	19	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
5	d1rhoa_	 Alignment		54.1	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
6	d2fhzb1	 Alignment		48.6	56	Fold: Colicin D/E5 nuclease domain Superfamily: Colicin D/E5 nuclease domain Family: Colicin E5 nuclease domain
7	c2nuhA_	 Alignment		37.6	18	PDB header: unknown function Chain: A: PDB Molecule: periplasmic divalent cation tolerance protein; PDBTitle: crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
8	c2v43A_	 Alignment		36.2	36	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
9	d1nzaa_	 Alignment		34.3	18	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
10	d1naqa_	 Alignment		33.2	26	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
11	c2zomC_	 Alignment		32.2	18	PDB header: unknown function Chain: C: PDB Molecule: protein cuta, chloroplast, putative, expressed; PDBTitle: crystal structure of cuta1 from oryza sativa

12	c3ahpA	 Alignment		31.1	14	PDB header: electron transport Chain: A: PDB Molecule: cuta1; PDBTitle: crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
13	d1k8ta	 Alignment		30.7	16	Fold: Adenylyl cyclase toxin (the edema factor) Superfamily: Adenylyl cyclase toxin (the edema factor) Family: Adenylyl cyclase toxin (the edema factor)
14	c3bb5B	 Alignment		30.2	20	PDB header: unknown function Chain: B: PDB Molecule: stress responsive alpha-beta protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
15	d2zfha1	 Alignment		29.5	16	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
16	c1xk8A	 Alignment		29.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: divalent cation tolerant protein cuta; PDBTitle: divalent cation tolerant protein cuta from homo sapiens2 o60888
17	c2zfha	 Alignment		29.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cuta; PDBTitle: crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
18	c3d0iA	 Alignment		28.5	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ca_c3497; PDBTitle: crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
19	c1fybA	 Alignment		27.2	60	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: proteinase inhibitor; PDBTitle: solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana alata
20	d1p1la	 Alignment		25.2	19	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
21	d1vhfa	 Alignment	not modelled	22.6	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
22	d1osce	 Alignment	not modelled	21.9	15	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
23	d1ukua	 Alignment	not modelled	20.5	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
24	d1kr4a	 Alignment	not modelled	19.7	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
25	d3bgea1	 Alignment	not modelled	18.7	18	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
26	d3ctda1	 Alignment	not modelled	18.2	21	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
27	d1ajwa	 Alignment	not modelled	18.2	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
28	c3et6A	 Alignment	not modelled	15.0	13	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
29	d1gpja1	 Alignment	not modelled	15.0	14	Fold: Glutamyl tRNA-reductase dimerization domain Superfamily: Glutamyl tRNA-reductase dimerization domain

					Family: Glutamyl tRNA-reductase dimerization domain
30	c3nj2B_	Alignment	not modelled	14.9	27 PDB header: unknown function Chain: B: PDB Molecule: duf269-containing protein; PDBTitle: crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
31	c3iyuY_	Alignment	not modelled	14.4	14 PDB header: virus Chain: Y: PDB Molecule: outer capsid protein vp4; PDBTitle: atomic model of an infectious rotavirus particle
32	c3g43F_	Alignment	not modelled	13.6	30 PDB header: metal binding protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel subunit PDBTitle: crystal structure of the calmodulin-bound cav1.2 c-terminal2 regulatory domain dimer
33	c3kolA_	Alignment	not modelled	13.2	44 PDB header: metal binding protein Chain: A: PDB Molecule: glyoxalase/bleomycin resistance PDBTitle: crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
34	dlpjua1	Alignment	not modelled	12.9	50 Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
35	c1h4tD_	Alignment	not modelled	12.6	24 PDB header: aminoacyl-trna synthetase Chain: D: PDB Molecule: prolyl-trna synthetase; PDBTitle: prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
36	c1wq6A_	Alignment	not modelled	12.5	29 PDB header: oncoprotein Chain: A: PDB Molecule: aml1-eto; PDBTitle: the tetramer structure of the nervy homolgy two (nhr2) domain of aml1-eto is critical for aml1-eto's activity
37	c2o61A_	Alignment	not modelled	12.3	32 PDB header: transcription/dna Chain: A: PDB Molecule: transcription factor p65/interferon regulatory factor PDBTitle: crystal structure of nfkb, irf7, irf3 bound to the interferon-b2 enhancer
38	c2q2kA_	Alignment	not modelled	12.0	9 PDB header: dna binding protein/dna Chain: A: PDB Molecule: hypothetical protein; PDBTitle: structure of nucleic-acid binding protein
39	d4sgbi_	Alignment	not modelled	11.8	60 Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
40	d1nr3a_	Alignment	not modelled	11.3	5 Fold: DNA-binding protein Tfx Superfamily: DNA-binding protein Tfx Family: DNA-binding protein Tfx
41	c3mcrA_	Alignment	not modelled	11.1	32 PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
42	c2qycA_	Alignment	not modelled	10.8	24 PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
43	d1oyvi_	Alignment	not modelled	10.7	50 Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
44	c2l1nA_	Alignment	not modelled	10.7	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
45	c3bn7A_	Alignment	not modelled	10.7	16 PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution
46	d1k3ka_	Alignment	not modelled	10.5	16 Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
47	c2khrA_	Alignment	not modelled	10.3	67 PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
48	c2xgfA_	Alignment	not modelled	9.9	26 PDB header: viral protein Chain: A: PDB Molecule: long tail fiber protein p37; PDBTitle: structure of the bacteriophage t4 long tail fibre needle-2 shaped receptor-binding tip
49	c3nsjA_	Alignment	not modelled	9.3	19 PDB header: immune system Chain: A: PDB Molecule: perforin-1; PDBTitle: the x-ray crystal structure of lymphocyte perforin
50	c1w36F_	Alignment	not modelled	9.1	12 PDB header: recombination Chain: F: PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
51	d1azsb_	Alignment	not modelled	8.8	14 Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
52	c2oevA_	Alignment	not modelled	8.3	15 PDB header: protein transport Chain: A: PDB Molecule: programmed cell death 6-interacting protein; PDBTitle: crystal structure of alix/aip1
53	d1leha2	Alignment	not modelled	8.3	20 Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
54	d2f23a1	Alignment	not modelled	8.2	22 Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
55	c2rmsB_	Alignment	not modelled	8.2	32 PDB header: transcription Chain: B: PDB Molecule: msin3a-binding protein;

						PDBTitle: solution structure of the msln3a pah1-sap25 sid complex
56	c2bf9A_	Alignment	not modelled	7.9	17	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic2 polypeptide at 0.99 angstroms resolution.
57	d1fyba1	Alignment	not modelled	7.7	60	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
58	d2ftxa1	Alignment	not modelled	7.5	53	Fold: Kinetochore globular domain-like Superfamily: Kinetochore globular domain Family: Spc25-like
59	c2hr5B_	Alignment	not modelled	7.3	20	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
60	c3ctdB_	Alignment	not modelled	7.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative atpase, aaa family; PDBTitle: crystal structure of a putative aaa family atpase from2 prochlorococcus marinus subsp. pastoris
61	d1g7oa1	Alignment	not modelled	7.1	21	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
62	c1tz5A_	Alignment	not modelled	7.1	17	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
63	d1tzfa_	Alignment	not modelled	7.0	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
64	c3u7vA_	Alignment	not modelled	7.0	36	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
65	c2xnsC_	Alignment	not modelled	6.8	71	PDB header: hydrolase/peptide Chain: C: PDB Molecule: regulator of g-protein signaling 14; PDBTitle: crystal structure of human g alpha i1 bound to a designed helical2 peptide derived from the goloco motif of rgs14
66	c1hk8A_	Alignment	not modelled	6.6	44	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
67	d1hk8a_	Alignment	not modelled	6.6	44	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
68	d1xpm2	Alignment	not modelled	6.5	14	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
69	d3erja1	Alignment	not modelled	6.5	22	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
70	c2hfvA_	Alignment	not modelled	6.3	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
71	c3f4yF_	Alignment	not modelled	6.3	26	PDB header: viral protein Chain: F: PDB Molecule: mutant peptide derived from hiv gp41 chr domain; PDBTitle: hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
72	d1f06a2	Alignment	not modelled	6.2	23	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
73	d1m8aa_	Alignment	not modelled	6.1	45	Fold: IL8-like Superfamily: Interleukin 8-like chemokines Family: Interleukin 8-like chemokines
74	c2rbca_	Alignment	not modelled	6.1	8	PDB header: transferase Chain: A: PDB Molecule: sugar kinase; PDBTitle: crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
75	d1tiha_	Alignment	not modelled	6.1	60	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
76	c1xtyD_	Alignment	not modelled	6.0	18	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
77	d1q7sa_	Alignment	not modelled	5.9	20	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
78	d1dl6a_	Alignment	not modelled	5.9	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
79	c3g7pA_	Alignment	not modelled	5.9	21	PDB header: unknown function Chain: A: PDB Molecule: nitrogen fixation protein; PDBTitle: crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
80	c2wx6B_	Alignment	not modelled	5.8	44	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxidase ycdb; PDBTitle: x-ray crystallographic structure of e. coli apo-efeb

81	c2dezA_	Alignment	not modelled	5.8	31	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy
82	c3be3A_	Alignment	not modelled	5.8	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
83	c1ronA_	Alignment	not modelled	5.7	13	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
84	d2gvka1	Alignment	not modelled	5.7	50	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like
85	d1rlka_	Alignment	not modelled	5.6	12	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
86	c2yy8B_	Alignment	not modelled	5.6	29	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
87	d1q4ra_	Alignment	not modelled	5.5	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
88	d2o3aa1	Alignment	not modelled	5.5	29	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
89	d2i2la1	Alignment	not modelled	5.4	24	Fold: YopX-like Superfamily: YopX-like Family: YopX-like
90	d1nrja_	Alignment	not modelled	5.4	41	Fold: Profilin-like Superfamily: SNARE-like Family: SRP alpha N-terminal domain-like
91	c3c18B_	Alignment	not modelled	5.4	9	PDB header: transferase Chain: B: PDB Molecule: nucleotidyltransferase-like protein; PDBTitle: crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
92	c1jsuC_	Alignment	not modelled	5.4	35	PDB header: complex (transferase/cyclin/inhibitor) Chain: C: PDB Molecule: p27; PDBTitle: p27(kip1)/cyclin a/cdk2 complex
93	c2om2B_	Alignment	not modelled	5.4	86	PDB header: signaling protein Chain: B: PDB Molecule: regulator of g-protein signalling 14 goloco PDBTitle: crystal structure of human g[alpha]i1 bound to the goloco2 motif of rgs14
94	d1wz3a1	Alignment	not modelled	5.4	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: APG12-like
95	d2o8sa1	Alignment	not modelled	5.3	21	Fold: AGR C 984p-like Superfamily: AGR C 984p-like Family: AGR C 984p-like
96	c2rp4C_	Alignment	not modelled	5.3	24	PDB header: transcription Chain: C: PDB Molecule: transcription factor p53; PDBTitle: solution structure of the oligomerization domain in dmp53
97	c2d3kA_	Alignment	not modelled	5.3	24	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2 horikoshii ot3
98	d1tr0a_	Alignment	not modelled	5.3	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
99	c2i4nA_	Alignment	not modelled	5.2	36	PDB header: cytokine Chain: A: PDB Molecule: c-c motif chemokine 21; PDBTitle: solution structure of the chemokine ccl21