






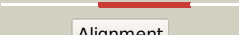

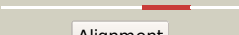






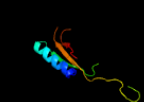






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1673c_(-) _1898307_1899239
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	d46c4c591350539b

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		100.0	19	<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		99.9	14	<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="#">c3kd4A_</a>	 Alignment		99.7	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 (bdj_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
5	<a href="#">d2q3za4</a>	 Alignment		99.7	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
6	<a href="#">d1g0da4</a>	 Alignment		99.7	25	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
7	<a href="#">d1ex0a4</a>	 Alignment		99.6	29	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
8	<a href="#">d2f4ma1</a>	 Alignment		99.6	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
9	<a href="#">d1vjja4</a>	 Alignment		99.6	23	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
10	<a href="#">c1g0dA_</a>	 Alignment		99.3	17	<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
11	<a href="#">d1x3za1</a>	 Alignment		99.3	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core

12	<a href="#">c1f13A_</a>	Alignment		99.2	31	<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="#">c19mB_</a>	Alignment		99.2	25	<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
14	<a href="#">c1kv3F_</a>	Alignment		99.2	29	<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
15	<a href="#">c4u65F_</a>	Alignment		99.0	16	<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
16	<a href="#">c3eswA_</a>	Alignment		98.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptide-n(4)-(n-acetyl-beta-glucosaminy)asparagine <b>PDBTitle:</b> complex of yeast pngase with glcnac2-iac.
17	<a href="#">c2qshA_</a>	Alignment		98.7	15	<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
18	<a href="#">c4fgpB_</a>	Alignment		97.9	16	<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		97.5	13	<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="#">c3lnbA_</a>	Alignment		97.4	10	<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
21	<a href="#">c2vfbA_</a>	Alignment	not modelled	97.2	18	<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
22	<a href="#">d1e2ta_</a>	Alignment	not modelled	97.1	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
23	<a href="#">d1w4ta1</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
24	<a href="#">d1w5ra1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
25	<a href="#">c4dmoB_</a>	Alignment	not modelled	96.9	10	<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
26	<a href="#">d2bsza1</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Arylamine N-acetyltransferase
27	<a href="#">c4guzA_</a>	Alignment	not modelled	96.7	13	<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
28	<a href="#">c3d9wA_</a>	Alignment	not modelled	96.5	12	<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

29	<a href="#">c5woyA</a>	Alignment	not modelled	64.8	29	<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
30	<a href="#">c1ezaA</a>	Alignment	not modelled	61.3	14	<b>PDB header:</b> phosphotransferase <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
31	<a href="#">c5t1oB</a>	Alignment	not modelled	60.6	20	<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) in2 complex with ein-ntr (170-424)
32	<a href="#">d2hlya1</a>	Alignment	not modelled	56.7	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Atu2299-like
33	<a href="#">c3re2A</a>	Alignment	not modelled	37.2	18	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of menin reveals the binding site for mixed lineage2 leukemia (mll) protein
34	<a href="#">d1ou9a</a>	Alignment	not modelled	35.4	27	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
35	<a href="#">d1ou8a</a>	Alignment	not modelled	35.3	27	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
36	<a href="#">d1zszc1</a>	Alignment	not modelled	34.1	27	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
37	<a href="#">c1vbhA</a>	Alignment	not modelled	33.5	11	<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
38	<a href="#">c4gq6A</a>	Alignment	not modelled	33.1	17	<b>PDB header:</b> transcription/transcription inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> menin; <b>PDBTitle:</b> human menin in complex with mll peptide
39	<a href="#">d1yfna1</a>	Alignment	not modelled	32.2	18	<b>Fold:</b> SspB-like <b>Superfamily:</b> SspB-like <b>Family:</b> Stringent starvation protein B, SspB
40	<a href="#">c3u88B</a>	Alignment	not modelled	31.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> menin; <b>PDBTitle:</b> crystal structure of human menin in complex with mll1 and ledgf
41	<a href="#">c3l0rA</a>	Alignment	not modelled	24.9	33	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cystatin-2; <b>PDBTitle:</b> crystal structure of salivary cystatin from the soft tick ornithodoros2 moubata
42	<a href="#">c3mwzA</a>	Alignment	not modelled	24.6	16	<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 I 22,47,2 100 m mutant of sialostatin I2
43	<a href="#">d2gzsa1</a>	Alignment	not modelled	24.4	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> IroE-like
44	<a href="#">c3j21k</a>	Alignment	not modelled	21.9	16	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 50s ribosomal protein I14e; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
45	<a href="#">d1zyma2</a>	Alignment	not modelled	21.8	14	<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
46	<a href="#">c4nwbA</a>	Alignment	not modelled	21.2	12	<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
47	<a href="#">c3j3bq</a>	Alignment	not modelled	19.7	15	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 60s ribosomal protein I18; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
48	<a href="#">c5o46A</a>	Alignment	not modelled	18.8	15	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> iristatin; <b>PDBTitle:</b> crystal structure of iristatin, a secreted salivary cystatin from the2 hard tick ixodes ricinus
49	<a href="#">c3iz5s</a>	Alignment	not modelled	18.5	11	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein I18a (I18ae); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
50	<a href="#">d1kbla2</a>	Alignment	not modelled	17.3	8	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
51	<a href="#">d1vbg2</a>	Alignment	not modelled	16.9	8	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
52	<a href="#">d1h6za2</a>	Alignment	not modelled	16.6	8	<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="#">d1jvaa3</a>	Alignment	not modelled	16.4	23	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
54	<a href="#">c1kq8A</a>	Alignment	not modelled	16.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte nuclear factor 3 forkhead homolog 1; <b>PDBTitle:</b> solution structure of winged helix protein hfh-1

55	<a href="#">d1kq8a_</a>	Alignment	not modelled	16.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
56	<a href="#">c4xvzB_</a>	Alignment	not modelled	16.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin iii 3''-o-methyltransferase; <b>PDBTitle:</b> mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
57	<a href="#">c1x4rA_</a>	Alignment	not modelled	15.3	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
58	<a href="#">c3iacA_</a>	Alignment	not modelled	15.3	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronate isomerase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
59	<a href="#">c3co7C_</a>	Alignment	not modelled	15.2	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> C: <b>PDB Molecule:</b> forkhead box protein o1; <b>PDBTitle:</b> crystal structure of foxo1 dbd bound to dbe2 dna
60	<a href="#">d1yuaa2</a>	Alignment	not modelled	15.1	45	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Prokaryotic DNA topoisomerase I, a C-terminal fragment
61	<a href="#">c3jsyA_</a>	Alignment	not modelled	15.1	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
62	<a href="#">c2j0wA_</a>	Alignment	not modelled	15.0	30	<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)
63	<a href="#">c2hroA_</a>	Alignment	not modelled	14.0	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
64	<a href="#">c2mbfA_</a>	Alignment	not modelled	13.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fork head domain containing protein; <b>PDBTitle:</b> solution structure of the forkhead domain of brugia malayi daf-16a
65	<a href="#">d3bpya1</a>	Alignment	not modelled	13.2	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
66	<a href="#">c5mjrA_</a>	Alignment	not modelled	13.0	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
67	<a href="#">c6cggA_</a>	Alignment	not modelled	12.8	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
68	<a href="#">c6ncmA_</a>	Alignment	not modelled	12.6	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> forkhead box protein n3; <b>PDBTitle:</b> crystal structure of the human foxn3 dna binding domain in complex2 with a forkhead-like (fhl) dna sequence
69	<a href="#">d2c6ya1</a>	Alignment	not modelled	12.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
70	<a href="#">c1e17A_</a>	Alignment	not modelled	12.5	13	<b>PDB header:</b> dna binding domain <b>Chain:</b> A: <b>PDB Molecule:</b> afx; <b>PDBTitle:</b> solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
71	<a href="#">c5b3kA_</a>	Alignment	not modelled	12.4	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
72	<a href="#">d1j0aa_</a>	Alignment	not modelled	12.2	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
73	<a href="#">c1yuaA_</a>	Alignment	not modelled	12.1	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> topoisomerase i; <b>PDBTitle:</b> c-terminal domain of escherichia coli topoisomerase i
74	<a href="#">c6h8mB_</a>	Alignment	not modelled	11.9	36	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neurotrypsin; <b>PDBTitle:</b> crystal structure of the third srcr domain of murine neurotrypsin.
75	<a href="#">c2avxA_</a>	Alignment	not modelled	11.8	12	<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
76	<a href="#">c5ocnG_</a>	Alignment	not modelled	11.7	16	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> forkhead box protein n1; <b>PDBTitle:</b> crystal structure of the forkhead domain of human foxn1
77	<a href="#">c4hubG_</a>	Alignment	not modelled	11.3	41	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l10e; <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 l7/l12 and l1 stalk, l5 and lx proteins
78	<a href="#">c3c1nA_</a>	Alignment	not modelled	10.9	10	<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
79	<a href="#">d1d5va_</a>	Alignment	not modelled	10.8	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
						<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein

80	<a href="#">c2hwgA_</a>	Alignment	not modelled	10.3	15	phosphotransferase; <b>PDBTitle:</b> structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
81	<a href="#">c6dsiB_</a>	Alignment	not modelled	10.3	14	<b>PDB header:</b> splicing <b>Chain:</b> B; <b>PDB Molecule:</b> consensus engineered intein catc; <b>PDBTitle:</b> consensus engineered intein (cat) with atypical split site
82	<a href="#">c5ancC_</a>	Alignment	not modelled	10.2	7	<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
83	<a href="#">c4wm8A_</a>	Alignment	not modelled	10.2	13	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> vp1; <b>PDBTitle:</b> crystal structure of human enterovirus d68
84	<a href="#">c3gafF_</a>	Alignment	not modelled	9.8	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> 7-alpha-hydroxysteroid dehydrogenase; <b>PDBTitle:</b> 2.2a crystal structure of 7-alpha-hydroxysteroid dehydrogenase from2 brucella melitensis
85	<a href="#">c3mxuA_</a>	Alignment	not modelled	9.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from bartonella2 henselae
86	<a href="#">c3g73A_</a>	Alignment	not modelled	9.8	13	<b>PDB header:</b> transcription/dna <b>Chain:</b> A; <b>PDB Molecule:</b> forkhead box protein m1; <b>PDBTitle:</b> structure of the foxm1 dna binding
87	<a href="#">d1p5ja_</a>	Alignment	not modelled	9.7	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
88	<a href="#">c1p5jA_</a>	Alignment	not modelled	9.7	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
89	<a href="#">c4bolA_</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
90	<a href="#">d2hfha_</a>	Alignment	not modelled	9.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
91	<a href="#">d1mxga1</a>	Alignment	not modelled	9.4	28	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
92	<a href="#">c6qfbB_</a>	Alignment	not modelled	9.4	25	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp
93	<a href="#">d1oa8a_</a>	Alignment	not modelled	9.0	46	<b>Fold:</b> AXH domain <b>Superfamily:</b> AXH domain <b>Family:</b> AXH domain
94	<a href="#">c6ei1A_</a>	Alignment	not modelled	8.8	17	<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
95	<a href="#">d2a07f1</a>	Alignment	not modelled	8.7	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
96	<a href="#">c3phzA_</a>	Alignment	not modelled	8.5	17	<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 to2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
97	<a href="#">c2rkbE_</a>	Alignment	not modelled	8.4	29	<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
98	<a href="#">c2d1fA_</a>	Alignment	not modelled	8.3	8	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
99	<a href="#">c4d8tC_</a>	Alignment	not modelled	8.2	4	<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