
























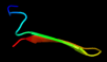


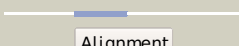

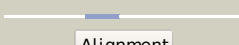
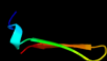
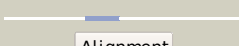

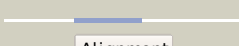
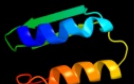
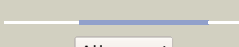


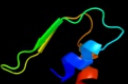



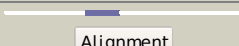
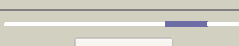

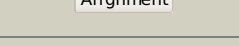
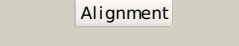



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AFH8
Date	Thu Jan 5 11:26:19 GMT 2012
Unique Job ID	1531707c00045d99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kgsA_	 Alignment		98.1	22	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
2	d1fe0a_	 Alignment		62.7	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
3	c2crlA_	 Alignment		53.8	16	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
4	c3rv2B_	 Alignment		49.3	19	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
5	d1qupa2	 Alignment		47.3	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
6	c2qfiB_	 Alignment		41.7	13	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yiiP
7	d1mxaa1	 Alignment		39.9	13	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
8	d1qm4a1	 Alignment		38.6	18	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase
9	c2rogA_	 Alignment		38.5	14	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
10	c1qupA_	 Alignment		36.3	14	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
11	d2p02a1	 Alignment		34.5	15	Fold: S-adenosylmethionine synthetase Superfamily: S-adenosylmethionine synthetase Family: S-adenosylmethionine synthetase

12	d1cc8a_	 Alignment		33.2	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
13	c2klrA_	 Alignment		32.5	18	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
14	c1jk9D_	 Alignment		28.3	14	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-ysod1 and yccs
15	c2k2pA_	 Alignment		27.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
16	c2wj7D_	 Alignment		27.1	18	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
17	c3q9qB_	 Alignment		26.4	27	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
18	c3ibwA_	 Alignment		25.9	16	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
19	c2l26A_	 Alignment		25.0	20	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein rv0899/mt0922; PDBTitle: rv0899 from mycobacterium tuberculosis contains two separated domains
20	d1sb6a_	 Alignment		23.7	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
21	c2zztA_	 Alignment	not modelled	23.5	9	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
22	d2cu6a1	 Alignment	not modelled	23.1	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
23	d2qfia1	 Alignment	not modelled	20.6	17	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
24	c2wj5A_	 Alignment	not modelled	16.8	23	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein beta-6; PDBTitle: rat alpha crystallin domain
25	c3imlB_	 Alignment	not modelled	15.7	21	PDB header: transferase Chain: B: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
26	c3glaA_	 Alignment	not modelled	15.7	22	PDB header: chaperone Chain: A: PDB Molecule: low molecular weight heat shock protein; PDBTitle: crystal structure of the hspa from xanthomonas axonopodis
27	c1rg9D_	 Alignment	not modelled	15.0	13	PDB header: transferase Chain: D: PDB Molecule: s-adenosylmethionine synthetase; PDBTitle: s-adenosylmethionine synthetase complexed with sam and ppnp
28	c3l1eA_	 Alignment	not modelled	14.6	23	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin a chain; PDBTitle: bovine alphaa crystallin zinc bound
						PDB header: transferase

29	c3so4C_	Alignment	not modelled	13.6	18	Chain: C: PDB Molecule: methionine-adenosyltransferase; PDBTitle: methionine-adenosyltransferase from entamoeba histolytica
30	c2obvA_	Alignment	not modelled	13.1	18	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine synthetase isoform type-1; PDBTitle: crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
31	d1xhja_	Alignment	not modelled	11.3	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
32	c2x36F_	Alignment	not modelled	10.0	13	PDB header: hydrolase Chain: F: PDB Molecule: Ion protease homolog, mitochondrial; PDBTitle: structure of the proteolytic domain of the human2 mitochondrial Ion protease
33	c3lnoA_	Alignment	not modelled	9.5	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis
34	d1gpma3	Alignment	not modelled	9.4	11	Fold: Alpha-lytic protease prodomain-like Superfamily: GMP synthetase C-terminal dimerisation domain Family: GMP synthetase C-terminal dimerisation domain
35	d1uwda_	Alignment	not modelled	9.3	20	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
36	d2joqa1	Alignment	not modelled	9.2	14	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
37	d1rwua_	Alignment	not modelled	9.0	17	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
38	c1rwuA_	Alignment	not modelled	9.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
39	c2bolA_	Alignment	not modelled	8.6	17	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
40	d2ffma1	Alignment	not modelled	8.4	21	Fold: Hypothetical protein SAV1430 Superfamily: Hypothetical protein SAV1430 Family: Hypothetical protein SAV1430
41	c2e3uA_	Alignment	not modelled	8.4	15	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein ph1566; PDBTitle: crystal structure analysis of dim2p from pyrococcus horikoshii ot3
42	c2k1hA_	Alignment	not modelled	7.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ser13; PDBTitle: solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
43	d2fmra_	Alignment	not modelled	7.6	29	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
44	d1m0sa2	Alignment	not modelled	7.5	27	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
45	c2ropA_	Alignment	not modelled	6.1	11	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
46	d1vyia_	Alignment	not modelled	6.1	23	Fold: Phosphoprotein M1, C-terminal domain Superfamily: Phosphoprotein M1, C-terminal domain Family: Phosphoprotein M1, C-terminal domain
47	c3fveA_	Alignment	not modelled	5.9	38	PDB header: isomerase Chain: A: PDB Molecule: diaminopimelate epimerase; PDBTitle: crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
48	d1lloa_	Alignment	not modelled	5.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
49	d1shsa_	Alignment	not modelled	5.8	9	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: HSP20
50	c1shsD_	Alignment	not modelled	5.8	9	PDB header: heat shock protein Chain: D: PDB Molecule: small heat shock protein; PDBTitle: small heat shock protein from methanococcus jannaschii