






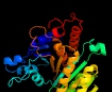



Phyre2

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 Description RVBD2995c_(leuB)_3352468_3353478
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w0da_	Alignment		100.0	100	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
2	c2d1cB_	Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of tt0538 protein from thermus thermophilus hb8
3	d1pb1a_	Alignment		100.0	32	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
4	c3fmX_	Alignment		100.0	41	PDB header: oxidoreductase Chain: X: PDB Molecule: tartrate dehydrogenase/decarboxylase; PDBTitle: crystal structure of tartrate dehydrogenase from pseudomonas putida2 complexed with nadh
5	c2d4vD_	Alignment		100.0	32	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase; PDBTitle: crystal structure of nad dependent isocitrate dehydrogenase2 from acidithiobacillus thiooxidans
6	d1cm7a_	Alignment		100.0	41	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
7	d1v53a1	Alignment		100.0	39	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
8	d1g2ua_	Alignment		100.0	43	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
9	d1cnza_	Alignment		100.0	41	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
10	d1a05a_	Alignment		100.0	42	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
11	d1hqsa_	Alignment		100.0	34	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases

12	d1xaca_	Alignment		100.0	42	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
13	c4iwhA_	Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of a 3-isopropylmalate dehydrogenase from2 burkholderia pseudomallei
14	d1vlca_	Alignment		100.0	41	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
15	c3r8wC_	Alignment		100.0	40	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-isopropylmalate dehydrogenase 2, chloroplastic; PDBTitle: structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
16	c2e0cA_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 409aa long hypothetical nadp-dependent isocitrate PDBTitle: crystal structure of isocitrate dehydrogenase from sulfobolus tokodaii2 strain7 at 2.0 a resolution
17	c3uduG_	Alignment		100.0	36	PDB header: oxidoreductase Chain: G: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of putative 3-isopropylmalate dehydrogenase from2 campylobacter jejuni
18	c3vl3A_	Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: 3-isopropylmalate dehydrogenase from shewanella oneidensis mr-1 at 3402 mpa
19	c3ty3A_	Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: probable homoisocitrate dehydrogenase; PDBTitle: crystal structure of homoisocitrate dehydrogenase from2 schizosaccharomyces pombe bound to glycyglycyl-glycine
20	c3u1hA_	Alignment		100.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of ipmdh from the last common ancestor of bacillus
21	d1wpwa_	Alignment	not modelled	100.0	35	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
22	c1x0lB_	Alignment	not modelled	100.0	43	PDB header: oxidoreductase Chain: B: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
23	c5grhA_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase [nad] subunit alpha, PDBTitle: crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)
24	c3blxL_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: L: PDB Molecule: isocitrate dehydrogenase [nad] subunit 2; PDBTitle: yeast isocitrate dehydrogenase (apo form)
25	c5grhB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase [nad] subunit gamma, PDBTitle: crystal structure of the alpha gamma heterodimer of human idh3 in2 complex with mg(2+)
26	c5hn6A_	Alignment	not modelled	100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of beta-decarboxylating dehydrogenase (tk0280) from2 thermococcus kodakarensis complexed with mn and 3-isopropylmalate
27	c3blxM_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: M: PDB Molecule: isocitrate dehydrogenase [nad] subunit 1; PDBTitle: yeast isocitrate dehydrogenase (apo form)
						PDB header: oxidoreductase

28	c1zorB	Alignment	not modelled	100.0	18	Chain: B: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile thermotoga maritima
29	c1tyoA	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase; PDBTitle: isocitrate dehydrogenase from the hyperthermophile aeropyrum pernix in2 complex with etheno-nadp
30	c2qfyE	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
31	c2uxqB	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase native; PDBTitle: isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
32	d1lwda	Alignment	not modelled	100.0	18	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
33	d1t0la	Alignment	not modelled	100.0	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
34	c3us8A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of an isocitrate dehydrogenase from sinorhizobium2 meliloti 1021
35	c2iv0A	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase; PDBTitle: thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
36	c4aoyD	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: open ctidh. the complex structures of isocitrate dehydrogenase from2 clostridium thermocellum and desulfotalea psychrophila, support a new3 active site locking mechanism
37	d1r8ka	Alignment	not modelled	97.6	27	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
38	c2b0tA	Alignment	not modelled	97.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp isocitrate dehydrogenase; PDBTitle: structure of monomeric nadp isocitrate dehydrogenase
39	c4jqpA	Alignment	not modelled	97.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: x-ray crystal structure of a 4-hydroxythreonine-4-phosphate2 dehydrogenase from burkholderia phymatum
40	c6g3uA	Alignment	not modelled	96.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase; PDBTitle: structure of pseudomonas aeruginosa isocitrate dehydrogenase, idh
41	d1itwa	Alignment	not modelled	96.8	20	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Monomeric isocitrate dehydrogenase
42	c2hi1A	Alignment	not modelled	96.7	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
43	c4atyA	Alignment	not modelled	96.6	42	PDB header: oxidoreductase Chain: A: PDB Molecule: terephthalate 1,2-cis-dihydrodiol dehydrogenase; PDBTitle: crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400
44	d1ptma	Alignment	not modelled	96.4	18	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
45	c1yxoB	Alignment	not modelled	96.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 1; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
46	c3tsnD	Alignment	not modelled	96.1	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: 4-hydroxythreonine-4-phosphate dehydrogenase from campylobacter jejuni
47	c3s40C	Alignment	not modelled	60.6	9	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
48	c6d6yA	Alignment	not modelled	56.0	15	PDB header: transferase Chain: A: PDB Molecule: apra methyltransferase 2; PDBTitle: apra methyltransferase 2 - gnat didomain in complex with sah
49	c3cfxA	Alignment	not modelled	53.0	18	PDB header: transport protein Chain: A: PDB Molecule: upf0100 protein ma_0280; PDBTitle: crystal structure of m. acetivorans periplasmic binding protein2 moda/wtpa with bound tungstate
50	d3thia	Alignment	not modelled	52.5	22	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	c3k6wA	Alignment	not modelled	47.2	18	PDB header: transport protein Chain: A: PDB Molecule: solute-binding protein ma_0280; PDBTitle: apo and ligand bound structures of moda from the archaeon2 methanosarcina acetivorans
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

52	d2fpoa1	Alignment	not modelled	44.6	11	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
53	d2onsa1	Alignment	not modelled	44.6	21	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
54	c1orhA	Alignment	not modelled	42.1	5	PDB header: transferase Chain: A; PDB Molecule: protein arginine n-methyltransferase 1; PDBTitle: structure of the predominant protein arginine methyltransferase prmt1
55	c4c0xA	Alignment	not modelled	41.9	32	PDB header: oxidoreductase Chain: A; PDB Molecule: frm-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
56	c5f4bB	Alignment	not modelled	41.9	18	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
57	c5odhH	Alignment	not modelled	39.6	22	PDB header: oxidoreductase Chain: H; PDB Molecule: heterodisulfide reductase, subunit b; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
58	c4kysA	Alignment	not modelled	39.1	18	PDB header: transferase Chain: A; PDB Molecule: thiamine pyridinylase i; PDBTitle: clostridium botulinum thiaminase i in complex with thiamin
59	d1oria	Alignment	not modelled	36.2	5	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
60	c2fyuE	Alignment	not modelled	35.0	26	PDB header: oxidoreductase Chain: E; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
61	c1p84E	Alignment	not modelled	34.8	32	PDB header: oxidoreductase Chain: E; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
62	c5xtuA	Alignment	not modelled	34.0	15	PDB header: hydrolase Chain: A; PDB Molecule: gdsl-family esterase; PDBTitle: crystal structure of gdsl esterase of photobacterium sp. j15
63	c6ccaA	Alignment	not modelled	32.6	18	PDB header: transferase Chain: A; PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
64	d2fiqa1	Alignment	not modelled	32.5	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
65	d1riea	Alignment	not modelled	32.1	26	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
66	c4p7cB	Alignment	not modelled	31.5	13	PDB header: transferase Chain: B; PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
67	c3cfzA	Alignment	not modelled	31.0	16	PDB header: transport protein Chain: A; PDB Molecule: upf0100 protein mj1186; PDBTitle: crystal structure of m. jannaschii periplasmic binding2 protein moda/wtpa with bound tungstate
68	c5mkbF	Alignment	not modelled	30.4	25	PDB header: sugar binding protein Chain: F; PDB Molecule: male1; PDBTitle: maltodextrin binding protein male1 from l. casei b123 without ligand
69	c4ptzC	Alignment	not modelled	30.0	13	PDB header: oxidoreductase Chain: C; PDB Molecule: frm reductase ssue; PDBTitle: crystal structure of the escherichia coli alkanesulfonate frm2 reductase ssue in frm-bound form
70	c4yccC	Alignment	not modelled	29.6	18	PDB header: hydrolase Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
71	c5ygeA	Alignment	not modelled	29.2	18	PDB header: transferase Chain: A; PDB Molecule: amino-acid acetyltransferase; PDBTitle: arga complexed with acecoa and glutamate
72	c1twyG	Alignment	not modelled	26.2	18	PDB header: structural genomics, unknown function Chain: G; PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of an abc-type phosphate transport receptor from2 vibrio cholerae
73	d1twya	Alignment	not modelled	26.2	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
74	d1ydga	Alignment	not modelled	26.2	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
75	c6fuvA	Alignment	not modelled	25.9	20	PDB header: transport protein Chain: A; PDB Molecule: solute binding protein, blmbp1 in complex with PDBTitle: structure of a manno-oligosaccharide specific solute binding protein,2 blmbp2 from bifidobacterium animalis subsp. lactis atcc 27673 in3 complex with mannose
76	c5f7vA	Alignment	not modelled	25.6	21	PDB header: cycloaltermann binding protein Chain: A; PDB Molecule: lmo0181 protein; PDBTitle: abc substrate-binding protein lmo0181 from listeria monocytogenes in2 complex with cycloaltermann Fold: S-adenosyl-L-methionine-dependent methyltransferases

77	d2esra1	Alignment	not modelled	25.2	16	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
78	c2k4mA	Alignment	not modelled	24.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0146 protein mth_1000; PDBTitle: solution nmr structure of m. thermoautotrophicum protein mth_1000,2 northeast structural genomics consortium target tr8
79	c4r81C	Alignment	not modelled	24.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
80	c4gd5B	Alignment	not modelled	23.9	9	PDB header: transport protein Chain: B: PDB Molecule: phosphate abc transporter, phosphate-binding protein; PDBTitle: x-ray crystal structure of a putative phosphate abc transporter2 substrate-binding protein with bound phosphate from clostridium3 perfringens
81	c5lkjA	Alignment	not modelled	23.9	15	PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of mouse carm1 in complex with ligand sa684
82	c2pebB	Alignment	not modelled	23.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dioxygenase; PDBTitle: crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
83	d3cx5e1	Alignment	not modelled	23.1	32	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
84	c3pvsA	Alignment	not modelled	23.0	25	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
85	c3lcmB	Alignment	not modelled	21.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
86	c6fjlD	Alignment	not modelled	21.8	13	PDB header: metal binding protein Chain: D: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of ibps from dickeya dadantii
87	d2r9ga1	Alignment	not modelled	21.6	31	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
88	d1j08a1	Alignment	not modelled	20.4	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
89	d2fyta1	Alignment	not modelled	20.1	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
90	c4r6hA	Alignment	not modelled	19.6	14	PDB header: transport protein Chain: A: PDB Molecule: solute binding protein msme; PDBTitle: crystal structure of putative binding protein msme from bacillus2 subtilis subsp. subtilis str. 168, target efi-510764, an open3 conformation
91	d1qapa1	Alignment	not modelled	19.4	26	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
92	c6dk9I	Alignment	not modelled	18.8	23	PDB header: lyase Chain: I: PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
93	d3bgea1	Alignment	not modelled	18.4	22	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
94	c5ftwA	Alignment	not modelled	18.0	46	PDB header: transferase Chain: A: PDB Molecule: chemotaxis protein methyltransferase; PDBTitle: crystal structure of glutamate o-methyltransferase in2 complex with s- adenosyl-l-homocysteine (sah) from3 bacillus subtilis
95	c5thyB	Alignment	not modelled	17.9	19	PDB header: transferase,lyase Chain: B: PDB Molecule: curj; PDBTitle: crystal structure of semet-substituted curj carbon methyltransferase
96	c3b3jA	Alignment	not modelled	17.7	15	PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
97	c2qhxB	Alignment	not modelled	17.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pteridine reductase 1; PDBTitle: structure of pteridine reductase from leishmania major2 complexed with a ligand
98	c4hwcC	Alignment	not modelled	17.2	20	PDB header: transferase Chain: C: PDB Molecule: thiaminase-i; PDBTitle: structure of a eukaryotic thiaminase-i
99	d1g6q1	Alignment	not modelled	17.1	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase