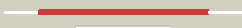




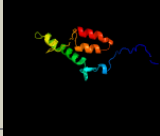

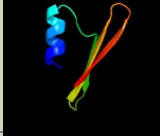


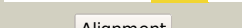
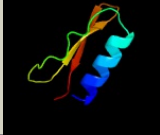
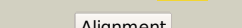

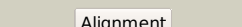

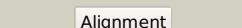

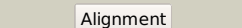
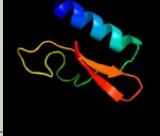


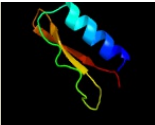


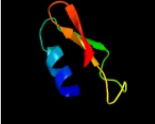


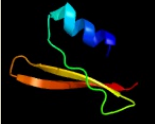




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2796c_(lppV)_3105066_3105629
Date	Wed Aug 7 12:50:45 BST 2019
Unique Job ID	70dc56be132429e3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2v7sA_</a>	 Alignment		100.0	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved lipoprotein lppa; <b>PDBTitle:</b> crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
2	<a href="#">c4mjgB_</a>	 Alignment		96.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf4853 family protein (actodq_00621) from2 actinomyces odontolyticus atcc 17982 at 2.65 a resolution
3	<a href="#">c3ls1A_</a>	 Alignment		89.0	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> sll1638 protein; <b>PDBTitle:</b> crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
4	<a href="#">c4n04B_</a>	 Alignment		80.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of glyoxalase / bleomycin resistance protein2 from catenulispora acidiphila dsm 44928
5	<a href="#">c2rk0B_</a>	 Alignment		79.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase domain; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
6	<a href="#">c1zswA_</a>	 Alignment		78.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of bacillus cereus metallo protein from glyoxalase2 family
7	<a href="#">c2zw7A_</a>	 Alignment		74.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bleomycin acetyltransferase; <b>PDBTitle:</b> crystal structure of bleomycin n-acetyltransferase complexed2 with bleomycin a2 and coenzyme a
8	<a href="#">c4pavA_</a>	 Alignment		73.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> structure of hypothetical protein sa1046 from s. aureus.
9	<a href="#">c4gymB_</a>	 Alignment		73.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from conexibacter woesei dsm 14684
10	<a href="#">c3ct8A_</a>	 Alignment		73.1	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glyoxalase; <b>PDBTitle:</b> crystal structure of a putative glyoxalase (np_243026.1) from bacillus2 halodurans at 2.10 a resolution
11	<a href="#">c3fcdB_</a>	 Alignment		69.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lyase; <b>PDBTitle:</b> crystal structure of a putative glyoxalase from an2 environmental bacteria

12	<a href="#">d1zswa2</a>	Alignment		69.5	17	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> BC1024-like
13	<a href="#">c4huzA_</a>	Alignment		68.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,6-dichloro-p-hydroquinone 1,2-dioxygenase; <b>PDBTitle:</b> 2,6-dichloro-p-hydroquinone 1,2-dioxygenase
14	<a href="#">c3rheA_</a>	Alignment		68.7	2	<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
15	<a href="#">c3g12A_</a>	Alignment		65.6	3	<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
16	<a href="#">d1twua_</a>	Alignment		65.3	7	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Hypothetical protein YycE
17	<a href="#">c3itwA_</a>	Alignment		63.7	14	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein tiox; <b>PDBTitle:</b> crystal structure of tiox from micromonospora sp. m1
18	<a href="#">c2qqzB_</a>	Alignment		62.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein, putative; <b>PDBTitle:</b> crystal structure of putative glyoxalase family protein from bacillus2 anthracis
19	<a href="#">c4g6xA_</a>	Alignment		62.5	5	<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.
20	<a href="#">c3ey7B_</a>	Alignment		61.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> biphenyl-2,3-diol 1,2-dioxygenase iii-related <b>PDBTitle:</b> structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1
21	<a href="#">c3r4qB_</a>	Alignment	not modelled	61.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of lactoylglutathione lyase from agrobacterium2 tumefaciens
22	<a href="#">c3oajA_</a>	Alignment	not modelled	60.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative ring-cleaving dioxygenase mhqo; <b>PDBTitle:</b> crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
23	<a href="#">c3bt3B_</a>	Alignment	not modelled	59.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase-related enzyme, arac type; <b>PDBTitle:</b> crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
24	<a href="#">c3sk1C_</a>	Alignment	not modelled	56.7	2	<b>PDB header:</b> griseoluteate-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ehpr; <b>PDBTitle:</b> crystal structure of phenazine resistance protein ehpr from2 enterobacter agglomerans (erwinia herbicola, pantoea agglomerans)3 eh1087, apo form
25	<a href="#">d1ecsa_</a>	Alignment	not modelled	52.4	10	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
26	<a href="#">d2i7ra1</a>	Alignment	not modelled	52.1	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
27	<a href="#">c3pkwA_</a>	Alignment	not modelled	52.0	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> toxoflavin lyase (tfla); <b>PDBTitle:</b> crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
28	<a href="#">c3r6aB_</a>	Alignment	not modelled	51.8	14	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein

						(hypothetical protein2 mm_3218) from methanosarcina mazei.
29	<a href="#">c4ro6A_</a>	Alignment	not modelled	50.8	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of glyoxalase i from zea mays
30	<a href="#">c3qghjA_</a>	Alignment	not modelled	50.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative integron gene cassette protein; <b>PDBTitle:</b> crystal structure from the mobile metagenome of halifax harbour sewage2 outfall: integron cassette protein hfx_cass4
31	<a href="#">d1lqta1</a>	Alignment	not modelled	49.9	10	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
32	<a href="#">d1qjpa_</a>	Alignment	not modelled	49.6	10	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Glyoxalase I (lactoylglutathione lyase)
33	<a href="#">c4iagA_</a>	Alignment	not modelled	49.4	10	<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
34	<a href="#">d1xrka_</a>	Alignment	not modelled	49.1	8	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
35	<a href="#">c3zi1A_</a>	Alignment	not modelled	48.2	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 4; <b>PDBTitle:</b> crystal structure of human glyoxalase domain-containing protein 42 (glod4)
36	<a href="#">d1nkia_</a>	Alignment	not modelled	47.7	12	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
37	<a href="#">c3zw5A_</a>	Alignment	not modelled	46.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 5; <b>PDBTitle:</b> crystal structure of the human glyoxalase domain-containing protein 5
38	<a href="#">c5umwA_</a>	Alignment	not modelled	45.0	11	<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
39	<a href="#">c4jh1B_</a>	Alignment	not modelled	44.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb; <b>PDBTitle:</b> crystal structure of fosb from bacillus cereus with zinc and sulfate2 at 1.55 a resolution -sad phasing
40	<a href="#">d1r9ca_</a>	Alignment	not modelled	43.9	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
41	<a href="#">c2rk9B_</a>	Alignment	not modelled	42.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01
42	<a href="#">c2qntA_</a>	Alignment	not modelled	41.2	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1872; <b>PDBTitle:</b> crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58
43	<a href="#">c4qb5A_</a>	Alignment	not modelled	41.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of a glyoxalase/bleomycin resistance protein from2 albidiferax ferrireducens t118
44	<a href="#">c4nb2B_</a>	Alignment	not modelled	39.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb; <b>PDBTitle:</b> crystal structure of fosb from staphylococcus aureus at 1.89 angstrom2 resolution - apo structure
45	<a href="#">c5vbnB_</a>	Alignment	not modelled	36.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
46	<a href="#">c3huhA_</a>	Alignment	not modelled	35.8	14	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence protein stm3117; <b>PDBTitle:</b> the structure of biphenyl-2,3-diol 1,2-dioxygenase iii-related protein2 from salmonella typhimurium
47	<a href="#">d1klla_</a>	Alignment	not modelled	35.3	11	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
48	<a href="#">c4z04A_</a>	Alignment	not modelled	35.1	4	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance /dioxygenase superfamily <b>PDBTitle:</b> crystal structure of a probable lactoylglutathione lyase from brucella2 melitensis in complex with glutathione
49	<a href="#">d1jifa_</a>	Alignment	not modelled	34.4	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
50	<a href="#">d1xrsb2</a>	Alignment	not modelled	33.0	15	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain <b>Family:</b> D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain

51	<a href="#">d2pjsa1</a>	Alignment	not modelled	31.8	10	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
52	<a href="#">d1aopa2</a>	Alignment	not modelled	31.5	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
53	<a href="#">c2kja_</a>	Alignment	not modelled	30.9	9	<b>PDB header:</b> unknown function <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="#">c4ps2A_</a>	Alignment	not modelled	29.3	25	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative type vi secretion protein; <b>PDBTitle:</b> structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
55	<a href="#">c2cpmA_</a>	Alignment	not modelled	28.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sperm-associated antigen 7; <b>PDBTitle:</b> solution structure of the r3h domain of human sperm-2 associated antigen 7
56	<a href="#">c3e5dA_</a>	Alignment	not modelled	27.4	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glyoxalase i; <b>PDBTitle:</b> crystal structure of a putative glyoxalase i (lmof2365_0426) from2 listeria monocytogenes str. 4b f2365 at 2.70 a resolution
57	<a href="#">d1bjna_</a>	Alignment	not modelled	26.7	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
58	<a href="#">c3bqxA_</a>	Alignment	not modelled	26.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase-related enzyme; <b>PDBTitle:</b> high resolution crystal structure of a glyoxalase-related enzyme from2 fulvimarina pelagi
59	<a href="#">d1kw3b1</a>	Alignment	not modelled	26.6	6	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
60	<a href="#">c3samB_</a>	Alignment	not modelled	25.4	21	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> rifampicin resistance protein; <b>PDBTitle:</b> structure of d13, the scaffolding protein of vaccinia virus (mutant2 d513g)
61	<a href="#">c2kxhB_</a>	Alignment	not modelled	24.8	22	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> peptide of far upstream element-binding protein 1; <b>PDBTitle:</b> solution structure of the first two rrm domains of fir in the complex2 with fbp nbx peptide
62	<a href="#">c2p7pB_</a>	Alignment	not modelled	24.7	22	<b>PDB header:</b> metal binding protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of genomically encoded fosfomycin resistance2 protein, fosx, from listeria monocytogenes complexed with mn(ii) and3 sulfate ion
63	<a href="#">c5ujpB_</a>	Alignment	not modelled	24.3	18	<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
64	<a href="#">c1wd6B_</a>	Alignment	not modelled	24.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydhr; <b>PDBTitle:</b> crystal structure of jw1657 from escherichia coli
65	<a href="#">c2otnB_</a>	Alignment	not modelled	23.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
66	<a href="#">d1mpya2</a>	Alignment	not modelled	23.4	11	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
67	<a href="#">c6a4zA_</a>	Alignment	not modelled	22.7	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> chap protein; <b>PDBTitle:</b> oxidase chap
68	<a href="#">c4hc5A_</a>	Alignment	not modelled	22.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of member of glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily from sphaerobacter thermophilus dsm3 20745
69	<a href="#">c5cb9A_</a>	Alignment	not modelled	22.6	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of c-as lyase with mercaptoethonal
70	<a href="#">c2r6uB_</a>	Alignment	not modelled	22.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of gene product rha04853 from rhodococcus sp. rha1
71	<a href="#">d1xqaa_</a>	Alignment	not modelled	21.1	22	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
72	<a href="#">c3uh9B_</a>	Alignment	not modelled	20.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> metallothiol transferase fosb 2; <b>PDBTitle:</b> crystal structure of metallothiol transferase fosb 2 from bacillus2 anthracis str. ames
73	<a href="#">c5k5wA_</a>	Alignment	not modelled	20.3	23	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> limiting co2-inducible protein lcib; <b>PDBTitle:</b> crystal structure of limiting co2-inducible protein lcib
						<b>PDB header:</b> oxidoreductase

74	<a href="#">c2p25A_</a>	Alignment	not modelled	19.8	13	<b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> the crystal structure of the glyoxalase family protein from2 enterococcus faecalis
75	<a href="#">c2wamB_</a>	Alignment	not modelled	19.6	26	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical alanine and leucine rich <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
76	<a href="#">c3kolA_</a>	Alignment	not modelled	19.2	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance <b>PDBTitle:</b> crystal structure of a glyoxalase/dioxygenase from nostoc2 punctiforme
77	<a href="#">c4nvsB_</a>	Alignment	not modelled	19.0	5	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative enzyme, glyoxalase family; <b>PDBTitle:</b> crystal structure of the q18cp6_clod6 protein from glyoxalase family.2 northeast structural genomics consortium target cfr3
78	<a href="#">c3zsuA_</a>	Alignment	not modelled	18.8	11	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> tl12057 protein; <b>PDBTitle:</b> structure of the cyanoq protein from thermosynechococcus elongatus
79	<a href="#">c4zgoA_</a>	Alignment	not modelled	18.5	33	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division cycle protein 123; <b>PDBTitle:</b> structure of c-terminally truncated cdc123 from schizosaccharomyces2 pombe
80	<a href="#">c5nlmB_</a>	Alignment	not modelled	18.1	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> indoxyl udp-glucosyltransferase; <b>PDBTitle:</b> complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
81	<a href="#">c3e77A_</a>	Alignment	not modelled	17.3	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> human phosphoserine aminotransferase in complex with plp
82	<a href="#">c3l7tB_</a>	Alignment	not modelled	17.3	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1112c
83	<a href="#">d2c0ra1</a>	Alignment	not modelled	17.2	13	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> GABA-aminotransferase-like
84	<a href="#">c4xvnC_</a>	Alignment	not modelled	17.2	31	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> small terminase; <b>PDBTitle:</b> crystal structure of the small terminase from thermophilic phage g20c
85	<a href="#">c4clvB_</a>	Alignment	not modelled	17.2	11	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nickel-cobalt-cadmium resistance protein nccx; <b>PDBTitle:</b> crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
86	<a href="#">c2rbbB_</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn
87	<a href="#">c5vb0E_</a>	Alignment	not modelled	17.1	12	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> fosfomycin resistance protein fosa3; <b>PDBTitle:</b> crystal structure of fosfomycin resistance protein fosa3
88	<a href="#">c6on3C_</a>	Alignment	not modelled	16.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> l-dopa extradiol dioxygenase; <b>PDBTitle:</b> a substrate bound structure of l-dopa dioxygenase from streptomyces2 sclerotialus
89	<a href="#">c3m2oB_</a>	Alignment	not modelled	16.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein; <b>PDBTitle:</b> crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
90	<a href="#">d2bgxa2</a>	Alignment	not modelled	15.7	14	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
91	<a href="#">c6hv8A_</a>	Alignment	not modelled	15.3	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase epsilon catalytic subunit a; <b>PDBTitle:</b> cryo-em structure of s. cerevisiae polymerase epsilon deltatcat mutant
92	<a href="#">c4b1xM_</a>	Alignment	not modelled	15.3	20	<b>PDB header:</b> structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> phosphatase and actin regulator 1; <b>PDBTitle:</b> structure of the phactr1 rpe1-2 bound to g-actin
93	<a href="#">c5n8nO_</a>	Alignment	not modelled	15.1	31	<b>PDB header:</b> structural protein <b>Chain:</b> Q: <b>PDB Molecule:</b> type vi secretion protein, family; <b>PDBTitle:</b> contracted sheath of a pseudomonas aeruginosa type six secretion2 system consisting of tssb1 and tssc1
94	<a href="#">c2oarA_</a>	Alignment	not modelled	15.1	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> mechanosensitive channel of large conductance (mscl)
95	<a href="#">d1lqta2</a>	Alignment	not modelled	15.0	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
96	<a href="#">c3rriB_</a>	Alignment	not modelled	14.7	4	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
97	<a href="#">c6iw6A_</a>	Alignment	not modelled	14.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> terminal uridylyltransferase 4,terminal uridylyltransferase <b>PDBTitle:</b> crystal structure of the lin28-interacting module of human tut4

98	<a href="#">c4mtsA</a>	<a href="#">Alignment</a>	not modelled	14.3	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> ni- and zn-bound gloa2 at high resolution
99	<a href="#">c5uhjA</a>	<a href="#">Alignment</a>	not modelled	14.1	13	<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