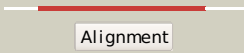
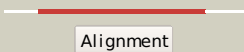
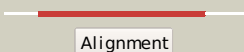
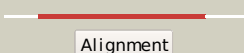
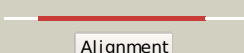
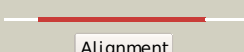
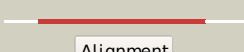
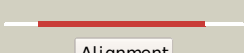
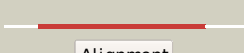
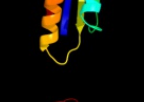


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jsxA_	 Alignment		100.0	100	PDB header: chaperone Chain: A; PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
2	d2cyya2	 Alignment		97.2	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
3	c2zbcH_	 Alignment		97.2	13	PDB header: transcription Chain: H; PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
4	c2e1aD_	 Alignment		96.9	22	PDB header: transcription Chain: D; PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
5	d1i1ga2	 Alignment		96.8	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
6	c2djwF_	 Alignment		96.8	17	PDB header: unknown function Chain: F; PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
7	c2e1cA_	 Alignment		96.8	17	PDB header: transcription/dna Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
8	c1i1ga_	 Alignment		96.3	22	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
9	d2cg4a2	 Alignment		96.3	9	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
10	c2dbbA_	 Alignment		94.5	9	PDB header: transcriptional regulator Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
11	c3ibwA_	 Alignment		94.3	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

12	c2e7xA	Alignment		93.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the Lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
13	c3i4pA	Alignment		93.9	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
14	d2cfxa2	Alignment		93.7	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
15	c2vbzA	Alignment		93.4	14	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
16	c2cg4B	Alignment		93.2	6	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
17	c2cfxD	Alignment		92.3	13	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpC; PDBTitle: structure of b.subtilis lrpC
18	c2p6tH	Alignment		91.7	7	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
19	d1sc6a3	Alignment		91.6	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
20	d2c5sa2	Alignment		90.6	17	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
21	d1o8ba2	Alignment	not modelled	88.7	22	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
22	c2gqgB	Alignment	not modelled	88.0	8	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
23	c2c5sA	Alignment	not modelled	86.8	17	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
24	c2ia0A	Alignment	not modelled	86.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
25	d1kona	Alignment	not modelled	84.3	26	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
26	d1vbka2	Alignment	not modelled	82.4	19	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
27	d1m0sa2	Alignment	not modelled	81.9	20	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
28	d1lk5a2	Alignment	not modelled	77.5	11	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain

29	d1mw7a_	Alignment	not modelled	76.6	9	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
30	c1uj6A_	Alignment	not modelled	74.3	14	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
31	c3u7jA_	Alignment	not modelled	71.3	23	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
32	d2p5ma1	Alignment	not modelled	65.1	7	Fold: DcoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
33	d1b4ba_	Alignment	not modelled	63.6	9	Fold: DcoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
34	d1s6la1	Alignment	not modelled	63.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
35	c1lk5C_	Alignment	not modelled	63.2	11	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
36	c2f8mB_	Alignment	not modelled	63.0	15	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
37	d1ygya3	Alignment	not modelled	60.7	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
38	c1rwuA_	Alignment	not modelled	59.6	15	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	d1rwua_	Alignment	not modelled	59.6	15	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
40	c3kwmC_	Alignment	not modelled	59.5	17	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
41	d1uj4a2	Alignment	not modelled	57.9	13	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
42	c3cagF_	Alignment	not modelled	57.2	16	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
43	c1vbkA_	Alignment	not modelled	56.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
44	d1lfpa_	Alignment	not modelled	56.0	15	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
45	c1xtzA_	Alignment	not modelled	53.7	8	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
46	c3sf5D_	Alignment	not modelled	50.2	23	PDB header: chaperone Chain: D: PDB Molecule: urease accessory protein ureh; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
47	c2pjmA_	Alignment	not modelled	49.8	18	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
48	c3l7oB_	Alignment	not modelled	49.0	11	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
49	d1mwza_	Alignment	not modelled	48.9	7	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
50	c3dxsX_	Alignment	not modelled	48.7	18	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
51	c3v4gA_	Alignment	not modelled	45.6	15	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
52	c2gcfA_	Alignment	not modelled	45.6	20	PDB header: hydrolase Chain: A: PDB Molecule: cation-transporting atpase pacs; PDBTitle: solution structure of the n-terminal domain of the coppfer(i) atpase2 pacs in its apo form
53	d1xxaa_	Alignment	not modelled	44.9	11	Fold: DcoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
54	c3l7pA_	Alignment	not modelled	44.8	20	PDB header: transcription Chain: A: PDB Molecule: putative nitrogen regulatory protein pii; PDBTitle: crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans

55	d1fe0a_	Alignment	not modelled	44.3	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
56	c3ptwA_	Alignment	not modelled	43.5	24	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
57	c2rogA_	Alignment	not modelled	43.1	25	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
58	c1m0sA_	Alignment	not modelled	42.5	20	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
59	c3ereD_	Alignment	not modelled	42.0	10	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
60	d1p6ta2	Alignment	not modelled	42.0	18	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
61	c2kt2A_	Alignment	not modelled	41.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
62	d1p6ta1	Alignment	not modelled	41.3	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
63	c2l3mA_	Alignment	not modelled	40.0	16	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
64	d2nzca1	Alignment	not modelled	39.7	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
65	d1czda2	Alignment	not modelled	39.2	17	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
66	d1osda_	Alignment	not modelled	37.5	9	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
67	c1b4aA_	Alignment	not modelled	36.8	9	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
68	d2aw0a_	Alignment	not modelled	36.7	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
69	c1yjrA_	Alignment	not modelled	36.7	9	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
70	c1y3kA_	Alignment	not modelled	33.3	13	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
71	c1lkzB_	Alignment	not modelled	32.8	21	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA)2 from escherichia coli.
72	d1vk2a_	Alignment	not modelled	32.4	16	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
73	d1afia_	Alignment	not modelled	32.1	9	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
74	c2crlA_	Alignment	not modelled	31.6	11	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
75	d1cpza_	Alignment	not modelled	30.5	6	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
76	c1ybaC_	Alignment	not modelled	29.6	14	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
77	d1qupa2	Alignment	not modelled	29.0	23	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
78	c2ofhX_	Alignment	not modelled	28.6	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
79	c1qupA_	Alignment	not modelled	27.1	23	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
80	d1b77a2	Alignment	not modelled	27.1	15	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor

81	c2aj1A_	Alignment	not modelled	26.3	13	PDB header: hydrolase Chain: A: PDB Molecule: probable cadmium-transporting atpase; PDBTitle: solution structure of apocada
82	c2ldiA_	Alignment	not modelled	24.2	22	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: nmr solution structure of ziaan sub mutant
83	c2kkhA_	Alignment	not modelled	24.0	18	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
84	d2qifa1	Alignment	not modelled	23.4	15	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
85	c3qatB_	Alignment	not modelled	23.1	21	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
86	c2ga7A_	Alignment	not modelled	23.0	29	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(ii) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
87	c2ew9A_	Alignment	not modelled	22.7	20	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
88	dls6ua_	Alignment	not modelled	20.1	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
89	d1q8la_	Alignment	not modelled	20.0	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
90	d2ggpb1	Alignment	not modelled	19.9	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
91	d1kvja_	Alignment	not modelled	19.8	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
92	c2rmlA_	Alignment	not modelled	19.6	16	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
93	d2pd1a1	Alignment	not modelled	18.2	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
94	c1vgvA_	Alignment	not modelled	17.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
95	c1u5tA_	Alignment	not modelled	17.5	9	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the esct-ii endosomal trafficking complex
96	d2d8xa2	Alignment	not modelled	17.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
97	c1b8hA_	Alignment	not modelled	16.9	13	PDB header: transferase Chain: A: PDB Molecule: dna polymerase processivity component; PDBTitle: sliding clamp, dna polymerase
98	c2k2pA_	Alignment	not modelled	16.9	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
99	c2yy3B_	Alignment	not modelled	16.8	18	PDB header: translation Chain: B: PDB Molecule: elongation factor 1-beta; PDBTitle: crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii