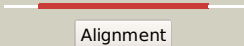

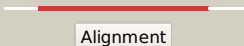

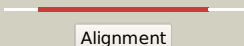







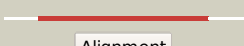




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3441c_(mrsA)_3860204_3861550
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	383fc4ee78816d3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pdkB_	 Alignment		100.0	48	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
2	c6gyzB_	 Alignment		100.0	47	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
3	c1wqaB_	 Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
4	c2f7IA_	 Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
5	c3i3wB_	 Alignment		100.0	37	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
6	c3c04A_	 Alignment		100.0	27	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
7	c3uw2A_	 Alignment		100.0	26	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
8	c5bmpA_	 Alignment		100.0	25	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
9	c2fuvB_	 Alignment		100.0	23	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
10	c1tuoA_	 Alignment		100.0	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
11	c1c4gB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex

12	c4hjhA	Alignment		100.0	26	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
13	c2z0fA	Alignment		100.0	24	PDB header: isomerase Chain: A: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
14	c1kfiA	Alignment		100.0	21	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
15	c4qg5D	Alignment		100.0	21	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	23	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	25	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	d1p5dx1	Alignment		100.0	31	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
19	d1kfi1	Alignment		100.0	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
20	d3pmga1	Alignment		100.0	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
21	d1p5dx3	Alignment	not modelled	99.9	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
22	d1kfi3	Alignment	not modelled	99.9	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	d1p5dx2	Alignment	not modelled	99.9	36	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
24	d3pmga3	Alignment	not modelled	99.9	14	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
25	d3pmga2	Alignment	not modelled	99.8	26	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
26	d1kfi2	Alignment	not modelled	99.8	25	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
27	d1p5dx4	Alignment	not modelled	99.7	19	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
28	d1wjwa	Alignment	not modelled	99.5	33	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
29	d3pmga4	Alignment	not modelled	97.5	27	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain

30	d1kfia4	Alignment	not modelled	97.5	24	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
31	d3bula2	Alignment	not modelled	91.4	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
32	d1vmea1	Alignment	not modelled	91.2	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
33	d1nn4a_	Alignment	not modelled	91.2	26	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
34	c3s5pA_	Alignment	not modelled	91.1	15	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpiB from giardia2 lamblia
35	c3he8A_	Alignment	not modelled	91.0	21	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
36	c3k7pA_	Alignment	not modelled	88.5	24	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.
37	c3m1pA_	Alignment	not modelled	88.5	24	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
38	c1k98A_	Alignment	not modelled	87.7	15	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
39	c4m6iA_	Alignment	not modelled	86.1	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
40	c3qayC_	Alignment	not modelled	85.0	18	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
41	c3hlyA_	Alignment	not modelled	82.4	19	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.
42	c4ifnD_	Alignment	not modelled	81.6	18	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
43	c4em8A_	Alignment	not modelled	81.4	24	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
44	c3whpA_	Alignment	not modelled	81.1	25	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
45	d1ccwa_	Alignment	not modelled	80.8	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
46	c1y80A_	Alignment	not modelled	80.2	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
47	d1ycga1	Alignment	not modelled	79.2	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
48	d2vvpA1	Alignment	not modelled	78.7	30	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
49	c4ifmA_	Alignment	not modelled	78.4	21	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
50	c3fniA_	Alignment	not modelled	78.3	16	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
51	c2i2xD_	Alignment	not modelled	78.1	13	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
52	c6mu0A_	Alignment	not modelled	76.8	14	PDB header: isomerase Chain: A: PDB Molecule: probable ribose-5-phosphate isomerase b; PDBTitle: crystal structure of ribose-5-phosphate isomerase b from mycoplasma2 genitalium with bound ribulose-5-phosphate
53	c1bmtB_	Alignment	not modelled	75.5	14	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
54	c3ne8A_	Alignment	not modelled	74.1	19	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
						Fold: Flavodoxin-like

55	d1xrsb1	Alignment	not modelled	72.5	16	Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
56	c3ezxA	Alignment	not modelled	70.8	13	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
57	c5emiA	Alignment	not modelled	67.9	16	PDB header: hydrolase Chain: A: PDB Molecule: cell wall hydrolase/autolysin; PDBTitle: n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
58	c4jgiB	Alignment	not modelled	63.3	15	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfotobacterium hafniense dcb-2
59	d1o1xa	Alignment	not modelled	63.2	23	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
60	c6apeA	Alignment	not modelled	56.8	17	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
61	c1xrsB	Alignment	not modelled	56.2	17	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
62	c2ppwA	Alignment	not modelled	56.1	15	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
63	c3qd5B	Alignment	not modelled	54.6	28	PDB header: isomerase Chain: B: PDB Molecule: putative ribose-5-phosphate isomerase; PDBTitle: crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
64	c2yh5A	Alignment	not modelled	53.9	11	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
65	d7reqa2	Alignment	not modelled	53.1	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
66	d2a5la1	Alignment	not modelled	52.6	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
67	d1d9ea	Alignment	not modelled	48.2	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
68	c5c8eC	Alignment	not modelled	46.5	25	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
69	c3nvtA	Alignment	not modelled	45.9	19	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
70	d1e5da1	Alignment	not modelled	44.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
71	c2yxbA	Alignment	not modelled	42.0	17	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
72	d1ml4a2	Alignment	not modelled	41.2	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
73	d1b1ca	Alignment	not modelled	40.7	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
74	c1vmeB	Alignment	not modelled	40.6	12	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
75	c3f93D	Alignment	not modelled	40.1	22	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
76	c6fxwA	Alignment	not modelled	39.2	22	PDB header: isomerase Chain: A: PDB Molecule: putative ribose 5-phosphate isomerase; PDBTitle: structure of leishmania infantum type b ribose 5-phosphate isomerase
77	c3qqzA	Alignment	not modelled	37.7	20	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
78	c3sz8D	Alignment	not modelled	36.0	19	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
79	c4binA	Alignment	not modelled	35.0	26	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase amic; PDBTitle: crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
80	c5npeA	Alignment	not modelled	34.9	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase;

80	c1h5A_	Alignment	not modelled	34.9	20	PDBTitle: structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa PDB header: oxidoreductase
81	c2ohiB_	Alignment	not modelled	34.6	14	Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
82	d1xk7a1	Alignment	not modelled	34.0	38	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
83	c6mdyC_	Alignment	not modelled	33.5	18	PDB header: hydrolase Chain: C: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a 2-dehydro-3-deoxyphosphooctonate aldolase from2 legionella pneumophila philadelphia 1
84	c4xfrB_	Alignment	not modelled	33.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a domain of unknown function (duf1537) from2 bordetella bronchiseptica (bb3215), target efi-511620, with bound3 citrate, domain swapped dimer, space group p6522
85	c2q9uB_	Alignment	not modelled	32.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
86	c4amuB_	Alignment	not modelled	31.9	13	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
87	c5mp4C_	Alignment	not modelled	31.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
88	c3tqkA_	Alignment	not modelled	31.5	16	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
89	c2pfsA_	Alignment	not modelled	31.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
90	d1dxha2	Alignment	not modelled	30.9	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
91	d1ak2a1	Alignment	not modelled	30.5	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
92	c2zkiH_	Alignment	not modelled	30.4	15	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)
93	c1xa3B_	Alignment	not modelled	30.1	38	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase; PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
94	c4heqB_	Alignment	not modelled	30.1	25	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from desulfovibrio gigas
95	c4khaA_	Alignment	not modelled	28.7	13	PDB header: chaperone/nuclear protein Chain: A: PDB Molecule: spt16m-histone h2b 1.1 chimera; PDBTitle: structural basis of histone h2a-h2b recognition by the essential2 chaperone fact
96	c4r3uD_	Alignment	not modelled	28.4	17	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
97	c1a4iB_	Alignment	not modelled	28.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
98	d1kjna_	Alignment	not modelled	27.9	24	Fold: Hypothetical protein MTH777 (MT0777) Superfamily: Hypothetical protein MTH777 (MT0777) Family: Hypothetical protein MTH777 (MT0777)
99	c3eglC_	Alignment	not modelled	27.7	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: degv family protein; PDBTitle: crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
100	c4xz6A_	Alignment	not modelled	27.1	12	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmox in complex with tmao
101	c3nolA_	Alignment	not modelled	27.0	24	PDB header: transferase Chain: A: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of zymomonas mobilis glutaminy cyclase (trigonal2 form)
102	d1f4pa_	Alignment	not modelled	26.8	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
103	c5o5oD_	Alignment	not modelled	26.1	27	PDB header: chaperone Chain: D: PDB Molecule: rnase adapter protein rapz; PDBTitle: x-ray crystal structure of rapz from escherichia coli (p32 space2 group)
104	c5vegC_	Alignment	not modelled	25.8	18	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment

105	c6h0cA_	Alignment	not modelled	25.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
106	d1q7ea_	Alignment	not modelled	25.7	24	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
107	c4h2dB_	Alignment	not modelled	25.5	7	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
108	c2g04B_	Alignment	not modelled	25.1	19	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
109	d1q77a_	Alignment	not modelled	25.1	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
110	c5z87B_	Alignment	not modelled	24.9	18	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
111	d1ykga1	Alignment	not modelled	24.9	5	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
112	c5oa1V_	Alignment	not modelled	24.9	21	PDB header: transcription Chain: V: PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: rna polymerase i pre-initiation complex
113	c1e5dA_	Alignment	not modelled	24.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
114	c4hh3C_	Alignment	not modelled	24.7	16	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
115	d1fmfa_	Alignment	not modelled	24.3	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
116	c4wnyA_	Alignment	not modelled	23.9	10	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
117	c2nz2A_	Alignment	not modelled	23.7	28	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
118	c4hl6D_	Alignment	not modelled	22.9	30	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein yfde; PDBTitle: yfde from escherichia coli
119	c3s3tD_	Alignment	not modelled	22.7	5	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
120	d2ak3a1	Alignment	not modelled	22.6	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases