

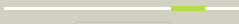




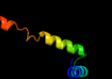

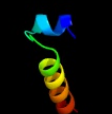

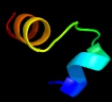





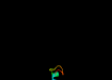

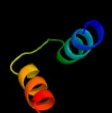


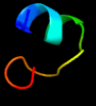






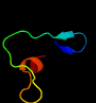
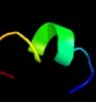


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1265_(-)_1413266_1413946
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	2ba239c69c7007eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2bj7a1</a>	 Alignment		78.2	14	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
2	<a href="#">d1h3fa2</a>	 Alignment		64.0	29	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
3	<a href="#">d1jh3a_</a>	 Alignment		60.8	35	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
4	<a href="#">c5cegC_</a>	 Alignment		59.4	18	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> addiction module antidote protein, copg/arc/metj family; <b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
5	<a href="#">d2hzaa1</a>	 Alignment		52.6	21	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
6	<a href="#">d2hza1</a>	 Alignment		48.8	27	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
7	<a href="#">c1q5vB_</a>	 Alignment		48.4	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
8	<a href="#">c2bj3D_</a>	 Alignment		48.0	19	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
9	<a href="#">c2janD_</a>	 Alignment		46.6	35	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
10	<a href="#">c2v6zM_</a>	 Alignment		45.4	21	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase epsilon subunit 2; <b>PDBTitle:</b> solution structure of amino-terminal domain of human dna polymerase2 epsilon subunit b
11	<a href="#">c2ca9B_</a>	 Alignment		45.3	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation

12	<a href="#">c6otjA_</a>	Alignment		40.3	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine--trna ligase; <b>PDBTitle:</b> crystal structure of tyrosyl-trna synthetase from neisseria2 gonorrhoeae with bound l-tyr
13	<a href="#">c1h3eA_</a>	Alignment		34.8	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
14	<a href="#">c4oudA_</a>	Alignment		33.8	35	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosyl-trna synthetase; <b>PDBTitle:</b> engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
15	<a href="#">c3hp7A_</a>	Alignment		26.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin, putative; <b>PDBTitle:</b> putative hemolysin from streptococcus thermophilus.
16	<a href="#">d1dm9a_</a>	Alignment		25.9	30	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Heat shock protein 15 kD
17	<a href="#">c1dm9A_</a>	Alignment		25.9	30	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 15.5 kd protein in mrca-pcka intergenic <b>PDBTitle:</b> heat shock protein 15 kd
18	<a href="#">d1uhwa_</a>	Alignment		25.4	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
19	<a href="#">c2v43A_</a>	Alignment		24.8	42	<b>PDB header:</b> regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sigma-e factor regulatory protein rseb; <b>PDBTitle:</b> crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
20	<a href="#">c2i6hA_</a>	Alignment		21.6	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0120; <b>PDBTitle:</b> structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
21	<a href="#">d2i6ha1</a>	Alignment	not modelled	21.6	38	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Atu0120-like
22	<a href="#">d1w4ma_</a>	Alignment	not modelled	20.5	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
23	<a href="#">d2axtz1</a>	Alignment	not modelled	18.3	30	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> PsbZ-like <b>Family:</b> PsbZ-like
24	<a href="#">c5z81A_</a>	Alignment	not modelled	17.9	35	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 15; <b>PDBTitle:</b> trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
25	<a href="#">c3nmeA_</a>	Alignment	not modelled	17.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sex4 glucan phosphatase; <b>PDBTitle:</b> structure of a plant phosphatase
26	<a href="#">c6bywB_</a>	Alignment	not modelled	16.7	26	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> goxa; <b>PDBTitle:</b> structure of goxa from pseudoalteromonas luteoviolacea
27	<a href="#">c6fhsH_</a>	Alignment	not modelled	16.5	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> les2; <b>PDBTitle:</b> cryoem structure of ino80core
28	<a href="#">c5t9yA_</a>	Alignment	not modelled	16.4	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> he protein; <b>PDBTitle:</b> crystal structure of the infectious salmon anemia virus (isav)2 hemagglutinin-esterase protein
29	<a href="#">d1mdah_</a>	Alignment	not modelled	15.9	20	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> YVTN repeat-like/Quinoprotein amine dehydrogenase

						<b>Family:</b> Methylamine dehydrogenase, H-chain
30	<a href="#">c1oeiA_</a>	Alignment	not modelled	13.8	62	<b>PDB header:</b> prion protein <b>Chain:</b> A: <b>PDB Molecule:</b> major prion protein; <b>PDBTitle:</b> human prion protein 61-84
31	<a href="#">c3kb8A_</a>	Alignment	not modelled	13.7	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
32	<a href="#">c6fmlH_</a>	Alignment	not modelled	13.7	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> les2; <b>PDBTitle:</b> cryoem structure ino80core nucleosome complex
33	<a href="#">d2ccaa1</a>	Alignment	not modelled	13.0	23	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
34	<a href="#">c2nsvA_</a>	Alignment	not modelled	12.9	75	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mating pheromone en-1; <b>PDBTitle:</b> nmr solution structure of the pheromone en-1
35	<a href="#">c3kxeD_</a>	Alignment	not modelled	12.8	29	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
36	<a href="#">c2cqjA_</a>	Alignment	not modelled	12.4	22	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u3 small nucleolar ribonucleoprotein protein <b>PDBTitle:</b> solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
37	<a href="#">d1c06a_</a>	Alignment	not modelled	11.3	33	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4
38	<a href="#">c5yhha_</a>	Alignment	not modelled	10.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein yim; <b>PDBTitle:</b> crystal structure of yim from geobacillus stearothermophilus
39	<a href="#">c2ys9A_</a>	Alignment	not modelled	10.1	37	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox and leucine zipper protein homez; <b>PDBTitle:</b> structure of the third homeodomain from the human homeobox2 and leucine zipper protein, homez
40	<a href="#">d1q0oa2</a>	Alignment	not modelled	9.9	15	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
41	<a href="#">d1v3fa_</a>	Alignment	not modelled	9.8	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
42	<a href="#">c3mmlE_</a>	Alignment	not modelled	9.4	42	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> allophanate hydrolase subunit 2; <b>PDBTitle:</b> allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
43	<a href="#">c4u65A_</a>	Alignment	not modelled	9.3	25	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> two component histidine kinase, ggdef domain protein/eal <b>PDBTitle:</b> structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
44	<a href="#">c5bs1C_</a>	Alignment	not modelled	9.1	27	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> crrbcx-iiia; <b>PDBTitle:</b> crystal structure of rbcx-iiia from chlamydomonas reinhardtii
45	<a href="#">c3clqC_</a>	Alignment	not modelled	9.1	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 enterococcus faecalis v583
46	<a href="#">c3j20D_</a>	Alignment	not modelled	8.8	38	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 30s ribosomal protein s4p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
47	<a href="#">d2csoa1</a>	Alignment	not modelled	8.4	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
48	<a href="#">c6a68A_</a>	Alignment	not modelled	8.3	31	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-dependent secretion activator 1; <b>PDBTitle:</b> the crystal structure of rat calcium-dependent activator protein for2 secretion (caps) damh domain
49	<a href="#">d2p6ra1</a>	Alignment	not modelled	8.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> RecQ helicase DNA-binding domain-like
50	<a href="#">d1vdca2</a>	Alignment	not modelled	8.0	17	<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
51	<a href="#">c5yysC_</a>	Alignment	not modelled	7.9	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> l-fucokinase, l-fucose-1-p guanylyltransferase; <b>PDBTitle:</b> cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
52	<a href="#">c1fryA_</a>	Alignment	not modelled	7.9	42	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> myeloid antimicrobial peptide; <b>PDBTitle:</b> the solution structure of sheep myeloid antimicrobial2 peptide, residues 1-29 (smap29)
53	<a href="#">c3tsyA_</a>	Alignment	not modelled	7.8	29	<b>PDB header:</b> ligase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein 4-coumarate--coa ligase 1, resveratrol <b>PDBTitle:</b> 4-coumaroyl-coa ligase::stilbene synthase fusion protein

54	<a href="#">c1lnsA</a>	Alignment	not modelled	7.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> x-prolyl dipeptidyl aminopeptidase; <b>PDBTitle:</b> crystal structure analysis of the x-prolyl dipeptidyl aminopeptidase2 from lactococcus lactis
55	<a href="#">c2jyaA</a>	Alignment	not modelled	7.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1810; <b>PDBTitle:</b> nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
56	<a href="#">c6in8A</a>	Alignment	not modelled	7.7	44	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sigma factor alga regulatory protein mucb; <b>PDBTitle:</b> crystal structure of mucb
57	<a href="#">c5n81B</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrocidine synthase 1; <b>PDBTitle:</b> crystal structure of an engineered tyca variant in complex with an o-2 propargyl-beta-tyr-amp analog
58	<a href="#">d1y88a1</a>	Alignment	not modelled	7.3	27	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> Hypothetical protein AF1548, C-terminal domain
59	<a href="#">c2k48A</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
60	<a href="#">d2j01p1</a>	Alignment	not modelled	7.2	27	<b>Fold:</b> Ribosomal proteins L15p and L18e <b>Superfamily:</b> Ribosomal proteins L15p and L18e <b>Family:</b> Ribosomal proteins L15p and L18e
61	<a href="#">d1p9ka</a>	Alignment	not modelled	6.9	26	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ybcj-like
62	<a href="#">c2l3oA</a>	Alignment	not modelled	6.9	43	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interleukin 3; <b>PDBTitle:</b> solution structure of murine interleukin 3
63	<a href="#">c1v0dA</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna fragmentation factor 40 kda subunit; <b>PDBTitle:</b> crystal structure of caspase-activated dnase (cad)
64	<a href="#">d1v0da</a>	Alignment	not modelled	6.8	15	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Caspase-activated DNase, CAD (DffB, DFF40)
65	<a href="#">c3jcuZ</a>	Alignment	not modelled	6.6	26	<b>PDB header:</b> membrane protein <b>Chain:</b> Z: <b>PDB Molecule:</b> photosystem ii reaction center protein z; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
66	<a href="#">d1fsha</a>	Alignment	not modelled	6.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> DEP domain
67	<a href="#">c2k8vA</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin domain-containing protein 12; <b>PDBTitle:</b> solution structure of oxidised erp18
68	<a href="#">c5wlqA</a>	Alignment	not modelled	6.5	22	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7,microtubule- <b>PDBTitle:</b> crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
69	<a href="#">c3pjd</a>	Alignment	not modelled	6.5	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclic dimeric gmp binding protein; <b>PDBTitle:</b> structure of pseudomonas fluorescence lapd periplasmic domain
70	<a href="#">d1o89a2</a>	Alignment	not modelled	6.3	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
71	<a href="#">c2dakA</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 5; <b>PDBTitle:</b> solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
72	<a href="#">c5z08C</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> cenp-k; <b>PDBTitle:</b> the crystal structure of kinetochore subunits cenp-h//k triple2 complex
73	<a href="#">c4aukB</a>	Alignment	not modelled	6.2	86	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase m; <b>PDBTitle:</b> crystal structure of c2498 2'-o-ribose methyltransferase rlmm from2 escherichia coli
74	<a href="#">d1zc3b1</a>	Alignment	not modelled	6.0	32	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
75	<a href="#">c2xvcA</a>	Alignment	not modelled	6.0	50	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> escrt-iii; <b>PDBTitle:</b> molecular and structural basis of escrt-iii recruitment to membranes2 during archaeal cell division
76	<a href="#">c2kkgA</a>	Alignment	not modelled	5.9	62	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> major prion protein; <b>PDBTitle:</b> nmr structure of the octarepeat region of prion protein2 bound to pentosan polysulfate
77	<a href="#">c2wttN</a>	Alignment	not modelled	5.8	31	<b>PDB header:</b> transcription <b>Chain:</b> N: <b>PDB Molecule:</b> tumor protein p73; <b>PDBTitle:</b> structure of the human p73 tetramerization domain (crystal form ii)
78	<a href="#">d1jmx5</a>	Alignment	not modelled	5.6	25	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3 <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domain 3
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioester reductase domain-containing

79	<a href="#">c5mstA</a>	Alignment	not modelled	5.5	21	protein; <b>PDBTitle:</b> structure of the a domain of carboxylic acid reductase (car) from <i>Mycobacterium tuberculosis</i> in complex with amp and a co-purified carboxylic acid
80	<a href="#">c5dudB</a>	Alignment	not modelled	5.4	100	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ybgj; <b>PDBTitle:</b> crystal structure of e. coli ybgjk
81	<a href="#">d1jmla</a>	Alignment	not modelled	5.4	75	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Immunoglobulin-binding domains <b>Family:</b> Immunoglobulin-binding domains
82	<a href="#">c2wtth</a>	Alignment	not modelled	5.3	31	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> tumor protein p73; <b>PDBTitle:</b> structure of the human p73 tetramerization domain (crystal form ii)
83	<a href="#">c3u1dA</a>	Alignment	not modelled	5.2	50	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the structure of a protein with a gntR superfamily winged-helix-turn-2 helix domain from <i>Halomicrobium mukohataei</i> .
84	<a href="#">d1mwva1</a>	Alignment	not modelled	5.1	20	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
85	<a href="#">d1v9va1</a>	Alignment	not modelled	5.1	31	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> MAST3 pre-PK domain-like <b>Family:</b> MAST3 pre-PK domain-like
86	<a href="#">d2uubd1</a>	Alignment	not modelled	5.1	40	<b>Fold:</b> Alpha-L RNA-binding motif <b>Superfamily:</b> Alpha-L RNA-binding motif <b>Family:</b> Ribosomal protein S4