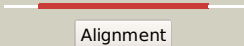



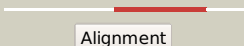

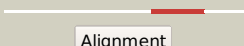

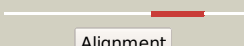
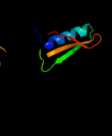
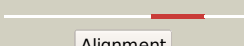

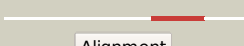
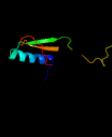









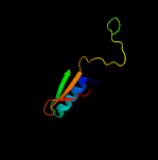

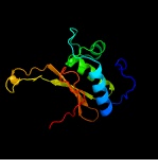


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2409c_(-)_2706504_2707343
Date	Wed Aug 7 12:50:02 BST 2019
Unique Job ID	4e51eb83247178dd

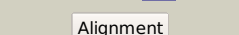


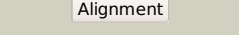
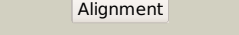

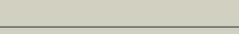
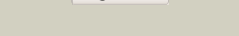



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3lsrB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transglutaminase-like enzymes, putative cysteine protease; <b>PDBTitle:</b> the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
2	<a href="#">c6g49A_</a>	 Alignment		99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of the periplasmic domain of tgpa from pseudomonas2 aeruginosa
3	<a href="#">c4xz7A_</a>	 Alignment		99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a tgase
4	<a href="#">d2q3za4</a>	 Alignment		99.6	35	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
5	<a href="#">d1g0da4</a>	 Alignment		99.6	37	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
6	<a href="#">d1vjja4</a>	 Alignment		99.5	32	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
7	<a href="#">d1ex0a4</a>	 Alignment		99.5	38	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
8	<a href="#">d2f4ma1</a>	 Alignment		99.5	30	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
9	<a href="#">c3kd4A_</a>	 Alignment		99.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative protease; <b>PDBTitle:</b> crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
10	<a href="#">d1x3za1</a>	 Alignment		99.1	32	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
11	<a href="#">c1l9mB_</a>	 Alignment		99.0	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein-glutamine glutamyltransferase e3; <b>PDBTitle:</b> three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation

12	<a href="#">c1f13A_</a>	Alignment		99.0	37	<b>PDB header:</b> coagulation factor <b>Chain:</b> A: <b>PDB Molecule:</b> cellular coagulation factor xiii zymogen; <b>PDBTitle:</b> recombinant human cellular coagulation factor xiii
13	<a href="#">c1g0dA_</a>	Alignment		99.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of red sea bream transglutaminase
14	<a href="#">c4u65F_</a>	Alignment		99.0	18	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> putative cystine protease; <b>PDBTitle:</b> structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
15	<a href="#">c1kv3F_</a>	Alignment		99.0	33	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> human tissue transglutaminase in gdp bound form
16	<a href="#">c2qshA_</a>	Alignment		98.7	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad4; <b>PDBTitle:</b> crystal structure of rad4-rad23 bound to a mismatch dna
17	<a href="#">c3eswA_</a>	Alignment		98.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine <b>PDBTitle:</b> complex of yeast pngase with glcnac2-iac.
18	<a href="#">c4fgpB_</a>	Alignment		98.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein; <b>PDBTitle:</b> legionella pneumophila lapg (egta-treated)
19	<a href="#">c2pfrB_</a>	Alignment		97.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arylamine n-acetyltransferase 2; <b>PDBTitle:</b> human n-acetyltransferase 2
20	<a href="#">c2vfbA_</a>	Alignment		96.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylamine n-acetyltransferase; <b>PDBTitle:</b> the structure of mycobacterium marinum arylamine n-2 acetyltransferase
21	<a href="#">d1w4ta1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
22	<a href="#">c3lnbA_</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase family protein; <b>PDBTitle:</b> crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
23	<a href="#">c4guzA_</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable arylamine n-acetyl transferase; <b>PDBTitle:</b> structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
24	<a href="#">d1e2ta_</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
25	<a href="#">c3d9wA_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase; <b>PDBTitle:</b> crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase
26	<a href="#">d1w5ra1</a>	Alignment	not modelled	96.0	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
27	<a href="#">d2bsza1</a>	Alignment	not modelled	96.0	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
28	<a href="#">c4dmoB_</a>	Alignment	not modelled	95.6	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-hydroxyarylamine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of the (baccr)nat3 arylamine n-acetyltransferase2 from bacillus cereus reveals a unique cys-his-glu catalytic triad

29	<a href="#">d2hlya1</a>	Alignment	not modelled	63.4	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Atu2299-like
30	<a href="#">d1kbla2</a>	Alignment	not modelled	49.5	14	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
31	<a href="#">c2lzoA</a>	Alignment	not modelled	40.8	24	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> ugt3; <b>PDBTitle:</b> spatial structure of pi-anmtx ugr 9a-1
32	<a href="#">c1kblA</a>	Alignment	not modelled	37.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase
33	<a href="#">d2f2ha3</a>	Alignment	not modelled	34.9	27	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> Putative glucosidase YicI, domain 3
34	<a href="#">c5x7rB</a>	Alignment	not modelled	34.7	20	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 31 alpha-glucosidase; <b>PDBTitle:</b> crystal structure of paenibacillus sp. 598k alpha-1,6-2 glucosyltransferase complexed with isomaltotetraose
35	<a href="#">c5vglA</a>	Alignment	not modelled	32.2	3	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> lachrymatory-factor synthase; <b>PDBTitle:</b> crystal structure of lachrymatory factor synthase from allium cepa
36	<a href="#">d1n2fa</a>	Alignment	not modelled	28.9	14	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
37	<a href="#">d2ftxa1</a>	Alignment	not modelled	26.4	43	<b>Fold:</b> Kinetochore globular domain-like <b>Superfamily:</b> Kinetochore globular domain <b>Family:</b> Spc25-like
38	<a href="#">d1u2ca1</a>	Alignment	not modelled	25.3	29	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cadherin-like <b>Family:</b> Dystroglycan, N-terminal domain
39	<a href="#">d1jvaa3</a>	Alignment	not modelled	23.3	14	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
40	<a href="#">c5mjrA</a>	Alignment	not modelled	22.4	12	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> protein thf1; <b>PDBTitle:</b> structure of psb29 at 1.55a
41	<a href="#">d1nyed</a>	Alignment	not modelled	22.2	13	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
42	<a href="#">c2ml7A</a>	Alignment	not modelled	22.1	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> specific abundant protein 3; <b>PDBTitle:</b> ginsentides: characterization, structure and application of a new 2 class of highly stable cystine knot peptides in ginseng
43	<a href="#">c4nwbA</a>	Alignment	not modelled	21.6	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mrna turnover protein 4; <b>PDBTitle:</b> crystal structure of mrt4
44	<a href="#">c3phzA</a>	Alignment	not modelled	21.4	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ricin b-related lectin; <b>PDBTitle:</b> crystal structure analysis of polyporus squamosus lectin bound to 2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
45	<a href="#">c1vbhA</a>	Alignment	not modelled	21.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate, orthophosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase with bound mg-pep from maize
46	<a href="#">c1rpcA</a>	Alignment	not modelled	21.2	50	<b>PDB header:</b> replication inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> tricyclic peptide rp 71955; <b>PDBTitle:</b> solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
47	<a href="#">d1h59b</a>	Alignment	not modelled	20.5	33	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Growth factor receptor domain <b>Family:</b> Growth factor receptor domain
48	<a href="#">c5t1oB</a>	Alignment	not modelled	20.4	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase ptsp; <b>PDBTitle:</b> solution-state nmr and saxs structural ensemble of npr (1-85) in 2 complex with ein-ntr (170-424)
49	<a href="#">c1rpbA</a>	Alignment	not modelled	20.3	50	<b>PDB header:</b> replication inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> tricyclic peptide rp 71955; <b>PDBTitle:</b> solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
50	<a href="#">c4dx94</a>	Alignment	not modelled	19.8	20	<b>PDB header:</b> protein binding <b>Chain:</b> 4: <b>PDB Molecule:</b> integrin beta-1-binding protein 1; <b>PDBTitle:</b> icap1 in complex with integrin beta 1 cytoplasmic tail
51	<a href="#">c6ak0A</a>	Alignment	not modelled	19.7	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cys-leu-gly-val-gly-ser-cys-val-asp-phe-alg-gly-cys-gly- <b>PDBTitle:</b> solution nmr structure of a new lasso peptide specialicin
52	<a href="#">d1vbga2</a>	Alignment	not modelled	19.5	14	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
53	<a href="#">d1mxga1</a>	Alignment	not modelled	19.4	41	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
54	<a href="#">c1xsf</a>	Alignment	not modelled	19.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> putative family 31 glucosidase yici; <b>PDBTitle:</b> structure of a family 31 alpha glucosidase
						<b>PDB header:</b> phosphotransferase

55	<a href="#">c1ezaA_</a>	Alignment	not modelled	18.5	25	<b>Chain:</b> A: <b>PDB Molecule:</b> enzyme i; <b>PDBTitle:</b> amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
56	<a href="#">c2j0wA_</a>	Alignment	not modelled	18.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-sensitive aspartokinase 3; <b>PDBTitle:</b> crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
57	<a href="#">d1w7ja1</a>	Alignment	not modelled	18.2	12	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
58	<a href="#">c6cggA_</a>	Alignment	not modelled	18.1	4	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
59	<a href="#">d1zyna2</a>	Alignment	not modelled	17.7	25	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
60	<a href="#">c3jsyA_</a>	Alignment	not modelled	16.8	41	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> acidic ribosomal protein p0 homolog; <b>PDBTitle:</b> n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
61	<a href="#">c4mh4B_</a>	Alignment	not modelled	16.2	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> osmc-like protein; <b>PDBTitle:</b> crystal structure of osmc-like protein from burkholderia cenocepacia2 j2315
62	<a href="#">c5f7sA_</a>	Alignment	not modelled	15.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 31; <b>PDBTitle:</b> cycloalternan-degrading enzyme from trueperella pyogenes
63	<a href="#">c3j3bq_</a>	Alignment	not modelled	15.5	14	<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
64	<a href="#">d1j0aa_</a>	Alignment	not modelled	15.4	12	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
65	<a href="#">d1ml8a_</a>	Alignment	not modelled	14.7	10	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> YhfA-like
66	<a href="#">c4xpsA_</a>	Alignment	not modelled	14.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of the mutant d365a of pedobacter saltans gh312 alpha-galactosidase complexed with p-nitrophenyl-alpha-3 galactopyranoside
67	<a href="#">d2ihoa2</a>	Alignment	not modelled	14.3	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> MOA C-terminal domain-like
68	<a href="#">d1p5ja_</a>	Alignment	not modelled	14.2	16	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	<a href="#">c1p5jA_</a>	Alignment	not modelled	14.2	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure analysis of human serine dehydratase
70	<a href="#">c5td8D_</a>	Alignment	not modelled	13.8	39	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> kinetochore protein spc25; <b>PDBTitle:</b> crystal structure of an extended dwarf ndc80 complex
71	<a href="#">c2gp4A_</a>	Alignment	not modelled	13.7	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydratase; <b>PDBTitle:</b> structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
72	<a href="#">c6mvhD_</a>	Alignment	not modelled	13.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of fmn-binding beta-glucuronidase from roseburia2 hominis
73	<a href="#">c1x4rA_</a>	Alignment	not modelled	13.6	7	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> parp14 protein; <b>PDBTitle:</b> solution structure of wwe domain in parp14 protein
74	<a href="#">c3idwA_</a>	Alignment	not modelled	13.6	37	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> actin cytoskeleton-regulatory complex protein sla1; <b>PDBTitle:</b> crystal structure of sla1 homology domain 2
75	<a href="#">c6d9nA_</a>	Alignment	not modelled	13.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> organic hydroperoxide resistance protein; <b>PDBTitle:</b> crystal structure of an organic hydroperoxide resistance protein from2 elizabethkingia anophelis with crystallant-derived thiocyanate bound
76	<a href="#">c5ancC_</a>	Alignment	not modelled	13.3	14	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> 60s acidic ribosomal protein p0; <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
77	<a href="#">c3j21k_</a>	Alignment	not modelled	13.3	35	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 50s ribosomal protein l14e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
78	<a href="#">c3iz5s_</a>	Alignment	not modelled	13.1	14	<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
79	<a href="#">c5woyA_</a>	Alignment	not modelled	13.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> nmr solution structure of enzyme i (neit) protein using two 4d-spectra

80	<a href="#">c3izcs</a>	 Alignment	not modelled	12.8	23	<b>PDB header:</b> ribosome <b>Chain:</b> S; <b>PDB Molecule:</b> 60s ribosomal protein rpl20 (I18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
81	<a href="#">c3c1nA</a>	 Alignment	not modelled	12.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable aspartokinase; <b>PDBTitle:</b> crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
82	<a href="#">c5iegA</a>	 Alignment	not modelled	12.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> neutral alpha-glucosidase ab; <b>PDBTitle:</b> murine endoplasmic reticulum alpha-glucosidase ii with n-9'-2 methoxynonyl-1-deoxynojirimycin
83	<a href="#">c3mwzA</a>	 Alignment	not modelled	12.6	20	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> sialostatin I2; <b>PDBTitle:</b> crystal structure of the selenomethionine derivative of the I22,47,2 100 m mutant of sialostatin I2
84	<a href="#">c2rkbE</a>	 Alignment	not modelled	12.4	20	<b>PDB header:</b> lyase <b>Chain:</b> E; <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
85	<a href="#">c4xz6A</a>	 Alignment	not modelled	12.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> glycine betaine/proline abc transporter, periplasmic <b>PDBTitle:</b> tmox in complex with tmao
86	<a href="#">c4hubG</a>	 Alignment	not modelled	12.3	22	<b>PDB header:</b> ribosome <b>Chain:</b> G; <b>PDB Molecule:</b> 50s ribosomal protein I10e; <b>PDBTitle:</b> the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the I7/I12 and I1 stalk, I5 and Ix proteins
87	<a href="#">c5zn6D</a>	 Alignment	not modelled	12.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> alpha-xylosidase mexyl31; <b>PDBTitle:</b> crystal structure of gh31 alpha-xylosidase from a soil metagenome
88	<a href="#">d1xafa</a>	 Alignment	not modelled	12.1	17	<b>Fold:</b> CNF1/Yfih-like putative cysteine hydrolases <b>Superfamily:</b> CNF1/Yfih-like putative cysteine hydrolases <b>Family:</b> Yfih-like
89	<a href="#">c2avxA</a>	 Alignment	not modelled	11.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> regulatory protein sdia; <b>PDBTitle:</b> solution structure of e coli sdia1-171
90	<a href="#">d1yuaa2</a>	 Alignment	not modelled	11.4	30	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Prokaryotic DNA topoisomerase I, a C-terminal fragment
91	<a href="#">c5xenB</a>	 Alignment	not modelled	11.2	8	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
92	<a href="#">c4kmgA</a>	 Alignment	not modelled	11.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> lmo2446 protein; <b>PDBTitle:</b> 1.9 angstrom resolution crystal structure of uncharacterized protein2 lmo2446 from listeria monocytogenes egd-e
93	<a href="#">c6ei1A</a>	 Alignment	not modelled	11.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> zinc finger with ufm1-specific peptidase domain protein; <b>PDBTitle:</b> crystal structure of the covalent complex between deubiquitinase zufsp2 (zup1) and ubiquitin-pa
94	<a href="#">d1h6za2</a>	 Alignment	not modelled	11.1	42	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
95	<a href="#">d1uspa</a>	 Alignment	not modelled	11.0	20	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
96	<a href="#">c5b3kA</a>	 Alignment	not modelled	11.0	12	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein pa3435; <b>PDBTitle:</b> c101a mutant of flavodoxin from pseudomonas aeruginosa
97	<a href="#">c4d8tC</a>	 Alignment	not modelled	10.7	16	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> d-cysteine desulfhydrase; <b>PDBTitle:</b> crystal structure of d-cysteine desulfhydrase from salmonella2 typhimurium at 2.2 a resolution
98	<a href="#">c5cvcB</a>	 Alignment	not modelled	10.6	16	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> structure of maize serine racemase
99	<a href="#">d2j0wa1</a>	 Alignment	not modelled	10.4	15	<b>Fold:</b> Carbamate kinase-like <b>Superfamily:</b> Carbamate kinase-like <b>Family:</b> PyrH-like