Phyre^2

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Description	RVBD1899c_(lppD)_2145221_2146252
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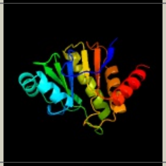
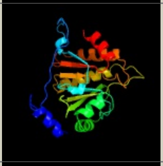
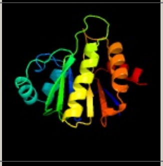
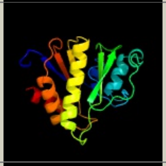
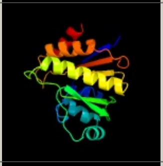
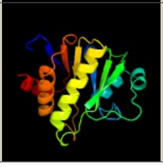
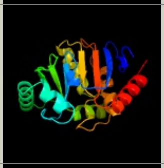
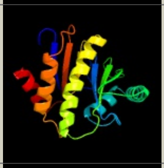
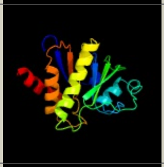
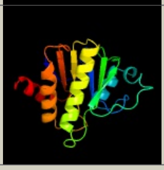
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fszA_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrodomain; **PDBTitle:** crystal structure of trypanosoma cruzi macrodomain
2	c5iitC_	Alignment		100.0	26	**PDB header:**inositol phosphate binding protein **Chain:** C: **PDB Molecule:**vacuolar transporter chaperone 4,core histone macro-h2a.1; **PDBTitle:** structure of spx domain of the yeast inorganic polyphophate polymerase2 vtc4 crystallized by carrier-driven crystallization in fusion with3 the macro domain of human histone macroh2a1.1
3	c5fsuA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrodomain; **PDBTitle:** crystal structure of trypanosoma brucei macrodomain2 (crystal form 1)
4	c4iqyB_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-acetyl-adp-ribose deacetylase macrod2; **PDBTitle:** crystal structure of the human protein-proximal adp-ribosyl-hydrolase2 macrod2
5	c5kivA_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-adp-ribose hydrolase; **PDBTitle:** crystal structure of saumacro (sav0325)
6	c2x47A_	Alignment		100.0	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**macro domain-containing protein 1; **PDBTitle:** crystal structure of human macrod1
7	d1zr5a1	Alignment		100.0	22	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
8	c3vfqA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8, bal2) - macro domains 1 and 2 in complex with2 adenosine-5-diphosphoribose
9	c4umlA_	Alignment		100.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ganglioside-induced differentiation-associated protein 2; **PDBTitle:** crystal structure of ganglioside induced differentiation2 associated protein 2 (gdap2) macro domain
10	c1zr5B_	Alignment		100.0	22	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
11	c2xd7B_	Alignment		100.0	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**core histone macro-h2a.2; **PDBTitle:** crystal structure of the macro domain of human core histone h2a

12	d1yd9a1	Alignment		100.0	24	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
13	c4ablA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8, bal2) - macro domain 3
14	c3q71A_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
15	c3kh6A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 15; **PDBTitle:** human poly(adp-ribose) polymerase 15, macro domain 2 in complex with2 adenosine-5-diphosphoribose
16	c3q6zA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
17	d1vhua_	Alignment		100.0	32	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
18	c5ailA_	Alignment		100.0	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 9; **PDBTitle:** human parp9 2nd macrodomain
19	c5l9kB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**macrod-type macrodomain; **PDBTitle:** oceanobacillus iheyensis macrodomain with adpr
20	d1spva_	Alignment		100.0	33	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
21	d2acfa1	Alignment	not modelled	100.0	26	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
22	c5dusA_	Alignment	not modelled	100.0	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**orf1a; **PDBTitle:** crystal structure of mers-cov macro domain in complex with adp-ribose
23	c2vriA_	Alignment	not modelled	100.0	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structure of the nsp3 x-domain of human coronavirus nl63
24	c3ejfA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of ibv x-domain at ph 8.5
25	c2dx6B_	Alignment	not modelled	100.0	39	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0132; **PDBTitle:** crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8
26	c3ew5B_	Alignment	not modelled	100.0	25	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**macro domain of non-structural protein 3; **PDBTitle:** structure of the tetragonal crystal form of x (adrp) domain2 from fcov
27	c3ejgA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of hcov-229e x-domain
28	c3gqeA_	Alignment	not modelled	100.0	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of venezuelan equine encephalitis2 virus
						PDB header:viral protein

29	c5iq5A_	Alignment	not modelled	100.0	22	**Chain:** A: **PDB Molecule:**macro domain; **PDBTitle:** nmr solution structure of mayaro virus macro domain
30	c3ewqA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** hcov-229e nsp3 adrp domain
31	c3gpqA_	Alignment	not modelled	100.0	19	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of chikungunya virus in complex with2 rna
32	c5m3iB_	Alignment	not modelled	100.0	19	**PDB header:**antitoxin **Chain:** B: **PDB Molecule:**rnase iii inhibitor; **PDBTitle:** macrodomain of mycobacterium tuberculosis darg
33	c5m31A_	Alignment	not modelled	100.0	22	**PDB header:**antitoxin **Chain:** A: **PDB Molecule:**appr-1-p processing domain protein; **PDBTitle:** macrodomain of thermus aquaticus darg
34	c4guaB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** alphavirus p23pro-zbd
35	c2eeeA_	Alignment	not modelled	99.9	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**uncharacterized protein c6orf130; **PDBTitle:** solution structure of the a1pp domain from human protein2 c6orf130
36	c5lw0A_	Alignment	not modelled	99.9	29	**PDB header:**adp-ribose-binding protein **Chain:** A: **PDB Molecule:**basic helix-loop-helix, putative, expressed; **PDBTitle:** oryza sativa apl macrodomain in complex with adp-ribose
37	d1njra_	Alignment	not modelled	99.9	19	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
38	c5e3bA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrodomain protein; **PDBTitle:** structure of macrodomain protein from streptomyces coelicolor
39	d2fg1a1	Alignment	not modelled	99.9	13	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
40	c5zdcL_	Alignment	not modelled	98.7	23	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**poly adp-ribose glycohydrolase; **PDBTitle:** crystal structure of poly(adp-ribose) glycohydrolase (parg) from2 deinococcus radiodurans in complex with adp-ribose (p32)
41	c3siiA_	Alignment	not modelled	98.5	32	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
42	c5lw6A_	Alignment	not modelled	98.4	8	**PDB header:**adp-ribose binding protein **Chain:** A: **PDB Molecule:**ddb_g0293866; **PDBTitle:** crystal structure of a se-met substituted dictyostelium discoideum2 adp-ribose binding macrodomain (residues 342-563) of ddb_g0293866
43	d1gyta1	Alignment	not modelled	97.6	13	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
44	c6omeA_	Alignment	not modelled	92.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from chlamydia trachomatis d/uw-3/cx
45	c1gytG_	Alignment	not modelled	91.4	13	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
46	c3jruB_	Alignment	not modelled	85.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
47	c3kzwD_	Alignment	not modelled	66.4	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
48	c3h8gC_	Alignment	not modelled	61.4	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
49	c5gukA_	Alignment	not modelled	49.1	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cyclolavandulyl diphosphate synthase; **PDBTitle:** crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
50	c2vg2C_	Alignment	not modelled	47.9	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
51	c5hc7A_	Alignment	not modelled	45.8	20	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**prenyltransference for protein; **PDBTitle:** crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenyldiphosphate
52	c4h8eA_	Alignment	not modelled	37.7	19	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
53	c5wggA_	Alignment	not modelled	30.9	11	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**radical sam domain protein; **PDBTitle:** structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
54	c4g56C_	Alignment	not modelled	30.0	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**hsl7 protein; **PDBTitle:** crystal structure of full length prmt5/mep50 complexes

						from xenopus2 laevis
55	c2k19A_	Alignment	not modelled	28.9	45	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
56	c3ua4A_	Alignment	not modelled	26.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 5; **PDBTitle:** crystal structure of protein arginine methyltransferase prmt5
57	c4dqvA_	Alignment	not modelled	26.5	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**probable peptide synthetase nrp (peptide synthase); **PDBTitle:** crystal structure of reductase (r) domain of non-ribosomal peptide2 synthetase from mycobacterium tuberculosis
58	c5v1tA_	Alignment	not modelled	23.5	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam; **PDBTitle:** crystal structure of streptococcus suis suib bound to precursor2 peptide suia
59	c5th5C_	Alignment	not modelled	21.0	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**7-carboxy-7-deazaguanine synthase; **PDBTitle:** crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
60	c2h8bB_	Alignment	not modelled	19.6	47	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**insulin-like 3; **PDBTitle:** solution structure of insl3
61	d1mlda1	Alignment	not modelled	19.1	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
62	c4q9mA_	Alignment	not modelled	18.5	14	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**isoprenyl transferase; **PDBTitle:** crystal structure of upps in complex with fpp and an allosteric2 inhibitor
63	c5n4kA_	Alignment	not modelled	17.8	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** n-terminal domain of a human coronavirus nl63 nucleocapsid protein
64	d1gnfa_	Alignment	not modelled	15.9	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
65	c3ugsB_	Alignment	not modelled	15.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
66	c4pg8B_	Alignment	not modelled	15.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of s. aureus homoserine dehydrogenase at ph8.5
67	c5msuC_	Alignment	not modelled	14.9	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carboxylic acid reductase; **PDBTitle:** structure of the r domain of carboxylic acid reductase (car) from2 mycobacterium marinum in complex with nadp, p21 form
68	d2vuti1	Alignment	not modelled	14.5	31	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
69	c6bxwA_	Alignment	not modelled	13.3	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitochondrial association factor 1; **PDBTitle:** crystal structure of toxoplasma gondii mitochondrial association2 factor 1 b (maf1b) in complex with adpribose
70	c2kaeA_	Alignment	not modelled	12.9	31	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**gata-type transcription factor; **PDBTitle:** data-driven model of med1:dna complex
71	c3a46B_	Alignment	not modelled	12.9	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of mvnei1/thf complex
72	c5b37A_	Alignment	not modelled	12.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophan dehydrogenase; **PDBTitle:** crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
73	d1hyea1	Alignment	not modelled	11.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
74	d1v5ma_	Alignment	not modelled	11.7	25	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
75	d2amxa1	Alignment	not modelled	11.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
76	d1sska_	Alignment	not modelled	11.4	56	**Fold:**Coronavirus RNA-binding domain **Superfamily:**Coronavirus RNA-binding domain **Family:**Coronavirus RNA-binding domain
77	c3g5rA_	Alignment	not modelled	11.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
78	c4c4aA_	Alignment	not modelled	10.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 7; **PDBTitle:** crystal structure of mouse protein arginine methyltransferase 7 in2 complex with sah
79	c5xk9F_	Alignment	not modelled	10.1	9	**PDB header:**transferase **Chain:** F: **PDB Molecule:**undecaprenyl diphosphate synthase; **PDBTitle:** crystal structure of isosesquilavandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gspp and dmapp
						PDB header:lyase

80	c4zr8B_	Alignment	not modelled	10.1	21	**Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
81	d1y0ja1	Alignment	not modelled	9.9	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
82	c2lo9A_	Alignment	not modelled	9.9	75	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mu-conotoxin buiiib; **PDBTitle:** nmr solution structure of mu-contoxin buiiib
83	c2mxfA_	Alignment	not modelled	9.9	45	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**mvat; **PDBTitle:** structure of the dna complex of the c-terminal domain of mvat
84	c5cw9A_	Alignment	not modelled	9.8	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed ferredoxin-ferredoxin domain insertion **PDBTitle:** crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
85	c1jpkA_	Alignment	not modelled	9.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
86	c5vslB_	Alignment	not modelled	9.5	11	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**radical s-adenosyl methionine domain-containing protein 2; **PDBTitle:** crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
87	c2locA_	Alignment	not modelled	9.4	75	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mu-conotoxin buiiib; **PDBTitle:** conotoxin analogue [d-ala2]buiiib
88	c6efnA_	Alignment	not modelled	9.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sporulation killing factor maturation protein skfb; **PDBTitle:** structure of a ripp maturase, skfb
89	c5imuA_	Alignment	not modelled	9.2	78	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tat (twin-arginine translocation) pathway signal sequence **PDBTitle:** a fragment of conserved hypothetical protein rv3899c (residues 184-2 410) from mycobacterium tuberculosis
90	d1r8ka_	Alignment	not modelled	9.1	12	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
91	c6nd1A_	Alignment	not modelled	9.1	50	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocation protein sec63; **PDBTitle:** cryoem structure of the sec complex from yeast
92	d1c0pa1	Alignment	not modelled	8.9	35	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
93	c4ndlC_	Alignment	not modelled	8.8	53	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**enh-c2b, computational designed homodimer; **PDBTitle:** computational design and experimental verification of a symmetric2 homodimer
94	c3hd4A_	Alignment	not modelled	8.8	53	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleoprotein; **PDBTitle:** mhv nucleocapsid protein ntd
95	c2vfwB_	Alignment	not modelled	8.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
96	c3ckvA_	Alignment	not modelled	8.5	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
97	d2cmda1	Alignment	not modelled	8.1	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
98	c3ingA_	Alignment	not modelled	8.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
99	c6pdmA_	Alignment	not modelled	7.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 9; **PDBTitle:** crystal structure of human protein arginine methyltransferase 92 (prmt9)