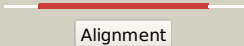

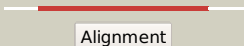

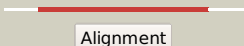







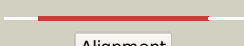




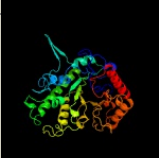








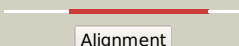

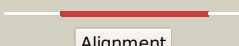

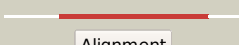

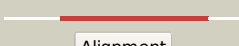







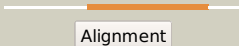
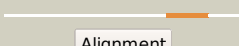



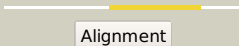
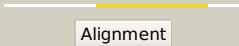
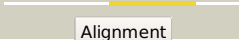


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3015c_(-)_3374661_3375674
Date	Thu Aug 8 16:20:18 BST 2019
Unique Job ID	1a55a7324e2001c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u22A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- PDBTitle: a. thaliana cobalamine independent methionine synthase
2	c1t71A_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- homocysteine PDBTitle: crystal structure of cobalamin-independent methionine synthase from t.2 maritima
3	c4ztxA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: cobalamin-independent methionine synthase; PDBTitle: neurospora crassa cobalamin-independent methionine synthase complexed2 with zn2+
4	c3l7sA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- homocysteine PDBTitle: crystal structure of mete coordinated with zinc from streptococcus2 mutans
5	c2nq5A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- homocysteine PDBTitle: crystal structure of methyltransferase from streptococcus mutans
6	d1u1ha2	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
7	c3ppgA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydropteroyltriglutamate-- homocysteine PDBTitle: crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
8	c3rpdB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: methionine synthase (b12-independent); PDBTitle: the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
9	c1ypxA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative vitamin-b12 independent methionine synthase family PDBTitle: crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
10	d1u1ha1	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
11	c4ay8B_	 Alignment		99.7	17	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin\): coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei

12	d1j93a_	 Alignment		99.7	13	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
13	c3cyvA_	 Alignment		99.6	13	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
14	c4exqA_	 Alignment		99.6	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
15	c1jpkA_	 Alignment		99.5	14	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
16	c4zr8B_	 Alignment		99.5	14	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
17	d1r3sa_	 Alignment		99.5	14	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
18	c2infB_	 Alignment		99.5	10	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
19	c2ejaB_	 Alignment		99.4	18	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
20	c3rhgA_	 Alignment		86.2	14	PDB header: hydrolase Chain: A: PDB Molecule: putative phophotriesterase; PDBTitle: crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
21	d1ajza_	 Alignment	not modelled	83.1	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
22	c5odcD_	 Alignment	not modelled	83.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: methyl-viologen reducing hydrogenase subunit d; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
23	d1rvga_	 Alignment	not modelled	81.1	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
24	d1qvfa_	 Alignment	not modelled	79.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
25	c3qc3B_	 Alignment	not modelled	74.9	16	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
26	d1h1ya_	 Alignment	not modelled	74.8	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
27	c6omzA_	 Alignment	not modelled	74.7	16	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
28	d1tqxa_	 Alignment	not modelled	74.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel

						Family: D-ribulose-5-phosphate 3-epimerase
29	c1tx2A_	Alignment	not modelled	73.1	9	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
30	d1tx2a_	Alignment	not modelled	73.1	9	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
31	c6ofuC_	Alignment	not modelled	72.3	11	PDB header: lyase Chain: C: PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from escherichia coli k12
32	d1f6ya_	Alignment	not modelled	72.0	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
33	d1rpxa_	Alignment	not modelled	71.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
34	c3k2gA_	Alignment	not modelled	70.5	15	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
35	c3ct7E_	Alignment	not modelled	70.3	16	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
36	c3c52B_	Alignment	not modelled	65.3	16	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
37	c5u4nA_	Alignment	not modelled	65.1	17	PDB header: lyase Chain: A: PDB Molecule: fructose-1; PDBTitle: crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
38	c2vp8A_	Alignment	not modelled	64.7	14	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
39	d1tqja_	Alignment	not modelled	64.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
40	c2bmbA_	Alignment	not modelled	58.2	14	PDB header: transferase Chain: A: PDB Molecule: folic acid synthesis protein fol1; PDBTitle: x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
41	c3tr9A_	Alignment	not modelled	56.7	11	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
42	c4mwaA_	Alignment	not modelled	56.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
43	c2iswB_	Alignment	not modelled	55.7	17	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-bisphosphate aldolase in2 complex with phosphoglycolohydroxamate
44	c4nu7C_	Alignment	not modelled	53.9	15	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
45	c3q94B_	Alignment	not modelled	52.1	20	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
46	c3inpA_	Alignment	not modelled	51.0	17	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
47	d1xrta2	Alignment	not modelled	47.9	11	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
48	c5umfB_	Alignment	not modelled	47.7	15	PDB header: isomerase Chain: B: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
49	d1ad1a_	Alignment	not modelled	46.2	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
50	c5uurA_	Alignment	not modelled	45.1	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
51	c2y5sA_	Alignment	not modelled	43.2	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
52	c2yciX_	Alignment	not modelled	43.1	17	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: 1.73 angstrom resolution crystal structure of
53	c5visB_	Alignment	not modelled	43.1	17	

						dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
54	c3nm3D_	Alignment	not modelled	39.1	12	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
55	c3ipwA_	Alignment	not modelled	37.7	16	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase tatd family protein; PDBTitle: crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
56	c5uswD_	Alignment	not modelled	37.6	8	PDB header: transferase Chain: D: PDB Molecule: dihydropteroate synthase; PDBTitle: the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
57	c3f4cA_	Alignment	not modelled	35.8	13	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearotherophilus strain 10, with glycerol bound
58	c4djdD_	Alignment	not modelled	34.3	11	PDB header: transferase/vitamin-binding protein Chain: D: PDB Molecule: corrinoide/iron-sulfur protein small subunit; PDBTitle: crystal structure of folate-free corrinoide iron-sulfur protein (cfesp)2 in complex with its methyltransferase (metr)
59	c6o5IA_	Alignment	not modelled	31.3	27	PDB header: dna binding protein Chain: A: PDB Molecule: ppra; PDBTitle: crystal structure of ppra filament from deinococcus peraridilitoris
60	c3ceuA_	Alignment	not modelled	29.8	21	PDB header: transferase Chain: A: PDB Molecule: thiamine phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamine phosphate pyrophosphorylase (bt_0647)2 from bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr268
61	c2d16B_	Alignment	not modelled	29.0	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ph1918; PDBTitle: crystal structure of ph1918 protein from pyrococcus horikoshii ot3
62	d1gkma_	Alignment	not modelled	28.9	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: HAL/PAL-like
63	c2h9aB_	Alignment	not modelled	28.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoide iron-sulfur protein
64	d1vgga_	Alignment	not modelled	26.5	27	Fold: Ta1353-like Superfamily: Ta1353-like Family: Ta1353-like
65	c2ekmC_	Alignment	not modelled	24.2	17	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein st1511; PDBTitle: structure of st1219 protein from sulfolobus tokodaii
66	c3unvB_	Alignment	not modelled	24.2	22	PDB header: lyase Chain: B: PDB Molecule: admh; PDBTitle: pantoea agglomerans phenylalanine aminomutase
67	c6s7qG_	Alignment	not modelled	23.7	18	PDB header: lyase Chain: G: PDB Molecule: ergothionase; PDBTitle: crystal structure of ergothioneine degrading enzyme ergothionase from2 treponema denticola in complex with desmethyl-ergothioneine sulfonic3 acid
68	c6cluC_	Alignment	not modelled	21.4	14	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
69	c2vefB_	Alignment	not modelled	21.2	12	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
70	c2o6yF_	Alignment	not modelled	20.7	22	PDB header: lyase Chain: F: PDB Molecule: putative histidine ammonia-lyase; PDBTitle: tyrosine ammonia-lyase from rhodobacter sphaeroides
71	d2flia1	Alignment	not modelled	20.7	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
72	c2qveA_	Alignment	not modelled	20.0	15	PDB header: transferase Chain: A: PDB Molecule: tyrosine aminomutase; PDBTitle: crystal structure of sgtam bound to mechanism based inhibitor
73	d3bofa1	Alignment	not modelled	19.1	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
74	d1rd5a_	Alignment	not modelled	19.0	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	c3k5pA_	Alignment	not modelled	19.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
76	d1dosa_	Alignment	not modelled	18.5	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
77	c6mc8A_	Alignment	not modelled	17.7	30	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein ppra; PDBTitle: crystal structure of ppra dimer from deinococcus deserti
78	c4exaD_	Alignment	not modelled	17.4	16	PDB header: oxidoreductase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the pa4992, the putative aldo-keto reductase from2 pseudomona aeruginosa
						Fold: TIM beta/alpha-barrel

79	d1ur4a_	Alignment	not modelled	17.4	18	Superfamily: (Trans)glycosidases Family: beta-glycanases
80	c3i5aA_	Alignment	not modelled	17.0	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
81	c3uowB_	Alignment	not modelled	15.8	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
82	c5n2pA_	Alignment	not modelled	15.7	8	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
83	c2gl0A_	Alignment	not modelled	14.9	14	PDB header: transferase Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: structure of pae2307 in complex with adenosine
84	c2eklA_	Alignment	not modelled	14.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
85	d1o9ga_	Alignment	not modelled	14.0	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
86	c3pm6B_	Alignment	not modelled	13.9	16	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
87	c4muza_	Alignment	not modelled	13.7	16	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp
88	c3exsB_	Alignment	not modelled	13.7	6	PDB header: lyase Chain: B: PDB Molecule: rmppd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
89	c5yf1A_	Alignment	not modelled	12.9	10	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of carnmt1 bound to carnosine and sfg
90	c3ufbA_	Alignment	not modelled	12.7	27	PDB header: transferase Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
91	d1gvea_	Alignment	not modelled	11.9	17	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
92	c3jr2D_	Alignment	not modelled	11.7	9	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
93	c2rdtA_	Alignment	not modelled	10.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
94	c4o1fB_	Alignment	not modelled	10.1	14	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
95	c5tw7E_	Alignment	not modelled	9.0	23	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
96	c1gpmD_	Alignment	not modelled	9.0	21	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
97	d2q02a1	Alignment	not modelled	9.0	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lol1-like
98	c5z79F_	Alignment	not modelled	8.8	15	PDB header: transferase Chain: F: PDB Molecule: hydroxymethylidihydropterin pyrophosphokinase- PDBTitle: crystal structure analysis of the hppk-dhps in complex with substrates
99	c5ybbA_	Alignment	not modelled	8.8	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: structural basis underlying complex assembly andconformational2 transition of the type i r-m system