

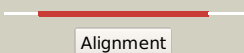
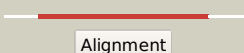


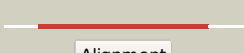





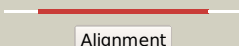

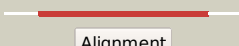

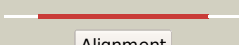

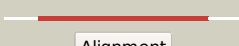







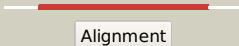
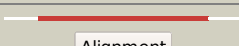

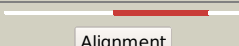

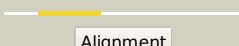




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0044c_(-)_48233_49027
Date	Tue Jul 23 14:50:07 BST 2019
Unique Job ID	34125b1e0335c4a5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b81D_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: D; PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
2	c3sdoB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B; PDB Molecule: nitrotriacetate monooxygenase; PDBTitle: structure of a nitrotriacetate monooxygenase from burkholderia2 pseudomallei
3	c5tlcA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
4	d1tvla_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
5	c1tvA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
6	c5w4zA_	 Alignment		100.0	17	PDB header: flavoprotein Chain: A; PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmh and2 substrate riboflavin
7	d1lucb_	 Alignment		100.0	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
8	d1luca_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
9	c3raoB_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
10	c1z69D_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: D; PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
11	c6friD_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: D; PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi

12	d1f07a_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
13	d1ezwa_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
14	c5dqpa_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
15	c3b9nB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
16	c2i7ga_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
17	c2wgka_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
18	c6ak1B_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
19	c3c8nB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
20	d1rhca_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
21	d1nqka_	 Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
22	c5wanA_	 Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
23	d1nfpa_	 Alignment	not modelled	99.3	10	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	 Alignment	not modelled	96.9	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3kwsB_	 Alignment	not modelled	83.6	18	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
26	c3ih1A_	 Alignment	not modelled	73.9	12	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
27	c3vniC_	 Alignment	not modelled	68.0	12	PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
28	c2hinA_	 Alignment	not modelled	61.2	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase;

28	c2tjpA	Alignment	not modelled	51.2	14	PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with 2 phosphonopyruvate and mg ⁺⁺ PDB header: hydrolase
29	c3qy6A	Alignment	not modelled	54.1	6	Chain: A; PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from streptococcus pneumoniae, unique metal-dependent tyrosine 3 phosphatases
30	c5zfsA	Alignment	not modelled	49.5	18	PDB header: isomerase Chain: A; PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase 2 which can produce d-allulose from d-fructose
31	c3b8fF	Alignment	not modelled	48.3	10	PDB header: lyase Chain: F; PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of pseudomonas 2 aeruginosa (pa4872) in complex with oxalate and mg ²⁺ .
32	c6daoB	Alignment	not modelled	48.2	11	PDB header: lyase Chain: B; PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
33	d1oyaa	Alignment	not modelled	47.3	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
34	c2ekcA	Alignment	not modelled	47.2	18	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
35	c1ps9A	Alignment	not modelled	45.8	16	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl 2 coa reductase
36	c4b5nA	Alignment	not modelled	45.7	20	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
37	c3eooL	Alignment	not modelled	45.4	16	PDB header: lyase Chain: L; PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from burkholderia pseudomallei
38	c5dxxA	Alignment	not modelled	45.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
39	c5tchG	Alignment	not modelled	44.0	26	PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
40	d1e0ta2	Alignment	not modelled	43.0	10	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
41	c4tmcB	Alignment	not modelled	41.6	25	PDB header: flavoprotein Chain: B; PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis 2 aku4588 complexed with p-hydroxybenzaldehyde
42	c4a3uB	Alignment	not modelled	41.2	20	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis 2 (ncr)
43	c1zlpA	Alignment	not modelled	40.9	14	PDB header: lyase Chain: A; PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming 2 a thiohemiacetal adduct
44	d1gwja	Alignment	not modelled	40.7	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
45	c2gq8A	Alignment	not modelled	40.3	20	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex 2 with p-hydroxyacetophenone
46	c3dcpB	Alignment	not modelled	38.5	11	PDB header: hydrolase Chain: B; PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from 2 listeria monocytogenes. northeast structural genomics consortium 3 target lmr141.
47	d1q45a	Alignment	not modelled	38.5	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
48	c6daqA	Alignment	not modelled	38.2	15	PDB header: lyase Chain: A; PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
49	c3l5aA	Alignment	not modelled	38.1	9	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase 2 from staphylococcus aureus
50	d1vjia	Alignment	not modelled	38.0	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
51	d1vyra	Alignment	not modelled	37.5	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
52	c4jicB	Alignment	not modelled	37.2	22	PDB header: oxidoreductase Chain: B; PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
53	c1bplA	Alignment	not modelled	37.2	11	PDB header: glycosyltransferase Chain: A; PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase

54	c5ocsB	Alignment	not modelled	37.1	4	PDB header: flavoprotein Chain: B: PDB Molecule: putative nadh-dependent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
55	d1muma	Alignment	not modelled	36.8	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
56	c3gkaB	Alignment	not modelled	36.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
57	c2ze3A	Alignment	not modelled	36.0	15	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
58	d1icpa	Alignment	not modelled	34.9	25	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	c2x7vA	Alignment	not modelled	34.9	14	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
60	c3e38A	Alignment	not modelled	34.5	14	PDB header: hydrolase Chain: A: PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bv_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
61	c3fa4D	Alignment	not modelled	34.3	13	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
62	d1oy0a	Alignment	not modelled	34.1	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
63	c4rnxA	Alignment	not modelled	34.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase 1; PDBTitle: k154 circular permutation of old yellow enzyme
64	d1djqa1	Alignment	not modelled	33.9	35	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
65	c3ag5A	Alignment	not modelled	33.0	23	PDB header: ligase Chain: A: PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantothenate synthetase from staphylococcus2 aureus
66	d1xp3a1	Alignment	not modelled	33.0	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
67	d1z41a1	Alignment	not modelled	32.8	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
68	c4df2A	Alignment	not modelled	32.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: p. stiptitis oye2.6 complexed with p-chlorophenol
69	c2qiWA	Alignment	not modelled	32.5	19	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
70	c4qnWA	Alignment	not modelled	31.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
71	c3bc9A	Alignment	not modelled	31.4	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
72	c6mywA	Alignment	not modelled	30.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: gluconobacter ene-reductase (gluer) mutant - t36a
73	c2p0oA	Alignment	not modelled	30.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
74	c3vndD	Alignment	not modelled	29.7	23	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
75	c2vk2A	Alignment	not modelled	29.3	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter periplasmic-binding protein ytfq; PDBTitle: crystal structure of a galactofuranose binding protein
76	c3kruC	Alignment	not modelled	29.1	25	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
77	c4rnvD	Alignment	not modelled	28.8	15	PDB header: oxidoreductase/inhibitor Chain: D: PDB Molecule: nadh dehydrogenase 1; PDBTitle: g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
78	d1x7fa2	Alignment	not modelled	28.6	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain PDB header: lyase

79	c3dz1A_	Alignment	not modelled	28.3	10	Chain: A; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>2 rhodopseudomonas palustris</i> at 1.87a resolution
80	d1m5wa_	Alignment	not modelled	27.7	20	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
81	c3innB_	Alignment	not modelled	27.4	15	PDB header: ligase Chain: B; PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
82	d1s2wa_	Alignment	not modelled	27.3	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
83	c2zvrA_	Alignment	not modelled	27.0	6	PDB header: isomerase Chain: A; PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from <i>2 thermotoga maritima</i>
84	c5epdA_	Alignment	not modelled	26.8	20	PDB header: oxidoreductase Chain: A; PDB Molecule: glycerol trinitrate reductase; PDBTitle: crystal structure of glycerol trinitrate reductase xdpb from <i>2 agrobacterium sp. r89-1</i> (apo form)
85	c2ejcA_	Alignment	not modelled	26.6	20	PDB header: ligase Chain: A; PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from <i>thermotoga maritima</i>
86	c2hk1D_	Alignment	not modelled	26.0	13	PDB header: isomerase Chain: D; PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
87	d1uoua2	Alignment	not modelled	25.1	17	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
88	c4ot7A_	Alignment	not modelled	25.0	22	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from <i>zymomonas mobilis</i>
89	c3gk0H_	Alignment	not modelled	24.8	23	PDB header: transferase Chain: H; PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from <i>2 burkholderia pseudomallei</i>
90	c2yb1A_	Alignment	not modelled	24.6	14	PDB header: hydrolase Chain: A; PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from <i>chromobacterium violaceum</i> (efi2 target efi-500202) with bound mn, amp and phosphate.
91	d1ua7a2	Alignment	not modelled	22.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	d1hl2a_	Alignment	not modelled	22.9	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	d1goxa_	Alignment	not modelled	22.8	9	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
94	c6k0aC_	Alignment	not modelled	22.7	0	PDB header: rna binding protein/rna Chain: C; PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
95	c2a7nA_	Alignment	not modelled	22.6	16	PDB header: oxidoreductase Chain: A; PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
96	d1ud2a2	Alignment	not modelled	22.6	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	d2gjpa2	Alignment	not modelled	22.6	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	c3khjE_	Alignment	not modelled	22.1	10	PDB header: oxidoreductase Chain: E; PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
99	d1ihoA_	Alignment	not modelled	21.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
100	c5dlcC_	Alignment	not modelled	21.4	20	PDB header: transferase Chain: C; PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from <i>pseudomonas aeruginosa</i>
101	c5kwvA_	Alignment	not modelled	21.4	15	PDB header: ligase Chain: A; PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of a pantoate-beta-alanine ligase from <i>neisseria2 gonorrhoeae</i> with bound amppnp
102	c6de6B_	Alignment	not modelled	21.2	25	PDB header: oxidoreductase Chain: B; PDB Molecule: histamine dehydrogenase; PDBTitle: 2.1 a resolution structure of histamine dehydrogenase from <i>rhizobium2 sp. 4-9</i>
103	d1ujga_	Alignment	not modelled	21.1	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
104	c3obeB_	Alignment	not modelled	20.4	12	PDB header: isomerase Chain: B; PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from <i>parabacteroides distasonis</i>

105	c6agzA_	Alignment	not modelled	20.4	15	atcc 8503 at 1.70 a resolution PDB header: oxidoreductase Chain: A: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from pichia sp. aku4542
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