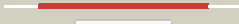



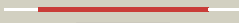






















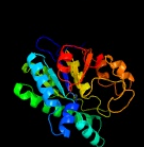





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2883c_(pyrH)_3192383_3193168
Date	Thu Aug 8 16:20:03 BST 2019
Unique Job ID	b6849e2b44bc8e9e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nwyB_	 Alignment		100.0	100	PDB header: transferase Chain: B; PDB Molecule: uridylate kinase; PDBTitle: structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
2	d1ybda1	 Alignment		100.0	45	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
3	c3ek5A_	 Alignment		100.0	47	PDB header: transferase Chain: A; PDB Molecule: uridylate kinase; PDBTitle: unique gtp-binding pocket and allosteric regulation of ump kinase from a gram-2 negative phytopathogen bacterium
4	d1z9da1	 Alignment		100.0	52	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
5	d2bnea1	 Alignment		100.0	46	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
6	c2jixC_	 Alignment		100.0	39	PDB header: transferase Chain: C; PDB Molecule: uridylate kinase; PDBTitle: the crystal structure of ump kinase from bacillus anthracis (ba1797)
7	d2a1fa1	 Alignment		100.0	44	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
8	c4a7xF_	 Alignment		100.0	44	PDB header: transferase Chain: F; PDB Molecule: uridylate kinase; PDBTitle: crystal structure of uridylate kinase from helicobacter pylori
9	c2j5tF_	 Alignment		100.0	21	PDB header: transferase Chain: F; PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
10	c2va1A_	 Alignment		100.0	33	PDB header: transferase Chain: A; PDB Molecule: uridylate kinase; PDBTitle: crystal structure of ump kinase from ureaplasma parvum
11	c2w21A_	 Alignment		100.0	21	PDB header: transferase Chain: A; PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.

12	d2brxa1	Alignment		100.0	25	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
13	c2j4kC	Alignment		100.0	23	PDB header: transferase Chain: C: PDB Molecule: uridylylate kinase; PDBTitle: crystal structure of uridylylate kinase from sulfolobus solfataricus in2 complex with ump to 2.2 angstrom resolution
14	d2ij9a1	Alignment		100.0	31	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
15	c2ogxB	Alignment		100.0	24	PDB header: metal binding protein Chain: B: PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
16	d2akoal	Alignment		100.0	13	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
17	c2ogxA	Alignment		100.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
18	c5yeiG	Alignment		100.0	27	PDB header: transferase Chain: G: PDB Molecule: aspartokinase; PDBTitle: mechanistic insight into the regulation of pseudomonas aeruginosa2 aspartate kinase
19	c2rd5A	Alignment		100.0	16	PDB header: protein binding Chain: A: PDB Molecule: acetylglutamate kinase-like protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
20	c3l76B	Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
21	c4axsA	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: carbamate kinase; PDBTitle: structure of carbamate kinase from mycoplasma penetrans
22	d2ap9a1	Alignment	not modelled	100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
23	c2v5hB	Alignment	not modelled	100.0	17	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
24	c4f6tA	Alignment	not modelled	100.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein (mosto) from2 azotobacter vinelandii loaded with various polyoxometalates
25	d2bufa1	Alignment	not modelled	100.0	15	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
26	c4q1tD	Alignment	not modelled	100.0	21	PDB header: transferase Chain: D: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of a glutamate 5-kinase from burkholderia2 thailandensis
27	d1e19a	Alignment	not modelled	100.0	26	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
28	c3ll5C	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyl kinase related protein;

28	c3l9C_	Alignment	not modelled	100.0	17	PDBTitle: crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex PDB header: transferase
29	c3ab4K_	Alignment	not modelled	100.0	25	Chain: K; PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
30	d2btya1	Alignment	not modelled	100.0	18	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
31	c3kzfC_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C; PDB Molecule: carbamate kinase; PDBTitle: structure of giardia carbamate kinase
32	c2e9yA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: carbamate kinase; PDBTitle: crystal structure of project ape1968 from aeropyrum pernix k1
33	c3d40A_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: foma protein; PDBTitle: crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
34	d2hmfa1	Alignment	not modelled	100.0	25	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
35	c3k4yB_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B; PDB Molecule: isopentenyl phosphate kinase; PDBTitle: crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
36	d1b7ba_	Alignment	not modelled	100.0	23	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
37	c2r98A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: putative acetylglutamate synthase; PDBTitle: crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
38	c3l9A_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: isopentenyl phosphate kinase; PDBTitle: x-ray structures of isopentenyl phosphate kinase
39	d1gs5a_	Alignment	not modelled	100.0	17	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
40	d2j0wa1	Alignment	not modelled	100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
41	c3c1nA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
42	c2egxA_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative acetylglutamate kinase; PDBTitle: crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
43	c3zzqC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C; PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of the amino acid kinase domain from saccharomyces2 cerevisiae acetylglutamate kinase without ligands
44	c3tviD_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D; PDB Molecule: aspartokinase; PDBTitle: crystal structure of clostridium acetobutylicum aspartate kinase2 (caak): an important allosteric enzyme for industrial amino acids3 production
45	d2cdqa1	Alignment	not modelled	100.0	23	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
46	c2j0wA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A; PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
47	c2cdqB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B; PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
48	c3l86A_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: acetylglutamate kinase; PDBTitle: the crystal structure of smu.665 from streptococcus mutans ua159
49	c3s7yX_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: X; PDB Molecule: n-acetylglutamate kinase / n-acetylglutamate synthase; PDBTitle: crystal structure of mmnags in space group p3121 at 4.3 a resolution
50	c4ab7C_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C; PDB Molecule: protein arg5,6, mitochondrial; PDBTitle: crystal structure of a tetrameric acetylglutamate kinase from2 saccharomyces cerevisiae complexed with its substrate n-3 acetylglutamate
51	c3s6kA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A; PDB Molecule: acetylglutamate kinase; PDBTitle: crystal structure of xcnags
52	c5dxiB_	Alignment	not modelled	85.9	13	PDB header: hydrolase Chain: B; PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain
53	c3dnpA_	Alignment	not modelled	83.4	14	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
54	c3zupB	Alignment	not modelled	82.1	19	PDB header: hydrolase Chain: B: PDB Molecule: mannosyl-3-phosphoglycerate phosphatase; PDBTitle: the 3-dimensional structure of mpgp from thermus2 thermophilus hb27, in complex with the alpha-3 mannosylglycerate and orthophosphate reaction products.
55	c5dxIA	Alignment	not modelled	81.6	16	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of aspergillus fumigatus trehalose-6-phosphate phosphatase2 crystal form 1
56	c3daoB	Alignment	not modelled	80.6	14	PDB header: hydrolase Chain: B: PDB Molecule: putative phosphate; PDBTitle: crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
57	d1p3y1	Alignment	not modelled	80.3	12	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
58	d1xvia	Alignment	not modelled	78.9	11	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
59	c1xviA	Alignment	not modelled	78.9	11	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
60	d1ovma1	Alignment	not modelled	78.8	8	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	c2p9jH	Alignment	not modelled	78.6	19	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein aq2171; PDBTitle: crystal structure of aq2171 from aquifex aeolicus
62	d1k1ea	Alignment	not modelled	77.0	20	Fold: HAD-like Superfamily: HAD-like Family: Probable phosphatase Yrbl
63	c2i55C	Alignment	not modelled	74.0	14	PDB header: isomerase Chain: C: PDB Molecule: phosphomannomutase; PDBTitle: complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
64	d1nrwa	Alignment	not modelled	72.5	22	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
65	c5gvxA	Alignment	not modelled	72.0	18	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-phosphate phosphatase; PDBTitle: structural insight into dephosphorylation by trehalose 6-phosphate2 phosphatase (otsb2) from mycobacterium tuberculosis
66	c3cetA	Alignment	not modelled	71.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: crystal structure of the pantheonate kinase-like protein q6m145 at the2 resolution 1.8 a. northeast structural genomics consortium target3 mrr63
67	c4umfC	Alignment	not modelled	69.8	13	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; PDBTitle: crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
68	c4zexA	Alignment	not modelled	69.7	14	PDB header: unknown function Chain: A: PDB Molecule: pfhad1; PDBTitle: crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate
69	c3bq9A	Alignment	not modelled	69.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted rossmann fold nucleotide-binding domain- PDBTitle: crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
70	d2b30a1	Alignment	not modelled	68.7	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
71	c5dx9A	Alignment	not modelled	67.2	13	PDB header: hydrolase Chain: A: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of trehalose-6-phosphate phosphatase from cryptococcus2 neoformans
72	c3niwA	Alignment	not modelled	67.0	12	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
73	c3mmzA	Alignment	not modelled	66.5	17	PDB header: hydrolase Chain: A: PDB Molecule: putative had family hydrolase; PDBTitle: crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
74	c3pgvB	Alignment	not modelled	65.4	10	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
75	c3r4cA	Alignment	not modelled	64.8	15	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like hydrolase; PDBTitle: divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
76	c6gfmA	Alignment	not modelled	64.7	16	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine/purine nucleotide 5'-monophosphate nucleosidase; PDBTitle: crystal structure of the escherichia coli nucleosidase ppnn (pppppp-2 form)

77	c3e8mD	Alignment	not modelled	62.3	13	PDB header: transferase Chain: D: PDB Molecule: acylneuraminate cytidylyltransferase; PDBTitle: structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
78	c3gygA	Alignment	not modelled	61.8	14	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
79	d1u02a	Alignment	not modelled	60.2	17	Fold: HAD-like Superfamily: HAD-like Family: Trehalose-phosphatase
80	c3mn1B	Alignment	not modelled	58.9	13	PDB header: hydrolase Chain: B: PDB Molecule: probable yrbi family phosphatase; PDBTitle: crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
81	c3ewiB	Alignment	not modelled	58.3	13	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidylyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
82	c3fzqA	Alignment	not modelled	58.1	23	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
83	d2fw2a1	Alignment	not modelled	56.8	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
84	c2r8zC	Alignment	not modelled	56.3	18	PDB header: hydrolase Chain: C: PDB Molecule: 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; PDBTitle: crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
85	c2qyhD	Alignment	not modelled	54.6	12	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical conserved protein, gk1056; PDBTitle: crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
86	c2fbmB	Alignment	not modelled	53.2	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: y chromosome chromodomain protein 1, telomeric isoform b; PDBTitle: acetyltransferase domain of cdy1
87	c2fu3A	Alignment	not modelled	53.1	15	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
88	d1xpja	Alignment	not modelled	52.7	13	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
89	c3n07B	Alignment	not modelled	51.6	22	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
90	c4hgnB	Alignment	not modelled	51.5	20	PDB header: hydrolase Chain: B: PDB Molecule: 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate PDBTitle: crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
91	c2hx1D	Alignment	not modelled	50.5	8	PDB header: hydrolase Chain: D: PDB Molecule: predicted sugar phosphatases of the had superfamily; PDBTitle: crystal structure of possible sugar phosphatase, had superfamily2 (zp_00311070.1) from cytophaga hutchinsonii atcc 33406 at 2.10 a3 resolution
92	d2obba1	Alignment	not modelled	49.3	2	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
93	d1s2oa1	Alignment	not modelled	47.5	8	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
94	d1rlma	Alignment	not modelled	42.1	12	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
95	d2nx2a1	Alignment	not modelled	41.2	19	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: YpsA-like
96	c3kc2A	Alignment	not modelled	40.6	27	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
97	d1rkqa	Alignment	not modelled	40.3	14	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
98	c5yloA	Alignment	not modelled	37.4	16	PDB header: hydrolase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structural of pseudomonas aeruginosa pa4980
99	c3hinA	Alignment	not modelled	37.3	21	PDB header: lyase Chain: A: PDB Molecule: putative 3-hydroxybutyryl-coa dehydratase; PDBTitle: crystal structure of putative enoyl-coa hydratase from2 rhodospseudomonas palustris cga009
100	c3mcf	Alignment	not modelled	36.4	8	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.

101	d2ftsa3	Alignment	not modelled	33.9	15	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
102	c3lqkA	Alignment	not modelled	31.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
103	c5wq3A	Alignment	not modelled	31.2	22	PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of type-ii log from corynebacterium glutamicum
104	c3zg6A	Alignment	not modelled	30.7	17	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
105	d1wpga2	Alignment	not modelled	30.7	16	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
106	c2gsiA	Alignment	not modelled	30.2	35	PDB header: hydrolase Chain: A: PDB Molecule: protein ppl-2; PDBTitle: cdna cloning and 1.75a crystal structure determination of ppl2, a2 novel chimerolectin from parkia platycephala seeds exhibiting3 endochitinolytic activity
107	d1wzca1	Alignment	not modelled	30.2	20	Fold: HAD-like Superfamily: HAD-like Family: Predicted hydrolases Cof
108	c4navB	Alignment	not modelled	30.1	13	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein xcc279; PDBTitle: crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
109	d2nqra3	Alignment	not modelled	30.1	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
110	c4gxtA	Alignment	not modelled	27.8	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
111	c2xucA	Alignment	not modelled	27.5	25	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: natural product-guided discovery of a fungal chitinase inhibitor
112	c2iexA	Alignment	not modelled	25.9	12	PDB header: lyase Chain: A: PDB Molecule: dihydroxynaphthoic acid synthetase; PDBTitle: crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
113	d1zpdA1	Alignment	not modelled	25.5	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
114	c4eggD	Alignment	not modelled	25.3	17	PDB header: ligase Chain: D: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase b from burkholderia2 pseudomallei
115	c3l7yA	Alignment	not modelled	25.2	9	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1108c; PDBTitle: the crystal structure of smu.1108c from streptococcus mutans ua159
116	c4i4zE	Alignment	not modelled	25.2	13	PDB header: lyase Chain: E: PDB Molecule: naphthoate synthase; PDBTitle: synechocystis sp. pcc 6803 1,4-dihydroxy-2-naphthoyl-coenzyme a2 synthase (menb) in complex with salicylyl-coa
117	c3rfqC	Alignment	not modelled	24.8	17	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
118	c2nqqA	Alignment	not modelled	24.6	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
119	c4qjbB	Alignment	not modelled	24.6	12	PDB header: hydrolase Chain: B: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of the sugar phosphatase pfhad1 from plasmodium2 falciparum
120	c2uy2A	Alignment	not modelled	23.4	25	PDB header: hydrolase Chain: A: PDB Molecule: endochitinase; PDBTitle: sccts1_apo crystal structure