
















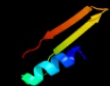

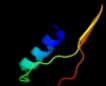


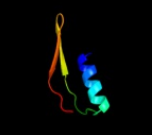
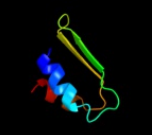



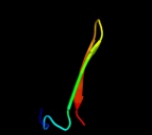

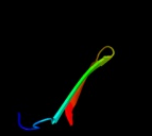



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kgsA_</a>	 Alignment		96.7	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv0899/mt0922; <b>PDBTitle:</b> solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
2	<a href="#">c2crlA_</a>	 Alignment		51.4	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> the apo form of hma domain of copper chaperone for2 superoxide dismutase
3	<a href="#">d1fe0a_</a>	 Alignment		47.2	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
4	<a href="#">c2qfiB_</a>	 Alignment		46.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous-iron efflux pump fief; <b>PDBTitle:</b> structure of the zinc transporter yiiip
5	<a href="#">d1qupa2</a>	 Alignment		38.2	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
6	<a href="#">d1gpma3</a>	 Alignment		36.3	22	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> GMP synthetase C-terminal dimerisation domain <b>Family:</b> GMP synthetase C-terminal dimerisation domain
7	<a href="#">c3rv2B_</a>	 Alignment		34.5	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine synthase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
8	<a href="#">c2rogA_</a>	 Alignment		32.6	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
9	<a href="#">d1qm4a1</a>	 Alignment		28.4	26	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
10	<a href="#">d1mxaal</a>	 Alignment		27.4	18	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
11	<a href="#">c1qupaA_</a>	 Alignment		25.2	7	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase 1 copper chaperone; <b>PDBTitle:</b> crystal structure of the copper chaperone for superoxide2 dismutase

12	<a href="#">d2p02a1</a>	Alignment		23.6	24	<b>Fold:</b> S-adenosylmethionine synthetase <b>Superfamily:</b> S-adenosylmethionine synthetase <b>Family:</b> S-adenosylmethionine synthetase
13	<a href="#">d1cc8a_</a>	Alignment		22.9	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
14	<a href="#">c2zztA_</a>	Alignment		20.9	0	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
15	<a href="#">d2qfia1</a>	Alignment		18.5	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Cation efflux protein cytoplasmic domain-like <b>Family:</b> Cation efflux protein cytoplasmic domain-like
16	<a href="#">c2wj7D_</a>	Alignment		15.9	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> human alphab crystallin
17	<a href="#">c2klrA_</a>	Alignment		15.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin b chain; <b>PDBTitle:</b> solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
18	<a href="#">c1jk9D_</a>	Alignment		14.8	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-ysod1 and yccs
19	<a href="#">c3q9qB_</a>	Alignment		13.3	23	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock protein beta-1; <b>PDBTitle:</b> hspb1 fragment second crystal form
20	<a href="#">c3ibwA_</a>	Alignment		12.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
21	<a href="#">c3e6qL_</a>	Alignment	not modelled	10.5	12	<b>PDB header:</b> isomerase <b>Chain:</b> L: <b>PDB Molecule:</b> putative 5-carboxymethyl-2-hydroxymuconate isomerase; <b>PDBTitle:</b> putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa.
22	<a href="#">c2k2pA_</a>	Alignment	not modelled	10.1	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1203; <b>PDBTitle:</b> solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
23	<a href="#">c1rg9D_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> s-adenosylmethionine synthetase complexed with sam and ppnp
24	<a href="#">d1otga_</a>	Alignment	not modelled	9.5	10	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
25	<a href="#">c3qlaA_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight heat shock protein; <b>PDBTitle:</b> crystal structure of the hspa from xanthomonas axonopodis
26	<a href="#">d1sb6a_</a>	Alignment	not modelled	9.4	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
27	<a href="#">c3imlB_</a>	Alignment	not modelled	9.2	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine synthetase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
						<b>PDB header:</b> chaperone

28	<a href="#">c2wj5A_</a>	Alignment	not modelled	8.8	9	<b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein beta-6; <b>PDBTitle:</b> rat alpha crystallin domain
29	<a href="#">c2bolA_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> heat shock protein <b>Chain:</b> A: <b>PDB Molecule:</b> small heat shock protein; <b>PDBTitle:</b> crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
30	<a href="#">c3so4C_</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine-adenosyltransferase; <b>PDBTitle:</b> methionine-adenosyltransferase from entamoeba histolytica
31	<a href="#">c1gpmD_</a>	Alignment	not modelled	8.5	24	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
32	<a href="#">c3uowB_</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
33	<a href="#">c2obvA_</a>	Alignment	not modelled	8.4	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine synthetase isoform type-1; <b>PDBTitle:</b> crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
34	<a href="#">d2fmra_</a>	Alignment	not modelled	8.0	31	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
35	<a href="#">d1vyia_</a>	Alignment	not modelled	7.1	15	<b>Fold:</b> Phosphoprotein M1, C-terminal domain <b>Superfamily:</b> Phosphoprotein M1, C-terminal domain <b>Family:</b> Phosphoprotein M1, C-terminal domain
36	<a href="#">d2c5sa2</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> THUMP domain <b>Superfamily:</b> THUMP domain-like <b>Family:</b> THUMP domain
37	<a href="#">c2dplA_</a>	Alignment	not modelled	6.9	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
38	<a href="#">c3l1eA_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-crystallin a chain; <b>PDBTitle:</b> bovine alphaa crystallin zinc bound