

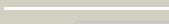
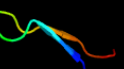







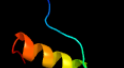






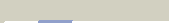


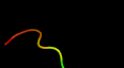






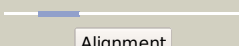

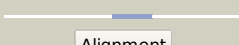

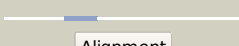

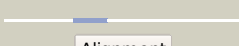





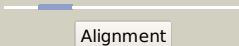
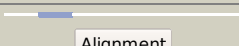
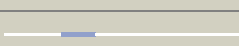
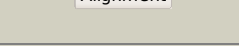
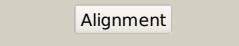

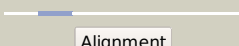



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1907c_(-)_2153242_2153889
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	d87cf65e4bfc6ac1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2l6pA_</a>	 Alignment		60.2	38	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phac1, phac2 and phad genes; <b>PDBTitle:</b> nmr solution structure of the protein np_253742.1
2	<a href="#">c3luuA_</a>	 Alignment		60.1	38	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
3	<a href="#">c2fb1A_</a>	 Alignment		53.6	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of protein bt0354 from bacteroides thetaiotaomicron
4	<a href="#">c2l6nA_</a>	 Alignment		45.9	38	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_001092504.1; <b>PDBTitle:</b> nmr solution structure of the protein yp_001092504.1
5	<a href="#">c4i62A_</a>	 Alignment		44.6	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> 1.05 angstrom crystal structure of an amino acid abc transporter2 substrate-binding protein abpa from streptococcus pneumoniae canada3 mdr_19a bound to l-arginine
6	<a href="#">c2yyhC_</a>	 Alignment		41.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 8-oxo-dgtpase domain; <b>PDBTitle:</b> crystal structure of nudix family protein from aquifex aeolicus
7	<a href="#">d1h9hi_</a>	 Alignment		36.2	43	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
8	<a href="#">c3uv1B_</a>	 Alignment		36.1	16	<b>PDB header:</b> allergen <b>Chain:</b> B: <b>PDB Molecule:</b> der f 7 allergen; <b>PDBTitle:</b> crystal structure a major allergen from dust mite
9	<a href="#">c3i9xA_</a>	 Alignment		33.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of a mutt/nudix family protein from listeria innocua
10	<a href="#">c2fm1B_</a>	 Alignment		29.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of mutt/nudix family protein from enterococcus2 faecalis
11	<a href="#">c2m2qA_</a>	 Alignment		26.9	70	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> inhibitor cystine knot peptide mch-1; <b>PDBTitle:</b> solution structure of mch-1: a novel inhibitor cystine knot peptide2 from momordica charantia

12	<a href="#">c1hw4A_</a>	 Alignment		26.5	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> structure of thymidylate synthase suggests advantages of chemotherapy2 with noncompetitive inhibitors
13	<a href="#">c3egyX_</a>	 Alignment		25.1	33	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> crystal structure of human thymidylate synthase a191k with loop 181-2 197 stabilized in the inactive conformation
14	<a href="#">d2fmla2</a>	 Alignment		25.0	26	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
15	<a href="#">c5t3pB_</a>	 Alignment		24.6	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal coenzyme a diphosphatase nudt7; <b>PDBTitle:</b> crystal structure of human peroxisomal coenzyme a diphosphatase nudt7
16	<a href="#">c5cw9A_</a>	 Alignment		24.0	37	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed ferredoxin-ferredoxin domain insertion <b>PDBTitle:</b> crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
17	<a href="#">c6btmB_</a>	 Alignment		23.8	50	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alternative complex iii subunit b; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
18	<a href="#">d1hvya_</a>	 Alignment		23.2	30	<b>Fold:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Superfamily:</b> Thymidylate synthase/dCMP hydroxymethylase <b>Family:</b> Thymidylate synthase/dCMP hydroxymethylase
19	<a href="#">d1mcvi_</a>	 Alignment		23.1	45	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
20	<a href="#">c1mcvl_</a>	 Alignment		23.1	45	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> hei-toe i; <b>PDBTitle:</b> crystal structure analysis of a hybrid squash inhibitor in2 complex with porcine pancreatic elastase
21	<a href="#">d2it7a1</a>	 Alignment	not modelled	22.1	45	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
22	<a href="#">c2it7A_</a>	 Alignment	not modelled	22.1	45	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin inhibitor 2; <b>PDBTitle:</b> solution structure of the squash trypsin inhibitor eeti-ii
23	<a href="#">c2ph5A_</a>	 Alignment	not modelled	22.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
24	<a href="#">c6n1nA_</a>	 Alignment	not modelled	22.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of class d beta-lactamase from sebaldeella termitidis2 atcc 33386
25	<a href="#">c6f0kB_</a>	 Alignment	not modelled	21.8	25	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> fe-s-cluster-containing hydrogenase; <b>PDBTitle:</b> alternative complex iii
26	<a href="#">c3gz6A_</a>	 Alignment	not modelled	21.6	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of shewanella oneidensis nrtr complexed with a 27mer2 dna
27	<a href="#">c2letA_</a>	 Alignment	not modelled	21.5	45	<b>PDB header:</b> proteinase inhibitor(trypsin) <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin inhibitor ii; <b>PDBTitle:</b> an 1h nmr determination of the three dimensional structures of mirror2 image forms of a leu-5 variant of the trypsin inhibitor ecballium3 elaterium (eeti-ii)
28	<a href="#">c4v14A_</a>	 Alignment	not modelled	19.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> structure and function analysis of mutt from the2

						psychrophile fish pathogen aliivibrio salmonicida and the3 mesophile vibrio cholerae
29	<a href="#">c1hw3A_</a>	Alignment	not modelled	19.3	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> structure of human thymidylate synthase suggests advantages of2 chemotherapy with noncompetitive inhibitors
30	<a href="#">c5o5jF_</a>	Alignment	not modelled	18.9	19	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 30s ribosomal protein s6; <b>PDBTitle:</b> structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
31	<a href="#">c3k5jA_</a>	Alignment	not modelled	18.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of fused family protein; <b>PDBTitle:</b> crystal structure of putative sufu (suppressor of fused protein)2 homolog (yp_208451.1) from neisseria gonorrhoeae fa 1090 at 1.40 a3 resolution
32	<a href="#">c6jczL_</a>	Alignment	not modelled	18.4	10	<b>PDB header:</b> isomerase <b>Chain:</b> L: <b>PDB Molecule:</b> putative ketol-acid reductoisomerase 2; <b>PDBTitle:</b> cryo-em structure of sulfobolus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd at3 ph7.5
33	<a href="#">c2pq1B_</a>	Alignment	not modelled	17.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ap4a hydrolase; <b>PDBTitle:</b> crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
34	<a href="#">c4plpB_</a>	Alignment	not modelled	17.6	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad
35	<a href="#">d2fb1a2</a>	Alignment	not modelled	17.4	29	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> BT0354 N-terminal domain-like
36	<a href="#">c5bonC_</a>	Alignment	not modelled	17.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> probable 8-oxo-dgtp diphosphatase nudt15; <b>PDBTitle:</b> crystal structure of human nudt15 (mth2)
37	<a href="#">d2c4ba2</a>	Alignment	not modelled	16.9	53	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
38	<a href="#">c3ef5A_</a>	Alignment	not modelled	16.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable pyrophosphohydrolase; <b>PDBTitle:</b> structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
39	<a href="#">c4h5fB_</a>	Alignment	not modelled	16.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc superfamily atp binding cassette <b>PDBTitle:</b> crystal structure of an amino acid abc transporter substrate-binding2 protein from streptococcus pneumoniae canada mdr_19a bound to l-3 arginine, form 1
40	<a href="#">d1iry_a_</a>	Alignment	not modelled	16.4	32	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
41	<a href="#">d1h9ii_</a>	Alignment	not modelled	16.2	39	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
42	<a href="#">c6g3bA_</a>	Alignment	not modelled	15.7	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii site-specific deoxyribonuclease; <b>PDBTitle:</b> avaii restriction endonuclease in complex with an rna/dna hybrid
43	<a href="#">c2m7tA_</a>	Alignment	not modelled	15.5	53	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cystine knot protein 2.5d; <b>PDBTitle:</b> solution nmr structure of engineered cystine knot protein 2.5d
44	<a href="#">c6gpcB_</a>	Alignment	not modelled	15.1	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> crystal structure of the arginine-bound form of domain 1 from tmargbp
45	<a href="#">c2aaazG_</a>	Alignment	not modelled	14.7	23	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> thymidylate synthase; <b>PDBTitle:</b> cryptococcus neoformans thymidylate synthase complexed with substrate2 and an antifolate
46	<a href="#">d1nqza_</a>	Alignment	not modelled	14.2	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
47	<a href="#">d2iela1</a>	Alignment	not modelled	14.1	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
48	<a href="#">c3p14C_</a>	Alignment	not modelled	14.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> l-rhamnose isomerase; <b>PDBTitle:</b> crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
49	<a href="#">c3exqA_</a>	Alignment	not modelled	14.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nudix family hydrolase; <b>PDBTitle:</b> crystal structure of a nudix family hydrolase from2 lactobacillus brevis
50	<a href="#">d1sjya_</a>	Alignment	not modelled	13.9	31	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
51	<a href="#">c3h95A_</a>	Alignment	not modelled	13.9	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside diphosphate-linked moiety x motif 6; <b>PDBTitle:</b> crystal structure of the nudix domain of nudt6
52	<a href="#">c1ttwB_</a>	Alignment	not modelled	13.2	43	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> yscm2; <b>PDBTitle:</b> crystal structure of the yersinia pestis type iii secretion chaperone2 sych in complex with a stable fragment of yscm2
53	<a href="#">c3n4iA_</a>	Alignment	not modelled	13.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohydrolase (mutt/nudix family

53	<a href="#">c0q4A_</a>	Alignment	not modelled	13.1	20	protein); <b>PDBTitle:</b> crystal structure of cdp-chase in complex with gd3+
54	<a href="#">c2fefB_</a>	Alignment	not modelled	12.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pa2201; <b>PDBTitle:</b> the crystal structure of protein pa2201 from pseudomonas aeruginosa
55	<a href="#">d1zgHa1</a>	Alignment	not modelled	12.9	20	<b>Fold:</b> FMT C-terminal domain-like <b>Superfamily:</b> FMT C-terminal domain-like <b>Family:</b> Post formyltransferase domain
56	<a href="#">d2b0va1</a>	Alignment	not modelled	12.7	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
57	<a href="#">d1x51a1</a>	Alignment	not modelled	12.6	19	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutY C-terminal domain-like
58	<a href="#">c3dclC_</a>	Alignment	not modelled	12.5	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> tm1086; <b>PDBTitle:</b> crystal structure of tm1086
59	<a href="#">c2r5wA_</a>	Alignment	not modelled	12.5	23	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenyllyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nm2 adenyllyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
60	<a href="#">c3mpbA_</a>	Alignment	not modelled	12.4	22	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar isomerase; <b>PDBTitle:</b> z5688 from e. coli o157:h7 bound to fructose
61	<a href="#">c3r03B_</a>	Alignment	not modelled	12.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nudix hydrolase; <b>PDBTitle:</b> the crystal structure of nudix hydrolase from rhodospirillum rubrum
62	<a href="#">c5gg7A_</a>	Alignment	not modelled	11.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family protein; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
63	<a href="#">d1ryaa_</a>	Alignment	not modelled	11.6	29	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> GDP-mannose mannosyl hydrolase NudD
64	<a href="#">c2rrkA_</a>	Alignment	not modelled	11.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp pyrophosphohydrolase; <b>PDBTitle:</b> solution structure of the e. coli orf135 protein
65	<a href="#">c3hbrD_</a>	Alignment	not modelled	11.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> oxa-48; <b>PDBTitle:</b> crystal structure of oxa-48 beta-lactamase
66	<a href="#">c4hfqB_</a>	Alignment	not modelled	11.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> crystal structure of udp-x diphosphatase
67	<a href="#">c4kyxA_</a>	Alignment	not modelled	11.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribose pyrophosphatase mutt; <b>PDBTitle:</b> crystal structure of adp-ribose pyrophosphatase mutt from rickettsia2 felis
68	<a href="#">c4zbpC_</a>	Alignment	not modelled	10.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> nudix hydrolase 7; <b>PDBTitle:</b> crystal structure of the ampccpr-bound atnudt7
69	<a href="#">c2ctuA_</a>	Alignment	not modelled	10.7	73	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 483; <b>PDBTitle:</b> solution structure of zinc finger domain from human zn2 finger protein 483
70	<a href="#">d1k2ea_</a>	Alignment	not modelled	10.7	21	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
71	<a href="#">c2lnbA_</a>	Alignment	not modelled	10.5	57	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> z-dna-binding protein 1; <b>PDBTitle:</b> solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a.
72	<a href="#">c4z9nB_</a>	Alignment	not modelled	10.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> amino acid abc transporter, periplasmic amino acid-binding <b>PDBTitle:</b> abc transporter / periplasmic binding protein from brucella ovis with2 glutathione bound
73	<a href="#">c5l82A_</a>	Alignment	not modelled	10.3	33	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> enterococin k1; <b>PDBTitle:</b> nmr structure of enterocin k1 in 50%/50% tfe/water
74	<a href="#">d1q33a_</a>	Alignment	not modelled	10.2	18	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like
75	<a href="#">c4ccvA_</a>	Alignment	not modelled	10.1	23	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> histidine-rich glycoprotein; <b>PDBTitle:</b> crystal structure of histidine-rich glycoprotein n2 domain2 reveals redox activity at an interdomain disulfide bridge:3 implications for the regulation of angiogenesis
76	<a href="#">c3fcmA_</a>	Alignment	not modelled	9.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family; <b>PDBTitle:</b> crystal structure of a nudix hydrolase from clostridium perfringens
77	<a href="#">c2qjoB_</a>	Alignment	not modelled	9.9	22	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nm2 adenyllyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nm2 adenyllyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
78	<a href="#">c2m4mA_</a>	Alignment	not modelled	9.8	24	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;

78	<a href="#">c2144nA</a>	Alignment	not modelled	9.8	24	<b>PDBTitle:</b> solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata <b>PDB header:</b> dna binding protein
79	<a href="#">c3gz8C</a>	Alignment	not modelled	9.7	22	<b>Chain:</b> C; <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> cocrystal structure of nudix domain of shewanella oneidensis nrtr2 complexed with adp ribose
80	<a href="#">c6nhsA</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of the beta lactamase class d ybxi from nostoc
81	<a href="#">c5g5tA</a>	Alignment	not modelled	9.6	8	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> argonaute; <b>PDBTitle:</b> structure of the argonaute protein from methanocaldococcus janaschii in2 complex with guide dna
82	<a href="#">c2p3nB</a>	Alignment	not modelled	9.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> inositol-1-monophosphatase; <b>PDBTitle:</b> thermotoga maritima impase tm1415
83	<a href="#">c3hhjA</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> crystal structure of mutator mutt from bartonella henselae
84	<a href="#">c5eq9A</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> inositol monophosphatase; <b>PDBTitle:</b> crystal structure of medicago truncatula histidinol-phosphate2 phosphatase (mthpp) in complex with l-histidinol phosphate and mg2+
85	<a href="#">d1qjha</a>	Alignment	not modelled	9.4	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Ribosomal protein S6 <b>Family:</b> Ribosomal protein S6
86	<a href="#">c2ylnA</a>	Alignment	not modelled	9.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative abc transporter, periplasmic binding protein, <b>PDBTitle:</b> crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
87	<a href="#">c2ieeB</a>	Alignment	not modelled	9.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> probable abc transporter extracellular-binding protein <b>PDBTitle:</b> crystal structure of yckb_bacsu from bacillus subtilis. northeast2 structural genomics consortium target sr574.
88	<a href="#">c5onkA</a>	Alignment	not modelled	9.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> yndl; <b>PDBTitle:</b> native yndl
89	<a href="#">d1pxza</a>	Alignment	not modelled	8.9	60	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Pectate lyase-like
90	<a href="#">c5zonA</a>	Alignment	not modelled	8.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> histidinol phosphate phosphatase from mycobacterium tuberculosis
91	<a href="#">c5x1xA</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mutator mutt protein; <b>PDBTitle:</b> solution nmr structure of dna mismatch repair protein mutt (family2 nudix hydrolase) from methicillin resistant staphylococcus aureus 252
92	<a href="#">c3grnB</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mutt related protein; <b>PDBTitle:</b> crystal structure of mutt protein from methanosarcina mazei go1
93	<a href="#">d2g7sa1</a>	Alignment	not modelled	8.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
94	<a href="#">c3n77B</a>	Alignment	not modelled	8.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> nucleoside triphosphatase nudi; <b>PDBTitle:</b> crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
95	<a href="#">c5ln5A</a>	Alignment	not modelled	8.4	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin and wlm domain-containing metalloprotease <b>PDBTitle:</b> crystal structure of the wss1 e203q mutant from s. pombe
96	<a href="#">c2xfmA</a>	Alignment	not modelled	8.3	67	<b>PDB header:</b> rna/protein <b>Chain:</b> A; <b>PDB Molecule:</b> piwi-like protein 1; <b>PDBTitle:</b> complex structure of the miwi paz domain bound to methylated single2 stranded rna
97	<a href="#">c5uxtC</a>	Alignment	not modelled	8.3	57	<b>PDB header:</b> de novo protein <b>Chain:</b> C; <b>PDB Molecule:</b> coiled-coil trimer with glu:trp:lys triad; <b>PDBTitle:</b> coiled-coil trimer with glu:trp:lys triad
98	<a href="#">d1kx5d</a>	Alignment	not modelled	8.1	11	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
99	<a href="#">d1puna</a>	Alignment	not modelled	8.1	16	<b>Fold:</b> Nudix <b>Superfamily:</b> Nudix <b>Family:</b> MutT-like