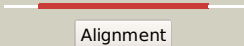

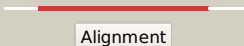

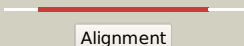







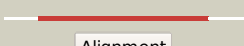











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3257c_(manB)_3637309_3638706
Date	Thu Aug 8 16:20:46 BST 2019
Unique Job ID	c12a66ecb901d299

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5bmpA_	 Alignment		100.0	39	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
2	c3c04A_	 Alignment		100.0	32	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
3	c1wqaB_	 Alignment		100.0	27	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
4	c3uw2A_	 Alignment		100.0	35	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
5	c2f7IA_	 Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
6	c3pdkB_	 Alignment		100.0	26	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
7	c6gyzB_	 Alignment		100.0	24	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
8	c1tuoA_	 Alignment		100.0	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
9	c3i3wB_	 Alignment		100.0	22	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
10	c4hjhA_	 Alignment		100.0	22	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
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	c2fuvB_	Alignment		100.0	19	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
13	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
14	c2z0fA_	Alignment		100.0	21	PDB header: isomerase Chain: A: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
15	c4qg5D_	Alignment		100.0	22	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	16	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-acetylphosphoglucosamine mutase as an antifungal target
18	d1p5dx1	Alignment		100.0	26	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
19	d1kfi1	Alignment		100.0	21	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
20	d3pmga1	Alignment		100.0	18	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
21	d1p5dx3	Alignment	not modelled	99.9	34	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
22	d1p5dx2	Alignment	not modelled	99.9	43	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	d3pmga3	Alignment	not modelled	99.9	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
24	d1kfi3	Alignment	not modelled	99.9	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
25	d3pmga2	Alignment	not modelled	99.9	26	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
26	d1kfi2	Alignment	not modelled	99.8	23	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
27	d1p5dx4	Alignment	not modelled	99.8	26	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
28	d1wjwa_	Alignment	not modelled	99.4	15	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
29	d1kfi4	Alignment	not modelled	96.6	20	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain

						Family: Phosphoglucomutase, C-terminal domain
30	d3pmga4	Alignment	not modelled	96.5	20	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
31	d3bula2	Alignment	not modelled	87.8	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
32	c3whpA_	Alignment	not modelled	82.1	13	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
33	c3he8A_	Alignment	not modelled	79.9	21	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
34	d2ebfx2	Alignment	not modelled	79.5	11	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
35	c2i2xD_	Alignment	not modelled	75.4	18	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
36	d1nn4a_	Alignment	not modelled	74.7	21	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
37	c4em8A_	Alignment	not modelled	74.2	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
38	c1k98A_	Alignment	not modelled	72.9	8	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
39	c1bmtB_	Alignment	not modelled	71.9	8	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
40	c2jpiA_	Alignment	not modelled	71.5	10	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical protein; PDBTitle: chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
41	c4pyrA_	Alignment	not modelled	70.7	17	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc transporter; PDBTitle: structure of a putative branched-chain amino acid abc transporter from2 chromobacterium violaceum atcc 12472
42	c6gzuA_	Alignment	not modelled	69.3	7	PDB header: transferase Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of chlamydia abortus effector protein chladub
43	c3s5pA_	Alignment	not modelled	69.1	13	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpiB from giardia2 lamblia
44	d1o1xa_	Alignment	not modelled	67.8	23	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
45	c1y80A_	Alignment	not modelled	67.5	15	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
46	c3brcA_	Alignment	not modelled	64.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
47	d1ccwa_	Alignment	not modelled	64.2	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
48	c5nbsA_	Alignment	not modelled	62.4	15	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
49	c2zkiH_	Alignment	not modelled	62.4	19	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)
50	c3m1pA_	Alignment	not modelled	62.3	22	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 allse-6-phosphate
51	c3k7pA_	Alignment	not modelled	62.3	22	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.
52	c3c5yD_	Alignment	not modelled	62.0	11	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
53	c4m6iA_	Alignment	not modelled	59.5	17	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
54	c5d5pC_	Alignment	not modelled	57.9	17	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
						Fold: Flavodoxin-like

55	d1ycga1	Alignment	not modelled	57.6	22	Superfamily: Flavoproteins Family: Flavodoxin-related
56	c5wabC	Alignment	not modelled	56.4	22	PDB header: hydrolase Chain: C: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
57	c3hlyA	Alignment	not modelled	55.8	21	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_syp6 protein. northeast structural genomics consortium target3 snr135d.
58	c3ezxA	Alignment	not modelled	55.8	8	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
59	c4blpD	Alignment	not modelled	54.4	5	PDB header: hydrolase Chain: D: PDB Molecule: packaging enzyme p4; PDBTitle: p4 protein from bacteriophage phi13
60	c3qayC	Alignment	not modelled	52.5	9	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd271 endolysin targeting clostridia difficile
61	c2ppwA	Alignment	not modelled	51.8	14	PDB header: isomerase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
62	c4e1rA	Alignment	not modelled	51.4	19	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
63	c4e1pA	Alignment	not modelled	51.4	19	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
64	c4lfnD	Alignment	not modelled	50.7	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-ribose
65	d1e5da1	Alignment	not modelled	49.3	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
66	d2vvpA1	Alignment	not modelled	49.0	12	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
67	c5wabD	Alignment	not modelled	48.9	21	PDB header: hydrolase Chain: D: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
68	c4lfnA	Alignment	not modelled	47.1	18	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
69	d1xrsb1	Alignment	not modelled	47.0	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
70	c5c8eC	Alignment	not modelled	45.1	13	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
71	c4khaA	Alignment	not modelled	45.0	20	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
72	c3qd5B	Alignment	not modelled	43.8	31	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
73	c4xz6A	Alignment	not modelled	43.6	18	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmoX in complex with tmao
74	d2a5la1	Alignment	not modelled	43.4	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
75	c6fxsA	Alignment	not modelled	43.2	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase
76	c6mr3C	Alignment	not modelled	42.7	14	PDB header: structural genomics Chain: C: PDB Molecule: putative competence-damage inducible protein; PDBTitle: crystal structure of the competence-damaged protein (cina) superfamily2 protein from streptococcus mutans
77	d1b1ca	Alignment	not modelled	42.2	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
78	c6mu0A	Alignment	not modelled	40.1	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
79	c4bloC	Alignment	not modelled	39.6	13	PDB header: hydrolase Chain: C: PDB Molecule: packaging enzyme p4; PDBTitle: p4 protein from bacteriophage phi6 in complex with adp PDB header: oxidoreductase

80	c2q9uB	Alignment	not modelled	39.4	18	Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
81	c4jgiB	Alignment	not modelled	39.1	9	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
82	c4hh3C	Alignment	not modelled	38.3	13	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
83	c3f93D	Alignment	not modelled	36.8	25	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
84	d1ws6a1	Alignment	not modelled	36.6	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
85	c3n0wA	Alignment	not modelled	36.6	9	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
86	d7reqa2	Alignment	not modelled	36.0	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
87	c3cinA	Alignment	not modelled	35.5	18	PDB header: isomerase Chain: A: PDB Molecule: myo-inositol-1-phosphate synthase-related protein; PDBTitle: crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
88	c3lopA	Alignment	not modelled	35.3	4	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
89	c3ne8A	Alignment	not modelled	35.2	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
90	c5oa1V	Alignment	not modelled	34.1	26	PDB header: transcription Chain: V: PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: rna polymerase i pre-initiation complex
91	d2qn6b1	Alignment	not modelled	34.1	14	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain
92	c3fniA	Alignment	not modelled	33.2	17	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
93	d2cc0a1	Alignment	not modelled	31.4	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
94	c2pfsA	Alignment	not modelled	31.3	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
95	c2x41A	Alignment	not modelled	31.2	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
96	c5x2oD	Alignment	not modelled	31.2	15	PDB header: signaling protein/immune system Chain: D: PDB Molecule: taste receptor, type 1, member 3; PDBTitle: crystal structure of the medaka fish taste receptor t1r2a-t1r3 ligand2 binding domains in complex with l-arginine
97	c4gxtA	Alignment	not modelled	30.7	15	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
98	d1gvfa	Alignment	not modelled	30.4	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
99	c4ffnA	Alignment	not modelled	29.6	5	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
100	c4d0jD	Alignment	not modelled	29.2	21	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
101	c4ne4A	Alignment	not modelled	28.7	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein PDBTitle: crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystallized with btb
102	c5mp4C	Alignment	not modelled	28.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
103	d3eeqa2	Alignment	not modelled	27.8	11	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
104	d1t6t1	Alignment	not modelled	27.3	15	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain

105	c1xrsB_	Alignment	not modelled	26.9	16	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
106	c4wnyA_	Alignment	not modelled	26.9	13	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
107	c3wo8B_	Alignment	not modelled	26.4	14	PDB header: hydrolase Chain: B; PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
108	c6ofuC_	Alignment	not modelled	25.5	12	PDB header: lyase Chain: C; PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from escherichia coli k12
109	c5z87B_	Alignment	not modelled	25.1	20	PDB header: hydrolase Chain: B; PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
110	c3i09A_	Alignment	not modelled	25.1	11	PDB header: transport protein Chain: A; PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
111	d1vr6a1	Alignment	not modelled	24.9	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
112	d1ur4a_	Alignment	not modelled	24.6	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
113	d1q77a_	Alignment	not modelled	24.4	4	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
114	c3ac0B_	Alignment	not modelled	23.9	21	PDB header: hydrolase Chain: B; PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
115	d1jf8a_	Alignment	not modelled	23.8	11	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
116	c3nvtA_	Alignment	not modelled	23.6	13	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
117	c1yz7A_	Alignment	not modelled	22.8	18	PDB header: translation Chain: A; PDB Molecule: probable translation initiation factor 2 alpha PDBTitle: crystal structure of a c-terminal segment of the alpha2 subunit of aif2 from pyrococcus abyssi
118	c5k6IA_	Alignment	not modelled	22.7	17	PDB header: hydrolase Chain: A; PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome
119	c4xasB_	Alignment	not modelled	22.5	15	PDB header: signaling protein Chain: B; PDB Molecule: metabotropic glutamate receptor 2; PDBTitle: mglur2 ecd ligand complex
120	c4m88A_	Alignment	not modelled	22.4	4	PDB header: transport protein Chain: A; PDB Molecule: extracellular ligand-binding receptor; PDBTitle: crystal structure of extracellular ligand-binding receptor from2 verminephrobacter eiseniae ef01-2