














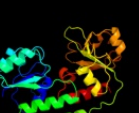








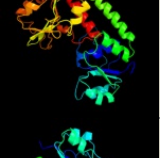
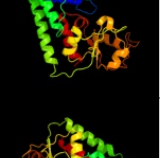
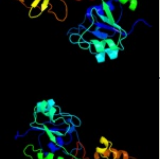
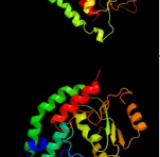
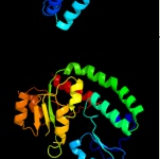
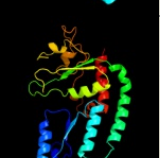
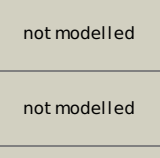
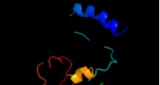
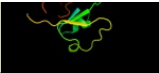




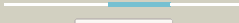
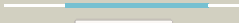



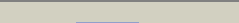



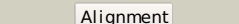

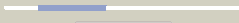

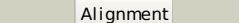
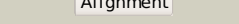
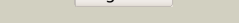


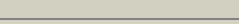

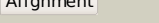


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlesza_	 Alignment		100.0	100	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Periplasmic ferric siderophore binding protein FhuD
2	c3eiwA_	 Alignment		100.0	21	PDB header: transport protein Chain: A: PDB Molecule: htsa protein; PDBTitle: crystal structure of staphylococcus aureus lipoprotein, htsa
3	c3gfvA_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized abc transporter solute-binding PDBTitle: crystal structure of petrobactin-binding protein yclq from2 bacillus subtilis
4	c2q8pA_	 Alignment		100.0	17	PDB header: metal transport Chain: A: PDB Molecule: iron-regulated surface determinant e; PDBTitle: crystal structure of selenomethionine labelled s. aureus isdE2 complexed with heme
5	c2r7aC_	 Alignment		100.0	17	PDB header: transport protein Chain: C: PDB Molecule: bacterial heme binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
6	d2chua1	 Alignment		100.0	17	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
7	c2r79A_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
8	c3md9A_	 Alignment		100.0	17	PDB header: transport protein Chain: A: PDB Molecule: hemin-binding periplasmic protein hmut; PDBTitle: structure of apo form of a periplasmic heme binding protein
9	c3pshA_	 Alignment		100.0	14	PDB header: metal transport Chain: A: PDB Molecule: protein hi_1472; PDBTitle: classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
10	c3mwgA_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: iron-regulated abc transporter siderophore-binding protein PDBTitle: crystal structure of staphylococcus aureus sira
11	c3be5D_	 Alignment		100.0	18	PDB header: metal transport Chain: D: PDB Molecule: putative iron compound-binding protein of abc transporter PDBTitle: crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein

12	d2phza1	Alignment		100.0	16	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
13	c2phzA_	Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: iron-uptake system-binding protein; PDBTitle: crystal structure of iron-uptake system-binding protein2 feua from bacillus subtilis. northeast structural genomics3 target sr580.
14	c3g9qA_	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: ferrichrome-binding protein; PDBTitle: crystal structure of the fhud fold-family bsu3320, a periplasmic2 binding protein component of a fep/fec-like ferrichrome abc3 transporter from bacillus subtilis. northeast structural genomics4 consortium target sr577a
15	d1n2za_	Alignment		100.0	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
16	c2x4lA_	Alignment		100.0	16	PDB header: transport Chain: A: PDB Molecule: ferric-siderophore receptor protein; PDBTitle: crystal structure of dese, a ferric-siderophore receptor2 protein from streptomyces coelicolor
17	d2etva1	Alignment		100.0	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TM0189-like
18	d1qh8a_	Alignment		96.7	17	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
19	d1m1na_	Alignment		96.3	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
20	c3pdiG_	Alignment		96.2	16	PDB header: protein binding Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
21	d1mioa_	Alignment	not modelled	95.4	13	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
22	d1qh8b_	Alignment	not modelled	95.1	13	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
23	d1m1nb_	Alignment	not modelled	93.8	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
24	d1mioB_	Alignment	not modelled	92.0	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
25	c3aerC_	Alignment	not modelled	91.7	14	PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
26	c3pdiB_	Alignment	not modelled	89.0	11	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
27	c1fmtA_	Alignment	not modelled	82.5	18	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
28	c3obiC_	Alignment		79.0	12	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase

					(np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
29	c1z7eC	Alignment	not modelled	73.5	16 PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
30	c3nrbD	Alignment	not modelled	72.2	17 PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
31	d1a6db2	Alignment	not modelled	70.9	8 Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
32	d1assa	Alignment	not modelled	70.5	8 Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
33	d1gm1a	Alignment	not modelled	70.0	14 Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
34	d1fmta2	Alignment	not modelled	69.9	18 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
35	d1q3qa2	Alignment	not modelled	69.7	6 Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
36	c3o1lB	Alignment	not modelled	67.3	15 PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
37	c3dcjA	Alignment	not modelled	66.8	20 PDB header: transferase Chain: A: PDB Molecule: probable 5'-phosphoribosylglycinamide PDBTitle: crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3,6,7,8-tetrahydrofolic acid derivative
38	d2blna2	Alignment	not modelled	66.1	16 Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
39	c3cx3A	Alignment	not modelled	64.9	10 PDB header: metal binding protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
40	c3tqrA	Alignment	not modelled	63.6	18 PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
41	d1a9xb2	Alignment	not modelled	60.9	25 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	d1xvla1	Alignment	not modelled	57.5	6 Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
43	c1yrwA	Alignment	not modelled	55.6	16 PDB header: transferase Chain: A: PDB Molecule: protein arna; PDBTitle: crystal structure of e.coli arna transformylase domain
44	c3aerB	Alignment	not modelled	52.7	5 PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
45	c2xdqB	Alignment	not modelled	46.6	13 PDB header: oxidoreductase Chain: B: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: dark operative protochlorophyllide oxidoreductase (chlN-2 chlB)2 complex
46	c2yxba	Alignment	not modelled	44.8	7 PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
47	c3rfoA	Alignment	not modelled	43.8	16 PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: crystal structure of methionyl-trna formyltransferase from bacillus2 anthracis
48	c3louB	Alignment	not modelled	43.7	9 PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
49	c3mfqB	Alignment	not modelled	43.6	11 PDB header: metal binding protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
50	c2r8rB	Alignment	not modelled	41.6	14 PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: crystal structure of the n-terminal region (19..243) of sensor protein2 kdpg from pseudomonas syringae pv. tomato str. dc3000
51	c1keeH	Alignment	not modelled	41.4	29 PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin

52	c3n0vD	 Alignment	not modelled	41.4	12	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
53	c2xdqA	 Alignment	not modelled	38.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: dark operative protochlorophyllide oxidoreductase (chlN-2 chlB)2 complex
54	c3kcgA	 Alignment	not modelled	34.8	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
55	c3q0iA	 Alignment	not modelled	33.9	17	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from vibrio cholerae
56	c3chgB	 Alignment	not modelled	33.3	9	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
57	c2ov3A	 Alignment	not modelled	32.3	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc2 bound
58	c2o1eB	 Alignment	not modelled	32.0	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ycdh; PDBTitle: crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
59	c2e76D	 Alignment	not modelled	30.6	18	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
60	c2qrvA	 Alignment	not modelled	29.2	19	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: structure of dnmt3a-dnmt3l c-terminal domain complex
61	c3cu5B	 Alignment	not modelled	27.8	6	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
62	d1psza	 Alignment	not modelled	25.6	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
63	c3ndjA	 Alignment	not modelled	24.3	10	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
64	d1zgha2	 Alignment	not modelled	23.8	13	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
65	d2czca2	 Alignment	not modelled	23.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c2jzcA	 Alignment	not modelled	22.7	9	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
67	d1s3ia2	 Alignment	not modelled	22.4	11	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
68	c3dapB	 Alignment	not modelled	19.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
69	d2bw0a2	 Alignment	not modelled	19.1	10	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
70	c3nhzA	 Alignment	not modelled	17.8	11	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
71	c2dc1A	 Alignment	not modelled	17.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
72	c1zghA	 Alignment	not modelled	17.1	12	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: methionyl-trna formyltransferase from clostridium thermocellum
73	c2fynO	 Alignment	not modelled	16.8	17	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
74	d1krwa	 Alignment	not modelled	15.1	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d1l7da1	 Alignment	not modelled	15.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain

76	c2ayxA	 Alignment	not modelled	14.2	8	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
77	d1q7ea	 Alignment	not modelled	12.8	25	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
78	c2gm2A	 Alignment	not modelled	12.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
79	d2cyja1	 Alignment	not modelled	12.5	16	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
80	c3ssoE	 Alignment	not modelled	12.5	21	PDB header: transferase Chain: E: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
81	d1jkxa	 Alignment	not modelled	12.5	14	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
82	c2zwrA	 Alignment	not modelled	12.2	15	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of tha1623 from thermus thermophilus hb8
83	c2g04B	 Alignment	not modelled	11.9	6	PDB header: isomerase Chain: B: PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
84	c2pq4B	 Alignment	not modelled	11.7	19	PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
85	c2rjnA	 Alignment	not modelled	11.3	16	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptunibacter caesariensis
86	d1ihna	 Alignment	not modelled	11.3	35	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
87	c2ph5A	 Alignment	not modelled	11.3	15	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
88	d1ys7a2	 Alignment	not modelled	11.0	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	cls3iA	 Alignment	not modelled	10.8	13	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 10-formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
90	c3tqqa	 Alignment	not modelled	10.8	11	PDB header: transferase Chain: A: PDB Molecule: methionyl-trna formyltransferase; PDBTitle: structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
91	c2ps3A	 Alignment	not modelled	10.7	12	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
92	c2z4dA	 Alignment	not modelled	10.6	20	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn13; PDBTitle: nmr structures of yeast proteasome component rpn13
93	d2q4qa1	 Alignment	not modelled	10.6	17	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
94	d7reqb2	 Alignment	not modelled	10.4	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
95	d1x74a1	 Alignment	not modelled	10.1	24	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
96	d1swva	 Alignment	not modelled	10.0	12	Fold: HAD-like Superfamily: HAD-like Family: Phosphonoacetaldehyde hydrolase-like
97	d1fmfa	 Alignment	not modelled	10.0	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
98	d1pq4a	 Alignment	not modelled	9.9	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
99	d1xk7a1	 Alignment	not modelled	9.8	18	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)