








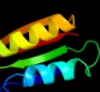














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1je3a_	 Alignment		99.9	100	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
2	d1dcja_	 Alignment		99.9	30	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
3	d1jdqa_	 Alignment		99.9	39	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
4	d1pava_	 Alignment		99.8	23	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
5	c3hz7A_	 Alignment		99.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the sirA-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
6	c1yg0A_	 Alignment		92.8	13	PDB header: metal transport Chain: A: PDB Molecule: cop associated protein; PDBTitle: solution structure of apo-copp from helicobacter pylori
7	d1cc8a_	 Alignment		92.1	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
8	c1y3kA_	 Alignment		89.9	11	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
9	c2l3mA_	 Alignment		89.3	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
10	d1p6ta1	 Alignment		88.9	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
11	d2qifa1	 Alignment		88.5	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain

12	c2kt2A_	Alignment		86.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
13	d1kvja_	Alignment		86.1	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
14	c2ldiA_	Alignment		85.8	24	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaa sub mutant
15	c2ofhX_	Alignment		85.2	20	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
16	d2aw0a_	Alignment		85.2	12	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
17	d1p6ta2	Alignment		84.9	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
18	d2ggpb1	Alignment		84.4	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
19	c2gcfA_	Alignment		83.2	16	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
20	d1q8la_	Alignment		82.5	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
21	d1mwza_	Alignment	not modelled	82.3	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
22	c3dxsX_	Alignment	not modelled	82.2	13	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
23	d1s6ua_	Alignment	not modelled	80.9	13	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
24	d2d9ia1	Alignment	not modelled	77.6	11	Fold: IF3-like Superfamily: SMR domain-like Family: Smr domain
25	c1yjrA_	Alignment	not modelled	76.2	10	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
26	c3qwua_	Alignment	not modelled	75.7	10	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: putative atp-dependent dna ligase from aquifex aeolicus.
27	d1cpza_	Alignment	not modelled	74.8	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
28	c2kyzA_	Alignment	not modelled	74.5	16	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
29	c2grzA_	Alignment	not modelled	73.4	10	PDB header: transferase Chain: A: PDB Molecule: ribosomal protein l11 methyltransferase;

29	c3gr2A	Alignment	not modelled	73.4	10	PDBTitle: crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
30	c2kkhA	Alignment	not modelled	72.6	10	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
31	d1osda	Alignment	not modelled	71.4	17	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
32	d1afia	Alignment	not modelled	70.7	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
33	d1sb6a	Alignment	not modelled	68.4	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
34	c2k2pA	Alignment	not modelled	67.9	18	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
35	c2vkCA	Alignment	not modelled	67.1	12	PDB header: hydrolase Chain: A: PDB Molecule: nedd4-binding protein 2; PDBTitle: solution structure of the b3bp smr domain
36	d2nxca1	Alignment	not modelled	64.1	9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ribosomal protein L11 methyltransferase PrmA
37	c3nf5A	Alignment	not modelled	58.9	3	PDB header: protein transport Chain: A: PDB Molecule: nucleoporin nup116; PDBTitle: crystal structure of the c-terminal domain of nuclear pore complex2 component nup116 from candida glabrata
38	c2aivA	Alignment	not modelled	58.0	11	PDB header: transport protein Chain: A: PDB Molecule: fragment of nucleoporin nup116/nsp116; PDBTitle: multiple conformations in the ligand-binding site of the2 yeast nuclear pore targeting domain of nup116p
39	c1ko6A	Alignment	not modelled	53.6	7	PDB header: transferase Chain: A: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: crystal structure of c-terminal autolytic domain of2 nucleoporin nup98
40	c2zqeA	Alignment	not modelled	52.8	16	PDB header: dna binding protein Chain: A: PDB Molecule: mutS2 protein; PDBTitle: crystal structure of the smr domain of thermus thermophilus mutS2
41	c3fryB	Alignment	not modelled	51.4	16	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
42	c2q5xA	Alignment	not modelled	50.8	7	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: crystal structure of the c-terminal domain of hnup98
43	c3kepA	Alignment	not modelled	49.2	6	PDB header: protein transport, rna binding protein Chain: A: PDB Molecule: nucleoporin nup145; PDBTitle: crystal structure of the autolytic domain from the2 nuclear pore complex component nup145 from saccharomyces3 cerevisiae
44	c2rogA	Alignment	not modelled	44.8	18	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
45	c2ga7A	Alignment	not modelled	43.6	9	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
46	d1fe0a	Alignment	not modelled	42.0	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
47	c2rmlA	Alignment	not modelled	38.9	14	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting p-type atpase copa; PDBTitle: solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
48	d2cc0a1	Alignment	not modelled	32.6	18	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
49	c2kngA	Alignment	not modelled	31.5	26	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
50	d1dusa	Alignment	not modelled	30.7	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
51	d1qupa2	Alignment	not modelled	28.1	11	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
52	c3iz6A	Alignment	not modelled	28.0	12	PDB header: ribosome Chain: A: PDB Molecule: 40s ribosomal protein sa (s2p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
53	c2ropA	Alignment	not modelled	27.6	13	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of domains 3 and 4 of human atp7b
54	c3qd7X	Alignment	not modelled	27.3	11	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized protein ydal; PDBTitle: crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli

55	dlnyla_	Alignment	not modelled	25.5	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
56	c3dlcA_	Alignment	not modelled	22.5	13	PDB header: transferase Chain: A: PDB Molecule: putative s-adenosyl-l-methionine-dependent PDBTitle: crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
57	d2clia1	Alignment	not modelled	20.8	24	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
58	d2obba1	Alignment	not modelled	20.7	14	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
59	c3fpnB_	Alignment	not modelled	19.2	15	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrB interaction PDBTitle: crystal structure of uvra-uvrB interaction domains
60	c3ntaA_	Alignment	not modelled	19.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
61	d1h8ca_	Alignment	not modelled	18.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
62	c3evzA_	Alignment	not modelled	17.7	27	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal strucure of methyltransferase from pyrococcus furiosus
63	d1l3ia_	Alignment	not modelled	17.5	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Precorrin-6Y methyltransferase (CbiT)
64	d1jvaa3	Alignment	not modelled	17.5	11	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
65	d1wj4a_	Alignment	not modelled	17.3	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
66	c2vyoA_	Alignment	not modelled	16.6	11	PDB header: hydrolase Chain: A: PDB Molecule: chitooligosaccharide deacetylase; PDBTitle: chitin deacetylase family member from encephalitozoon2 cuniculi
67	c2eseA_	Alignment	not modelled	16.2	22	PDB header: protein/rna complex Chain: A: PDB Molecule: vts1p; PDBTitle: structure of the sam domain of vts1p in complex with rna
68	c2aj1A_	Alignment	not modelled	16.1	11	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
69	d2naca2	Alignment	not modelled	15.5	10	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
70	c3lteH_	Alignment	not modelled	14.9	20	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
71	d2j13a1	Alignment	not modelled	14.2	20	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
72	c2b6gA_	Alignment	not modelled	14.1	22	PDB header: rna binding protein Chain: A: PDB Molecule: vts1p; PDBTitle: rna recognition by the vts1 sam domain
73	d2cr5a1	Alignment	not modelled	13.4	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
74	c3qq5A_	Alignment	not modelled	13.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [feFe]-hydrogenase maturation protein hydf
75	c3njrB_	Alignment	not modelled	13.2	17	PDB header: transferase Chain: B: PDB Molecule: precorrin-6y methylase; PDBTitle: crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
76	c3c5yD_	Alignment	not modelled	13.2	16	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
77	c2yvaB_	Alignment	not modelled	12.9	15	PDB header: dna binding protein Chain: B: PDB Molecule: dnaa initiator-associating protein diaa; PDBTitle: crystal structure of escherichia coli diaa
78	c3hjhA_	Alignment	not modelled	12.9	13	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair-coupling factor; PDBTitle: a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
79	c3hm2G_	Alignment	not modelled	12.6	17	PDB header: transferase Chain: G: PDB Molecule: precorrin-6y c5,15-methyltransferase; PDBTitle: crystal structure of putative precorrin-6y c5,15-2 methyltransferase targeted domain from corynebacterium3 diphtheriae
						Fold: P-loop containing nucleoside triphosphate hydrolases

80	d2b2na1	Alignment	not modelled	12.0	13	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
81	c2pwyB	Alignment	not modelled	11.8	15	PDB header: transferase Chain: B: PDB Molecule: trna (adenine-n(1)-)-methyltransferase; PDBTitle: crystal structure of a mla58 trna methyltransferase
82	d1ofla	Alignment	not modelled	11.6	13	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
83	c3e05B	Alignment	not modelled	11.4	15	PDB header: transferase Chain: B: PDB Molecule: precocorrin-6y c5,15-methyltransferase (decarboxylating); PDBTitle: crystal structure of precocorrin-6y c5,15-methyltransferase from2 geobacter metallireducens gs-15
84	c3trjC	Alignment	not modelled	10.9	15	PDB header: isomerase Chain: C: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of a phosphoheptose isomerase from francisella tularensis
85	d1tk9a	Alignment	not modelled	10.6	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
86	c3icrA	Alignment	not modelled	10.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
87	c2ziuA	Alignment	not modelled	10.5	9	PDB header: hydrolase Chain: A: PDB Molecule: mus81 protein; PDBTitle: crystal structure of the mus81-eme1 complex
88	c3ndjA	Alignment	not modelled	10.4	20	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
89	d1o54a	Alignment	not modelled	9.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
90	c3cxjB	Alignment	not modelled	9.7	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
91	c2ew9A	Alignment	not modelled	9.6	12	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
92	c1w17A	Alignment	not modelled	9.5	16	PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
93	c3cg6A	Alignment	not modelled	9.4	7	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible 45 gamma; PDBTitle: crystal structure of gadd45 gamma
94	c2rpiA	Alignment	not modelled	9.1	14	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
95	d1jg5a	Alignment	not modelled	9.0	24	Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP
96	c3dh0B	Alignment	not modelled	8.9	16	PDB header: transferase Chain: B: PDB Molecule: sam dependent methyltransferase; PDBTitle: crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
97	d1x92a	Alignment	not modelled	8.9	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
98	c1dbgA	Alignment	not modelled	8.9	13	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
99	c2fe9A	Alignment	not modelled	8.8	21	PDB header: rna binding protein Chain: A: PDB Molecule: protein vts1; PDBTitle: solution structure of the vts1 sam domain in the presence2 of rna