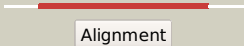

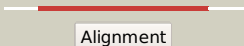

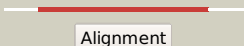







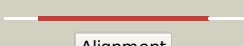













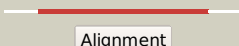

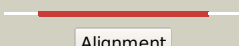

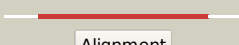

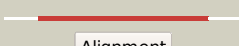








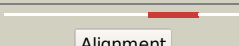
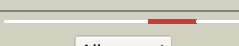


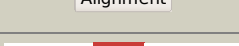
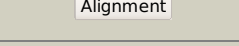

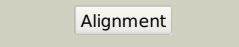


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3068c_(pgmA)_3431976_3433619
Date	Thu Aug 8 16:20:24 BST 2019
Unique Job ID	b485097a160a4548

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fuvB_	 Alignment		100.0	56	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
2	c2z0fA_	 Alignment		100.0	55	PDB header: isomerase Chain: A: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
3	c1c4gB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex
4	c1kfiA_	 Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
5	c1wqaB_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
6	c2f7IA_	 Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
7	c3pdkB_	 Alignment		100.0	18	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
8	c3c04A_	 Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
9	c6gyzB_	 Alignment		100.0	17	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
10	c1tuoA_	 Alignment		100.0	26	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
11	c3uw2A_	 Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_i1489)from burkholderia thailandensis

12	c5bmpA	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
13	c3i3wB	 Alignment		100.0	18	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: structure of a phosphoglucomutase from francisella tularensis
14	c4hjhA	 Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
15	c4qg5D	 Alignment		100.0	25	PDB header: isomerase Chain: D: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
16	c2dkdA	 Alignment		100.0	19	PDB header: isomerase Chain: A: PDB Molecule: phosphoacetylglucosamine mutase; PDBTitle: crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
17	c4bjuB	 Alignment		100.0	18	PDB header: isomerase Chain: B: PDB Molecule: n-acetylglucosamine-phosphate mutase; PDBTitle: genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucomutase as an antifungal target
18	d1kfia1	 Alignment		100.0	25	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
19	d3pmga1	 Alignment		100.0	27	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
20	d1p5dx1	 Alignment		100.0	23	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
21	d1kfia3	 Alignment	not modelled	99.9	27	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
22	d3pmga3	 Alignment	not modelled	99.9	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	d1p5dx3	 Alignment	not modelled	99.9	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
24	d3pmga2	 Alignment	not modelled	99.8	18	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
25	d1p5dx2	 Alignment	not modelled	99.8	16	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
26	d1kfia2	 Alignment	not modelled	99.8	15	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
27	d1p5dx4	 Alignment	not modelled	99.7	18	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
28	d1wjwa	 Alignment	not modelled	99.4	25	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
29	d3pmga4	 Alignment	not modelled	97.9	16	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain

						Family: Phosphoglucomutase, C-terminal domain
30	d1kfia4	Alignment	not modelled	97.9	17	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
31	c3qayC_	Alignment	not modelled	78.0	13	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
32	c2zf8A_	Alignment	not modelled	73.8	13	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of moty
33	c5emiA_	Alignment	not modelled	70.6	19	PDB header: hydrolase Chain: A: PDB Molecule: cell wall hydrolase/autolysin; PDBTitle: n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
34	c4m6iA_	Alignment	not modelled	64.8	19	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
35	c4xgiA_	Alignment	not modelled	58.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a domain of unknown function (duf1537) from2 pectobacterium atrosepticum (eca3761), target efi-511609, apo3 structure, domain swapped dimer
36	d1nn4a_	Alignment	not modelled	54.7	12	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
37	c5nbsA_	Alignment	not modelled	54.6	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa
38	c5mp4C_	Alignment	not modelled	53.3	11	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
39	c1qdu_	Alignment	not modelled	53.1	13	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: caspase-8 alpha-chain; PDBTitle: crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
40	c3ne8A_	Alignment	not modelled	52.6	17	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
41	c2w37A_	Alignment	not modelled	50.5	15	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
42	d1vmea1	Alignment	not modelled	49.5	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
43	c5a7mA_	Alignment	not modelled	49.1	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: the structure of hypocrea jecorina beta-xylosidase xyl3a (bx1)
44	c3hlyA_	Alignment	not modelled	47.5	17	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
45	c3zz1A_	Alignment	not modelled	41.9	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-glucoside glucohydrolase; PDBTitle: crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
46	c3he8A_	Alignment	not modelled	41.6	11	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
47	c3f93D_	Alignment	not modelled	40.9	18	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
48	c1vmeB_	Alignment	not modelled	38.7	16	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
49	c2p2gD_	Alignment	not modelled	38.5	18	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
50	d1e5da1	Alignment	not modelled	38.5	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
51	d1ykgal	Alignment	not modelled	38.4	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
52	c2zkiH_	Alignment	not modelled	37.8	12	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
53	c1vlvA_	Alignment	not modelled	36.8	14	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
54	c4amuB_	Alignment	not modelled	36.1	16	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group

55	c3s5pA	Alignment	not modelled	35.5	10	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
56	c5k6IA	Alignment	not modelled	34.5	22	PDB header: hydrolase Chain: A: PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome
57	c3m1pA	Alignment	not modelled	34.3	14	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
58	c3k7pA	Alignment	not modelled	34.3	14	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
59	d3eeqa2	Alignment	not modelled	33.9	11	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
60	c1a1sA	Alignment	not modelled	33.5	17	PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
61	c4heqB	Alignment	not modelled	33.0	12	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from desulfovibrio gigas
62	d3bula2	Alignment	not modelled	33.0	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
63	d2vvpA1	Alignment	not modelled	32.9	20	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
64	c3a9rA	Alignment	not modelled	32.6	14	PDB header: isomerase Chain: A: PDB Molecule: d-arabinose isomerase; PDBTitle: x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
65	d1gy8a	Alignment	not modelled	30.8	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	d1o1xa	Alignment	not modelled	30.1	11	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
67	c5vegC	Alignment	not modelled	29.6	16	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
68	d1dxha2	Alignment	not modelled	29.6	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
69	c3c52B	Alignment	not modelled	29.6	27	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolhydroxamic acid, a competitive3 inhibitor
70	c1fvoB	Alignment	not modelled	29.1	14	PDB header: transferase Chain: B: PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
71	c4lfmA	Alignment	not modelled	28.8	13	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-psicose
72	c2q9uB	Alignment	not modelled	28.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
73	c4em8A	Alignment	not modelled	28.2	14	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
74	c4lfnD	Alignment	not modelled	27.4	12	PDB header: isomerase Chain: D: PDB Molecule: galactose-6-phosphate isomerase subunit b; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-ribulose
75	c3noIA	Alignment	not modelled	27.2	10	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
76	d1t6t1	Alignment	not modelled	27.0	13	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
77	c3gd5D	Alignment	not modelled	26.9	22	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
78	c2ql5A	Alignment	not modelled	26.8	8	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7; PDBTitle: crystal structure of caspase-7 with inhibitor ac-dmqd-cho
79	d1f4pa	Alignment	not modelled	26.7	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
80	c5z87B	Alignment	not modelled	26.6	18	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3

						angstrom from2 erythrobacter marinus PDB header: choline-binding protein Chain: A: PDB Molecule: putative glycine betaine abc transporter protein; PDBTitle: abc-transporter choline binding protein in unliganded semi-2 closed conformation
81	c2rejA_	Alignment	not modelled	26.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
82	c3fniA_	Alignment	not modelled	26.3	5	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphoocatonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphoocatonate aldolase from2 burkholderia pseudomallei
83	c3sz8D_	Alignment	not modelled	26.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
84	c4h2dB_	Alignment	not modelled	25.9	12	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
85	c2otcA_	Alignment	not modelled	25.5	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
86	d1gvfa_	Alignment	not modelled	25.3	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
87	d1b1ca_	Alignment	not modelled	25.3	6	PDB header: hydrolase Chain: A: PDB Molecule: large terminase protein; PDBTitle: structure of p22 large terminase nuclease domain
88	c4dkwA_	Alignment	not modelled	24.3	14	PDB header: hydrolase Chain: B: PDB Molecule: cell death protein 3; PDBTitle: crystal structure of ced-3
89	c4m9rB_	Alignment	not modelled	24.3	10	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l21-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
90	c4b6at_	Alignment	not modelled	24.3	13	PDB header: transferase Chain: A: PDB Molecule: transcarbamylase; PDBTitle: structure of ygew encoded protein from e. coli
91	c3q98A_	Alignment	not modelled	23.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hughd with a104l substitution
92	c6c4jA_	Alignment	not modelled	23.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
93	c1dliA_	Alignment	not modelled	23.3	14	PDB header: transferase Chain: F: PDB Molecule: cad protein; PDBTitle: aspartate transcarbamoylase domain of human cad in apo form
94	c5g1oF_	Alignment	not modelled	23.1	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: caspase-7 subunit p20; PDBTitle: crystal structure of caspase-7 complexed with xiap
95	c1i51A_	Alignment	not modelled	23.1	8	PDB header: transferase Chain: A: PDB Molecule: aspartate/ornithine carbamoyltransferase; PDBTitle: crystal structure of a putative transcarbamoylase from2 enterococcus faecalis
96	c2yfkA_	Alignment	not modelled	22.4	16	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
97	c5yw2D_	Alignment	not modelled	22.4	16	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase
98	c6fxwA_	Alignment	not modelled	22.2	13	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein yfde; PDBTitle: yfde from escherichia coli
99	c4hl6D_	Alignment	not modelled	22.1	11	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from beutenbergia2 cavernae dsm 12333
100	c5bu9B_	Alignment	not modelled	22.1	18	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan glcnae deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant.
101	c2c1iA_	Alignment	not modelled	21.7	20	PDB header: hydrolase Chain: I: PDB Molecule: caspase-6; PDBTitle: crystal structure of apo-caspase-6 at physiological ph
102	c3p45I_	Alignment	not modelled	21.2	7	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
103	c3q94B_	Alignment	not modelled	20.9	22	PDB header: isomerase Chain: B: PDB Molecule: probable fatty-acid-coa racemase far; PDBTitle: crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
104	c2g04B_	Alignment	not modelled	20.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: putative uncharacterized protein yjik; PDBTitle: crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
105	c3qqzA_	Alignment	not modelled	20.7	5	PDB header: membrane protein

106	c4iiiA_	Alignment	not modelled	20.6	10	Chain: A: PDB Molecule: membrane lipoprotein tpn38(b); PDBTitle: crystal structure of rfua (tp0298) of t. pallidum bound to riboflavin
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