
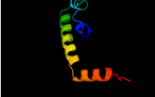


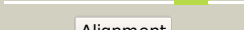

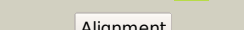







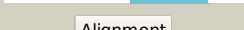

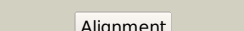

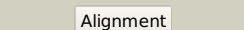


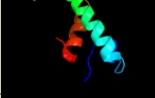











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0360c (-) _438303_438740
Date	Tue Jul 23 14:50:43 BST 2019
Unique Job ID	b4ef6b5315ac380c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1bxca_</a>	 Alignment		76.6	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
2	<a href="#">c5v2gB_</a>	 Alignment		61.2	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> 20-mer peptide; <b>PDBTitle:</b> de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
3	<a href="#">c5v2gA_</a>	 Alignment		61.2	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> 20-mer peptide; <b>PDBTitle:</b> de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
4	<a href="#">c5v2gC_</a>	 Alignment		61.2	50	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> 20-mer peptide; <b>PDBTitle:</b> de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
5	<a href="#">c5fjsB_</a>	 Alignment		58.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosylceramidase; <b>PDBTitle:</b> bacterial beta-glucosidase reveals the structural and functional2 basis of genetic defects in human glucocerebrosidase 2 (gba2)3 disorders
6	<a href="#">d1bxba_</a>	 Alignment		55.7	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
7	<a href="#">c2ww1B_</a>	 Alignment		53.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
8	<a href="#">c5swiD_</a>	 Alignment		37.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sugar hydrolase; <b>PDBTitle:</b> crystal structure of spgh92 in complex with mannose
9	<a href="#">c3f1iS_</a>	 Alignment		36.4	28	<b>PDB header:</b> protein binding <b>Chain:</b> S: <b>PDB Molecule:</b> signal transducing adapter molecule 1; <b>PDBTitle:</b> human escrt-0 core complex
10	<a href="#">c3ktcB_</a>	 Alignment		30.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
11	<a href="#">c4ozwA_</a>	 Alignment		30.4	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> alginate lyase; <b>PDBTitle:</b> crystal structure of the periplasmic alginate lyase alg h202a mutant

12	<a href="#">c2l3gA_</a>	Alignment		21.7	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rho guanine nucleotide exchange factor 7; <b>PDBTitle:</b> solution nmr structure of ch domain of rho guanine nucleotide exchange2 factor 7 from homo sapiens, northeast structural genomics consortium3 target hr4495e
13	<a href="#">d1iq0a1</a>	Alignment		21.2	22	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
14	<a href="#">c3mkqB_</a>	Alignment		20.2	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
15	<a href="#">c4madA_</a>	Alignment		17.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382
16	<a href="#">c2ihmA_</a>	Alignment		16.9	42	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase mu; <b>PDBTitle:</b> polymerase mu in ternary complex with gapped 11mer dna duplex and2 bound incoming nucleotide
17	<a href="#">d1f7ua1</a>	Alignment		16.2	17	<b>Fold:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Superfamily:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases <b>Family:</b> Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
18	<a href="#">c4c9bB_</a>	Alignment		15.6	19	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc22 homolog; <b>PDBTitle:</b> crystal structure of eif4aiii-cwc22 complex
19	<a href="#">c2m35A_</a>	Alignment		15.4	78	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> k-ssm1a; <b>PDBTitle:</b> nmr study of k-ssm1a
20	<a href="#">d1muwa_</a>	Alignment		14.9	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
21	<a href="#">c4zlgA_</a>	Alignment	not modelled	14.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative b-glycan phosphorylase; <b>PDBTitle:</b> cellobionic acid phosphorylase - gluconic acid complex
22	<a href="#">d1c6vx_</a>	Alignment	not modelled	13.6	71	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
23	<a href="#">c1c6vX_</a>	Alignment	not modelled	13.6	71	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> protein (siu89134); <b>PDBTitle:</b> siv integrase (catalytic domain + dna biding domain comprising2 residues 50-293) mutant with phe 185 replaced by his (f185h)
24	<a href="#">d1qt1a_</a>	Alignment	not modelled	12.9	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
25	<a href="#">c4gmnA_</a>	Alignment	not modelled	12.1	13	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structural basis of rpl5 recognition by syo1
26	<a href="#">c2gm4B_</a>	Alignment	not modelled	12.0	30	<b>PDB header:</b> recombination, dna <b>Chain:</b> B: <b>PDB Molecule:</b> transposon gamma-delta resolvase; <b>PDBTitle:</b> an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
27	<a href="#">c3ty8A_</a>	Alignment	not modelled	11.6	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide 2',3'-cyclic phosphate phosphodiesterase / <b>PDBTitle:</b> crystal structure of c. thermocellum pnkp ligase domain apo form
28	<a href="#">c4e6nC_</a>	Alignment	not modelled	11.4	32	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> metallophosphoesterase; <b>PDBTitle:</b> crystal structure of bacterial pnkp-c/hen1-n heterodimer
						<b>PDB header:</b> structural protein

29	<a href="#">c1wynA</a>	Alignment	not modelled	11.1	24	<b>Chain:</b> A: <b>PDB Molecule:</b> calponin-2; <b>PDBTitle:</b> solution structure of the ch domain of human calponin-2
30	<a href="#">c5wftA</a>	Alignment	not modelled	9.9	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> pelb; <b>PDBTitle:</b> pelb 319-436 from pseudomonas aeruginosa pao1
31	<a href="#">c4luqD</a>	Alignment	not modelled	9.3	45	<b>PDB header:</b> protein binding/toxin inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of virulence effector tse3 in complex with2 neutralizer tsi3
32	<a href="#">d2pqrB1</a>	Alignment	not modelled	9.3	21	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
33	<a href="#">c5a1uC</a>	Alignment	not modelled	9.2	28	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> coatomer subunit alpha; <b>PDBTitle:</b> the structure of the copi coat triad
34	<a href="#">d1y8ma1</a>	Alignment	not modelled	9.2	21	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
35	<a href="#">c5dseC</a>	Alignment	not modelled	9.1	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> tetratricopeptide repeat protein 7b; <b>PDBTitle:</b> crystal structure of the ttc7b/hyccin complex
36	<a href="#">c3p6IA</a>	Alignment	not modelled	9.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distansonic atcc 8503 at 1.85 a resolution
37	<a href="#">c5ikjB</a>	Alignment	not modelled	8.7	71	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cryptic loci regulator protein 1; <b>PDBTitle:</b> structure of clr2 bound to the clr1 c-terminus
38	<a href="#">c2i2oB</a>	Alignment	not modelled	8.7	57	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> eif4g-like protein; <b>PDBTitle:</b> crystal structure of an eif4g-like protein from danio rerio
39	<a href="#">c2hk1D</a>	Alignment	not modelled	8.6	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
40	<a href="#">d1ex4a1</a>	Alignment	not modelled	8.5	71	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
41	<a href="#">d1kpta</a>	Alignment	not modelled	8.3	37	<b>Fold:</b> Yeast killer toxins <b>Superfamily:</b> Yeast killer toxins <b>Family:</b> Virally encoded KP4 toxin
42	<a href="#">d1ihwa</a>	Alignment	not modelled	8.3	71	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
43	<a href="#">c6f90A</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,2-mannosidase, putative; <b>PDBTitle:</b> structure of the family gh92 alpha-mannosidase bt3130 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)
44	<a href="#">c2rbaB</a>	Alignment	not modelled	8.0	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> g/t mismatch-specific thymine dna glycosylase; <b>PDBTitle:</b> structure of human thymine dna glycosylase bound to abasic and2 undamaged dna
45	<a href="#">c1wymA</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> transgelin-2; <b>PDBTitle:</b> solution structure of the ch domain of human transgelin-2
46	<a href="#">c4I3uA</a>	Alignment	not modelled	7.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3571 family protein (abaye3784) from2 acinetobacter baumannii aye at 1.95 a resolution
47	<a href="#">c3nzkB</a>	Alignment	not modelled	7.3	39	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine <b>PDBTitle:</b> structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
48	<a href="#">c5lc5D</a>	Alignment	not modelled	7.2	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
49	<a href="#">c3thdD</a>	Alignment	not modelled	7.2	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
50	<a href="#">d1mpga2</a>	Alignment	not modelled	7.2	22	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> DNA repair glycosylase, N-terminal domain
51	<a href="#">d1zu2a1</a>	Alignment	not modelled	7.1	9	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
52	<a href="#">d1v29b</a>	Alignment	not modelled	7.1	33	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
53	<a href="#">c3hluA</a>	Alignment	not modelled	7.1	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf2179; <b>PDBTitle:</b> crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
54	<a href="#">c3j3vE</a>	Alignment	not modelled	7.1	31	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 50s ribosomal protein I4; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
						<b>PDB header:</b> transferase

55	<a href="#">c3c66C</a>	Alignment	not modelled	7.0	63	<b>Chain:</b> C: <b>PDB Molecule:</b> pre-mrna polyadenylation factor fip1; <b>PDBTitle:</b> yeast poly(a) polymerase in complex with fip1 residues 80-105
56	<a href="#">c6gcsC</a>	Alignment	not modelled	6.9	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 49-kda protein (nucm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
57	<a href="#">c3c66D</a>	Alignment	not modelled	6.9	63	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pre-mrna polyadenylation factor fip1; <b>PDBTitle:</b> yeast poly(a) polymerase in complex with fip1 residues 80-105
58	<a href="#">c4yl8B</a>	Alignment	not modelled	6.9	32	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> protein crumbs; <b>PDBTitle:</b> crystal structure of the crumbs/moesin complex
59	<a href="#">c3j3bq</a>	Alignment	not modelled	6.7	6	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein l18; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
60	<a href="#">c6bs7A</a>	Alignment	not modelled	6.7	53	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
61	<a href="#">d1hh5a</a>	Alignment	not modelled	6.5	28	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Cytochrome c3-like
62	<a href="#">c4e8cA</a>	Alignment	not modelled	6.4	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 35; <b>PDBTitle:</b> crystal structure of streptococcal beta-galactosidase in complex with2 galactose
63	<a href="#">d1pc2a</a>	Alignment	not modelled	6.3	16	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TPR-like <b>Family:</b> Tetratricopeptide repeat (TPR)
64	<a href="#">d2btva</a>	Alignment	not modelled	6.3	38	<b>Fold:</b> Reovirus inner layer core protein p3 <b>Superfamily:</b> Reovirus inner layer core protein p3 <b>Family:</b> Orbivirus core
65	<a href="#">d2cy3a</a>	Alignment	not modelled	6.2	30	<b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Cytochrome c3-like
66	<a href="#">c2btvB</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> protein (vp3 core protein); <b>PDBTitle:</b> atomic model for bluetongue virus (btv) core
67	<a href="#">c3iz5s</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein l18a (l18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
68	<a href="#">d1hx7a</a>	Alignment	not modelled	6.1	32	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> Resolvase-like <b>Family:</b> gamma,delta resolvase, catalytic domain
69	<a href="#">d1te4a</a>	Alignment	not modelled	6.0	20	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> PBS lyase HEAT-like repeat
70	<a href="#">c5mlc2</a>	Alignment	not modelled	6.0	36	<b>PDB header:</b> ribosome <b>Chain:</b> 2: <b>PDB Molecule:</b> 50s ribosomal protein l32, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
71	<a href="#">c5f5nA</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> the structure of monooxygenase ksta11 in complex with nad and its2 substrate
72	<a href="#">c4ijyA</a>	Alignment	not modelled	5.7	55	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cofj; <b>PDBTitle:</b> crystal structure of the etec secreted protein cofj
73	<a href="#">c4cimQ</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> apoptosis <b>Chain:</b> Q: <b>PDB Molecule:</b> bcl-2-like protein 2; <b>PDBTitle:</b> complex of a bcl-w bh3 mutant with a bh3 domain
74	<a href="#">c4cimP</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> apoptosis <b>Chain:</b> P: <b>PDB Molecule:</b> bcl-2-like protein 2; <b>PDBTitle:</b> complex of a bcl-w bh3 mutant with a bh3 domain
75	<a href="#">c3h4nB</a>	Alignment	not modelled	5.5	27	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c7; <b>PDBTitle:</b> ppcd, a cytochrome c7 from geobacter sulfurreducens
76	<a href="#">c2lsqA</a>	Alignment	not modelled	5.4	63	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> analog of the fragment 197-221 of beta-1 adrenoreceptor; <b>PDBTitle:</b> analog of the fragment 197-221 of beta-1 adrenoreceptor
77	<a href="#">c1lv4A</a>	Alignment	not modelled	5.4	50	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> catestatin; <b>PDBTitle:</b> human catestatin 21-mer
78	<a href="#">c5n4aA</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport protein 80; <b>PDBTitle:</b> crystal structure of chlamydomonas ift80
79	<a href="#">c2c2pA</a>	Alignment	not modelled	5.3	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> g/u mismatch-specific dna glycosylase; <b>PDBTitle:</b> the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
80	<a href="#">c5ncrA</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine phosphatase; <b>PDBTitle:</b> oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
81	<a href="#">c3izcs</a>	Alignment	not modelled	5.3	6	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein rpl20 (l18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s

				ribosome	
82	<a href="#">d1hu3a_</a>	Alignment	not modelled	5.2	30 <b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
83	<a href="#">d1rwja_</a>	Alignment	not modelled	5.1	40 <b>Fold:</b> Multiheme cytochromes <b>Superfamily:</b> Multiheme cytochromes <b>Family:</b> Cytochrome c3-like
84	<a href="#">c6f92B_</a>	Alignment	not modelled	5.1	23 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of the family gh92 alpha-mannosidase bt3965 from bacteroides2 thetaiotaomicron in complex with mannoimidazole (mani)