
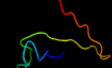
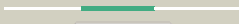




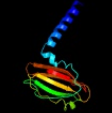







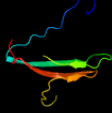





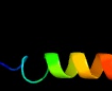


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0875c (- )_973809_974297
Date	Fri Jul 26 01:50:46 BST 2019
Unique Job ID	a4b55957fe8330fd

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1hx0a1</a>	 Alignment		42.9	24	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
2	<a href="#">d1g94a1</a>	 Alignment		41.5	24	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
3	<a href="#">d3dhp1</a>	 Alignment		39.9	30	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
4	<a href="#">c1xmeB</a>	 Alignment		39.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
5	<a href="#">c4d7pa</a>	 Alignment		32.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide reductase; <b>PDBTitle:</b> superoxide reductase (1fe-sor) from giardia intestinalis
6	<a href="#">c1f3ka</a>	 Alignment		32.1	50	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> omega-conotoxin txvii; <b>PDBTitle:</b> three-dimensional solution structure of omega-conotoxin2 txvii, an l-type calcium channel blocker
7	<a href="#">c5o4uK</a>	 Alignment		30.9	37	<b>PDB header:</b> cell adhesion <b>Chain:</b> K: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> the flagellin of pyrococcus furiosus
8	<a href="#">d2q9oa2</a>	 Alignment		30.3	12	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
9	<a href="#">c4bv1D</a>	 Alignment		28.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> neq011; <b>PDBTitle:</b> superoxide reductase (neelaredoxin) from nanoarchaeum2 equitans
10	<a href="#">c1y07A</a>	 Alignment		28.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> desulfoferrodoxin (rbo); <b>PDBTitle:</b> crystal structure of the superoxide reductase from treponema pallidum
11	<a href="#">c5z1L</a>	 Alignment		27.4	37	<b>PDB header:</b> protein fibril <b>Chain:</b> L: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> cryo-em structure of methanoccus maripaludis archaellum

12	<a href="#">c4u3qA_</a>			26.2	23	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 17 kda lipoprotein; <b>PDBTitle:</b> crystal structure of recombinant tp0435 from treponema pallidum
13	<a href="#">c2q5tA_</a>			25.6	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> cholix toxin; <b>PDBTitle:</b> full-length cholix toxin from vibrio cholerae
14	<a href="#">d1jaea1</a>			25.2	23	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
15	<a href="#">d1umga_</a>			24.3	29	<b>Fold:</b> Sulfolobus fructose-1,6-bisphosphatase-like <b>Superfamily:</b> Sulfolobus fructose-1,6-bisphosphatase-like <b>Family:</b> Sulfolobus fructose-1,6-bisphosphatase-like
16	<a href="#">c6exnc_</a>			22.1	38	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> post-catalytic p complex spliceosome with 3' splice site docked
17	<a href="#">c5tfyl_</a>			21.3	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> J: <b>PDB Molecule:</b> flagellin; <b>PDBTitle:</b> the archaeal flagellum of methanospirillum hungatei strain jf1.
18	<a href="#">c1fu3A_</a>			18.4	40	<b>PDB header:</b> metal transport inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> delta-conotoxin txvia; <b>PDBTitle:</b> three-dimensional structure in solution of the sodium2 channel agonist/antagonist delta-conotoxin txvia
19	<a href="#">d1fu3a_</a>			18.4	40	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> omega toxin-like <b>Family:</b> Conotoxin
20	<a href="#">d2cuaa_</a>			17.8	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
21	<a href="#">c1yz2A_</a>		not modelled	17.1	22	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-conotoxin am 2766; <b>PDBTitle:</b> solution structure of am2766
22	<a href="#">d1qcsa1</a>		not modelled	15.3	27	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Cdc48 N-terminal domain-like
23	<a href="#">c6cfwE_</a>		not modelled	15.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
24	<a href="#">c5ujpB_</a>		not modelled	14.8	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a glyoxalase/bleomycin resistance protein2 from streptomyces sp. cb03234
25	<a href="#">d1dfxa1</a>		not modelled	14.4	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Superoxide reductase-like <b>Family:</b> Superoxide reductase-like
26	<a href="#">c4f2fA_</a>		not modelled	13.8	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase, e1-e2 family protein; <b>PDBTitle:</b> crystal structure of the metal binding domain (mbd) of the2 streptococcus pneumoniae d39 cu(i) exporting p-type atpase copa with3 cu(i)
27	<a href="#">c2mm5A_</a>		not modelled	12.8	24	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase alstotide s4; <b>PDBTitle:</b> solution structure of alpha-amylase inhibitor peptide as4 from2 allatide scholaris
28	<a href="#">c6irz7_</a>		not modelled	12.5	42	<b>PDB header:</b> splicing <b>Chain:</b> Z: <b>PDB Molecule:</b> pre-mrna-splicing factor slu7;

28	<a href="#">c0ltz2_</a>	Alignment	not modelled	12.5	42	<b>PDBTitle:</b> cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
29	<a href="#">d1isua_</a>	Alignment	not modelled	12.5	27	<b>Fold:</b> HIPIP (high potential iron protein) <b>Superfamily:</b> HIPIP (high potential iron protein) <b>Family:</b> HIPIP (high potential iron protein)
30	<a href="#">c4bffK_</a>	Alignment	not modelled	12.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> superoxide reductase; <b>PDBTitle:</b> superoxide reductase (neelaredoxin) from archaeoglobus2 fulgidus in the reduced form
31	<a href="#">c4g6xA_</a>	Alignment	not modelled	12.0	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance protein from2 catenulispora acidiphila.
32	<a href="#">c5umwA_</a>	Alignment	not modelled	11.5	13	<b>PDB header:</b> tiancimycin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of tnms2, an antibiotic binding protein from2 streptomyces sp. cb03234
33	<a href="#">c4rdmB_</a>	Alignment	not modelled	11.4	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease r.ngovii; <b>PDBTitle:</b> crystal structure of r.ngoavii restriction endonuclease b3 domain with2 cognate dna
34	<a href="#">d1zvpa1</a>	Alignment	not modelled	11.0	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> VC0802-like
35	<a href="#">c3m1uB_</a>	Alignment	not modelled	10.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase; <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
36	<a href="#">c2mm6A_</a>	Alignment	not modelled	10.4	40	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase alstotide s1; <b>PDBTitle:</b> solution structure of alpha amylase inhibitor peptide as1 from2 allatide scholaris
37	<a href="#">d1nh2d2</a>	Alignment	not modelled	10.3	40	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
38	<a href="#">c4bk8A_</a>	Alignment	not modelled	10.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> desulfoferredoxin, ferrous iron-binding region; <b>PDBTitle:</b> superoxide reductase (neelaredoxin) from ignicoccus2 hospitalis
39	<a href="#">c4r11D_</a>	Alignment	not modelled	9.9	33	<b>PDB header:</b> cell adhesion/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> cadherin-related hmr-1; <b>PDBTitle:</b> a conserved phosphorylation switch controls the interaction between2 cadherin and beta-catenin in vitro and in vivo
40	<a href="#">d1okia1</a>	Alignment	not modelled	9.6	8	<b>Fold:</b> gamma-Crystallin-like <b>Superfamily:</b> gamma-Crystallin-like <b>Family:</b> Crystallins/Ca-binding development proteins
41	<a href="#">d1kyaa2</a>	Alignment	not modelled	9.6	8	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
42	<a href="#">d1djrd_</a>	Alignment	not modelled	9.5	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
43	<a href="#">c5gyyB_</a>	Alignment	not modelled	9.4	39	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> s-receptor kinase srk9; <b>PDBTitle:</b> plant receptor complex
44	<a href="#">c4iaagA_</a>	Alignment	not modelled	9.1	30	<b>PDB header:</b> zorbamycin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zbm binding protein; <b>PDBTitle:</b> crystal structure of zbma, the zorbamycin binding protein from2 streptomyces flavoviridis
45	<a href="#">c5b4sA_</a>	Alignment	not modelled	8.7	55	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitosanase; <b>PDBTitle:</b> crystal structure of gh80 chitosanase from mitsuaria chitosanitabida
46	<a href="#">c3rx9A_</a>	Alignment	not modelled	8.7	9	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 3d structure of scin from an escherichia coli patotype
47	<a href="#">c6e5cA_</a>	Alignment	not modelled	8.6	22	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo beta protein; <b>PDBTitle:</b> solution nmr structure of a de novo designed double-stranded beta-2 helix
48	<a href="#">d1nvpd2</a>	Alignment	not modelled	8.5	40	<b>Fold:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Superfamily:</b> Transcription factor IIA (TFIIA), beta-barrel domain <b>Family:</b> Transcription factor IIA (TFIIA), beta-barrel domain
49	<a href="#">c3u22B_</a>	Alignment	not modelled	8.3	12	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative hmuy_like heme binding protein; <b>PDBTitle:</b> crystal structure of a putative hmuy_like heme binding protein2 (bvu_2192) from bacteroides vulgatus atcc 8482 at 2.12 a resolution
50	<a href="#">c2p28A_</a>	Alignment	not modelled	8.2	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> structure of the phe2 and phe3 fragments of the integrin beta2 subunit
51	<a href="#">c4bjia_</a>	Alignment	not modelled	8.0	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor tau subunit sfc1; <b>PDBTitle:</b> sfc1-dbd
52	<a href="#">c3rheA_</a>	Alignment	not modelled	7.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent benzaldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of nad-dependent benzaldehyde dehydrogenase from2 legionella pneumophila <b>PDB header:</b> unknown function

53	<a href="#">c2kzjA_</a>	Alignment	not modelled	7.7	7	<b>Chain:</b> A; <b>PDB Molecule:</b> atc0852; <b>PDBTitle:</b> solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
54	<a href="#">d1vzia1</a>	Alignment	not modelled	7.5	24	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Superoxide reductase-like <b>Family:</b> Superoxide reductase-like
55	<a href="#">d2h8pc1</a>	Alignment	not modelled	7.4	24	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
56	<a href="#">c2yhgA_</a>	Alignment	not modelled	7.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cellulose-binding protein; <b>PDBTitle:</b> ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
57	<a href="#">c5uhjA_</a>	Alignment	not modelled	7.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a natural product biosynthetic enzyme from2 streptomyces sp. cb03234
58	<a href="#">c3mk7F_</a>	Alignment	not modelled	7.1	0	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
59	<a href="#">c5k21C_</a>	Alignment	not modelled	7.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> pyocyanin demethylase; <b>PDBTitle:</b> pyocyanin demethylase
60	<a href="#">d1mpya2</a>	Alignment	not modelled	6.9	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
61	<a href="#">c5ikuA_</a>	Alignment	not modelled	6.7	8	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> collagenase; <b>PDBTitle:</b> crystal structure of the clostridium histolyticum colg tandem2 collagen-binding domain s3as3b in the presence of calcium at 1.93 angstrom resolution
62	<a href="#">c5k26A_</a>	Alignment	not modelled	6.6	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> mitogen-activated protein kinase kinase kinase 11,chimera <b>PDBTitle:</b> structure of the sh3 domain of mlk3 bound to peptide generated from2 phage display
63	<a href="#">c2zouB_</a>	Alignment	not modelled	6.6	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> spondin-1; <b>PDBTitle:</b> crystal structure of human f-spondin reeler domain (fragment 2)
64	<a href="#">c1b5fD_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> protein (cardosin a); <b>PDBTitle:</b> native cardosin a from cynara cardunculus l.
65	<a href="#">c3ossC_</a>	Alignment	not modelled	6.3	7	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> type 2 secretion system, gspc; <b>PDBTitle:</b> the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
66	<a href="#">c6f0kA_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
67	<a href="#">c5ezdB_</a>	Alignment	not modelled	6.1	44	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> kunitz-type protease inhibitor 1; <b>PDBTitle:</b> crystal structure of a hepatocyte growth factor activator inhibitor-12 (hai-1) fragment covering the pkd-like 'internal' domain and kunitz3 domain 1
68	<a href="#">c3n6yA_</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> immunoglobulin-like protein; <b>PDBTitle:</b> crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
69	<a href="#">c1okiB_</a>	Alignment	not modelled	6.1	8	<b>PDB header:</b> eye lens protein <b>Chain:</b> B; <b>PDB Molecule:</b> beta crystallin b1; <b>PDBTitle:</b> crystal structure of truncated human beta-b1-crystallin
70	<a href="#">c3jqoV_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> V; <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
71	<a href="#">d2cuab_</a>	Alignment	not modelled	6.0	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Periplasmic domain of cytochrome c oxidase subunit II
72	<a href="#">c4bfhA_</a>	Alignment	not modelled	5.9	45	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> wrightide r1; <b>PDBTitle:</b> crystal structure of alpha-amylase inhibitor wrightide r1 (wr1)2 peptide from wrightia religiosa
73	<a href="#">c2mauA_</a>	Alignment	not modelled	5.9	45	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> wrightide r1; <b>PDBTitle:</b> solution structure of alpha-amylase inhibitor wrightide r1 (wr1)2 peptide from wrightia religiosa
74	<a href="#">c5tvzA_</a>	Alignment	not modelled	5.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> nucleoporin pom152; <b>PDBTitle:</b> solution nmr structure of saccharomyces cerevisiae pom152 ig-like2 repeat, residues 718-820
75	<a href="#">c5yi8B_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> pon peptide from partner of numb; <b>PDBTitle:</b> crystal structure of drosophila numb ptb domain and pon peptide2 complex
76	<a href="#">c6cctA_</a>	Alignment	not modelled	5.9	17	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> glucose-induced degradation protein 4 homolog; <b>PDBTitle:</b> fragment of gid4 in complex with a short peptide
77	<a href="#">c3h8tA_</a>	Alignment	not modelled	5.6	13	<b>PDB header:</b> heme-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> hmuY; <b>PDBTitle:</b> structure of porphyromonas gingivalis heme-binding

						protein hmuY in2 complex with heme
78	<a href="#">d1qnia1</a>	Alignment	not modelled	5.6	14	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Nitrosocyanin
79	<a href="#">c3g12A</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
80	<a href="#">c1vzhB</a>	Alignment	not modelled	5.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> desulfoferrodoxin; <b>PDBTitle:</b> structure of superoxide reductase bound to ferrocyanide and active2 site expansion upon x-ray induced photoreduction
81	<a href="#">d2fi9a1</a>	Alignment	not modelled	5.5	40	<b>Fold:</b> MTH938-like <b>Superfamily:</b> MTH938-like <b>Family:</b> MTH938-like
82	<a href="#">c3zhaA</a>	Alignment	not modelled	5.5	11	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pa_0080; <b>PDBTitle:</b> crystal structure of the t6ss lipoprotein tssj1 from2 pseudomonas aeruginosa
83	<a href="#">d1xrka</a>	Alignment	not modelled	5.4	30	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
84	<a href="#">c3jvfC</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> signaling protein / cytokine <b>Chain:</b> C: <b>PDB Molecule:</b> interleukin-17 receptor a; <b>PDBTitle:</b> crystal structure of an interleukin-17 receptor complex
85	<a href="#">c6nbxG</a>	Alignment	not modelled	5.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
86	<a href="#">c2hb5A</a>	Alignment	not modelled	5.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reverse transcriptase/ribonuclease h; <b>PDBTitle:</b> crystal structure of the moloney murine leukemia virus rnase h domain
87	<a href="#">d1f1xa2</a>	Alignment	not modelled	5.2	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases