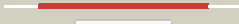



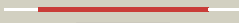


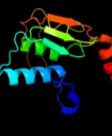
















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0828c_(-)_921194_921616
Date	Fri Jul 26 01:50:41 BST 2019
Unique Job ID	61d0a6c0016bfa34

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2g84a1</a>	 Alignment		100.0	27	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
2	<a href="#">d1wkqa_</a>	 Alignment		100.0	29	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
3	<a href="#">c2nx8A_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific adenosine deaminase; <b>PDBTitle:</b> the crystal structure of the trna-specific adenosine deaminase from2 streptococcus pyogenes
4	<a href="#">c3ocqA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytosine/adenosine deaminase; <b>PDBTitle:</b> crystal structure of trna-specific adenosine deaminase from salmonella2 enterica
5	<a href="#">d1z3aa1</a>	 Alignment		99.9	23	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
6	<a href="#">d1wwra1</a>	 Alignment		99.9	26	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
7	<a href="#">d2b3ja1</a>	 Alignment		99.9	24	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
8	<a href="#">c3dh1D_</a>	 Alignment		99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> trna-specific adenosine deaminase 2; <b>PDBTitle:</b> crystal structure of human trna-specific adenosine-34 deaminase2 subunit adat2
9	<a href="#">c5xkrA_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cmp/dcmp deaminase, zinc-binding protein; <b>PDBTitle:</b> crystal structure of msmeg3575 in complex with benzoguanamine
10	<a href="#">c5jfyC_</a>	 Alignment		99.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidine deaminase; <b>PDBTitle:</b> crystal structure of a plant cytidine deaminase
11	<a href="#">d2a8na1</a>	 Alignment		99.9	30	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like

12	<a href="#">d1p6oa_</a>	Alignment		99.9	18	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
13	<a href="#">d2b3za2</a>	Alignment		99.9	19	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
14	<a href="#">c2o7pA_</a>	Alignment		99.9	23	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
15	<a href="#">c2d5nB_</a>	Alignment		99.8	18	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
16	<a href="#">c4p9eA_</a>	Alignment		99.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from the cyanophage s-tim5 in apo2 form
17	<a href="#">c2w4lC_</a>	Alignment		99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> human dcmp deaminase
18	<a href="#">c3zpgA_</a>	Alignment		99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribd; <b>PDBTitle:</b> acinetobacter baumannii ribd, form 2
19	<a href="#">c2hxvA_</a>	Alignment		99.8	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- <b>PDBTitle:</b> crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
20	<a href="#">d1vq2a_</a>	Alignment		99.8	19	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
21	<a href="#">c2hvwC_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> deoxycytidylate deaminase; <b>PDBTitle:</b> crystal structure of dcmp deaminase from streptococcus mutans
22	<a href="#">d2hxva2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
23	<a href="#">c5k83C_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> apolipoprotein b mrna editing enzyme, catalytic peptide- <b>PDBTitle:</b> crystal structure of a primate apobec3g n-domain, in complex with2 ssdna
24	<a href="#">c3g8qA_</a>	Alignment	not modelled	96.3	31	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> predicted rna-binding protein, contains thump <b>PDBTitle:</b> a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
25	<a href="#">c3vowB_</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable dna dc->du-editing enzyme apobec-3c; <b>PDBTitle:</b> crystal structure of the human apobec3c having hiv-1 vif-binding2 interface
26	<a href="#">c5tkmA_</a>	Alignment	not modelled	95.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna dc->du-editing enzyme apobec-3b; <b>PDBTitle:</b> crystal structure of human apobec3b n-terminal domain
27	<a href="#">c2nytB_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable c->u-editing enzyme apobec-2; <b>PDBTitle:</b> the apobec2 crystal structure and functional implications2 for aid
						<b>Fold:</b> Cytidine deaminase-like

28	<a href="#">d2fr5a1</a>	Alignment	not modelled	94.7	23	<b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
29	<a href="#">d1mq0a_</a>	Alignment	not modelled	94.6	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
30	<a href="#">d1r5ta_</a>	Alignment	not modelled	94.1	10	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
31	<a href="#">c6b0bE_</a>	Alignment	not modelled	94.0	24	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> apobec3h; <b>PDBTitle:</b> crystal structure of human apobec3h
32	<a href="#">c2kboA_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna dc->du-editing enzyme apobec-3g; <b>PDBTitle:</b> structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
33	<a href="#">d2d30a1</a>	Alignment	not modelled	93.0	21	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
34	<a href="#">c3jifX_</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase from mycobacterium2 tuberculosis
35	<a href="#">d1uwza_</a>	Alignment	not modelled	92.3	21	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
36	<a href="#">d1alna1</a>	Alignment	not modelled	92.0	29	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
37	<a href="#">c3r2nC_</a>	Alignment	not modelled	91.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase from mycobacterium leprae
38	<a href="#">c6bwyA_</a>	Alignment	not modelled	91.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protection of telomeres protein 1, dna dc->du-editing <b>PDBTitle:</b> dna substrate selection by apobec3g
39	<a href="#">c2m65A_</a>	Alignment	not modelled	90.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dna dc->du-editing enzyme apobec-3a; <b>PDBTitle:</b> nmr structure of human restriction factor apobec3a
40	<a href="#">c2mzZA_</a>	Alignment	not modelled	90.3	19	<b>PDB header:</b> hydrolase, antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein b mrna-editing enzyme, catalytic <b>PDBTitle:</b> nmr structure of apobec3g ntd variant, sntd
41	<a href="#">c3dmoD_</a>	Alignment	not modelled	89.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 1.6 a crystal structure of cytidine deaminase from burkholderia2 pseudomallei
42	<a href="#">c3oj6C_</a>	Alignment	not modelled	88.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> blasticidin-s deaminase; <b>PDBTitle:</b> crystal structure of blasticidin s deaminase from coccidioides immitis
43	<a href="#">c3b8fB_</a>	Alignment	not modelled	88.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative blasticidin s deaminase; <b>PDBTitle:</b> crystal structure of the cytidine deaminase from bacillus anthracis
44	<a href="#">c1alnA_</a>	Alignment	not modelled	84.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> crystal structure of cytidine deaminase complexed with 3-deazacytidine
45	<a href="#">d2z3ga1</a>	Alignment	not modelled	81.4	19	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
46	<a href="#">c4eg2G_</a>	Alignment	not modelled	81.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> cytidine deaminase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of cytidine deaminase from vibrio2 cholerae in complex with zinc and uridine
47	<a href="#">d1alna2</a>	Alignment	not modelled	80.6	10	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Cytidine deaminase
48	<a href="#">c1zy7A_</a>	Alignment	not modelled	73.5	44	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rna-specific adenosine deaminase b1, isoform <b>PDBTitle:</b> crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
49	<a href="#">d2hi7b1</a>	Alignment	not modelled	49.1	43	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> DsbB-like <b>Family:</b> DsbB-like
50	<a href="#">c3e9jC_</a>	Alignment	not modelled	49.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thiol/disulfide oxidoreductase dsbb; <b>PDBTitle:</b> structure of the charge-transfer intermediate of the2 transmembrane redox catalyst dsbb
51	<a href="#">c2k74A_</a>	Alignment	not modelled	43.8	29	<b>PDB header:</b> membrane protein, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> disulfide bond formation protein b; <b>PDBTitle:</b> solution nmr structure of dsbb-ubiquinone complex
52	<a href="#">c3nznA_</a>	Alignment	not modelled	25.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
53	<a href="#">d2hqya1</a>	Alignment	not modelled	24.6	19	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> FemXAB nonribosomal peptidyltransferases
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphatase (duf442);

54	<a href="#">c3gxgA</a>	Alignment	not modelled	19.8	15	<b>PDBTitle:</b> crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
55	<a href="#">c3d5jB</a>	Alignment	not modelled	19.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-2, mitochondrial; <b>PDBTitle:</b> structure of yeast grx2-c30s mutant with glutathionyl mixed disulfide
56	<a href="#">c5y4uA</a>	Alignment	not modelled	19.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-3; <b>PDBTitle:</b> crystal structure of grx domain of grx3 from saccharomyces cerevisiae
57	<a href="#">c2muqA</a>	Alignment	not modelled	14.7	50	<b>PDB header:</b> ubiquitin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia-associated protein of 20 kda; <b>PDBTitle:</b> solution structure of the human faap20 ubz
58	<a href="#">c2murA</a>	Alignment	not modelled	14.1	50	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fanconi anemia-associated protein of 20 kda; <b>PDBTitle:</b> solution structure of the human faap20 ubz-ubiquitin complex
59	<a href="#">c3ld0Q</a>	Alignment	not modelled	14.1	63	<b>PDB header:</b> gene regulation <b>Chain:</b> Q: <b>PDB Molecule:</b> inhibitor of trap, regulated by t-box (trp) sequence rtpa; <b>PDBTitle:</b> crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
60	<a href="#">c5cx2B</a>	Alignment	not modelled	13.7	43	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> coronin; <b>PDBTitle:</b> structure of coiled coil domain of leishmania donovani coronin
61	<a href="#">c5cx2C</a>	Alignment	not modelled	13.3	43	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> coronin; <b>PDBTitle:</b> structure of coiled coil domain of leishmania donovani coronin
62	<a href="#">c4tr1A</a>	Alignment	not modelled	12.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin 3; <b>PDBTitle:</b> crystal structure of gsh-bound cgrx2/c15s
63	<a href="#">c3ipzA</a>	Alignment	not modelled	12.7	10	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monothiol glutaredoxin-s14, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
64	<a href="#">c4e17B</a>	Alignment	not modelled	11.7	46	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> catenin alpha-1; <b>PDBTitle:</b> alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
65	<a href="#">d1tza</a>	Alignment	not modelled	11.5	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
66	<a href="#">d1vdda</a>	Alignment	not modelled	11.0	20	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
67	<a href="#">c1vddC</a>	Alignment	not modelled	9.8	20	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
68	<a href="#">c5xftA</a>	Alignment	not modelled	9.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydroascorbate reductase; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii dehydroascorbate2 reductase
69	<a href="#">c5yt6B</a>	Alignment	not modelled	9.3	80	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tax1-binding protein 1; <b>PDBTitle:</b> crystal structure of tax1bp1 ubz2 in complex with mono-ubiquitin
70	<a href="#">d1egoa</a>	Alignment	not modelled	9.1	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
71	<a href="#">c5aj3p</a>	Alignment	not modelled	8.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> mitoribosomal protein bs16m, mrps16; <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
72	<a href="#">d2drpa2</a>	Alignment	not modelled	8.3	80	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
73	<a href="#">c3ve5D</a>	Alignment	not modelled	8.0	27	<b>PDB header:</b> recombination <b>Chain:</b> D: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> structure of recombination mediator protein recr16-196 deletion mutant
74	<a href="#">c5y7iB</a>	Alignment	not modelled	8.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride intracellular channel protein 2; <b>PDBTitle:</b> structure of tilapia fish clic2
75	<a href="#">c3h8qB</a>	Alignment	not modelled	7.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 3; <b>PDBTitle:</b> crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
76	<a href="#">c3lq9B</a>	Alignment	not modelled	7.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-damage-inducible transcript 4 protein; <b>PDBTitle:</b> crystal structure of human redd1, a hypoxia-induced regulator of mtor
77	<a href="#">c2khpA</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> solution structure of glutaredoxin from brucella melitensis
78	<a href="#">c6gv7A</a>	Alignment	not modelled	7.0	43	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> metallothionein; <b>PDBTitle:</b> cadmium(ii) form of a44h mutant of shortened metallothionein from2 pseudomonas fluorescens q2-87 (residues 1-52)
79	<a href="#">c5z2vB</a>	Alignment	not modelled	7.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recr from pseudomonas aeruginosa

					pao1
80	<a href="#">c2kixA_</a>	Alignment	not modelled	7.0	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> solution structure of glutaredoxin from bartonella henselae str.2 houston
81	<a href="#">d1nuia2</a>	Alignment	not modelled	7.0	27 <b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> DNA primase zinc finger
82	<a href="#">c2i7uA_</a>	Alignment	not modelled	6.9	14 <b>PDB header:</b> de novo protein/ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> four-alpha-helix bundle; <b>PDBTitle:</b> structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
83	<a href="#">c2bx9J_</a>	Alignment	not modelled	6.5	71 <b>PDB header:</b> transcription regulation <b>Chain:</b> J: <b>PDB Molecule:</b> tryptophan rna-binding attenuator protein-inhibitory <b>PDBTitle:</b> crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
84	<a href="#">c3zywB_</a>	Alignment	not modelled	6.1	11 <b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutaredoxin-3; <b>PDBTitle:</b> crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)
85	<a href="#">c2c4rL_</a>	Alignment	not modelled	5.7	56 <b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ribonuclease e; <b>PDBTitle:</b> catalytic domain of e. coli rnase e
86	<a href="#">d1h75a_</a>	Alignment	not modelled	5.6	18 <b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase