
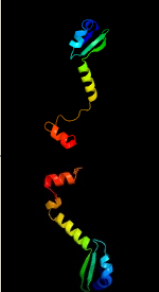

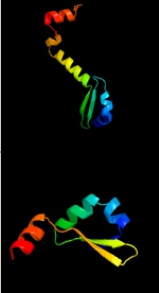
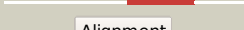
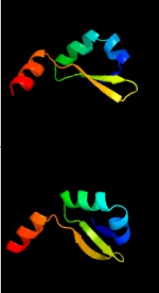

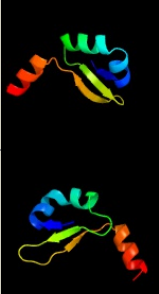

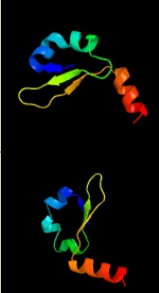

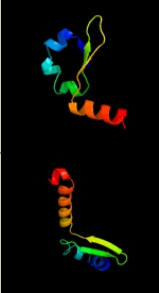



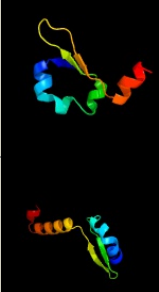

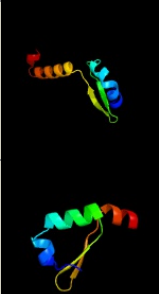






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0268c_(-)_322764_323273
Date	Tue Jul 23 14:50:33 BST 2019
Unique Job ID	9daf0e4ff7338876

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3g5oA_</a>	 Alignment		99.6	31	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv2865; <b>PDBTitle:</b> the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
2	<a href="#">c3oeiB_</a>	 Alignment		99.4	26	<b>PDB header:</b> toxin, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> relj (antitoxin rv3357); <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
3	<a href="#">c2odkD_</a>	 Alignment		99.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative prevent-host-death protein from nitrosomonas europaea
4	<a href="#">d2odka1</a>	 Alignment		99.3	17	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
5	<a href="#">d2a6qb1</a>	 Alignment		99.2	29	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
6	<a href="#">c3hs2H_</a>	 Alignment		99.2	24	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
7	<a href="#">d2a6qa1</a>	 Alignment		99.2	28	<b>Fold:</b> YefM-like <b>Superfamily:</b> YefM-like <b>Family:</b> YefM-like
8	<a href="#">c3hryA_</a>	 Alignment		99.1	23	<b>PDB header:</b> antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> prevent host death protein; <b>PDBTitle:</b> crystal structure of phd in a trigonal space group and partially2 disordered
9	<a href="#">c3d55A_</a>	 Alignment		98.9	26	<b>PDB header:</b> toxin inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv3357/mt3465; <b>PDBTitle:</b> crystal structure of m. tuberculosis yefm antitoxin
10	<a href="#">c3k6qB_</a>	 Alignment		91.0	16	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative ligand binding protein; <b>PDBTitle:</b> crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	<a href="#">c1lvaA_</a>	 Alignment		63.0	14	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of a c-terminal fragment of moorella2 thermoacetica elongation factor selb

12	<a href="#">c4g6vE_</a>	Alignment		54.2	13	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> adhesin/hemolysin; <b>PDBTitle:</b> cdia-ct/cdii toxin and immunity complex from burkholderia pseudomallei
13	<a href="#">c6nkoA_</a>	Alignment		43.1	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> forh; <b>PDBTitle:</b> crystal structure of forh
14	<a href="#">d1g8ma1</a>	Alignment		41.9	13	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
15	<a href="#">d1pkx1</a>	Alignment		40.6	13	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
16	<a href="#">c2v9vA_</a>	Alignment		37.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of moorella thermoacetica selb(377-511)
17	<a href="#">c3kzqE_</a>	Alignment		35.8	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein vp2116; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
18	<a href="#">d2hfda1</a>	Alignment		29.3	13	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> HyaE-like
19	<a href="#">c3lciA_</a>	Alignment		28.9	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminase lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
20	<a href="#">d1m9dc_</a>	Alignment		28.7	17	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
21	<a href="#">c4iapB_</a>	Alignment	not modelled	27.2	21	<b>PDB header:</b> lipid binding protein/ hydorrase <b>Chain:</b> B: <b>PDB Molecule:</b> oxysterol-binding protein homolog 3, endolysin, oxysterol- <b>PDBTitle:</b> crystal structure of ph domain of osh3 from saccharomyces cerevisiae
22	<a href="#">d1hl2a_</a>	Alignment	not modelled	27.2	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
23	<a href="#">c3zbeA_</a>	Alignment	not modelled	27.2	15	<b>PDB header:</b> toxin-antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> paaa2; <b>PDBTitle:</b> e. coli o157 pare2-associated antitoxin 2 (paaa2)
24	<a href="#">c5b42A_</a>	Alignment	not modelled	27.1	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein mutl; <b>PDBTitle:</b> crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
25	<a href="#">c5c54D_</a>	Alignment	not modelled	27.0	9	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase/n-acetylneuraminase lyase; <b>PDBTitle:</b> crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
26	<a href="#">c3bpqA_</a>	Alignment	not modelled	25.5	24	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin relb3; <b>PDBTitle:</b> crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
27	<a href="#">c2w1tB_</a>	Alignment	not modelled	25.3	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> stage v sporulation protein t; <b>PDBTitle:</b> crystal structure of b. subtilis spovt
28	<a href="#">c4a1oB_</a>	Alignment	not modelled	23.0	17	<b>PDB header:</b> transferase-hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh;

28	<a href="#">c9a10B</a>	Alignment	not modelled	23.0	17	<b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
29	<a href="#">c3gabC</a>	Alignment	not modelled	22.8	41	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein mutl; <b>PDBTitle:</b> c-terminal domain of bacillus subtilis mutl crystal form i
30	<a href="#">c1thzA</a>	Alignment	not modelled	22.5	13	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
31	<a href="#">c3mk7B</a>	Alignment	not modelled	21.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit o; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
32	<a href="#">c3gnjD</a>	Alignment	not modelled	21.9	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin domain protein; <b>PDBTitle:</b> the crystal structure of a thioredoxin-related protein from2 desulfotobacterium hafniense dcb
33	<a href="#">d1zcza1</a>	Alignment	not modelled	20.8	6	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
34	<a href="#">c2o8xA</a>	Alignment	not modelled	20.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
35	<a href="#">d2pxrc1</a>	Alignment	not modelled	20.4	17	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
36	<a href="#">c4ehiB</a>	Alignment	not modelled	20.0	22	<b>PDB header:</b> hydrolase,transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional purine biosynthesis protein purh; <b>PDBTitle:</b> an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
37	<a href="#">c3msqC</a>	Alignment	not modelled	19.1	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative ubiquinone biosynthesis protein; <b>PDBTitle:</b> crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
38	<a href="#">c3cynC</a>	Alignment	not modelled	19.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable glutathione peroxidase 8; <b>PDBTitle:</b> the structure of human gpX8
39	<a href="#">c1v98A</a>	Alignment	not modelled	17.4	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> crystal structure analysis of thioredoxin from thermus thermophilus
40	<a href="#">c3bpqC</a>	Alignment	not modelled	17.0	26	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> antitoxin relB3; <b>PDBTitle:</b> crystal structure of relB-rele antitoxin-toxin complex from2 methanococcus jannaschii
41	<a href="#">c2m4hA</a>	Alignment	not modelled	16.2	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> feline calicivirus vpg protein; <b>PDBTitle:</b> solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
42	<a href="#">c2qsiB</a>	Alignment	not modelled	15.8	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative hydrogenase expression/formation protein hupg; <b>PDBTitle:</b> crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
43	<a href="#">d1o9ya</a>	Alignment	not modelled	15.8	11	<b>Fold:</b> Surface presentation of antigens (SPOA) <b>Superfamily:</b> Surface presentation of antigens (SPOA) <b>Family:</b> Surface presentation of antigens (SPOA)
44	<a href="#">c3kb4D</a>	Alignment	not modelled	15.7	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr8543 protein; <b>PDBTitle:</b> crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
45	<a href="#">c4tt9A</a>	Alignment	not modelled	15.5	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> surface presentation of antigens protein spao; <b>PDBTitle:</b> structure of the c-terminal spoa domain of shigella flexneri spa33
46	<a href="#">d1or7a1</a>	Alignment	not modelled	15.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
47	<a href="#">c3ncvB</a>	Alignment	not modelled	14.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein mutl; <b>PDBTitle:</b> ngol
48	<a href="#">d1pcfa</a>	Alignment	not modelled	14.6	25	<b>Fold:</b> ssDNA-binding transcriptional regulator domain <b>Superfamily:</b> ssDNA-binding transcriptional regulator domain <b>Family:</b> Transcriptional coactivator PC4 C-terminal domain
49	<a href="#">c4pa5A</a>	Alignment	not modelled	14.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> tgl - a bacterial spore coat transglutaminase - cystamine complex
50	<a href="#">c6ghbB</a>	Alignment	not modelled	13.9	23	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> upf0413 protein gk0824; <b>PDBTitle:</b> crystal structure of spx in complex with yjhb (oxidized)
51	<a href="#">c4aghA</a>	Alignment	not modelled	13.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mosub1, transcription cofactor; <b>PDBTitle:</b> structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae
						<b>Fold:</b> ATP-grasp

52	<a href="#">d1ta8a_</a>	Alignment	not modelled	13.7	17	<b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD <sup>+</sup> -dependent DNA ligase
53	<a href="#">c3nojA_</a>	Alignment	not modelled	13.6	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate <b>PDBTitle:</b> the structure of hmg/cha aldolase from the protocatechuete degradation2 pathway of pseudomonas putida
54	<a href="#">c3noeA_</a>	Alignment	not modelled	13.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
55	<a href="#">c4evmA_</a>	Alignment	not modelled	13.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin family protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of soluble domain of membrane-anchored2 thioredoxin family protein from streptococcus pneumoniae strain3 canada mdr_19a
56	<a href="#">c5ngwA_</a>	Alignment	not modelled	13.5	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> opgh99a; <b>PDBTitle:</b> glycoside hydrolase-like protein
57	<a href="#">c3vepA_</a>	Alignment	not modelled	12.8	28	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
58	<a href="#">c5ktiA_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
59	<a href="#">c5a4nB_</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bpsl1147; <b>PDBTitle:</b> crystal structure of bpsl1147, a pc4 homolog from burkholderia2 pseudomallei k96243 (tetragonal crystal form)
60	<a href="#">c1l6nA_</a>	Alignment	not modelled	12.6	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gag polyprotein; <b>PDBTitle:</b> structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
61	<a href="#">c1n0ff_</a>	Alignment	not modelled	12.5	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> F: <b>PDB Molecule:</b> protein mraz; <b>PDBTitle:</b> crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
62	<a href="#">d2j7pe1</a>	Alignment	not modelled	12.4	26	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
63	<a href="#">c5by3A_</a>	Alignment	not modelled	12.2	29	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> btgh115a; <b>PDBTitle:</b> a novel family gh115 4-o-methyl-alpha-glucuronidase, btgh115a, with2 specificity for decorated arabinogalactans
64	<a href="#">c3pueA_</a>	Alignment	not modelled	12.2	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
65	<a href="#">c2kucA_</a>	Alignment	not modelled	12.1	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative disulphide-isomerase; <b>PDBTitle:</b> solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
66	<a href="#">d1nw2a_</a>	Alignment	not modelled	11.8	31	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
67	<a href="#">c3g0sA_</a>	Alignment	not modelled	11.8	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from salmonella typhimurium lt2
68	<a href="#">c2hyjl_</a>	Alignment	not modelled	11.6	35	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> J: <b>PDB Molecule:</b> protein casc3; <b>PDBTitle:</b> structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna
69	<a href="#">c3ex7l_</a>	Alignment	not modelled	11.5	35	<b>PDB header:</b> hydrolase/rna binding protein/rna <b>Chain:</b> I: <b>PDB Molecule:</b> protein casc3; <b>PDBTitle:</b> the crystal structure of ejc in its transition state
70	<a href="#">c3cuoB_</a>	Alignment	not modelled	11.5	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
71	<a href="#">d1j93a_</a>	Alignment	not modelled	11.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
72	<a href="#">d2ns0a1</a>	Alignment	not modelled	11.4	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RHA1 ro06458-like
73	<a href="#">d7mdha2</a>	Alignment	not modelled	11.2	11	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
74	<a href="#">c4ph6A_</a>	Alignment	not modelled	11.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> structure of 3-dehydroquinate dehydratase from enterococcus faecalis
75	<a href="#">c3ihjA_</a>	Alignment	not modelled	10.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine aminotransferase 2; <b>PDBTitle:</b> human alanine aminotransferase 2 in complex with plp
76	<a href="#">c3ul3A_</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery <b>PDB header:</b> oxidoreductase

77	<a href="#">c3qdnA</a>	Alignment	not modelled	10.6	23	<b>Chain:</b> A: <b>PDB Molecule:</b> putative thioredoxin protein; <b>PDBTitle:</b> putative thioredoxin protein from salmonella typhimurium
78	<a href="#">c2x8qA</a>	Alignment	not modelled	10.6	21	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> capsid protein p27; <b>PDBTitle:</b> cryo-em 3d model of the icosahedral particle composed of rous sarcoma2 virus capsid protein pentamers
79	<a href="#">d1rj9a1</a>	Alignment	not modelled	10.6	26	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
80	<a href="#">c4yxaB</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> surface presentation of antigens protein spao; <b>PDBTitle:</b> complex of spao(spoa1,2 semet) and orgb(apar)::t4lysozyme fusion2 protein
81	<a href="#">d1n0ea</a>	Alignment	not modelled	10.6	9	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Hypothetical protein MraZ
82	<a href="#">c4e6zA</a>	Alignment	not modelled	10.5	4	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> apicoplast tic22, putative; <b>PDBTitle:</b> tic22 from plasmodium falciparum
83	<a href="#">c3erwG</a>	Alignment	not modelled	10.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> sporulation thiol-disulfide oxidoreductase a; <b>PDBTitle:</b> crystal structure of stoa from bacillus subtilis
84	<a href="#">d2isyA1</a>	Alignment	not modelled	10.3	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
85	<a href="#">c3feuA</a>	Alignment	not modelled	10.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
86	<a href="#">c3razA</a>	Alignment	not modelled	10.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin-related protein; <b>PDBTitle:</b> the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b
87	<a href="#">c2w7nA</a>	Alignment	not modelled	10.1	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
88	<a href="#">c2mwqA</a>	Alignment	not modelled	9.9	16	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 3, chloroplastic; <b>PDBTitle:</b> solution structure of psbq from spinacia oleracea
89	<a href="#">c1nzeA</a>	Alignment	not modelled	9.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 3; <b>PDBTitle:</b> crystal structure of psbq polypeptide of photosystem ii2 from higher plants
90	<a href="#">d1nzea</a>	Alignment	not modelled	9.9	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Oxygen-evolving enhancer protein 3, <b>Family:</b> Oxygen-evolving enhancer protein 3,
91	<a href="#">c3fggA</a>	Alignment	not modelled	9.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bce2196; <b>PDBTitle:</b> crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
92	<a href="#">d2dcfa1</a>	Alignment	not modelled	9.8	13	<b>Fold:</b> beta-lactamase/transpeptidase-like <b>Superfamily:</b> beta-lactamase/transpeptidase-like <b>Family:</b> beta-Lactamase/D-ala carboxypeptidase
93	<a href="#">d2fug51</a>	Alignment	not modelled	9.8	18	<b>Fold:</b> Nqo5-like <b>Superfamily:</b> Nqo5-like <b>Family:</b> Nqo5-like
94	<a href="#">c3t72o</a>	Alignment	not modelled	9.7	26	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
95	<a href="#">c5j9uG</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> enhancer of polycomb-like protein 1; <b>PDBTitle:</b> crystal structure of the nua4 core complex
96	<a href="#">c1qysA</a>	Alignment	not modelled	9.6	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> top7; <b>PDBTitle:</b> crystal structure of top7: a computationally designed2 protein with a novel fold
97	<a href="#">c3vufA</a>	Alignment	not modelled	9.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> granule-bound starch synthase 1, <b>PDBTitle:</b> crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
98	<a href="#">c1t00A</a>	Alignment	not modelled	9.6	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin; <b>PDBTitle:</b> the structure of thioredoxin from s. coelicolor
99	<a href="#">d1knga</a>	Alignment	not modelled	9.5	15	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like