

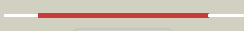












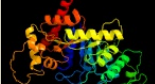

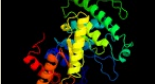




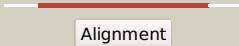

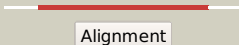

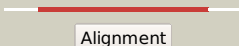



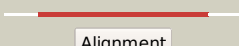

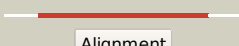

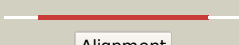





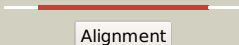


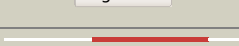
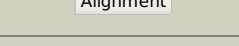


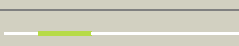


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1936 (-) _2187391_2188500
Date	Mon Aug 5 13:25:02 BST 2019
Unique Job ID	42690df5e9e766cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wgkA_	 Alignment		100.0	35	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
2	d1luca_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
3	d1lucb_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
4	c2i7gA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
5	c6friD_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
6	d1ezwa_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
7	c5tlcA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
8	c3raoB_	 Alignment		100.0	17	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.
9	d1tvla_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
10	c1tvIA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
11	c3sdoB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrotriacetate monooxygenase; PDBTitle: structure of a nitrotriacetate monooxygenase from burkholderia2 pseudomallei

12	d1nqka_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
13	c1z69D_	 Alignment		100.0	17	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
14	c5wanA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
15	d1rhca_	 Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
16	d1f07a_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
17	c5dqpA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
18	c5w4zA_	 Alignment		100.0	19	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
19	c3b9nB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
20	c3c8nB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
21	c6ak1B_	 Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
22	c2b81D_	 Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
23	d1nfpa_	 Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	 Alignment	not modelled	99.6	14	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3qy6A_	 Alignment	not modelled	78.5	10	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
26	d1xkya1	 Alignment	not modelled	75.2	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
27	c3s5oA_	 Alignment	not modelled	65.2	13	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
28	c3d0cB_	 Alignment	not modelled	65.1	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from

						oceanobacillus2 iheyensis at 1.9 a resolution
29	d1o5ka_	Alignment	not modelled	58.1	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
30	c2ekcA_	Alignment	not modelled	55.8	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
31	c4xkyC_	Alignment	not modelled	55.2	13	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
32	c3e96B_	Alignment	not modelled	54.9	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
33	d1p4ca_	Alignment	not modelled	54.7	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
34	c2a7nA_	Alignment	not modelled	54.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: (+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
35	c3vniC_	Alignment	not modelled	51.5	16	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
36	c6mqhA_	Alignment	not modelled	49.8	13	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
37	c1bplA_	Alignment	not modelled	48.8	8	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
38	c4ur7B_	Alignment	not modelled	44.9	12	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
39	c2r8wB_	Alignment	not modelled	44.8	9	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
40	c2infB_	Alignment	not modelled	42.4	17	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
41	c3cnyA_	Alignment	not modelled	42.1	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
42	c4n4qD_	Alignment	not modelled	42.1	12	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
43	c4lsbA_	Alignment	not modelled	37.8	7	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
44	c6dvhF_	Alignment	not modelled	37.7	9	PDB header: oxidoreductase Chain: F: PDB Molecule: lactate 2-monooxygenase; PDBTitle: lactate monooxygenase from mycobacterium smegmatis - c203a mutant
45	c3b4uB_	Alignment	not modelled	37.3	4	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
46	c3dcpB_	Alignment	not modelled	35.7	26	PDB header: hydrolase Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
47	c2yb1A_	Alignment	not modelled	34.9	21	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
48	c3wqoB_	Alignment	not modelled	34.8	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
49	c2ejaB_	Alignment	not modelled	34.4	13	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
50	c3lerA_	Alignment	not modelled	34.0	13	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
51	c2wjeA_	Alignment	not modelled	33.7	8	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
52	d1j93a_	Alignment	not modelled	33.5	22	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
						Fold: TIM beta/alpha-barrel

53	d1goxa_	Alignment	not modelled	33.5	15	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
54	c1e40A_	Alignment	not modelled	32.8	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
55	c1mwoA_	Alignment	not modelled	32.2	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
56	c5ktiA_	Alignment	not modelled	32.2	12	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
57	c2x7vA_	Alignment	not modelled	31.9	14	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
58	c6k0aC_	Alignment	not modelled	31.2	13	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
59	c3fkkA_	Alignment	not modelled	30.5	13	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
60	c3h5dD_	Alignment	not modelled	30.1	13	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
61	c4n6eA_	Alignment	not modelled	29.6	11	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
62	c4uxdC_	Alignment	not modelled	29.6	9	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
63	c3ikzA_	Alignment	not modelled	29.0	24	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenyltransferase; PDBTitle: crystal structure of phosphopantetheine adenyltransferase from2 burkholderia pseudomallei
64	c2gg8A_	Alignment	not modelled	28.7	5	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, frn-binding; PDBTitle: structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
65	c3qfeB_	Alignment	not modelled	28.6	18	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
66	c3l5aA_	Alignment	not modelled	28.2	8	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
67	c4exqA_	Alignment	not modelled	27.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
68	c4nq1B_	Alignment	not modelled	27.1	17	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
69	c6ahuJ_	Alignment	not modelled	26.7	22	PDB header: hydrolase/rna Chain: J: PDB Molecule: ribonuclease p protein subunit p30; PDBTitle: cryo-em structure of human ribonuclease p with mature trna
70	d1f74a_	Alignment	not modelled	26.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	c2qiwa_	Alignment	not modelled	25.7	14	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncg11015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
72	c5tchG_	Alignment	not modelled	25.0	11	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
73	c3e38A_	Alignment	not modelled	24.3	13	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 (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
74	c2rdtA_	Alignment	not modelled	23.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
75	c3lyeA_	Alignment	not modelled	23.1	20	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
76	c1zlpA_	Alignment	not modelled	23.0	20	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
77	d1m65a_	Alignment	not modelled	22.6	32	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: PHP domain
						PDB header: hydrolase

78	c3e0fA	Alignment	not modelled	22.3	25	Chain: A: PDB Molecule: putative metal-dependent phosphoesterase; PDBTitle: crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
79	d1tb3a1	Alignment	not modelled	21.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
80	c1wpcA	Alignment	not modelled	21.5	8	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltonaose
81	c5i4rA	Alignment	not modelled	21.2	12	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
82	c3kwsB	Alignment	not modelled	21.0	23	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
83	c2vc6A	Alignment	not modelled	20.8	9	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
84	c2ejcA	Alignment	not modelled	20.7	15	PDB header: ligase Chain: A: PDB Molecule: pantoate--beta-alanine ligase; PDBTitle: crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
85	c1hvxA	Alignment	not modelled	20.5	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
86	c5k9hA	Alignment	not modelled	19.6	18	PDB header: hydrolase Chain: A: PDB Molecule: 0940_gh29; PDBTitle: crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium
87	c3fa4D	Alignment	not modelled	19.6	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
88	c5ud6B	Alignment	not modelled	19.3	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
89	c6gvbC	Alignment	not modelled	19.2	23	PDB header: hydrolase Chain: C: PDB Molecule: exo-beta-1,4-mannosidase; PDBTitle: crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase
90	c3cqkB	Alignment	not modelled	18.8	26	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
91	c3g0sA	Alignment	not modelled	18.8	18	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
92	c1kbiB	Alignment	not modelled	18.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
93	d1r46a2	Alignment	not modelled	18.5	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	c3cyvA	Alignment	not modelled	18.5	6	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexneri: new insights into its catalytic3 mechanism
95	d1ulza2	Alignment	not modelled	18.3	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
96	c3si9B	Alignment	not modelled	18.1	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
97	d1jpm1	Alignment	not modelled	17.9	20	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
98	c3lciA	Alignment	not modelled	17.8	12	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
99	d1muma	Alignment	not modelled	17.7	27	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like