








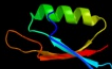




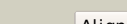

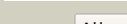




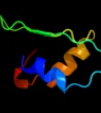


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yf5L_	 Alignment		99.9	16	PDB header: transport protein Chain: L: PDB Molecule: general secretion pathway protein I; PDBTitle: cyto-epsI: the cytoplasmic domain of epsI, an inner membrane component2 of the type ii secretion system of vibrio cholerae
2	c2w7vB_	 Alignment		99.8	29	PDB header: transport protein Chain: B: PDB Molecule: general secretion pathway protein I; PDBTitle: periplasmic domain of epsI from vibrio parahaemolyticus
3	d2bh1a1	 Alignment		99.6	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Cyto-EpsL domain
4	d1uv7a_	 Alignment		78.8	11	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
5	c1uv7A_	 Alignment		78.8	11	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
6	c2l3mA_	 Alignment		33.8	20	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
7	d1p6ta2	 Alignment		29.6	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
8	d2aw0a_	 Alignment		27.1	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
9	d1cpza_	 Alignment		21.5	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
10	d1s6ua_	 Alignment		20.9	4	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
11	d1sb6a_	 Alignment		20.5	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain

12	c2kt2A_	Alignment		17.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
13	c2jpiA_	Alignment		17.3	13	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical protein; PDBTitle: chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
14	d1p6ta1	Alignment		17.1	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
15	d2qifa1	Alignment		16.0	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
16	d1f44a1	Alignment		14.5	19	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
17	c2k2pA_	Alignment		14.4	6	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
18	c3dxsX_	Alignment		13.7	4	PDB header: hydrolase Chain: X: PDB Molecule: copper-transporting atpase ran1; PDBTitle: crystal structure of a copper binding domain from hma7, a p-2 type atpase
19	d1mwza_	Alignment		13.5	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
20	d1j5ya2	Alignment		13.2	8	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
21	c1yg0A_	Alignment	not modelled	12.9	14	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
22	c2x29A_	Alignment	not modelled	11.9	22	PDB header: cell adhesion Chain: A: PDB Molecule: tumor necrosis factor ligand superfamily member PDBTitle: crystal structure of human4-1bb ligand ectodomain
23	d1kvja_	Alignment	not modelled	11.5	4	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
24	c3hd7A_	Alignment	not modelled	11.1	12	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
25	d2ggpb1	Alignment	not modelled	10.7	3	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
26	c2gcfA_	Alignment	not modelled	9.8	5	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copppe(i) atpase2 pacs in its apo form
27	c3ibwA_	Alignment	not modelled	9.6	17	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
28	c2rrlA_	Alignment	not modelled	9.4	16	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the flik

29	dlje3a_	Alignment	not modelled	9.2	15	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
30	c2kyzA_	Alignment	not modelled	9.1	15	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
31	d2vzsa2	Alignment	not modelled	9.0	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
32	c2ofhX_	Alignment	not modelled	9.0	11	PDB header: hydrolase, membrane protein Chain: X: PDB Molecule: zinc-transporting atpase; PDBTitle: solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
33	c2yciX_	Alignment	not modelled	8.8	16	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
34	d1losda_	Alignment	not modelled	8.3	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
35	c2l3wA_	Alignment	not modelled	7.7	7	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome rod linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
36	c3h0dB_	Alignment	not modelled	7.5	25	PDB header: transcription/dna Chain: B: PDB Molecule: ctsr; PDBTitle: crystal structure of ctrs in complex with a 26bp dna duplex
37	d1afia_	Alignment	not modelled	7.3	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
38	c3k13A_	Alignment	not modelled	7.2	9	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
39	c1yjrA_	Alignment	not modelled	7.1	3	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
40	c3fryB_	Alignment	not modelled	7.1	14	PDB header: hydrolase Chain: B: PDB Molecule: probable copper-exporting p-type atpase a; PDBTitle: crystal structure of the copa c-terminal metal binding domain
41	c3nklA_	Alignment	not modelled	6.9	14	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
42	c2rjzA_	Alignment	not modelled	6.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
43	c2ldiA_	Alignment	not modelled	6.5	11	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant
44	c2ropA_	Alignment	not modelled	6.5	14	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
45	c2ychA_	Alignment	not modelled	6.5	10	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
46	d1q8la_	Alignment	not modelled	6.2	5	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
47	c1y3kA_	Alignment	not modelled	5.8	8	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the apo form of the fifth domain of2 menkes protein
48	c2k42B_	Alignment	not modelled	5.4	30	PDB header: signaling protein Chain: B: PDB Molecule: espfu; PDBTitle: solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
49	d1tlea2	Alignment	not modelled	5.1	10	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors