Phyre^2

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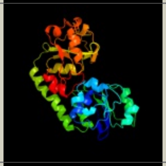
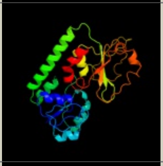
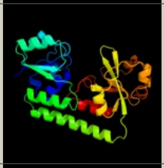
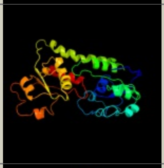
Description	P0AEL6
Date	Thu Jan 5 11:23:38 GMT 2012
Unique Job ID	3a454f0a499c1711

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eiwA_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**htsa protein; **PDBTitle:** crystal structure of staphylococcus aureus lipoprotein, htsa
2	c3pshA_	Alignment		100.0	15	**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)
3	c3be5D_	Alignment		100.0	21	**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
4	d2chua1	Alignment		100.0	23	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
5	c3gfvA_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized abc transporter solute-binding **PDBTitle:** crystal structure of petrobactin-binding protein yclq from2 bacillu subtilis
6	c2phzA_	Alignment		100.0	18	**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.
7	d2phza1	Alignment		100.0	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
8	c2x4lA_	Alignment		100.0	17	**PDB header:**transport **Chain:** A: **PDB Molecule:**ferric-siderophore receptor protein; **PDBTitle:** crystal structure of dese, a ferric-siderophore receptor2 protein from streptomyces coelicolor
9	d1esza_	Alignment		100.0	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Periplasmic ferric siderophore binding protein FhuD
10	c2q8pA_	Alignment		100.0	22	**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
11	c3g9qA_	Alignment		100.0	21	**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

12	c3mwgA_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated abc transporter siderophore-binding protein **PDBTitle:** crystal structure of staphylococcus aureus sira
13	c2r79A_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
14	c2r7aC_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
15	c3md9A_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hemin-binding periplasmic protein hmut; **PDBTitle:** structure of apo form of a periplasmic heme binding protein
16	d2etva1	Alignment		100.0	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
17	d1n2za_	Alignment		100.0	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
18	c3pdiG_	Alignment		97.6	11	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
19	d1mioa_	Alignment		97.2	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
20	c3pdiB_	Alignment		97.1	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
21	d1qh8a_	Alignment	not modelled	97.0	10	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
22	d1m1na_	Alignment	not modelled	96.8	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
23	d1m1nb_	Alignment	not modelled	95.9	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
24	c3aerC_	Alignment	not modelled	95.8	9	**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
25	d1miob_	Alignment	not modelled	95.8	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
26	d1qh8b_	Alignment	not modelled	93.9	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
27	c2xdqB_	Alignment	not modelled	90.4	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
28	d1a9xb2	Alignment	not modelled	74.8	28	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)

29	c2yxbA_	Alignment	not modelled	58.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
30	c1keeH_	Alignment	not modelled	43.2	28	**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
31	c3ndjA_	Alignment	not modelled	42.6	7	**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
32	c3obiC_	Alignment	not modelled	36.2	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
33	c3czpA_	Alignment	not modelled	35.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
34	c3rfoA_	Alignment	not modelled	32.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
35	c1z7eC_	Alignment	not modelled	27.6	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
36	d7reqa2	Alignment	not modelled	22.1	11	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
37	d1q3qa2	Alignment	not modelled	21.6	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
38	c2z4dA_	Alignment	not modelled	21.5	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn13; **PDBTitle:** nmr structures of yeast proteasome component rpn13
39	d1gmla_	Alignment	not modelled	21.5	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
40	c2r8rB_	Alignment	not modelled	20.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
41	c2g04B_	Alignment	not modelled	19.3	16	**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
42	d1zgha2	Alignment	not modelled	18.8	24	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
43	c3cu5B_	Alignment	not modelled	18.6	8	**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
44	d1a6db2	Alignment	not modelled	18.3	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
45	d1xvla1	Alignment	not modelled	18.2	10	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
46	c2z59A_	Alignment	not modelled	17.7	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** complex structures of mouse rpn13 (22-130aa) and ubiquitin
47	c3o1lB_	Alignment	not modelled	16.9	11	**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
48	c2r2yA_	Alignment	not modelled	16.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein adrm1; **PDBTitle:** crystal structure of the proteasomal rpn13 pru-domain
49	c1ohhH_	Alignment	not modelled	16.8	29	**PDB header:**synthase **Chain:** H: **PDB Molecule:**atpase inhibitor, mitochondrial; **PDBTitle:** bovine mitochondrial f1-atpase complexed with the inhibitor2 protein if1
50	d1q7ea_	Alignment	not modelled	16.5	17	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
51	c3rhfB_	Alignment	not modelled	16.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative polyphosphate kinase 2 family protein; **PDBTitle:** crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
52	c3n0vD_	Alignment	not modelled	16.1	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	c1fmtA_	Alignment	not modelled	15.8	19	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli

54	d1assa_	Alignment	not modelled	15.7	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
55	d1toaa_	Alignment	not modelled	15.1	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
56	c1toaA_	Alignment	not modelled	15.1	15	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
57	c2xdqA_	Alignment	not modelled	14.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
58	c1zghA_	Alignment	not modelled	13.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
59	c3dapB_	Alignment	not modelled	13.1	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
60	c1xeaD_	Alignment	not modelled	12.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
61	d1s3ia2	Alignment	not modelled	12.8	13	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
62	c2kr0A_	Alignment	not modelled	12.6	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**proteasomal ubiquitin receptor adrm1; **PDBTitle:** a proteasome protein
63	c2yfqA_	Alignment	not modelled	12.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
64	c1e0mA_	Alignment	not modelled	12.2	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
65	c2dc1A_	Alignment	not modelled	12.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
66	d2a9pa1	Alignment	not modelled	12.1	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3czqA_	Alignment	not modelled	11.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
68	d1ccwa_	Alignment	not modelled	11.7	19	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
69	d1hwxa1	Alignment	not modelled	11.6	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
70	c2v7qJ_	Alignment	not modelled	11.2	21	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**atpase inhibitor; **PDBTitle:** the structure of f1-atpase inhibited by i1-60his, a2 monomeric form of the inhibitor protein, if1.
71	d1k9ra_	Alignment	not modelled	10.8	15	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
72	c2ayxA_	Alignment	not modelled	10.4	6	**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
73	d1tk7a2	Alignment	not modelled	10.2	10	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
74	c3jvvA_	Alignment	not modelled	9.8	13	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
75	c2yscA_	Alignment	not modelled	9.6	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
76	d1x74a1	Alignment	not modelled	9.6	15	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
77	c3aerB_	Alignment	not modelled	9.2	20	**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
78	d1f06a1	Alignment	not modelled	8.9	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

79	c2djyA_	Alignment	not modelled	8.8	15	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
80	d1xk7a1	Alignment	not modelled	8.5	16	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
81	c2ysgA_	Alignment	not modelled	8.5	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**syntaxin-binding protein 4; **PDBTitle:** solution structure of the ww domain from the human syntaxin-2 binding protein 4
82	c2l4jA_	Alignment	not modelled	8.4	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**yes-associated protein 2 (yap2); **PDBTitle:** yap ww2
83	d2cyja1	Alignment	not modelled	8.4	11	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
84	c2kykA_	Alignment	not modelled	8.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
85	d1i5hw_	Alignment	not modelled	8.3	10	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
86	c3lo3E_	Alignment	not modelled	8.3	12	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
87	c2ixaA_	Alignment	not modelled	8.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
88	d1ihna_	Alignment	not modelled	8.1	18	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
89	d1fmta2	Alignment	not modelled	8.1	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
90	c1yiuA_	Alignment	not modelled	7.8	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
91	d1xeaa1	Alignment	not modelled	7.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	c1wr7A_	Alignment	not modelled	7.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
93	c2kq0A_	Alignment	not modelled	7.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase nedd4; **PDBTitle:** human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeymea
94	d1y5ia2	Alignment	not modelled	7.5	11	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
95	c2gm2A_	Alignment	not modelled	7.4	30	**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
96	d2q4qa1	Alignment	not modelled	6.9	9	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
97	d2f21a1	Alignment	not modelled	6.8	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
98	d2itka1	Alignment	not modelled	6.7	19	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
99	d1edza2	Alignment	not modelled	6.6	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase