











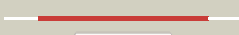

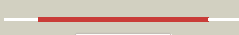







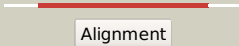

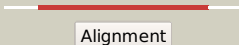
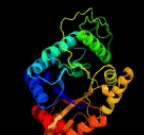
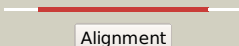



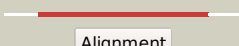

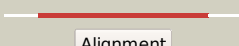

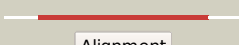






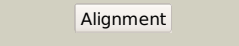
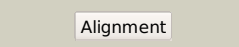


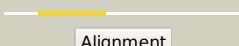
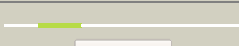



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1855c (-)_2103191_2104114
Date	Fri Aug 2 13:30:47 BST 2019
Unique Job ID	1ba65e3bee014d22

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sdoB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
2	d1luca_	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
3	c1tvIA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
4	d1tvIA_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
5	c3raoB_	 Alignment		100.0	24	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.
6	c5tlcA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
7	c5wanA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
8	c5dqgA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelatorans sp. bnc1
9	d1lucB_	 Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
10	c2i7gA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
11	c2wgkA_	 Alignment		100.0	20	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

12	c5w4zA_	 Alignment		100.0	20	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
13	d1ezwa_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
14	c3b9nB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
15	c6friD_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
16	c1z69D_	 Alignment		100.0	21	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
17	c2b81D_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
18	d1nqka_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
19	c6ak1B_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
20	c3c8nB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
21	d1rhca_	 Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
22	d1f07a_	 Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
23	d1nfpa_	 Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	 Alignment	not modelled	99.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3kwsB_	 Alignment	not modelled	84.3	19	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	c4xkyC_	 Alignment	not modelled	71.9	15	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
27	c3qy6A_	 Alignment	not modelled	64.8	16	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
28	c3noyA_	 Alignment	not modelled	51.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase;

						PDBTitle: crystal structure of ispg (gcpe)
29	c4k3zA_	Alignment	not modelled	50.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
30	c3ez4B_	Alignment	not modelled	48.7	26	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
31	c3d0cB_	Alignment	not modelled	44.5	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
32	d1xp3a1	Alignment	not modelled	41.4	20	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
33	c3e38A_	Alignment	not modelled	39.0	12	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
34	c3ilvA_	Alignment	not modelled	38.6	16	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
35	c3ih1A_	Alignment	not modelled	38.6	16	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
36	c3e96B_	Alignment	not modelled	36.7	21	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
37	c1jpkA_	Alignment	not modelled	34.1	21	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
38	c2wjeA_	Alignment	not modelled	33.9	9	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from2 streptococcus pneumoniae tigr4.
39	d1o5ka_	Alignment	not modelled	33.8	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	c2zvrA_	Alignment	not modelled	30.0	23	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
41	d1jdfa1	Alignment	not modelled	28.8	13	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
42	d1r3sa_	Alignment	not modelled	28.8	21	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
43	d1j93a_	Alignment	not modelled	28.5	28	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
44	c2ze3A_	Alignment	not modelled	27.6	39	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
45	c3wqoB_	Alignment	not modelled	26.8	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
46	c1zlpA_	Alignment	not modelled	26.5	8	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
47	d1ujqa_	Alignment	not modelled	25.3	25	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
48	c2hjpA_	Alignment	not modelled	25.1	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
49	c3b8iF_	Alignment	not modelled	24.3	15	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
50	c3fa4D_	Alignment	not modelled	24.1	21	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
51	c3auoB_	Alignment	not modelled	23.1	16	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
52	c2qiwa_	Alignment	not modelled	22.9	11	PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cg11060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
						Fold: TIM beta/alpha-barrel

53	d1m3ua_	Alignment	not modelled	22.8	22	Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
54	d1muma_	Alignment	not modelled	22.8	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
55	c3lyeA_	Alignment	not modelled	21.9	21	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
56	c3na8A_	Alignment	not modelled	20.7	22	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
57	c3qfeB_	Alignment	not modelled	20.3	14	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
58	c4ur7B_	Alignment	not modelled	19.3	13	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
59	c3bh1A_	Alignment	not modelled	18.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae
60	d2d69a1	Alignment	not modelled	18.7	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
61	c2yb1A_	Alignment	not modelled	18.3	16	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.
62	c3eooL_	Alignment	not modelled	17.0	17	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
63	c2ehhE_	Alignment	not modelled	16.9	12	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
64	c2ejaB_	Alignment	not modelled	16.7	12	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
65	c3pueA_	Alignment	not modelled	16.5	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
66	c3vniC_	Alignment	not modelled	16.0	10	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 ketoheose sugars
67	d1jpdx1	Alignment	not modelled	15.2	26	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
68	c3cqkB_	Alignment	not modelled	15.1	23	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
69	c4exqA_	Alignment	not modelled	15.1	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
70	c3dcpB_	Alignment	not modelled	14.8	16	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.
71	d2noca1	Alignment	not modelled	14.4	21	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
72	c3qvjB_	Alignment	not modelled	14.3	31	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
73	d1oy0a_	Alignment	not modelled	14.2	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
74	c6k0aC_	Alignment	not modelled	13.8	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
75	c6arhA_	Alignment	not modelled	13.8	24	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: crystal structure of human nal at a resolution of 1.6 angstrom
76	c2nuxB_	Alignment	not modelled	13.6	5	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
77	c2hmcA_	Alignment	not modelled	13.1	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens

78	c6mqhA_	Alignment	not modelled	13.1	15	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
79	c5dxxA_	Alignment	not modelled	12.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: artemisinic aldehyde delta(11(13)) reductase; PDBTitle: crystal structure of dbr2
80	d1oyaa_	Alignment	not modelled	12.8	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	c2r94B_	Alignment	not modelled	12.7	29	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
82	d1z41a1	Alignment	not modelled	12.3	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	d1bqga1	Alignment	not modelled	12.2	13	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
84	c2r8wB_	Alignment	not modelled	12.2	24	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
85	c4a3uB_	Alignment	not modelled	12.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh\flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
86	c4n4qD_	Alignment	not modelled	11.8	12	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
87	d2a6na1	Alignment	not modelled	11.6	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
88	d1x7fa2	Alignment	not modelled	11.5	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
89	c3si9B_	Alignment	not modelled	11.0	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
90	c3daqB_	Alignment	not modelled	11.0	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
91	c1rcxH_	Alignment	not modelled	10.9	10	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
92	c4tmcB_	Alignment	not modelled	10.8	17	PDB header: flavoprotein Chain: B: PDB Molecule: old yellow enzyme; PDBTitle: crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
93	c3n05B_	Alignment	not modelled	10.7	12	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
94	d1e8ca2	Alignment	not modelled	10.6	18	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
95	c4zr8B_	Alignment	not modelled	10.5	28	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
96	c4b5nA_	Alignment	not modelled	10.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sy4)
97	c2infB_	Alignment	not modelled	10.2	19	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
98	d1xxa1	Alignment	not modelled	10.2	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c6daqA_	Alignment	not modelled	10.1	25	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate