
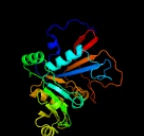








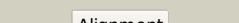









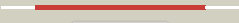



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2671_(ribD)_2986849_2987625
Date	Wed Aug 7 12:50:32 BST 2019
Unique Job ID	6498384ce81f4a02

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xt6A_	 Alignment		100.0	98	PDB header: oxidoreductase Chain: A: PDB Molecule: rv2671; PDBTitle: crystal structure of rv2671 from mycobacterium tuberculosis in complex2 with the tetrahydropteridine ring of tetrahydrofolate (thf)
2	c2p4gA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
3	c2d5nB_	 Alignment		100.0	19	PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
4	c2o7pA_	 Alignment		100.0	22	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
5	c5xuxC_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: conserved protein; PDBTitle: crystal structure of rib7 from methanosarcina mazei
6	c2h xvA_	 Alignment		100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
7	c3zpgA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ribd; PDBTitle: acinetobacter baumannii ribd, form 2
8	d2b3za1	 Alignment		100.0	20	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
9	d2azna1	 Alignment		100.0	20	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
10	c4ha7B_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 2,5-diamino-6-ribosylamino-4(3h)-pyrimidinone 5'-phosphate PDBTitle: structural insights into the reduction mechanism of saccharomyces2 cerevisia riboflavin biosynthesis reductase rib7
11	d2hxva1	 Alignment		100.0	19	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like

12	c3kgyA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional deaminase-reductase domain protein; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_001636057.1)2 from chloroflexus aurantiacus j-10-fl at 1.50 a resolution
13	c3jtwB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution
14	c2gd9A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein yyap; PDBTitle: crystal structure of a putative dihydrofolate reductase (bsu40760,2 yyap) from bacillus subtilis at 2.30 a resolution
15	d1d1ga_	Alignment		100.0	19	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
16	c2xw7A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of mycobacterium smegmatis putative reductase ms0308
17	c3ky8B_	Alignment		100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative riboflavin biosynthesis protein; PDBTitle: crystal structure of putative riboflavin biosynthesis protein2 (yp_001092907.1) from shewanella sp. pv-4 at 2.12 a resolution
18	d1seja1	Alignment		99.6	16	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
19	d1vdra_	Alignment		99.4	24	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
20	c5eccA_	Alignment		99.3	19	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dehydrofolate reductase type i; PDBTitle: klebsiella pneumoniae dfra1 complexed with nadph and 6-ethyl-5-(3-(2-2 methoxy-5-(pyridin-4-yl)phenyl)prop-1-yn-1-yl)pyrimidine-2,4-diamine
21	c3ix9B_	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of streptococcus pneumoniae dihydrofolate2 reductase - sp9 mutant
22	d1kmva_	Alignment	not modelled	99.1	13	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
23	d3dfra_	Alignment	not modelled	99.1	21	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
24	d1df7a_	Alignment	not modelled	99.0	15	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
25	c3k2hA_	Alignment	not modelled	99.0	17	PDB header: transferase Chain: A: PDB Molecule: dihydrofolate reductase/thymidylate synthase; PDBTitle: co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp
26	d8dfra_	Alignment	not modelled	99.0	12	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
27	d2fzia1	Alignment	not modelled	98.9	16	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
28	c3e0bA_	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: bacillus anthracis dihydrofolate reductase complexed with nadph and 2,2 4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)

29	d1ra9a_	Alignment	not modelled	98.8	15	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
30	c3tq8A_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of the dihydrofolate reductase (foIa) from coxiella burnetii2 in complex with trimethoprim
31	c1zdrB_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearothermophilus
32	c3vcoA_	Alignment	not modelled	98.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: schistosoma mansoni dihydrofolate reductase
33	c4m7vA_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: dihydrofolate reductase from enterococcus faecalis complexed with2 nadp(h)and rab-propyl
34	c3ia5A_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: moritella profunda dihydrofolate reductase (dhfr)
35	c2oipE_	Alignment	not modelled	98.6	18	PDB header: transferase, oxidoreductase Chain: E: PDB Molecule: chain a, crystal structure of dhfr; PDBTitle: crystal structure of the s290g active site mutant of ts-dhfr from2 cryptosporidium hominis
36	c6cxmA_	Alignment	not modelled	98.6	19	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of a dihydrofolate reductase from mycobacterium2 smegmatis in complex with nadp and p218
37	c3f0uX_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: X: PDB Molecule: trimethoprim-sensitive dihydrofolate reductase; PDBTitle: staphylococcus aureus f98y mutant dihydrofolate reductase complexed2 with nadph and 2,4-diamino-5-[3-(3-methoxy-5-phenylphenyl)but-1-3 ynyl]-6-methylpyrimidine
38	c3clbA_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dhfr-ts; PDBTitle: structure of bifunctional tcdhfr-ts in complex with tmq
39	d1aoea_	Alignment	not modelled	98.4	12	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
40	c4eckB_	Alignment	not modelled	98.3	10	PDB header: transferase, oxidoreductase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: crystal structure of the toxoplasma gondii ts-dhfr
41	d1j3ka_	Alignment	not modelled	98.3	16	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
42	c2blcA_	Alignment	not modelled	98.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in complex with2 des-chloropyrimethamine
43	c3cseA_	Alignment	not modelled	98.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with nadph and 2,4-2 diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-ynyl)-6-ethylpyrimidine3 (ucp120b)
44	c3dg8B_	Alignment	not modelled	98.0	13	PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase (pfdhfr-ts) complexed3 with rjf670, nadph, and dump
45	c3jsuA_	Alignment	not modelled	97.7	16	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: quadruple mutant(n51i+c59r+s108n+i164l) plasmodium falciparum2 dihydrofolate reductase-thymidylate synthase(pfdhfr-ts) complexed3 with qn254, nadph, and dump
46	c6drsA_	Alignment	not modelled	97.6	17	PDB header: antifungal protein/inhibitor Chain: A: PDB Molecule: dihydrofolate reductase, putative; PDBTitle: dihydrofolate reductase (dhfr) of aspergillus flavus in complex with a2 small molecule inhibitor
47	c3rg9A_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210
48	d1juva_	Alignment	not modelled	95.5	17	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
49	c4mcaB_	Alignment	not modelled	53.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
50	d1xk7a1	Alignment	not modelled	46.8	17	Fold: CoA-transferase family III (CaiB/BaiF) Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
51	c3uhjE_	Alignment	not modelled	45.9	19	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
52	c5yx6D_	Alignment	not modelled	41.9	17	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein rv3272; PDBTitle: crystal structure of rv3272 from m. tuberculosis orthorhombic form
						Fold: CoA-transferase familv III (CaiB/BaiF)

53	d2vjma1	Alignment	not modelled	36.1	17	Superfamily: CoA-transferase family III (CaiB/BaiF) Family: CoA-transferase family III (CaiB/BaiF)
54	c3ghfA_	Alignment	not modelled	30.1	23	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
55	c3fpnA_	Alignment	not modelled	29.2	11	PDB header: dna binding protein Chain: A: PDB Molecule: geobacillus stearothermophilus uvra interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
56	d1piaa2	Alignment	not modelled	27.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
57	d1w0ma_	Alignment	not modelled	27.1	9	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
58	c3ubmB_	Alignment	not modelled	26.7	14	PDB header: transferase Chain: B: PDB Molecule: formyl-coa:oxalate coa-transferase; PDBTitle: formyl-coa:oxalate coa-transferase from acetobacter aceti
59	c4dfcB_	Alignment	not modelled	26.6	16	PDB header: hydrolase/dna binding protein Chain: B: PDB Molecule: uvrabc system protein a; PDBTitle: core uvra/trcf complex
60	c2q5cA_	Alignment	not modelled	24.1	14	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
61	c1piiA_	Alignment	not modelled	23.3	13	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
62	d1e0ta3	Alignment	not modelled	23.2	13	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
63	d1i4na_	Alignment	not modelled	23.0	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
64	c2r3bA_	Alignment	not modelled	23.0	20	PDB header: transferase Chain: A: PDB Molecule: yjef-related protein; PDBTitle: crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
65	c1xa3B_	Alignment	not modelled	22.0	17	PDB header: transferase Chain: B: PDB Molecule: crotonobetainyl-coa:carnitine coa-transferase; PDBTitle: crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
66	c5cssA_	Alignment	not modelled	21.6	19	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate
67	d1a53a_	Alignment	not modelled	20.3	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
68	c3iwpK_	Alignment	not modelled	19.5	30	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
69	c5zxlD_	Alignment	not modelled	19.5	18	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of gldA from e.coli
70	c6csiD_	Alignment	not modelled	18.9	14	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity
71	d1hg3a_	Alignment	not modelled	17.7	9	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
72	c3h10B_	Alignment	not modelled	17.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
73	c2nv2U_	Alignment	not modelled	17.0	31	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
74	c6reqB_	Alignment	not modelled	17.0	13	PDB header: isomerase Chain: B: PDB Molecule: protein (methylmalonyl-coa mutase); PDBTitle: methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
75	c3lloA_	Alignment	not modelled	16.2	11	PDB header: motor protein Chain: A: PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
76	d1twda_	Alignment	not modelled	15.6	30	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
77	c4adsF_	Alignment	not modelled	15.3	31	PDB header: transferase/transferase Chain: F: PDB Molecule: pyridoxine biosynthetic enzyme pdx1 homologue, putative; PDBTitle: crystal structure of plasmodial plp synthase complex
78	d1znaa1	Alignment	not modelled	15.3	30	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like

79	c1znnF_	Alignment	not modelled	15.3	30	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
80	c3obeB_	Alignment	not modelled	15.0	16	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distazonis atcc 8503 at 1.70 a resolution
81	c2zbtB_	Alignment	not modelled	14.8	28	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
82	c6hyeF_	Alignment	not modelled	14.8	35	PDB header: plant protein Chain: F: PDB Molecule: pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a)
83	c6bmaA_	Alignment	not modelled	14.8	19	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
84	c5ydmA_	Alignment	not modelled	14.3	32	PDB header: transferase Chain: A: PDB Molecule: pks; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
85	d1vc4a_	Alignment	not modelled	14.2	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
86	c5z9yB_	Alignment	not modelled	14.1	9	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of staphylococcus aureus thiazole synthase2 (thig) complexed with dxp
87	d1j5ta_	Alignment	not modelled	14.1	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
88	c3qjaA_	Alignment	not modelled	14.0	24	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
89	d7reqa2	Alignment	not modelled	13.9	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
90	d1jq5a_	Alignment	not modelled	13.8	9	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
91	c1xahA_	Alignment	not modelled	13.3	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of staphylococcus aureus 3-dehydroquinase2 synthase (dhqs) in complex with zn2+ and nad+
92	d2pjua1	Alignment	not modelled	13.0	15	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
93	c3femB_	Alignment	not modelled	12.9	28	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
94	d1vlja_	Alignment	not modelled	12.8	11	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
95	c2yztB_	Alignment	not modelled	12.7	31	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from2 methanocaldococcus jannaschii
96	c3labA_	Alignment	not modelled	12.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpG (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpG (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
97	c3rihB_	Alignment	not modelled	12.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: short chain dehydrogenase or reductase; PDBTitle: crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
98	c4g07A_	Alignment	not modelled	12.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
99	c4l8nA_	Alignment	not modelled	12.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pdz domain protein; PDBTitle: crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distazonis atcc 8503 at 2.50 a resolution