


















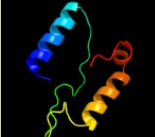

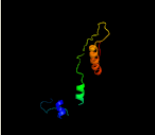

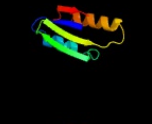






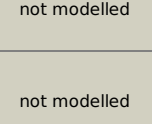


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2603c (- )_2930815_2931570
Date	Wed Aug 7 12:50:24 BST 2019
Unique Job ID	4eeb73a748b98cd6

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1fpa_</a>	 Alignment		100.0	46	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
2	<a href="#">c4f3qA_</a>	 Alignment		100.0	44	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cbu_1566; <b>PDBTitle:</b> structure of a yebc family protein (cbu_1566) from coxiella burnetii
3	<a href="#">d1kona_</a>	 Alignment		100.0	48	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
4	<a href="#">d1mw7a_</a>	 Alignment		100.0	29	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
5	<a href="#">c1u8sB_</a>	 Alignment		68.9	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> glycine cleavage system transcriptional <b>PDBTitle:</b> crystal structure of putative glycine cleavage system2 transcriptional repressor
6	<a href="#">c2jsxA_</a>	 Alignment		65.6	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein nappd; <b>PDBTitle:</b> solution structure of the e. coli tat proofreading2 chaperone protein nappd
7	<a href="#">c6bwqB_</a>	 Alignment		63.9	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel <b>PDBTitle:</b> larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
8	<a href="#">c6fqbd_</a>	 Alignment		63.3	13	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> mur ligase family protein; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
9	<a href="#">c3ibwA_</a>	 Alignment		60.1	9	<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 gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
10	<a href="#">d2auna2</a>	 Alignment		53.4	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> LD-carboxypeptidase A N-terminal domain-like
11	<a href="#">c2zf8A_</a>	 Alignment		51.0	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> component of sodium-driven polar flagellar motor; <b>PDBTitle:</b> crystal structure of moty

12	<a href="#">c2e1cA</a>	Alignment		50.2	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
13	<a href="#">d2cyya2</a>	Alignment		50.1	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
14	<a href="#">c2nyiB</a>	Alignment		48.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> unknown protein; <b>PDBTitle:</b> crystal structure of an unknown protein from galdieria sulphuraria
15	<a href="#">c2zbcH</a>	Alignment		47.5	16	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 83aa long hypothetical transcriptional regulator asnc; <b>PDBTitle:</b> crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfobolus tokodaii strain7.
16	<a href="#">c3fiaA</a>	Alignment		44.4	15	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intersectin-1; <b>PDBTitle:</b> crystal structure of the eh 1 domain from human intersectin-1 protein.2 northeast structural genomics consortium target hr3646e.
17	<a href="#">c2y9kG</a>	Alignment		43.4	8	<b>PDB header:</b> protein transport <b>Chain:</b> G: <b>PDB Molecule:</b> protein invg; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at subnanometer2 resolution
18	<a href="#">c2w0cS</a>	Alignment		43.1	28	<b>PDB header:</b> virus <b>Chain:</b> S: <b>PDB Molecule:</b> protein p3; <b>PDBTitle:</b> x-ray structure of the entire lipid-containing bacteriophage pm2
19	<a href="#">c2cveA</a>	Alignment		40.4	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ttha1053; <b>PDBTitle:</b> crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
20	<a href="#">c3k85B</a>	Alignment		37.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> d-glycero-d-manno-heptose 1-phosphate kinase; <b>PDBTitle:</b> crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
21	<a href="#">c4h1hB</a>	Alignment	not modelled	36.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1638 protein; <b>PDBTitle:</b> crystal structure of mccf homolog from listeria monocytogenes egd-e
22	<a href="#">c3k7A</a>	Alignment	not modelled	36.1	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
23	<a href="#">c3c19A</a>	Alignment	not modelled	35.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mk0293; <b>PDBTitle:</b> crystal structure of protein mk0293 from methanopyrus kandleri av19
24	<a href="#">c1vi7A</a>	Alignment	not modelled	35.2	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yigz; <b>PDBTitle:</b> crystal structure of an hypothetical protein
25	<a href="#">c2p6tH</a>	Alignment	not modelled	34.9	7	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
26	<a href="#">d1xp3a1</a>	Alignment	not modelled	34.2	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
27	<a href="#">c1zrsB</a>	Alignment	not modelled	33.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> wild-type ld-carboxypeptidase
28	<a href="#">d1ilga2</a>	Alignment	not modelled	33.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
29	<a href="#">c2kerA</a>	Alignment	not modelled	32.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intersectin-1;

29	<a href="#">c2xylA</a>	Alignment	not modelled	32.8	13	<b>PDBTitle:</b> solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a <b>PDB header:</b> hydrolase
30	<a href="#">c4e5sC</a>	Alignment	not modelled	31.9	25	<b>Chain:</b> C: <b>PDB Molecule:</b> mcccflake protein (ba_5613); <b>PDBTitle:</b> crystal structure of mcclike protein (ba_5613) from bacillus2 anthracis str. ames
31	<a href="#">d2nzca1</a>	Alignment	not modelled	31.2	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> TM1266-like
32	<a href="#">d1ewqa2</a>	Alignment	not modelled	30.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
33	<a href="#">c2f06B</a>	Alignment	not modelled	29.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0572 from bacteroides thetaiotaomicron
34	<a href="#">c1fpqA</a>	Alignment	not modelled	29.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isoliquiritigenin 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
35	<a href="#">c2lvwA</a>	Alignment	not modelled	29.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetolactate synthase isozyme 1 small subunit; <b>PDBTitle:</b> solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetoxyhydroxyacid synthase i (ahas i)
36	<a href="#">c6nkoA</a>	Alignment	not modelled	29.0	26	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> forh; <b>PDBTitle:</b> crystal structure of forh
37	<a href="#">d1zl0a2</a>	Alignment	not modelled	29.0	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> LD-carboxypeptidase A N-terminal domain-like
38	<a href="#">c3lmzA</a>	Alignment	not modelled	28.6	7	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distansonis atcc 8503 at 1.44 a resolution
39	<a href="#">c4yajA</a>	Alignment	not modelled	28.5	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
40	<a href="#">c3k2qA</a>	Alignment	not modelled	28.3	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrophosphate-dependent phosphofructokinase; <b>PDBTitle:</b> crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
41	<a href="#">c2vsaA</a>	Alignment	not modelled	27.4	45	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> mosquitocidal toxin; <b>PDBTitle:</b> structure and mode of action of a mosquitocidal holotoxin
42	<a href="#">c2kzza</a>	Alignment	not modelled	27.0	24	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (dna polymerase i); <b>PDBTitle:</b> klenow fragment with normal substrate and zinc only
43	<a href="#">c1lvaA</a>	Alignment	not modelled	26.1	11	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb
44	<a href="#">c3dx5A</a>	Alignment	not modelled	25.9	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
45	<a href="#">d1ub9a</a>	Alignment	not modelled	25.2	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
46	<a href="#">c2plyB</a>	Alignment	not modelled	25.2	13	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
47	<a href="#">d2ex4a1</a>	Alignment	not modelled	25.1	24	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> AD-003 protein-like
48	<a href="#">c1i1gA</a>	Alignment	not modelled	25.0	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
49	<a href="#">c3bzqA</a>	Alignment	not modelled	24.8	35	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
50	<a href="#">c3thzA</a>	Alignment	not modelled	24.3	33	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein msh2; <b>PDBTitle:</b> human mutsbeta complexed with an idl of 6 bases (loop6) and adp
51	<a href="#">d1kkca2</a>	Alignment	not modelled	24.0	37	<b>Fold:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Superfamily:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain <b>Family:</b> Fe,Mn superoxide dismutase (SOD), C-terminal domain
52	<a href="#">d1qmha1</a>	Alignment	not modelled	23.7	21	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> RNA 3'-terminal phosphate cyclase, RPTC, insert domain <b>Family:</b> RNA 3'-terminal phosphate cyclase, RPTC, insert domain
53	<a href="#">d1sc6a3</a>	Alignment	not modelled	23.6	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain <b>Fold:</b> HPr-like <b>Superfamily:</b> Putative transcriptional regulator TM1602, C-terminal

54	<a href="#">d1j5ya2</a>	Alignment	not modelled	23.6	20	domain <b>Family:</b> Putative transcriptional regulator TM1602, C-terminal domain
55	<a href="#">d1cc8a_</a>	Alignment	not modelled	23.5	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
56	<a href="#">c2khnA_</a>	Alignment	not modelled	23.1	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> intersectin-1; <b>PDBTitle:</b> nmr solution structure of the eh 1 domain from human2 intersectin-1 protein. northeast structural genomics3 consortium target hr3646e.
57	<a href="#">d1mwza_</a>	Alignment	not modelled	22.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> HMA, heavy metal-associated domain <b>Family:</b> HMA, heavy metal-associated domain
58	<a href="#">c2e7xA_</a>	Alignment	not modelled	22.2	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
59	<a href="#">c2e1aD_</a>	Alignment	not modelled	21.9	11	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> 75aa long hypothetical regulatory protein asnc; <b>PDBTitle:</b> crystal structure of ffrp-dm1
60	<a href="#">c5d4pA_</a>	Alignment	not modelled	21.8	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrogen regulatory protein p-ii glnb; <b>PDBTitle:</b> structure of cpil bound to adp and bicarbonate, from thiomonas2 intermedia k12
61	<a href="#">c1p65A_</a>	Alignment	not modelled	21.8	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleocapsid protein; <b>PDBTitle:</b> crystal structure of the nucleocapsid protein of porcine reproductive2 and respiratory syndrome virus (prsv)
62	<a href="#">d1p65a_</a>	Alignment	not modelled	21.8	31	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Arterivirus nucleocapsid protein
63	<a href="#">c3i7pA_</a>	Alignment	not modelled	20.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitrogen regulatory protein pii; <b>PDBTitle:</b> crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
64	<a href="#">c3n4sC_</a>	Alignment	not modelled	20.5	11	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> monopolin complex subunit csm1; <b>PDBTitle:</b> structure of csm1 c-terminal domain, p21212 form
65	<a href="#">c2djwF_</a>	Alignment	not modelled	20.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> probable transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of ttha0845 from thermus thermophilus hb8
66	<a href="#">d1gtra1</a>	Alignment	not modelled	20.4	26	<b>Fold:</b> Ribosomal protein L25-like <b>Superfamily:</b> Ribosomal protein L25-like <b>Family:</b> Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
67	<a href="#">c3fybA_</a>	Alignment	not modelled	20.3	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function (duf1244); <b>PDBTitle:</b> crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
68	<a href="#">c1b4aA_</a>	Alignment	not modelled	20.3	14	<b>PDB header:</b> repressor <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> structure of the arginine repressor from bacillus stearothermophilus
69	<a href="#">c3uagA_</a>	Alignment	not modelled	20.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
70	<a href="#">d1wb9a2</a>	Alignment	not modelled	20.0	39	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
71	<a href="#">d1jr3d2</a>	Alignment	not modelled	19.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
72	<a href="#">d4pfka_</a>	Alignment	not modelled	19.7	30	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
73	<a href="#">c4ozIA_</a>	Alignment	not modelled	19.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> glnk2 from haloferax mediterranei complexed with amp
74	<a href="#">c3canA_</a>	Alignment	not modelled	19.3	26	<b>PDB header:</b> lyase activator <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-formate lyase-activating enzyme; <b>PDBTitle:</b> crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
75	<a href="#">c5n9jB_</a>	Alignment	not modelled	19.2	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mediator of rna polymerase ii transcription subunit 10; <b>PDBTitle:</b> core mediator of transcriptional regulation
76	<a href="#">c3i4pA_</a>	Alignment	not modelled	18.7	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
77	<a href="#">c1ewrA_</a>	Alignment	not modelled	17.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of taq muts
78	<a href="#">d2cg4a2</a>	Alignment	not modelled	17.8	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
79	<a href="#">d1fima_</a>	Alignment	not modelled	17.7	11	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF

						<b>Family:</b> MIF-related
80	<a href="#">d1lxja_</a>	Alignment	not modelled	17.2	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
81	<a href="#">d2o35a1</a>	Alignment	not modelled	17.0	33	<b>Fold:</b> SMc04008-like <b>Superfamily:</b> SMc04008-like <b>Family:</b> SMc04008-like
82	<a href="#">c2o35A_</a>	Alignment	not modelled	17.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf1244; <b>PDBTitle:</b> protein of unknown function (duf1244) from sinorhizobium melloti
83	<a href="#">d1lxna_</a>	Alignment	not modelled	16.6	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
84	<a href="#">c2hw5F_</a>	Alignment	not modelled	16.5	21	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> enoyl-coa hydratase; <b>PDBTitle:</b> the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
85	<a href="#">c5z01A_</a>	Alignment	not modelled	16.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> murein tetrapeptide carboxypeptidase; <b>PDBTitle:</b> native escherichia coli l,d-carboxypeptidase a (ldca)
86	<a href="#">c2o8dB_</a>	Alignment	not modelled	16.3	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein msh6; <b>PDBTitle:</b> human mutsalpha (msh2/msh6) bound to adp and a g du mispair
87	<a href="#">c5xoeA_</a>	Alignment	not modelled	15.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent 6-phosphofructokinase; <b>PDBTitle:</b> crystal structure of the apo staphylococcus aureus phosphofructokinase
88	<a href="#">c5ubba_</a>	Alignment	not modelled	15.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha n-terminal protein methyltransferase 1b; <b>PDBTitle:</b> crystal structure of human alpha n-terminal protein methyltransferase2 1b
89	<a href="#">c1zxxA_</a>	Alignment	not modelled	15.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructokinase; <b>PDBTitle:</b> the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
90	<a href="#">d1ul3a_</a>	Alignment	not modelled	15.6	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
91	<a href="#">c5odcD_</a>	Alignment	not modelled	15.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> methyl-viologen reducing hydrogenase subunit d; <b>PDBTitle:</b> heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
92	<a href="#">d2r9ga1</a>	Alignment	not modelled	15.3	25	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> MgsA/YrvN C-terminal domain-like
93	<a href="#">c4bucA_</a>	Alignment	not modelled	15.3	5	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of murd ligase from thermotoga maritima in apo form
94	<a href="#">d1pfka_</a>	Alignment	not modelled	15.2	22	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
95	<a href="#">d2cfxa2</a>	Alignment	not modelled	15.0	13	<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="#">d1k47a2</a>	Alignment	not modelled	14.9	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Phosphomevalonate kinase (PMK)
97	<a href="#">d1hwua_</a>	Alignment	not modelled	14.9	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
98	<a href="#">d1uwva2</a>	Alignment	not modelled	14.6	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> (Uracil-5-)-methyltransferase
99	<a href="#">c2m45A_</a>	Alignment	not modelled	14.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> nmr solution structure of the c-terminus of the minichromosome2 maintenance protein mcm from sulfobolus solfataricus