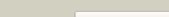
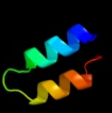


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4C2
Date	Sun Jul 8 11:45:08 BST 2012
Unique Job ID	c3369780539f1c21

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cw6B_	 Alignment		61.1	20	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
2	c2wqjM_	 Alignment		44.1	53	PDB header: transcription Chain: M: PDB Molecule: tumor protein p73; PDBTitle: crystal structure of a truncated variant of the human p732 tetramerization domain
3	c3hpxB_	 Alignment		35.9	17	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644)
4	c2wttL_	 Alignment		34.8	47	PDB header: transcription Chain: L: PDB Molecule: tumor protein p73; PDBTitle: structure of the human p73 tetramerization domain (crystal2 form ii)
5	c2waqQ_	 Alignment		34.7	27	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
6	c3hkzY_	 Alignment		33.1	27	PDB header: transferase Chain: Y: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
7	c2ftpA_	 Alignment		29.9	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
8	c3hkzZ_	 Alignment		29.9	27	PDB header: transferase Chain: Z: PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
9	c1ydoC_	 Alignment		26.0	17	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
10	d1sr9a2	 Alignment		25.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
11	c1zawX_	 Alignment		24.7	40	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a

12	c2y0sj_	Alignment		23.9	27	PDB header: transferase Chain: J: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
13	c2y0sQ_	Alignment		23.9	27	PDB header: transferase Chain: Q: PDB Molecule: rna polymerase subunit 13; PDBTitle: crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
14	c3he4A_	Alignment		23.3	36	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
15	c4a9zD_	Alignment		22.8	53	PDB header: transcription Chain: D: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of human p63 tetramerization domain
16	c3zy1A_	Alignment		22.4	53	PDB header: transcription Chain: A: PDB Molecule: tumor protein 63; PDBTitle: crystal structure of the human p63 tetramerization domain
17	c1zawY_	Alignment		22.3	40	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
18	c2odkD_	Alignment		21.6	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
19	c3s63B_	Alignment		19.4	34	PDB header: lipid binding protein Chain: B: PDB Molecule: saposin-like protein; PDBTitle: saposin-like protein na-slp-1
20	c1sr9A_	Alignment		18.9	17	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
21	c3hlsE_	Alignment	not modelled	16.5	13	PDB header: signaling protein Chain: E: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: crystal structure of the signaling helix coiled-coil doimain2 of the beta-1 subunit of the soluble guanylyl cyclase
22	d2odka1	Alignment	not modelled	15.0	19	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
23	c1zaxU_	Alignment	not modelled	13.2	40	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
24	dlzavu1	Alignment	not modelled	13.2	40	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
25	c1zavU_	Alignment	not modelled	13.2	40	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
26	c1zavY_	Alignment	not modelled	13.2	40	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
27	c2jq5A_	Alignment	not modelled	12.7	63	PDB header: structural genomics Chain: A: PDB Molecule: sec-c motif; PDBTitle: solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097

28	d2i9wa1	Alignment	not modelled	12.5	50	Fold: Cystatin-like Superfamily: NTF2-like Family: SEC-C associated NTF2-like domain
29	c2i9wA	Alignment	not modelled	11.9	50	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
30	dlzavz1	Alignment	not modelled	11.8	47	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
31	clzavZ	Alignment	not modelled	11.8	47	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
32	c3ivuB	Alignment	not modelled	11.3	17	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
33	c3bbpF	Alignment	not modelled	11.1	36	PDB header: protein transport/splicing Chain: F: PDB Molecule: grip and coiled-coil domain-containing protein 2; PDBTitle: rab6-gtp:gcc185 rab binding domain complex
34	clzaxZ	Alignment	not modelled	10.9	47	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
35	clzawW	Alignment	not modelled	10.8	47	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
36	clzawU	Alignment	not modelled	10.8	47	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
37	clzawZ	Alignment	not modelled	10.8	47	PDB header: structural protein Chain: Z: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
38	c3zyQC	Alignment	not modelled	10.7	47	PDB header: transcription Chain: C: PDB Molecule: tumor protein p63; PDBTitle: crystal structure of a truncated variant of the human p632 tetramerization domain lacking the c-terminal helix
39	clzaxX	Alignment	not modelled	10.7	47	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
40	clzavX	Alignment	not modelled	10.7	47	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
41	clzawV	Alignment	not modelled	10.6	47	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
42	clzaxW	Alignment	not modelled	10.6	47	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
43	clzavW	Alignment	not modelled	10.6	47	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
44	clzaxY	Alignment	not modelled	10.4	47	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
45	clzaxV	Alignment	not modelled	10.3	47	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
46	clzavV	Alignment	not modelled	10.3	47	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
47	cldd3C	Alignment	not modelled	10.2	47	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
48	cldd3D	Alignment	not modelled	10.2	47	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
49	c2zyfA	Alignment	not modelled	8.9	12	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
50	dldd4c	Alignment	not modelled	8.5	47	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
51	c2zxxA	Alignment	not modelled	7.8	32	PDB header: cell cycle/replication Chain: A: PDB Molecule: geminin; PDBTitle: crystal structure of cdt1/geminin complex
52	clyv0l	Alignment	not modelled	7.8	27	PDB header: contractile protein Chain: I: PDB Molecule: troponin i, fast skeletal muscle; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-2 free state

53	c3mk4B_	Alignment	not modelled	7.6	43	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray structure of human pex3 in complex with a pex19 derived peptide
54	c3batB_	Alignment	not modelled	7.5	31	PDB header: contractile protein Chain: B: PDB Molecule: myosin heavy chain, striated muscle/general PDBTitle: crystal structure of the n-terminal region of the scallop2 myosin rod, monoclinic (p21) form
55	d3pmga4	Alignment	not modelled	7.3	21	Fold: TBP-like Superfamily: Phosphoglucumutase, C-terminal domain Family: Phosphoglucumutase, C-terminal domain
56	c2wb1Q_	Alignment	not modelled	7.1	35	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
57	c1rweC_	Alignment	not modelled	7.0	31	PDB header: hormone/growth factor Chain: C: PDB Molecule: insulin; PDBTitle: enhancing the activity of insulin at receptor edge: crystal structure2 and photo-cross-linking of a8 analogues
58	c1rweA_	Alignment	not modelled	7.0	31	PDB header: hormone/growth factor Chain: A: PDB Molecule: insulin; PDBTitle: enhancing the activity of insulin at receptor edge: crystal structure2 and photo-cross-linking of a8 analogues
59	c3q4fG_	Alignment	not modelled	6.9	16	PDB header: dna binding protein/protein binding Chain: G: PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of xrcc4/xf-cernunnos complex
60	c2wb1J_	Alignment	not modelled	6.6	35	PDB header: transcription Chain: J: PDB Molecule: dna-directed rna polymerase rpo13 subunit; PDBTitle: the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
61	c4aj5M_	Alignment	not modelled	6.6	13	PDB header: cell cycle Chain: M: PDB Molecule: spindle and kinetochore-associated protein 2; PDBTitle: crystal structure of the ska core complex
62	c3he4F_	Alignment	not modelled	6.5	31	PDB header: de novo protein Chain: F: PDB Molecule: synzip5; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
63	d1v95a_	Alignment	not modelled	6.5	22	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
64	d1bk8a_	Alignment	not modelled	6.4	30	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Plant defensins
65	d1a1ua_	Alignment	not modelled	6.3	40	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
66	c2wvrB_	Alignment	not modelled	6.3	25	PDB header: replication Chain: B: PDB Molecule: geminin; PDBTitle: human cdt1:geminin complex
67	d1dd4d_	Alignment	not modelled	6.0	47	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
68	d1rqba2	Alignment	not modelled	6.0	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
69	c1zikA_	Alignment	not modelled	5.8	45	PDB header: leucine zipper Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
70	c1zikB_	Alignment	not modelled	5.8	45	PDB header: leucine zipper Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant asn16lys in the dimeric2 state
71	c2qlwA_	Alignment	not modelled	5.6	10	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
72	c2qlxA_	Alignment	not modelled	5.6	10	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
73	c1u2uB_	Alignment	not modelled	5.3	44	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
74	d1hs5a_	Alignment	not modelled	5.2	40	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain