

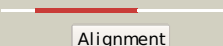

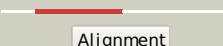



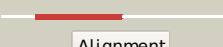
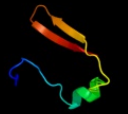
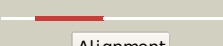


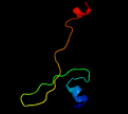



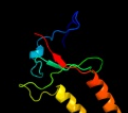

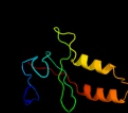










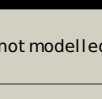


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P15373
Date	Thu Jan 5 11:34:46 GMT 2012
Unique Job ID	192fa70646c8c03e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w1tB_	 Alignment		98.6	21	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
2	c2l66B_	 Alignment		98.2	29	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrB family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrB2 superfamily from archaea.
3	c2ro5B_	 Alignment		97.5	23	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
4	d2fy9a1	 Alignment		97.2	26	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
5	d1yfa1	 Alignment		97.1	21	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
6	c2glwA_	 Alignment		97.0	27	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
7	d1ub4c_	 Alignment		95.6	22	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addition antidote
8	d1mvfd_	 Alignment		94.9	24	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Kis/PemI addition antidote
9	d1n0ea_	 Alignment		90.6	14	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
10	c1n0ff_	 Alignment		90.4	14	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
11	d2d9ra1	 Alignment		84.6	32	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like

12	d1ylea1	Alignment		83.7	14	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
13	d2vbua1	Alignment		78.2	41	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
14	c2c45F_	Alignment		76.0	20	PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase precursor; PDBTitle: native precursor of pyruvoyl dependent aspartate2 decarboxylase
15	c3o27B_	Alignment		73.8	29	PDB header: dna binding protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of c68 from the hybrid virus-plasmid pssvx
16	d1ppya_	Alignment		71.6	18	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
17	c1pt1B_	Alignment		71.6	16	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
18	c2155A_	Alignment		67.6	27	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
19	c1zeqX_	Alignment		67.1	19	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
20	c2pjhB_	Alignment		61.1	16	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
21	d2p19a1	Alignment	not modelled	55.5	17	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
22	c2kdoA_	Alignment	not modelled	49.4	18	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome maturation protein sbds; PDBTitle: structure of the human shwachman-bodian-diamond syndrome protein, sbds
23	d2c4ka1	Alignment	not modelled	48.4	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
24	d2fa1a1	Alignment	not modelled	48.3	14	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
25	c3l17A_	Alignment	not modelled	47.0	15	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
26	d1u9ya1	Alignment	not modelled	45.9	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
27	d2ikka1	Alignment	not modelled	44.2	17	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
28	c2ra5A_	Alignment	not modelled	44.0	19	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
						Fold: Chorismate lyase-like

29	d2ra5a1	Alignment	not modelled	44.0	19	Superfamily: Chorismate lyase-like Family: UTRA domain
30	d1cz5a1	Alignment	not modelled	42.1	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
31	d3cnva1	Alignment	not modelled	41.8	24	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
32	c1zc1A_	Alignment	not modelled	41.5	24	PDB header: protein turnover Chain: A: PDB Molecule: ubiquitin fusion degradation protein 1; PDBTitle: ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
33	d2pkha1	Alignment	not modelled	40.8	12	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
34	c3pjyB_	Alignment	not modelled	40.5	25	PDB header: transcription regulator Chain: B: PDB Molecule: hypothetical signal peptide protein; PDBTitle: crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
35	c3m7aA_	Alignment	not modelled	39.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of saro_0823 (yp_496102.1) a protein of2 unknown function from novosphingobium aromaticivorans dsm3 12444 at 1.22 a resolution
36	d3bwga2	Alignment	not modelled	36.8	20	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
37	d1dkua1	Alignment	not modelled	35.4	8	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
38	c1cz5A_	Alignment	not modelled	34.8	18	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
39	d1vlfm1	Alignment	not modelled	33.4	28	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c1zzvA_	Alignment	not modelled	33.4	15	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: iron(iii) dicitrate transport protein fecA; PDBTitle: solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter fecA from3 escherichia coli.
41	d2axti1	Alignment	not modelled	32.5	36	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein I, Psbl Family: Psbl-like
42	c2yujA_	Alignment	not modelled	31.3	16	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
43	c2ki8A_	Alignment	not modelled	30.5	28	PDB header: oxidoreductase Chain: A: PDB Molecule: tungsten formylmethanofuran dehydrogenase, PDBTitle: solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
44	c2k4vA_	Alignment	not modelled	30.5	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1076; PDBTitle: solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
45	d1zq1a1	Alignment	not modelled	28.3	14	Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
46	d1we0a1	Alignment	not modelled	27.6	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
47	d2fug21	Alignment	not modelled	24.8	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: NQO2-like
48	d2f23a2	Alignment	not modelled	24.6	21	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
49	c2jwB_	Alignment	not modelled	24.6	14	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
50	c3lhaA_	Alignment	not modelled	23.7	23	PDB header: transcription regulator Chain: A: PDB Molecule: gntR family transcriptional regulator; PDBTitle: the crystal structure of the c-terminal domain of a gntR2 family transcriptional regulator from bacillus anthracis3 str. sterne
51	d1yexa1	Alignment	not modelled	23.4	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
52	c2oqkA_	Alignment	not modelled	23.4	14	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
53	c1q6xA_	Alignment	not modelled	23.0	9	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
						Fold: OB-fold

54	d1u0la1	Alignment	not modelled	23.0	17	Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
55	d1zvvl1	Alignment	not modelled	22.1	15	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
56	c2c4kD	Alignment	not modelled	22.0	11	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
57	c3hvxB	Alignment	not modelled	21.7	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
58	d1qr5a	Alignment	not modelled	21.7	13	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
59	d2ifea	Alignment	not modelled	21.6	14	Fold: IF3-like Superfamily: Translation initiation factor IF3, C-terminal domain Family: Translation initiation factor IF3, C-terminal domain
60	d1ka5a	Alignment	not modelled	21.5	13	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
61	c1t95A	Alignment	not modelled	21.5	12	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein af0491; PDBTitle: crystal structure of the shwachman-bodian-diamond syndrome2 protein orthologue from archaeoglobus fulgidus
62	d3d31a1	Alignment	not modelled	20.8	18	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
63	c3hfiA	Alignment	not modelled	20.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative regulator; PDBTitle: the crystal structure of the putative regulator from escherichia coli2 cft073
64	c3dahB	Alignment	not modelled	20.3	11	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
65	c3ho6B	Alignment	not modelled	19.9	16	PDB header: toxin Chain: B: PDB Molecule: toxin a; PDBTitle: structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
66	c3f8lC	Alignment	not modelled	19.7	11	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional repressor phnf; PDBTitle: crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
67	c2wbmA	Alignment	not modelled	19.4	16	PDB header: rna-binding protein Chain: A: PDB Molecule: ribosome maturation protein sdo1 homolog; PDBTitle: crystal structure of mthsbds, the homologue of the2 shwachman-bodian-diamond syndrome protein in the3 euriarchaeon methanothermobacter thermautotrophicus
68	c3ougA	Alignment	not modelled	19.4	10	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
69	d1mola	Alignment	not modelled	19.4	17	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
70	d1ptfa	Alignment	not modelled	19.2	15	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
71	d2hpra	Alignment	not modelled	18.8	17	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
72	c3bmbB	Alignment	not modelled	18.7	36	PDB header: rna binding protein Chain: B: PDB Molecule: regulator of nucleoside diphosphate kinase; PDBTitle: crystal structure of a new rna polymerase interacting2 protein
73	d1hr0w	Alignment	not modelled	18.6	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
74	d1y7qa1	Alignment	not modelled	18.4	19	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: SCAN domain
75	d2jioa1	Alignment	not modelled	17.6	16	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
76	d1jt8a	Alignment	not modelled	17.5	9	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
77	d1ihra	Alignment	not modelled	16.8	19	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
78	d1g8ka1	Alignment	not modelled	16.8	13	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
79	d2eifa2	Alignment	not modelled	16.5	37	Fold: OB-fold Superfamily: Nucleic acid-binding proteins

				Family: Cold shock DNA-binding domain-like	
80	c3zvK_G	Alignment	not modelled	16.5	13 PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
81	c3le1B	Alignment	not modelled	16.4	11 PDB header: transferase Chain: B: PDB Molecule: phosphotransferase system, hpr-related proteins; PDBTitle: crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
82	c3lotC	Alignment	not modelled	16.3	39 PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
83	c1u9yD	Alignment	not modelled	16.3	16 PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
84	c3i4oA	Alignment	not modelled	16.1	26 PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-1; PDBTitle: crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
85	c3efhB	Alignment	not modelled	15.9	8 PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
86	d1kqfa1	Alignment	not modelled	15.8	12 Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
87	c1h0hA	Alignment	not modelled	15.5	13 PDB header: dehydrogenase Chain: A: PDB Molecule: formate dehydrogenase (large subunit); PDBTitle: tungsten containing formate dehydrogenase from2 desulfovibrio gigas
88	d1kbla3	Alignment	not modelled	15.3	17 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Pyruvate phosphate dikinase, N-terminal domain
89	d2iv2x1	Alignment	not modelled	15.2	10 Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
90	c2pn0D	Alignment	not modelled	14.6	38 PDB header: transcription Chain: D: PDB Molecule: prokaryotic transcription elongation factor PDBTitle: prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
91	c1dkrB	Alignment	not modelled	14.6	8 PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
92	d1h9ma2	Alignment	not modelled	14.5	32 Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
93	d1t9ha1	Alignment	not modelled	14.5	14 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
94	c3lpnB	Alignment	not modelled	14.5	21 PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
95	d2nzul1	Alignment	not modelled	14.5	18 Fold: HPr-like Superfamily: HPr-like Family: HPr-like
96	c3e02A	Alignment	not modelled	14.4	28 PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
97	c1h9mB	Alignment	not modelled	14.3	27 PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
98	c1vlfO	Alignment	not modelled	14.2	28 PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
99	d2etna2	Alignment	not modelled	13.9	21 Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain