

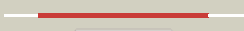
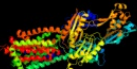















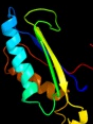



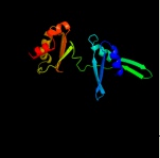
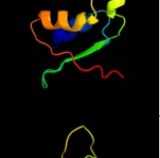

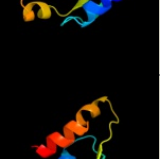
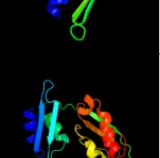
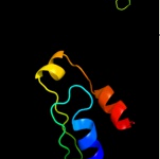

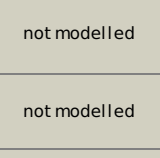


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">cloy8A_</a>	 Alignment		100.0	78	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b; <b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
2	<a href="#">c3k07A_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa; <b>PDBTitle:</b> crystal structure of cusa
3	<a href="#">c3aqpB_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein; <b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
4	<a href="#">dliwga8</a>	 Alignment		100.0	73	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
5	<a href="#">dliwga7</a>	 Alignment		100.0	82	<b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain <b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain
6	<a href="#">dliwga1</a>	 Alignment		99.9	88	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
7	<a href="#">dliwga2</a>	 Alignment		99.7	49	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
8	<a href="#">dliwga5</a>	 Alignment		99.7	68	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
9	<a href="#">dliwga6</a>	 Alignment		99.2	67	<b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains <b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
10	<a href="#">dliwga3</a>	 Alignment		98.9	65	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
11	<a href="#">dliwga4</a>	 Alignment		98.0	85	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains

12	<a href="#">c2ropA_</a>	Alignment		96.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> solution structure of domains 3 and 4 of human atp7b
13	<a href="#">c2ew9A_</a>	Alignment		95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 2; <b>PDBTitle:</b> solution structure of apowln5-6
14	<a href="#">d1s6ua_</a>	Alignment		91.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
15	<a href="#">d2qifa1</a>	Alignment		91.3	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
16	<a href="#">d2aw0a_</a>	Alignment		91.0	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
17	<a href="#">c2kkhA_</a>	Alignment		90.3	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative heavy metal transporter; <b>PDBTitle:</b> structure of the zinc binding domain of the atpase hma4
18	<a href="#">c2rmlA_</a>	Alignment		90.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting p-type atpase copa; <b>PDBTitle:</b> solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
19	<a href="#">d1p6ta2</a>	Alignment		89.4	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
20	<a href="#">d1p6ta1</a>	Alignment		89.4	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
21	<a href="#">c3dxsX_</a>	Alignment	not modelled	89.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> copper-transporting atpase ran1; <b>PDBTitle:</b> crystal structure of a copper binding domain from hma7, a p-2 type atpase
22	<a href="#">d1cpza_</a>	Alignment	not modelled	89.1	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
23	<a href="#">d1kvja_</a>	Alignment	not modelled	88.5	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
24	<a href="#">c2ga7A_</a>	Alignment	not modelled	88.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
25	<a href="#">d1q8la_</a>	Alignment	not modelled	88.1	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
26	<a href="#">c2l3mA_</a>	Alignment	not modelled	88.0	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> copper-ion-binding protein; <b>PDBTitle:</b> solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
27	<a href="#">c2ldiA_</a>	Alignment	not modelled	87.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> nmr solution structure of ziaan sub mutant
28	<a href="#">c1yjrA_</a>	Alignment	not modelled	87.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
						<b>PDB header:</b> hydrolase, membrane protein

29	<a href="#">c2ofhX_</a>	Alignment	not modelled	87.1	15	<b>Chain:</b> X: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
30	<a href="#">d1afia_</a>	Alignment	not modelled	86.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
31	<a href="#">c1yg0A_</a>	Alignment	not modelled	86.1	12	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> cop associated protein; <b>PDBTitle:</b> solution structure of apo-copp from helicobacter pylori
32	<a href="#">c2kt2A_</a>	Alignment	not modelled	86.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
33	<a href="#">d1osda_</a>	Alignment	not modelled	85.8	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
34	<a href="#">c1y3kA_</a>	Alignment	not modelled	83.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-transporting atpase 1; <b>PDBTitle:</b> solution structure of the apo form of the fifth domain of2 menkes protein
35	<a href="#">c2k2pA_</a>	Alignment	not modelled	77.7	9	<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
36	<a href="#">d1qupa2</a>	Alignment	not modelled	77.3	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
37	<a href="#">d2ggpb1</a>	Alignment	not modelled	76.4	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
38	<a href="#">c1jk9D_</a>	Alignment	not modelled	73.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-yso1 and yccs
39	<a href="#">d1mwza_</a>	Alignment	not modelled	73.6	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
40	<a href="#">d1sb6a_</a>	Alignment	not modelled	73.5	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
41	<a href="#">c2gcfA_</a>	Alignment	not modelled	72.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase pacs; <b>PDBTitle:</b> solution structure of the n-terminal domain of the copper(i) atpase2 pacs in its apo form
42	<a href="#">d1cc8a_</a>	Alignment	not modelled	70.0	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
43	<a href="#">c2rogA_</a>	Alignment	not modelled	68.6	14	<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
44	<a href="#">c2aj1A_</a>	Alignment	not modelled	68.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable cadmium-transporting atpase; <b>PDBTitle:</b> solution structure of apocada
45	<a href="#">c2crlA_</a>	Alignment	not modelled	66.8	21	<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
46	<a href="#">c3j09A_</a>	Alignment	not modelled	65.9	15	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
47	<a href="#">c1qupA_</a>	Alignment	not modelled	65.6	19	<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
48	<a href="#">c2yvxD_</a>	Alignment	not modelled	61.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
49	<a href="#">d2cu6a1</a>	Alignment	not modelled	55.8	25	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
50	<a href="#">d1uwda_</a>	Alignment	not modelled	53.9	14	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
51	<a href="#">c1yj7A_</a>	Alignment	not modelled	49.8	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escj; <b>PDBTitle:</b> crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
52	<a href="#">c2kyzA_</a>	Alignment	not modelled	39.9	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heavy metal binding protein; <b>PDBTitle:</b> nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
53	<a href="#">d2vv5a2</a>	Alignment	not modelled	38.3	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
54	<a href="#">c2yy3B_</a>	Alignment	not modelled	32.3	12	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-beta; <b>PDBTitle:</b> crystal structure of translation elongation factor ef-1

						beta from2 pyrococcus horikoshii
55	<a href="#">c3c6fD_</a>	Alignment	not modelled	29.7	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> yetf protein; <b>PDBTitle:</b> crystal structure of protein bsu07140 from bacillus subtilis
56	<a href="#">c1ciiA_</a>	Alignment	not modelled	26.4	17	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
57	<a href="#">c1vs3B_</a>	Alignment	not modelled	25.0	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trna pseudouridine synthase a; <b>PDBTitle:</b> crystal structure of the trna pseudouridine synthase trua from thermus2 thermophilus hb8
58	<a href="#">c3lnoA_</a>	Alignment	not modelled	23.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis
59	<a href="#">c3fryB_</a>	Alignment	not modelled	21.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable copper-exporting p-type atpase a; <b>PDBTitle:</b> crystal structure of the copa c-terminal metal binding domain
60	<a href="#">d2nwwa1</a>	Alignment	not modelled	20.9	7	<b>Fold:</b> Proton glutamate symport protein <b>Superfamily:</b> Proton glutamate symport protein <b>Family:</b> Proton glutamate symport protein
61	<a href="#">c2k9yB_</a>	Alignment	not modelled	19.6	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
62	<a href="#">c2k9yA_</a>	Alignment	not modelled	19.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 2; <b>PDBTitle:</b> epha2 dimeric structure in the lipidic bicelle at ph 5.0
63	<a href="#">c2mltA_</a>	Alignment	not modelled	18.0	23	<b>PDB header:</b> toxin (hemolytic polypeptide) <b>Chain:</b> A: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> melittin
64	<a href="#">c2mltB_</a>	Alignment	not modelled	18.0	23	<b>PDB header:</b> toxin (hemolytic polypeptide) <b>Chain:</b> B: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> melittin
65	<a href="#">c2hdiA_</a>	Alignment	not modelled	17.9	35	<b>PDB header:</b> protein transport, antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin i receptor; <b>PDBTitle:</b> crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
66	<a href="#">d1fe0a_</a>	Alignment	not modelled	16.6	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
67	<a href="#">c1bh1A_</a>	Alignment	not modelled	15.6	23	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> melittin; <b>PDBTitle:</b> structural studies of d-pro melittin, nmr, 20 structures
68	<a href="#">d1jb0i_</a>	Alignment	not modelled	12.7	19	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit VIII of photosystem I reaction centre, Psal <b>Family:</b> Subunit VIII of photosystem I reaction centre, Psal
69	<a href="#">c1a87A_</a>	Alignment	not modelled	12.7	11	<b>PDB header:</b> bacteriocin <b>Chain:</b> A: <b>PDB Molecule:</b> colicin n; <b>PDBTitle:</b> colicin n
70	<a href="#">d1a87a_</a>	Alignment	not modelled	12.7	11	<b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
71	<a href="#">c3lkbB_</a>	Alignment	not modelled	12.5	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> nascent polypeptide-associated complex subunit alpha; <b>PDBTitle:</b> human nac dimerization domain
72	<a href="#">d2gufa1</a>	Alignment	not modelled	12.0	30	<b>Fold:</b> Transmembrane beta-barrels <b>Superfamily:</b> Porins <b>Family:</b> Ligand-gated protein channel
73	<a href="#">d2yvxa3</a>	Alignment	not modelled	12.0	9	<b>Fold:</b> MgtE membrane domain-like <b>Superfamily:</b> MgtE membrane domain-like <b>Family:</b> MgtE membrane domain-like
74	<a href="#">d1f7ua3</a>	Alignment	not modelled	11.9	11	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain <b>Family:</b> Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain
75	<a href="#">c2bbjB_</a>	Alignment	not modelled	11.0	11	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
76	<a href="#">d1qmgal</a>	Alignment	not modelled	10.9	22	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
77	<a href="#">d2b3ya2</a>	Alignment	not modelled	10.9	48	<b>Fold:</b> Aconitase iron-sulfur domain <b>Superfamily:</b> Aconitase iron-sulfur domain <b>Family:</b> Aconitase iron-sulfur domain
78	<a href="#">c1f7uA_</a>	Alignment	not modelled	10.8	11	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-tRNA synthetase; <b>PDBTitle:</b> crystal structure of the arginyl-tRNA synthetase complexed with the2 trna(arg) and l-arg
79	<a href="#">c2k1hA_</a>	Alignment	not modelled	10.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ser13; <b>PDBTitle:</b> solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
80	<a href="#">d1xhja_</a>	Alianment	not modelled	10.6	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like

					<b>Family:</b> NifU C-terminal domain-like
81	<a href="#">c2ki0A_</a>	Alignment	not modelled	10.6	13 <b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> ds119; <b>PDBTitle:</b> nmr structure of a de novo designed beta alpha beta
82	<a href="#">c3ibwA_</a>	Alignment	not modelled	10.4	29 <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
83	<a href="#">d1ydx2</a>	Alignment	not modelled	10.2	15 <b>Fold:</b> DNA methylase specificity domain <b>Superfamily:</b> DNA methylase specificity domain <b>Family:</b> Type I restriction modification DNA specificity domain
84	<a href="#">c2e2xA_</a>	Alignment	not modelled	10.0	11 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> neurofibromin; <b>PDBTitle:</b> sec14 homology module of neurofibromin in complex with2 phosphatitylethanolamine
85	<a href="#">c3g74B_</a>	Alignment	not modelled	9.9	33 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of unknown function; <b>PDBTitle:</b> crystal structure of a functionally unknown protein from eubacterium2 ventriosum atcc 27560
86	<a href="#">c3gdzA_</a>	Alignment	not modelled	9.8	18 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> arginyl-trna synthetase; <b>PDBTitle:</b> crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
87	<a href="#">d2ffma1</a>	Alignment	not modelled	9.6	5 <b>Fold:</b> Hypothetical protein SAV1430 <b>Superfamily:</b> Hypothetical protein SAV1430 <b>Family:</b> Hypothetical protein SAV1430
88	<a href="#">c3qlbA_</a>	Alignment	not modelled	9.6	20 <b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> enantio-pyochelin receptor; <b>PDBTitle:</b> enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
89	<a href="#">d1s7ba_</a>	Alignment	not modelled	9.6	16 <b>Fold:</b> Multidrug resistance efflux transporter EmrE <b>Superfamily:</b> Multidrug resistance efflux transporter EmrE <b>Family:</b> Multidrug resistance efflux transporter EmrE
90	<a href="#">d2phcb2</a>	Alignment	not modelled	9.5	17 <b>Fold:</b> DCoH-like <b>Superfamily:</b> PH0987 N-terminal domain-like <b>Family:</b> PH0987 N-terminal domain-like
91	<a href="#">c3g7sA_</a>	Alignment	not modelled	9.3	11 <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> long-chain-fatty-acid--coa ligase (fadd-1); <b>PDBTitle:</b> crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
92	<a href="#">d1ciia1</a>	Alignment	not modelled	9.2	15 <b>Fold:</b> Toxins' membrane translocation domains <b>Superfamily:</b> Colicin <b>Family:</b> Colicin
93	<a href="#">c3iplB_</a>	Alignment	not modelled	8.9	10 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-succinylbenzoate--coa ligase; <b>PDBTitle:</b> crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
94	<a href="#">d1cz5a1</a>	Alignment	not modelled	8.7	22 <b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
95	<a href="#">d2cfxa2</a>	Alignment	not modelled	8.7	7 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
96	<a href="#">c2jnvA_</a>	Alignment	not modelled	8.6	11 <b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> nifu-like protein 1, chloroplast; <b>PDBTitle:</b> solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
97	<a href="#">d2cyya2</a>	Alignment	not modelled	8.2	4 <b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
98	<a href="#">c2y9jt_</a>	Alignment	not modelled	8.2	16 <b>PDB header:</b> protein transport <b>Chain:</b> T: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at2 subnanometer resolution
99	<a href="#">d1dd5a_</a>	Alignment	not modelled	8.1	12 <b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> Ribosome recycling factor, RRF <b>Family:</b> Ribosome recycling factor, RRF