

















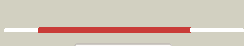
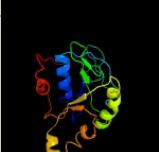
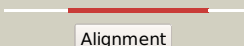
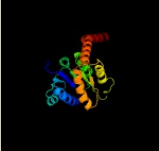





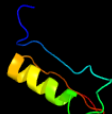


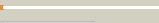
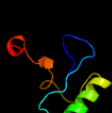



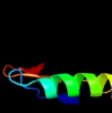
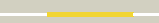
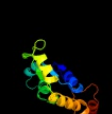


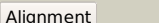
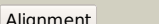
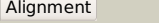
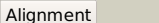
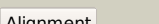
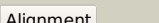
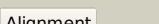
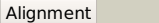


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2125 (-) _2386301_2387179
Date	Mon Aug 5 13:25:24 BST 2019
Unique Job ID	07730be48e4862ba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wamB_	 Alignment		100.0	26	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical alanine and leucine rich PDBTitle: crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
2	c2p90B_	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein cgl1923; PDBTitle: the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
3	c3e35A_	 Alignment		100.0	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein sco1997; PDBTitle: actinobacteria-specific protein of unknown function, sco1997
4	d2p90a1	 Alignment		100.0	25	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
5	c5un02_	 Alignment		100.0	100	PDB header: apoptosis Chain: 2: PDB Molecule: proteasome assembly chaperone 2 (pac2) homologue rv2125; PDB Fragment: unp residues 17-260; PDBTitle: crystal structure of mycobacterium tuberculosis proteasome-assembly2 chaperone homologue rv2125
6	c3mnfA_	 Alignment		100.0	58	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pac2 family protein; PDBTitle: crystal structure of pac2 family protein from streptomyces avermitilis2 ma
7	c3vr0D_	 Alignment		100.0	16	PDB header: protein binding Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbab, an archaeal proteasome2 activator
8	c3wz2C_	 Alignment		100.0	18	PDB header: chaperone Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
9	c3gaaB_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ta1441; PDBTitle: the crystal structure of the protein with unknown function from2 thermoplasma acidophilum
10	c4g4sP_	 Alignment		97.5	15	PDB header: hydrolase/chaperone Chain: P: PDB Molecule: proteasome assembly chaperone 2; PDBTitle: structure of proteasome-pba1-pba2 complex
11	c2p6pB_	 Alignment		93.1	14	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2

12	c3k7dA	 Alignment		85.5	16	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenylyltransferase; PDBTitle: c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenylyltransferase
13	c3khsB	 Alignment		83.3	18	PDB header: hydrolase Chain: B: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
14	d1gtma1	 Alignment		81.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
15	d1b26a1	 Alignment		80.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
16	c1pj6A	 Alignment		80.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
17	d1bvua1	 Alignment		77.5	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
18	c1bvuf	 Alignment		77.3	14	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
19	c5du2B	 Alignment		75.0	21	PDB header: transferase Chain: B: PDB Molecule: espg2 glycosyltransferase; PDBTitle: structural analysis of espg2 glycosyltransferase
20	c5hxdB	 Alignment		74.3	15	PDB header: hydrolase Chain: B: PDB Molecule: protein mpaa; PDBTitle: crystal structure of murein-tripeptide amidase mpaa from escherichia2 coli o157
21	c3tqkA	 Alignment	not modelled	73.5	18	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
22	c2tmgD	 Alignment	not modelled	72.2	14	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
23	d1euza1	 Alignment	not modelled	71.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
24	d1hwxal	 Alignment	not modelled	70.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
25	d1b5ta	 Alignment	not modelled	68.7	15	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Methylenetetrahydrofolate reductase
26	c2fmoA	 Alignment	not modelled	67.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
27	c3iaaB	 Alignment	not modelled	66.3	18	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
28	c3ia7A	 Alignment	not modelled	59.8	18	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase

29	d1s4ea1	Alignment	not modelled	55.7	12	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
30	c4p9sA	Alignment	not modelled	55.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgh
31	c1nr1A	Alignment	not modelled	49.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate dehydrogenase
32	c3ew7A	Alignment	not modelled	49.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo0794 protein; PDBTitle: crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
33	c3vp8B	Alignment	not modelled	47.7	13	PDB header: transcription Chain: B: PDB Molecule: general transcriptional corepressor tup1; PDBTitle: crystal structure of the n-terminal domain of the yeast general2 corepressor tup1p
34	d1of8a	Alignment	not modelled	47.7	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
35	d1fi4a1	Alignment	not modelled	45.4	10	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
36	c5gl5B	Alignment	not modelled	45.0	12	PDB header: transferase Chain: B: PDB Molecule: sterol 3-beta-glucosyltransferase; PDBTitle: sterol 3-beta-glucosyltransferase (ugt51) from saccharomyces2 cerevisiae (strain atcc 204508 / s288c): udpg complex
37	c1ofaB	Alignment	not modelled	44.0	21	PDB header: lyase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: crystal structure of the tyrosine-regulated2 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase3 from saccharomyces cerevisiae in complex with4 phosphoenolpyruvate and cobalt(ii)
38	c5xviA	Alignment	not modelled	43.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of aspergillus niger apo- glutamate dehydrogenase
39	c3r3jC	Alignment	not modelled	43.1	24	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
40	c3othB	Alignment	not modelled	43.1	10	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
41	c1v9lA	Alignment	not modelled	41.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
42	d1a3xa3	Alignment	not modelled	41.8	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
43	d1bgva1	Alignment	not modelled	40.9	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
44	c3sboA	Alignment	not modelled	40.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: structure of e.coli gdh from native source
45	c1yn9B	Alignment	not modelled	39.8	13	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
46	d1n8fa	Alignment	not modelled	39.3	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
47	c5jvsA	Alignment	not modelled	38.5	30	PDB header: motor protein Chain: A: PDB Molecule: chimera protein of kinesin heavy chain and microtubule- PDBTitle: the neck-linker + dal and alpha 7 helix of drosophila melanogaster2 kinesin-1 fused to eb1
48	d1ohea2	Alignment	not modelled	37.9	9	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
49	c1hrdA	Alignment	not modelled	37.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
50	c3aogA	Alignment	not modelled	37.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
51	c6agmA	Alignment	not modelled	37.3	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase, tyr-sensitive; PDBTitle: molecular basis for feedback inhibition of tyrosine-regulated 3-deoxy-2 d-arabino-heptulosonate-7-phosphate synthase from escherichia coli
52	d1i9sa	Alignment	not modelled	36.2	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
53	d1v9la1	Alignment	not modelled	35.9	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain

54	c3wg9D	Alignment	not modelled	35.8	9	PDB header: transcription Chain: D: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of rsp, a rex-family repressor
55	c4d9jl	Alignment	not modelled	35.4	21	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
56	c3i28A	Alignment	not modelled	35.2	20	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
57	c4lxgA	Alignment	not modelled	35.1	19	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
58	c2c46B	Alignment	not modelled	34.8	13	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2 phosphatase
59	c1u2eA	Alignment	not modelled	34.8	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
60	c1tcvB	Alignment	not modelled	34.8	17	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
61	c2iyaB	Alignment	not modelled	34.7	16	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a blueprint2 for antibiotic engineering
62	c5n6yE	Alignment	not modelled	34.7	12	PDB header: oxidoreductase Chain: E: PDB Molecule: nitrogenase vanadium-iron protein beta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
63	c2h04A	Alignment	not modelled	34.6	20	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase, receptor type, b,; PDBTitle: structural studies of protein tyrosine phosphatase beta catalytic2 domain in complex with inhibitors
64	c2p4sA	Alignment	not modelled	34.5	11	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
65	d1pkla3	Alignment	not modelled	34.4	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
66	c4xgiA	Alignment	not modelled	34.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
67	c3ketA	Alignment	not modelled	33.9	10	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
68	d1oj4a1	Alignment	not modelled	33.2	7	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
69	c4axvA	Alignment	not modelled	32.9	18	PDB header: hydrolase Chain: A: PDB Molecule: mpaa; PDBTitle: biochemical and structural characterization of the mpaa2 amidase as part of a conserved scavenging pathway for3 peptidoglycan derived peptides in gamma-proteobacteria
70	c4kyrA	Alignment	not modelled	32.2	23	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
71	c5ijzH	Alignment	not modelled	31.9	17	PDB header: oxidoreductase Chain: H: PDB Molecule: nadp-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase(gdh) from corynebacterium2 glutamicum
72	c2bmaA	Alignment	not modelled	31.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
73	c3aoeC	Alignment	not modelled	31.2	9	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
74	d2g50a3	Alignment	not modelled	30.9	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
75	c5zfsA	Alignment	not modelled	30.7	16	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
76	c2jfoB	Alignment	not modelled	30.4	20	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
77	c4hsnA	Alignment	not modelled	30.2	16	PDB header: transferase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: crystal structure of dah7ps from neisseria meningitidis PDB header: chaperone

78	c5sxyA_	Alignment	not modelled	30.2	18	Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
79	c1u2uA_	Alignment	not modelled	29.6	29	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: nmr solution structure of a designed heterodimeric leucine2 zipper
80	c5li3A_	Alignment	not modelled	29.5	15	PDB header: signaling protein Chain: A: PDB Molecule: acetoin utilization protein; PDBTitle: crystal structure of hdac-like protein from p. aeruginosa in complex2 with a photo-switchable inhibitor.
81	c4nyhB_	Alignment	not modelled	29.3	9	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core
82	c4rpfA_	Alignment	not modelled	27.8	10	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
83	c3lrxC_	Alignment	not modelled	27.8	24	PDB header: oxidoreductase Chain: C: PDB Molecule: putative hydrogenase; PDBTitle: crystal structure of the c-terminal domain (residues 78-226) of pf19112 hydrogenase from pyrococcus furiosus, northeast structural genomics3 consortium target pfr246a
84	c3fobA_	Alignment	not modelled	27.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
85	d1auga_	Alignment	not modelled	27.7	17	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
86	c2gzmB_	Alignment	not modelled	27.4	24	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus anthracis
87	d1o5ka_	Alignment	not modelled	27.2	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
88	c2jfzB_	Alignment	not modelled	26.8	18	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
89	c3dz1A_	Alignment	not modelled	26.6	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
90	d1f74a_	Alignment	not modelled	26.5	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c3k8zD_	Alignment	not modelled	26.5	16	PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a deacylated secondary glutamate2 dehydrogenase from b. subtilis
92	c5xw4A_	Alignment	not modelled	26.1	20	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
93	c1us2A_	Alignment	not modelled	25.9	23	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-xylanase; PDBTitle: xylanase10c (mutant e385a) from cellvibrio japonicus in complex with2 xylopentaose
94	c4lnaA_	Alignment	not modelled	25.7	13	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosema2 linguale dsm 74, nysgrc target 029362
95	c2qs8A_	Alignment	not modelled	25.2	17	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
96	d1h72c1	Alignment	not modelled	25.2	10	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
97	c1oheA_	Alignment	not modelled	25.0	10	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
98	c5kojD_	Alignment	not modelled	25.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase femo beta subunit protein nifk; PDBTitle: nitrogenase mofep protein in the ids oxidized state
99	c2lkiA_	Alignment	not modelled	24.7	15	PDB header: lipid transport Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.
100	c5cxsA_	Alignment	not modelled	24.3	12	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
101	d1qe5a_	Alignment	not modelled	24.2	11	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
						Fold: (Phosphotyrosine protein) phosphatases II

102	d1mkpa_	Alignment	not modelled	24.1	20	Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
103	c4icnB_	Alignment	not modelled	23.7	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
104	c5ud6B_	Alignment	not modelled	23.6	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhps from cyanidioschyzon merolae with lysine2 bound
105	c1cr6A_	Alignment	not modelled	23.5	27	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
106	c3pdiB_	Alignment	not modelled	22.9	17	PDB header: protein binding Chain: B: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nifn; PDBTitle: precursor bound nifen
107	c4ki9A_	Alignment	not modelled	22.8	20	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
108	d1hkha_	Alignment	not modelled	22.8	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
109	c3s3fA_	Alignment	not modelled	22.8	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: tyrosine-protein phosphatase 10d; PDBTitle: crystal structure of the catalytic domain of ptp10d from drosophila2 melanogaster with a small molecule inhibitor vanadate
110	c1oj4B_	Alignment	not modelled	22.4	6	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol PDBTitle: ternary complex of 2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase
111	c5czdB_	Alignment	not modelled	22.1	19	PDB header: transferase Chain: B: PDB Molecule: acyl-carrier-protein; PDBTitle: the complex structure of vink with vinl
112	d1bxca_	Alignment	not modelled	22.0	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
113	c2vf2A_	Alignment	not modelled	21.6	21	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis
114	d1liua3	Alignment	not modelled	21.5	15	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
115	c5c3lC_	Alignment	not modelled	21.4	13	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup62; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
116	c2oudA_	Alignment	not modelled	21.4	13	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
117	c2i6oA_	Alignment	not modelled	21.3	13	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
118	c3d0qB_	Alignment	not modelled	21.2	15	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
119	d1ppjb2	Alignment	not modelled	21.2	7	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
120	c3hulA_	Alignment	not modelled	21.2	10	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: structure of putative homoserine kinase thrb from listeria2 monocytogenes