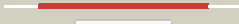



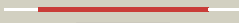







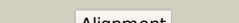







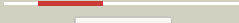







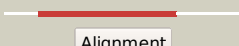

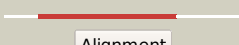

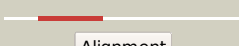








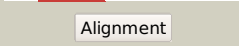
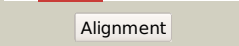
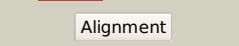
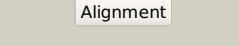





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1099c_glpX_1227601_1228689
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	0b655100de8924ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ayyB_	 Alignment		100.0	99	PDB header: hydrolase Chain: B; PDB Molecule: fructose-1,6-bisphosphatase class 2; PDBTitle: crystal structure of apo fructose-1,6-bisphosphatase from2 mycobacterium tuberculosis
2	c3rojD_	 Alignment		100.0	42	PDB header: hydrolase Chain: D; PDB Molecule: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7- PDBTitle: d-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase2 of synechocystis sp. pcc 6803
3	d1ni9a_	 Alignment		100.0	47	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: GlpX-like bacterial fructose-1,6-bisphosphatase
4	c3luzA_	 Alignment		97.6	19	PDB header: hydrolase Chain: A; PDB Molecule: extragenic suppressor protein subh; PDBTitle: crystal structure of extragenic suppressor protein subh from2 bartonella henselae, via combined iodide sad molecular replacement
5	c3t0jB_	 Alignment		97.5	16	PDB header: hydrolase Chain: B; PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of inositol monophosphatase - ii from staphylococcus2 aureus mssa476
6	d1lbva_	 Alignment		97.0	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
7	c2qf1A_	 Alignment		96.9	16	PDB header: hydrolase Chain: A; PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of subh: inositol monophosphatase and extragenic2 suppressor from e. coli
8	c5eq9A_	 Alignment		96.9	25	PDB header: biosynthetic protein Chain: A; PDB Molecule: inositol monophosphatase; PDBTitle: crystal structure of medicago truncatula histidinol-phosphate2 phosphatase (mthpp) in complex with l-histidinol phosphate and mg2+
9	c2czhB_	 Alignment		96.9	20	PDB header: hydrolase Chain: B; PDB Molecule: inositol monophosphatase 2; PDBTitle: crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
10	d1xi6a_	 Alignment		96.8	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	c2fvzB_	 Alignment		96.7	19	PDB header: hydrolase Chain: B; PDB Molecule: inositol monophosphatase 2; PDBTitle: human inositol monophosphatase 2

12	c5zhbB	 Alignment		96.7	22	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
13	c5zonA	 Alignment		96.7	26	PDB header: hydrolase Chain: A: PDB Molecule: histidinol-phosphatase; PDBTitle: histidinol phosphate phosphatase from mycobacterium tuberculosis
14	d1g0ha	 Alignment		96.6	25	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	c3rydA	 Alignment		96.6	13	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal strucutre of ca bound impase family protein from2 staphylococcus aureus
16	c2p3nB	 Alignment		96.5	18	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: thermotoga maritima impase tm1415
17	c2pcrA	 Alignment		96.5	27	PDB header: hydrolase Chain: A: PDB Molecule: inositol-1-monophosphatase; PDBTitle: crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
18	c2q74B	 Alignment		96.4	19	PDB header: hydrolase Chain: B: PDB Molecule: inositol-1-monophosphatase; PDBTitle: mycobacterium tuberculosis subh
19	c3qmfA	 Alignment		96.3	15	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase family protein; PDBTitle: crystal structure of an inositol monophosphatase family protein2 (sas2203) from staphylococcus aureus mssa476
20	c3b8bA	 Alignment		96.3	19	PDB header: hydrolase Chain: A: PDB Molecule: cysq, sulfite synthesis pathway protein; PDBTitle: crystal structure of cysq from bacteroides thetaiotaomicron, a2 bacterial member of the inositol monophosphatase family
21	c5djjA	 Alignment	not modelled	96.0	23	PDB header: hydrolase Chain: A: PDB Molecule: 3'-phosphoadenosine 5'-phosphate phosphatase; PDBTitle: structure of m. tuberculosis cysq, a pap phosphatase with po4 and 2mg2 bound
22	c4n81A	 Alignment	not modelled	96.0	28	PDB header: hydrolase Chain: A: PDB Molecule: inositol monophosphatase; PDBTitle: another flexible region at the active site of an inositol2 monophosphatase from zymomonas mobilis
23	c4j13B	 Alignment	not modelled	95.7	16	PDB header: hydrolase Chain: B: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase2 from entamoeba histolytica
24	d2hhma	 Alignment	not modelled	95.6	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
25	d1vdwa	 Alignment	not modelled	95.5	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
26	c4gdgA	 Alignment	not modelled	95.5	17	PDB header: hydrolase Chain: A: PDB Molecule: 3'(2'),5'-bisphosphate nucleotidase, putative; PDBTitle: structural and functional characterization of 3'(2'),5'-bisphosphate2 nucleotidase1 from entamoeba histolytica
27	c5iz3B	 Alignment	not modelled	94.2	17	PDB header: hydrolase Chain: B: PDB Molecule: predicted protein; PDBTitle: p. patens sedoheptulose-1,7-bisphosphatase
28	d1inpa	 Alignment	not modelled	94.1	31	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase

						Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
29	d1jp4a_	Alignment	not modelled	91.9	16	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
30	d1d9qa_	Alignment	not modelled	91.6	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	c5esyA_	Alignment	not modelled	91.3	25	PDB header: hydrolase Chain: A: PDB Molecule: sal1 phosphatase; PDBTitle: arabidopsis thaliana sal1
32	d1ka1a_	Alignment	not modelled	90.7	28	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
33	c3uksB_	Alignment	not modelled	88.8	23	PDB header: hydrolase Chain: B: PDB Molecule: sedoheptulose-1,7 bisphosphatase, putative; PDBTitle: 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
34	d1v8ba2	Alignment	not modelled	82.8	27	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
35	c3j08A_	Alignment	not modelled	80.1	23	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
36	c3j09A_	Alignment	not modelled	80.0	23	PDB header: hydrolase, metal transport Chain: A: PDB Molecule: copper-exporting p-type atpase a; PDBTitle: high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
37	d1g6sa_	Alignment	not modelled	71.4	18	Fold: IF3-like Superfamily: EPT/RTPC-like Family: Enolpyruvate transferase, EPT
38	c6i7tB_	Alignment	not modelled	65.5	27	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: eif2b:eif2 complex
39	c5xwbB_	Alignment	not modelled	60.3	17	PDB header: transferase Chain: B: PDB Molecule: 3-phosphoshikimate 1-carboxyvinyltransferase; PDBTitle: crystal structure of 5-enolpyruvylshikimate-3-phosphate synthase from2 a psychrophilic bacterium, colwellia psychrerythraea
40	c2yvka_	Alignment	not modelled	58.0	27	PDB header: isomerase Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
41	d1j5ta_	Alignment	not modelled	56.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
42	c4zemB_	Alignment	not modelled	55.5	14	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
43	c4umwA_	Alignment	not modelled	54.9	29	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
44	c3ht4B_	Alignment	not modelled	54.0	20	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
45	c3a11D_	Alignment	not modelled	53.7	9	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
46	d1t5oa_	Alignment	not modelled	53.3	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
47	d1spia_	Alignment	not modelled	51.2	19	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
48	c3ecsd_	Alignment	not modelled	50.8	8	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
49	c6a34B_	Alignment	not modelled	50.2	19	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i
50	c3rf7A_	Alignment	not modelled	48.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
51	d2a0ua1	Alignment	not modelled	46.9	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
52	c3rfuC_	Alignment	not modelled	46.2	21	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
						PDB header: lyase Chain: A: PDB Molecule: carbon-sulfur lyase involved in aluminum

53	c3gwpA_	Alignment	not modelled	45.3	26	resistance; PDBTitle: crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
54	d1ld1a_	Alignment	not modelled	42.6	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
55	c2kg4A_	Alignment	not modelled	42.2	18	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible protein gadd45 PDBTitle: three-dimensional structure of human gadd45alpha in solution by nmr
56	c3aerC_	Alignment	not modelled	42.0	15	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
57	c6i3mF_	Alignment	not modelled	41.7	7	PDB header: translation Chain: F: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
58	c3pajA_	Alignment	not modelled	40.2	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
59	c3vvpC_	Alignment	not modelled	39.2	10	PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
60	c6i3mD_	Alignment	not modelled	38.1	11	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
61	c5uebA_	Alignment	not modelled	37.7	8	PDB header: unknown function Chain: A: PDB Molecule: negoa.19184.a; PDBTitle: novel crystal structure of a hypothetical protein from neisseria2 gonorrhoeae
62	c2k2wA_	Alignment	not modelled	37.0	17	PDB header: cell cycle Chain: A: PDB Molecule: recombination and dna repair protein; PDBTitle: second brct domain of nbs1
63	d7reqa2	Alignment	not modelled	35.7	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
64	c3roiA_	Alignment	not modelled	35.5	16	PDB header: transferase Chain: A: PDB Molecule: 3-phosphoshikimate 1-carboxyvinyltransferase; PDBTitle: 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
65	c3n91A_	Alignment	not modelled	34.8	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a structural genomics, unknown function2 (bacova_03430) from bacteroides ovatus at 2.40 a resolution
66	c2gq1A_	Alignment	not modelled	32.8	17	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
67	c5wi5C_	Alignment	not modelled	32.5	12	PDB header: transferase Chain: C: PDB Molecule: udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; PDBTitle: 2.0 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from streptococcus pneumoniae in complex3 with uridine-diphosphate-2(n-acetylglucosaminy) butyric acid, (2r)-4 2-(phosphonoxy)propanoic acid and magnesium.
68	c2b8eB_	Alignment	not modelled	32.2	23	PDB header: membrane protein Chain: B: PDB Molecule: cation-transporting atpase; PDBTitle: copa atp binding domain
69	d1vb5a_	Alignment	not modelled	31.7	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: !F2B-like
70	d1m1na_	Alignment	not modelled	31.6	16	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
71	c2ejaB_	Alignment	not modelled	31.4	13	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
72	c1ml4A_	Alignment	not modelled	31.4	17	PDB header: transferase Chain: A: PDB Molecule: aspartate transcarbamoylase; PDBTitle: the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
73	c2hdiB_	Alignment	not modelled	30.7	33	PDB header: protein transport,antimicrobial protein Chain: B: PDB Molecule: colicin-ia; PDBTitle: crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
74	c5mrwF_	Alignment	not modelled	30.4	19	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
75	d1ekxa2	Alignment	not modelled	29.6	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase PDB header: protein binding

76	c3pdiB_	Alignment	not modelled	29.0	20	Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
77	c5bq2C_	Alignment	not modelled	27.9	10	PDB header: transferase Chain: C: PDB Molecule: udp-n-acetylglucosamine 1-carboxyvinyltransferase; PDBTitle: crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 (udp-n-acetylglucosamine enolpyruvyl transferase, ept) from3 pseudomonas aeruginosa
78	c5ujsB_	Alignment	not modelled	27.9	9	PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: udp-n-acetylglucosamine 1-carboxyvinyltransferase; PDBTitle: 2.45 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase from campylobacter jejuni.
79	d1vlja_	Alignment	not modelled	27.8	12	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
80	d1cjca2_	Alignment	not modelled	27.6	15	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
81	d1lmb3_	Alignment	not modelled	26.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	c4ldrA_	Alignment	not modelled	26.0	21	PDB header: isomerase, cell invasion Chain: A: PDB Molecule: methylthioribose-1-phosphate isomerase; PDBTitle: structure of the s283y mutant of mrdi
83	c5kojD_	Alignment	not modelled	25.8	14	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state
84	c1w2wj_	Alignment	not modelled	25.7	26	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
85	c2decA_	Alignment	not modelled	25.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 325aa long hypothetical protein; PDBTitle: crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
86	d1d7ka2_	Alignment	not modelled	25.4	18	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
87	d1qh8a_	Alignment	not modelled	25.0	15	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
88	c3d6jA_	Alignment	not modelled	24.6	24	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
89	c6c76A_	Alignment	not modelled	24.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
90	c3ox4D_	Alignment	not modelled	24.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
91	d1m1nb_	Alignment	not modelled	24.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
92	c3bfjK_	Alignment	not modelled	23.5	18	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
93	c6qq0G_	Alignment	not modelled	23.3	11	PDB header: translation Chain: G: PDB Molecule: translation initiation factor eif-2b subunit delta; PDBTitle: structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
94	c3bicA_	Alignment	not modelled	23.3	18	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
95	d1miob_	Alignment	not modelled	23.2	21	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
96	c3knzA_	Alignment	not modelled	23.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
97	c3n07B_	Alignment	not modelled	22.9	18	PDB header: hydrolase Chain: B: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
98	c5b04C_	Alignment	not modelled	22.9	13	PDB header: translation Chain: C: PDB Molecule: probable translation initiation factor eif-2b subunit beta; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
99	d1uc8a1_	Alignment	not modelled	22.9	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
100	d1wpga2_	Alignment	not modelled	22.7	30	Fold: HAD-like Superfamily: HAD-like

				Family:Meta-cation ATPase, catalytic domain P		
101	d1t9ka_	Alignment	not modelled	22.5	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
102	c2ewtA_	Alignment	not modelled	22.5	14	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
103	c3fd0B_	Alignment	not modelled	22.4	14	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
104	c2infB_	Alignment	not modelled	22.2	10	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
105	c1gpiA_	Alignment	not modelled	22.2	19	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
106	c4s1wA_	Alignment	not modelled	21.8	20	PDB header: transferase Chain: A: PDB Molecule: glutamine--fructose-6-phosphate aminotransferase PDBTitle: structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus subsp. aureus mu50
107	c3oj0A_	Alignment	not modelled	21.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
108	c2rtyA_	Alignment	not modelled	21.0	50	PDB header: toxin Chain: A: PDB Molecule: navitoxin; PDBTitle: solution structure of navitoxin