Phyre^2

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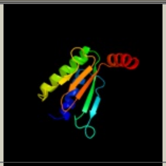
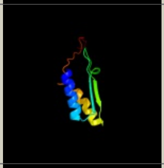
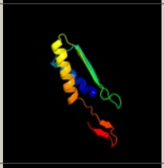
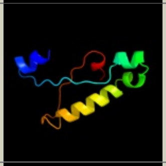
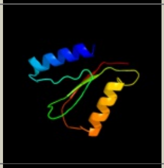
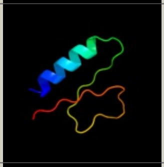
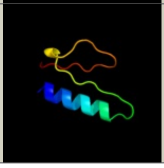
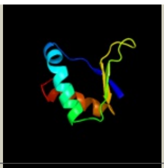
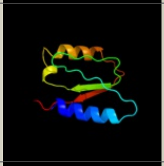
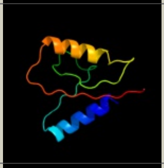
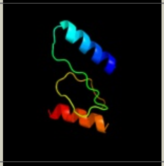
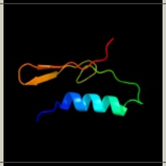
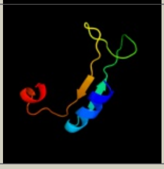
Description	P0AAT6
Date	Thu Jan 5 11:13:47 GMT 2012
Unique Job ID	ee14c3f52109cbd3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3upsA_	Alignment		100.0	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
2	d2id1a1	Alignment		100.0	36	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
3	d2o5aa1	Alignment		100.0	36	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
4	c2omdB_	Alignment		86.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
5	c2qieA_	Alignment		74.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
6	d1fm0e_	Alignment		69.9	12	**Fold:**alpha/beta-Hammerhead **Superfamily:**Molybdopterin synthase subunit MoaE **Family:**Molybdopterin synthase subunit MoaE
7	d1ex9a_	Alignment		51.8	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
8	d1vmea1	Alignment		51.4	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
9	c3b6iB_	Alignment		40.4	21	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
10	d1n0ua4	Alignment		39.3	8	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
11	d2arka1	Alignment		34.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like

12	d2dy1a4	Alignment		29.7	11	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
13	c3fniA_	Alignment		29.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
14	d2bm0a4	Alignment		28.7	5	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
15	d1e5da1	Alignment		28.0	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
16	c3hlyA_	Alignment		27.4	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
17	d1ycga1	Alignment		25.5	5	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	d1nvja_	Alignment		20.2	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**Molybdopterin synthase subunit MoaE **Family:**Molybdopterin synthase subunit MoaE
19	d1k8kd1	Alignment		20.2	28	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
20	d1lk5a2	Alignment		20.1	14	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
21	d2fz5a1	Alignment	not modelled	19.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
22	d1xpja_	Alignment	not modelled	19.3	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
23	c2zkiH_	Alignment	not modelled	18.7	15	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
24	c2wp4A_	Alignment	not modelled	16.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**molybdopterin-converting factor subunit 2 1; **PDBTitle:** crystal structure of rv3119 from mycobacterium tuberculosis
25	c3b8hA_	Alignment	not modelled	15.0	8	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
26	d2fcra_	Alignment	not modelled	14.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	d1mp9a1	Alignment	not modelled	14.2	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
28	c2xexA_	Alignment	not modelled	13.9	8	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g

29	c2pjmA_	Alignment	not modelled	13.4	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
30	d2obba1	Alignment	not modelled	13.0	5	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
31	c3dnpA_	Alignment	not modelled	12.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
32	c3f4aA_	Alignment	not modelled	12.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ygr203w; **PDBTitle:** structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
33	d1llda1	Alignment	not modelled	11.4	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
34	c1lk5C_	Alignment	not modelled	11.4	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
35	d2z1ca1	Alignment	not modelled	10.7	23	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
36	d2ot2a1	Alignment	not modelled	10.7	19	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
37	c2c5iP_	Alignment	not modelled	10.6	50	**PDB header:**protein transport **Chain:** P: **PDB Molecule:**vacuolar protein sorting protein 51; **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation
38	d5nula_	Alignment	not modelled	10.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
39	c2c5kP_	Alignment	not modelled	10.3	50	**PDB header:**protein transport **Chain:** P: **PDB Molecule:**vacuolar protein sorting protein 51; **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51
40	d1wzca1	Alignment	not modelled	10.3	5	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
41	c1vmeB_	Alignment	not modelled	10.3	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
42	d1e4ea1	Alignment	not modelled	10.2	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
43	d1ydga_	Alignment	not modelled	9.8	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
44	c3o2eA_	Alignment	not modelled	9.4	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
45	c3hheA_	Alignment	not modelled	9.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
46	c2kz0A_	Alignment	not modelled	9.2	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bola family protein; **PDBTitle:** solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
47	d1t57a_	Alignment	not modelled	8.7	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
48	c2rdo7_	Alignment	not modelled	8.6	13	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
49	c2q9uB_	Alignment	not modelled	8.4	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
50	c1ychD_	Alignment	not modelled	8.1	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
51	c1zn0B_	Alignment	not modelled	7.9	5	**PDB header:**translation/biosynthetic protein/rna **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf
52	c3tqtB_	Alignment	not modelled	7.7	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
53	c3f6sI_	Alignment	not modelled	7.7	10	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
54	d1nh8a2	Alignment	not modelled	7.7	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain

55	c2zf8A_	Alignment	not modelled	7.5	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
56	c1e5dA_	Alignment	not modelled	7.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
57	d2fvta1	Alignment	not modelled	7.4	19	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
58	c3cioA_	Alignment	not modelled	7.3	13	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
59	d2qwxa1	Alignment	not modelled	7.3	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
60	d2fi9a1	Alignment	not modelled	7.2	11	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
61	c2hnbA_	Alignment	not modelled	7.2	7	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
62	c3l7oB_	Alignment	not modelled	7.2	15	**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
63	c3o3nB_	Alignment	not modelled	7.1	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
64	d2hd3a1	Alignment	not modelled	7.0	25	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
65	c3pgvB_	Alignment	not modelled	6.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
66	d1nh2a1	Alignment	not modelled	6.9	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
67	c3bzqA_	Alignment	not modelled	6.9	18	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
68	d1j98a_	Alignment	not modelled	6.9	17	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
69	d1kqfa1	Alignment	not modelled	6.8	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
70	c1olsB_	Alignment	not modelled	6.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
71	c3niwA_	Alignment	not modelled	6.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
72	d1umya_	Alignment	not modelled	6.5	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
73	d2a5la1	Alignment	not modelled	6.5	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
74	d2bfdb2	Alignment	not modelled	6.4	10	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
75	d2cfxa2	Alignment	not modelled	6.4	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
76	d1qnaa1	Alignment	not modelled	6.3	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
77	d1uj4a2	Alignment	not modelled	6.3	12	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
78	c2bm0A_	Alignment	not modelled	6.3	5	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
79	d1nrwa_	Alignment	not modelled	6.2	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
80	d1nf2a_	Alignment	not modelled	6.1	5	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof

81	d1x4ma1	Alignment	not modelled	6.0	17	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
82	d1ny8a_	Alignment	not modelled	6.0	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
83	c3gygA_	Alignment	not modelled	5.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon putative hydrolase ntdb; **PDBTitle:** crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
84	d3d3ra1	Alignment	not modelled	5.8	19	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
85	c3d0oA_	Alignment	not modelled	5.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
86	c1uj6A_	Alignment	not modelled	5.7	13	**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
87	d2guma1	Alignment	not modelled	5.6	26	**Fold:**Viral glycoprotein ectodomain-like **Superfamily:**Viral glycoprotein ectodomain-like **Family:**Glycoprotein B-like
88	d1m7ja2	Alignment	not modelled	5.5	13	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**D-aminoacylase
89	d1otga_	Alignment	not modelled	5.5	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**5-carboxymethyl-2-hydroxymuconate isomerase (CHMI)
90	c1zosE_	Alignment	not modelled	5.5	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
91	c1byyA_	Alignment	not modelled	5.4	36	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein (sodium channel alpha-subunit); **PDBTitle:** sodium channel iia inactivation gate
92	d1iowa1	Alignment	not modelled	5.4	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
93	c3e5nA_	Alignment	not modelled	5.3	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
94	d2a6aa1	Alignment	not modelled	5.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**YeaZ-like
95	c1xviA_	Alignment	not modelled	5.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
96	d1xvia_	Alignment	not modelled	5.1	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
97	c3fojA_	Alignment	not modelled	5.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.