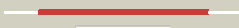












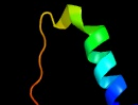








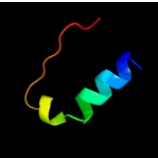


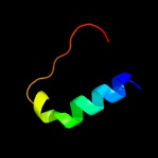

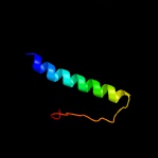
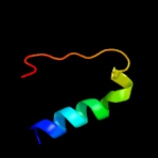
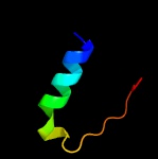
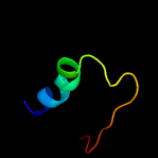


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1889c (-) _2138668_2139024
Date	Fri Aug 2 13:30:50 BST 2019
Unique Job ID	93f10ef73a5d9532

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2uyoa1</a>	 Alignment		100.0	47	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> ML2640-like
2	<a href="#">c3ieiD</a>	 Alignment		99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
3	<a href="#">c3mntA</a>	 Alignment		99.3	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxyl methyltransferase 1
4	<a href="#">d1rjda</a>	 Alignment		99.3	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Leucine carboxy methyltransferase Ppm1
5	<a href="#">c2zwaA</a>	 Alignment		98.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 2; <b>PDBTitle:</b> crystal structure of trna wybutosine synthesizing enzyme2 tyw4
6	<a href="#">c2qe6B</a>	 Alignment		92.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein tfu_2867; <b>PDBTitle:</b> crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
7	<a href="#">c5fwaA</a>	 Alignment		60.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 2; <b>PDBTitle:</b> crystal structure of mus musculus protein arginine methyltransferase 22 with cp1
8	<a href="#">d1f3la</a>	 Alignment		58.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
9	<a href="#">c4y30B</a>	 Alignment		56.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein arginine n-methyltransferase 6; <b>PDBTitle:</b> crystal structure of human protein arginine methyltransferase prmt62 bound to sah and epz020411
10	<a href="#">c5lkjA</a>	 Alignment		53.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1; <b>PDBTitle:</b> crystal structure of mouse carm1 in complex with ligand sa684
11	<a href="#">d1g6q1</a>	 Alignment		52.8	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase

12	<a href="#">c2v7eB_</a>	Alignment		49.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> histone-arginine methyltransferase arm1; <b>PDBTitle:</b> crystal structure of coactivator-associated arginine2 methyltransferase 1 (arm1), unliganded
13	<a href="#">d1oria_</a>	Alignment		48.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
14	<a href="#">d2fyta1</a>	Alignment		48.4	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
15	<a href="#">c3b3jA_</a>	Alignment		47.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase arm1; <b>PDBTitle:</b> the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
16	<a href="#">c1orhA_</a>	Alignment		46.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 1; <b>PDBTitle:</b> structure of the predominant protein arginine methyltransferase prmt1
17	<a href="#">c3giwA_</a>	Alignment		45.1	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf574; <b>PDBTitle:</b> crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
18	<a href="#">c5fubA_</a>	Alignment		44.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine methyltransferase 2; <b>PDBTitle:</b> crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah
19	<a href="#">c4hc4A_</a>	Alignment		43.2	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 6; <b>PDBTitle:</b> human hmt1 hnrnp methyltransferase-like protein 6 (s. cerevisiae)
20	<a href="#">c6dnzA_</a>	Alignment		42.2	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> arginine n-methyltransferase, putative; <b>PDBTitle:</b> trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy
21	<a href="#">c3r0qA_</a>	Alignment	not modelled	35.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable protein arginine n-methyltransferase 4.2; <b>PDBTitle:</b> a uniquely open conformation revealed in the crystal structure of2 arabidopsis thaliana protein arginine methyltransferase 10
22	<a href="#">c4c4aA_</a>	Alignment	not modelled	29.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of mouse protein arginine methyltransferase 7 in2 complex with sah
23	<a href="#">c3c3jA_</a>	Alignment	not modelled	26.6	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
24	<a href="#">c3thgA_</a>	Alignment	not modelled	26.4	35	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase/oxygenase activase 1, <b>PDBTitle:</b> crystal structure of the creosote rubisco activase c-domain
25	<a href="#">c3uqzB_</a>	Alignment	not modelled	24.8	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna processing protein dpra; <b>PDBTitle:</b> x-ray structure of dna processing protein a (dpra) from streptococcus2 pneumoniae
26	<a href="#">c4yaja_</a>	Alignment	not modelled	24.4	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
27	<a href="#">c4m38A_</a>	Alignment	not modelled	23.0	12	<b>PDB header:</b> transferase/transferase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of trypanosoma brucei protein arginine2

						methyltransferase 7 complex with adohcy and histone h4 peptide
28	<a href="#">d1m6ia2</a>	Alignment	not modelled	21.8	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
29	<a href="#">c3wssA</a>	Alignment	not modelled	21.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of c.elegans prmt7 in complex with sah (p43212)
30	<a href="#">c3k35D</a>	Alignment	not modelled	20.8	4	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> crystal structure of human sirt6
31	<a href="#">d1rssa</a>	Alignment	not modelled	20.3	6	<b>Fold:</b> Ribosomal protein S7 <b>Superfamily:</b> Ribosomal protein S7 <b>Family:</b> Ribosomal protein S7
32	<a href="#">c2e1mA</a>	Alignment	not modelled	18.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
33	<a href="#">c3we0A</a>	Alignment	not modelled	17.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase/monooxygenase; <b>PDBTitle:</b> l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
34	<a href="#">d1d7ya2</a>	Alignment	not modelled	17.3	10	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
35	<a href="#">c2csuB</a>	Alignment	not modelled	15.5	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
36	<a href="#">c6dnzB</a>	Alignment	not modelled	15.3	26	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> arginine n-methyltransferase, putative; <b>PDBTitle:</b> trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy
37	<a href="#">c3majA</a>	Alignment	not modelled	14.5	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna processing chain a; <b>PDBTitle:</b> crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
38	<a href="#">d1ojta2</a>	Alignment	not modelled	13.6	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
39	<a href="#">c3wz2C</a>	Alignment	not modelled	13.5	12	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
40	<a href="#">c3odpA</a>	Alignment	not modelled	13.3	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
41	<a href="#">c3qtyS</a>	Alignment	not modelled	13.1	20	<b>PDB header:</b> chaperone/ribosomal protein <b>Chain:</b> S: <b>PDB Molecule:</b> 30s ribosomal protein s7; <b>PDBTitle:</b> promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
42	<a href="#">d1r74a</a>	Alignment	not modelled	12.2	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
43	<a href="#">c3g68A</a>	Alignment	not modelled	12.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphosugar isomerase; <b>PDBTitle:</b> crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
44	<a href="#">c5ol0B</a>	Alignment	not modelled	12.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative silent information regulator 2,putative silent <b>PDBTitle:</b> structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
45	<a href="#">c6cn0B</a>	Alignment	not modelled	11.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 16s rrna (guanine(1405)-n(7))-methyltransferase; <b>PDBTitle:</b> 2.95 angstrom crystal structure of 16s rrna methylase from proteus2 mirabilis
46	<a href="#">d1q1ra2</a>	Alignment	not modelled	11.8	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
47	<a href="#">d2csua1</a>	Alignment	not modelled	11.6	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
48	<a href="#">c3zq6A</a>	Alignment	not modelled	11.6	4	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-6; <b>PDBTitle:</b> the novel de-long chain fatty acid function of human sirt6
49	<a href="#">c3b89A</a>	Alignment	not modelled	11.3	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 16s rrna methylase; <b>PDBTitle:</b> crystal structure of rrna methylase from escherichia coli
50	<a href="#">c2a3nA</a>	Alignment	not modelled	11.2	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative glucosamine-fructose-6-phosphate aminotransferase; <b>PDBTitle:</b> crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
51	<a href="#">c4iaoB</a>	Alignment	not modelled	11.1	13	<b>PDB header:</b> hydrolase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
						<b>Fold:</b> Flavodoxin-like

52	<a href="#">d1gdha2</a>	Alignment	not modelled	10.7	17	<b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
53	<a href="#">c4a69A</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> histone deacetylase 3;; <b>PDBTitle:</b> structure of hdac3 bound to corepressor and inositol tetraphosphate
54	<a href="#">c2amIB</a>	Alignment	not modelled	10.5	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
55	<a href="#">d1xhca2</a>	Alignment	not modelled	10.4	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
56	<a href="#">d1rp0a1</a>	Alignment	not modelled	10.1	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like
57	<a href="#">c2yv2A</a>	Alignment	not modelled	10.1	33	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
58	<a href="#">c5odcD</a>	Alignment	not modelled	10.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> methyl-viologen reducing hydrogenase subunit d; <b>PDBTitle:</b> heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
59	<a href="#">d1xvaa</a>	Alignment	not modelled	9.7	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
60	<a href="#">c5zdcL</a>	Alignment	not modelled	9.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> poly adp-ribose glycohydrolase; <b>PDBTitle:</b> crystal structure of poly(adp-ribose) glycohydrolase (parg) from2 deinococcus radiodurans in complex with adp-ribose (p32)
61	<a href="#">c3wrwE</a>	Alignment	not modelled	9.5	11	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> tm-1 protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of resistance protein
62	<a href="#">d1dxia2</a>	Alignment	not modelled	9.2	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
63	<a href="#">c1zz0C</a>	Alignment	not modelled	9.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> histone deacetylase-like amidohydrolase; <b>PDBTitle:</b> crystal structure of a hdac-like protein with acetate bound
64	<a href="#">c5hijA</a>	Alignment	not modelled	9.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine sarcosine n-methyltransferase; <b>PDBTitle:</b> crystal structure of glycine sarcosine n-methyltransferase from2 methanohalophilus portucalensis in complex with betaine
65	<a href="#">c3knzA</a>	Alignment	not modelled	8.9	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar binding protein; <b>PDBTitle:</b> crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
66	<a href="#">c6meIA</a>	Alignment	not modelled	8.9	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate--coa ligase subunit alpha; <b>PDBTitle:</b> succinyl-coa synthase from campylobacter jejuni
67	<a href="#">d2dlda2</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
68	<a href="#">c3pa8A</a>	Alignment	not modelled	8.5	11	<b>PDB header:</b> toxin/peptide inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> toxin b; <b>PDBTitle:</b> structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
69	<a href="#">c2z1dA</a>	Alignment	not modelled	8.4	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase expression/formation protein hypd; <b>PDBTitle:</b> crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
70	<a href="#">c3ho6B</a>	Alignment	not modelled	8.3	13	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> toxin a; <b>PDBTitle:</b> structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
71	<a href="#">c5oj7A</a>	Alignment	not modelled	8.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent protein deacylase; <b>PDBTitle:</b> sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
72	<a href="#">c3pkIF</a>	Alignment	not modelled	7.9	4	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-6; <b>PDBTitle:</b> human sirt6 crystal structure in complex with adp ribose
73	<a href="#">c3siiA</a>	Alignment	not modelled	7.9	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> poly(adp-ribose) glycohydrolase; <b>PDBTitle:</b> the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
74	<a href="#">c2fpgA</a>	Alignment	not modelled	7.8	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa synthetase in2 complex with gdp
75	<a href="#">c6h1dA</a>	Alignment	not modelled	7.8	22	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hemk methyltransferase family member 2; <b>PDBTitle:</b> crystal structure of c21orf127-trmt112 in complex with sah
						<b>PDB header:</b> transferase

76	<a href="#">c3busB_</a>	Alignment	not modelled	7.7	8	<b>Chain:</b> B: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> crystal structure of rebm
77	<a href="#">c4kdcA_</a>	Alignment	not modelled	7.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-demethylubiquinone-9 3-methyltransferase; <b>PDBTitle:</b> crystal structure of ubig
78	<a href="#">c5n6mA_</a>	Alignment	not modelled	7.6	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apolipoprotein n-acyltransferase; <b>PDBTitle:</b> structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa
79	<a href="#">d1nhpa2</a>	Alignment	not modelled	7.3	13	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
80	<a href="#">c6hxaA_</a>	Alignment	not modelled	7.3	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> citryl-coa synthetase small subunit; <b>PDBTitle:</b> structure of citryl-coa synthetase from hydrogenobacter thermophilus
81	<a href="#">d1yza1</a>	Alignment	not modelled	7.1	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TrmB-like
82	<a href="#">c2nu8D_</a>	Alignment	not modelled	7.1	24	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase
83	<a href="#">c5btrB_</a>	Alignment	not modelled	7.0	9	<b>PDB header:</b> hydrolase/substrate <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent protein deacetylase sirtuin-1; <b>PDBTitle:</b> crystal structure of sirt1 in complex with resveratrol and an amc-2 containing peptide
84	<a href="#">d1gv4a2</a>	Alignment	not modelled	6.9	5	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
85	<a href="#">c2we7A_</a>	Alignment	not modelled	6.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
86	<a href="#">d2d59a1</a>	Alignment	not modelled	6.8	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
87	<a href="#">c1f8sA_</a>	Alignment	not modelled	6.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
88	<a href="#">c2hjhB_</a>	Alignment	not modelled	6.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of the sir2 deacetylase
89	<a href="#">c5li3A_</a>	Alignment	not modelled	6.6	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetoin utilization protein; <b>PDBTitle:</b> crystal structure of hdac-like protein from p. aeruginosa in complex2 with a photo-switchable inhibitor.
90	<a href="#">c2yr6A_</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-enzyme of l-phenylalanine oxidase; <b>PDBTitle:</b> crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
91	<a href="#">c4gutA_</a>	Alignment	not modelled	6.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1b; <b>PDBTitle:</b> crystal structure of lsd2-npac
92	<a href="#">d1to6a_</a>	Alignment	not modelled	6.2	22	<b>Fold:</b> Glycerate kinase I <b>Superfamily:</b> Glycerate kinase I <b>Family:</b> Glycerate kinase I
93	<a href="#">d1xria_</a>	Alignment	not modelled	6.1	18	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
94	<a href="#">c2vvdD_</a>	Alignment	not modelled	6.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> monoamine oxidase n; <b>PDBTitle:</b> the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
95	<a href="#">c2hkoA_</a>	Alignment	not modelled	6.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1
96	<a href="#">c2v1dA_</a>	Alignment	not modelled	6.0	30	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-corest selectivity in histone h32 recognition
97	<a href="#">c2xagA_</a>	Alignment	not modelled	6.0	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
98	<a href="#">c6pdmA_</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 9; <b>PDBTitle:</b> crystal structure of human protein arginine methyltransferase 92 (prmt9)
99	<a href="#">c2lehB_</a>	Alignment	not modelled	6.0	43	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> solution structure of the core smn-gemin2 complex