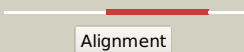
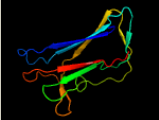
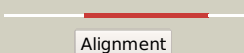




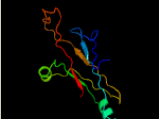

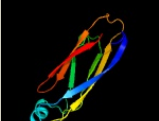




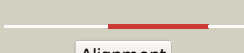









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3587c_(-)_4029147_4029941
Date	Fri Aug 9 18:20:27 BST 2019
Unique Job ID	21b04aaa4a69fdea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3isyA_</a>	 Alignment		98.5	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor; <b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
2	<a href="#">d1g4ma2</a>	 Alignment		97.3	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Arrestin/Vps26-like
3	<a href="#">c2kl6A_</a>	 Alignment		96.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
4	<a href="#">c2kutA_</a>	 Alignment		96.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
5	<a href="#">d1w8oa1</a>	 Alignment		96.3	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
6	<a href="#">c2p9rA_</a>	 Alignment		96.2	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3
7	<a href="#">c2i0dA_</a>	 Alignment		95.9	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
8	<a href="#">c5z87B_</a>	 Alignment		95.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> emgh1; <b>PDBTitle:</b> structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
9	<a href="#">d1ayra2</a>	 Alignment		95.4	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Arrestin/Vps26-like
10	<a href="#">c1jsyA_</a>	 Alignment		95.4	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bovine arrestin-2 (full length); <b>PDBTitle:</b> crystal structure of bovine arrestin-2
11	<a href="#">c5z9sB_</a>	 Alignment		95.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3 protein; <b>PDBTitle:</b> functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria

12	<a href="#">c5x7hA_</a>	Alignment		95.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cycloisomaltooligosaccharide glucanotransferase; <b>PDBTitle:</b> crystal structure of paenibacillus sp. 598k2 cycloisomaltooligosaccharide glucanotransferase complexed with3 cycloisomaltoheptaose
13	<a href="#">d1cf1a2</a>	Alignment		94.6	28	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Arrestin/Vps26-like
14	<a href="#">c5tf0B_</a>	Alignment		94.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 3 n-terminal domain protein; <b>PDBTitle:</b> crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
15	<a href="#">c3osvC_</a>	Alignment		94.3	19	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> flagellar basal-body rod modification protein flgd; <b>PDBTitle:</b> the crytsal structure of flgd from p. aeruginosa
16	<a href="#">c5a7mA_</a>	Alignment		94.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> the structure of hypocrea jecorina beta-xylosidase xyl3a (bx11)
17	<a href="#">c5yotB_</a>	Alignment		94.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> isoprimeverose-producing enzyme; <b>PDBTitle:</b> isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
18	<a href="#">c4zwiA_</a>	Alignment		93.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
19	<a href="#">c4zwiC_</a>	Alignment		92.7	23	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> chimera protein of human rhodopsin, mouse s-arrestin, and <b>PDBTitle:</b> crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser
20	<a href="#">c1ayrA_</a>	Alignment		92.7	23	<b>PDB header:</b> sensory transduction <b>Chain:</b> A: <b>PDB Molecule:</b> arrestin; <b>PDBTitle:</b> arrestin from bovine rod outer segments
21	<a href="#">c3u48A_</a>	Alignment	not modelled	92.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> jmb19063; <b>PDBTitle:</b> from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis
22	<a href="#">c3pvmB_</a>	Alignment	not modelled	92.4	12	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> structure of complement c5 in complex with cvf
23	<a href="#">c6q7jB_</a>	Alignment	not modelled	92.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-1,4-beta-xylosidase xInd; <b>PDBTitle:</b> gh3 exo-beta-xylosidase (xInd) in complex with xylobiose aziridine2 activity based probe
24	<a href="#">c2pn5A_</a>	Alignment	not modelled	92.3	14	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> thioester-containing protein i; <b>PDBTitle:</b> crystal structure of tep1r
25	<a href="#">c1sujA_</a>	Alignment	not modelled	91.9	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cone arrestin; <b>PDBTitle:</b> x-ray crystal structure of ambystoma tigrinum cone arrestin
26	<a href="#">c5axhA_</a>	Alignment	not modelled	91.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dextranase; <b>PDBTitle:</b> crystal structure of thermophilic dextranase from thermoanaerobacter2 pseudethanolicus, d312g mutant in complex with isomaltohexaose
27	<a href="#">c5jp0A_</a>	Alignment	not modelled	90.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase bogh3b; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh3b with bound glucose
28	<a href="#">c5nbsA_</a>	Alignment	not modelled	90.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa

29	<a href="#">c5wabD</a>	Alignment	not modelled	90.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
30	<a href="#">c4acqA</a>	Alignment	not modelled	90.2	20	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> alpha-2 macroglobulin
31	<a href="#">c2r5oA</a>	Alignment	not modelled	90.1	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp binding component of abc-transporter; <b>PDBTitle:</b> crystal structure of the c-terminal domain of wzt
32	<a href="#">c4i3gB</a>	Alignment	not modelled	90.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
33	<a href="#">c3zz1A</a>	Alignment	not modelled	89.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-d-glucoside glucohydrolase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
34	<a href="#">c4d0jD</a>	Alignment	not modelled	89.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
35	<a href="#">c1g4mA</a>	Alignment	not modelled	89.0	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-arrestin1; <b>PDBTitle:</b> crystal structure of bovine beta-arrestin 1
36	<a href="#">c6i2xB</a>	Alignment	not modelled	88.6	13	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> structure of complement c5 in complex with small molecule inhibitor2 and cvf
37	<a href="#">c2x41A</a>	Alignment	not modelled	87.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
38	<a href="#">c3cu7A</a>	Alignment	not modelled	87.6	10	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c5; <b>PDBTitle:</b> human complement component 5
39	<a href="#">c4zo9B</a>	Alignment	not modelled	86.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lin1840 protein; <b>PDBTitle:</b> crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
40	<a href="#">c3hrzA</a>	Alignment	not modelled	86.5	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b
41	<a href="#">c3c12A</a>	Alignment	not modelled	86.3	7	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein; <b>PDBTitle:</b> crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
42	<a href="#">c1l9mB</a>	Alignment	not modelled	86.3	12	<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
43	<a href="#">d1g0da2</a>	Alignment	not modelled	85.8	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
44	<a href="#">c2qsvA</a>	Alignment	not modelled	85.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
45	<a href="#">d1ex0a2</a>	Alignment	not modelled	85.2	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
46	<a href="#">c4rtdA</a>	Alignment	not modelled	83.7	11	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized lipoprotein yfhm; <b>PDBTitle:</b> escherichia coli alpha-2-macroglobulin activated by porcine elastase
47	<a href="#">c2b39B</a>	Alignment	not modelled	83.5	13	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> c3; <b>PDBTitle:</b> structure of mammalian c3 with an intact thioester at 3a resolution
48	<a href="#">c4acqC</a>	Alignment	not modelled	83.4	18	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-2-macroglobulin; <b>PDBTitle:</b> alpha-2 macroglobulin
49	<a href="#">c4iidB</a>	Alignment	not modelled	82.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase 1; <b>PDBTitle:</b> crystal structure of beta-glucosidase 1 from aspergillus aculeatus in2 complex with 1-deoxynojirimycin
50	<a href="#">c4zzkA</a>	Alignment	not modelled	82.2	10	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> basal-body rod modification protein flgd; <b>PDBTitle:</b> crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
51	<a href="#">c1cf1B</a>	Alignment	not modelled	82.1	25	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (arrestin); <b>PDBTitle:</b> arrestin from bovine rod outer segments
52	<a href="#">c4a5wA</a>	Alignment	not modelled	82.0	11	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c5; <b>PDBTitle:</b> crystal structure of c5b6
53	<a href="#">c5wvpA</a>	Alignment	not modelled	80.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> expression, characterization and crystal structure of a novel beta-2 glucosidase from paenibacillus barengoltzii
54	<a href="#">c3ac0B</a>	Alignment	not modelled	80.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase i; <b>PDBTitle:</b> crystal structure of beta-glucosidase from kluveromyces marxianus in2 complex with glucose

55	<a href="#">d1qfha2</a>	Alignment	not modelled	79.8	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
56	<a href="#">c5k6lA</a>	Alignment	not modelled	79.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> b-glucosidase; <b>PDBTitle:</b> structure of a gh3 b-glucosidase from cow rumen metagenome
57	<a href="#">c4fxgA</a>	Alignment	not modelled	77.2	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c4 beta chain; <b>PDBTitle:</b> complement c4 in complex with masp-2
58	<a href="#">c1yewl</a>	Alignment	not modelled	76.9	21	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
59	<a href="#">c3rgbA</a>	Alignment	not modelled	76.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase subunit b2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
60	<a href="#">d2vzsa2</a>	Alignment	not modelled	75.2	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
61	<a href="#">c3rfrl</a>	Alignment	not modelled	73.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
62	<a href="#">c3vmpA</a>	Alignment	not modelled	70.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dextranase; <b>PDBTitle:</b> crystal structure of dextranase from streptococcus mutans in complex2 with 4,5-epoxyphenyl alpha-d-glucopyranoside
63	<a href="#">c6ajjA</a>	Alignment	not modelled	69.9	17	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
64	<a href="#">c4m9pA</a>	Alignment	not modelled	69.8	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> crystal structure of the human filamin a ig-like domains 3-5
65	<a href="#">c5wabC</a>	Alignment	not modelled	69.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative beta-glucosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
66	<a href="#">d1kyaa2</a>	Alignment	not modelled	65.2	8	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
67	<a href="#">c3o0rC</a>	Alignment	not modelled	62.2	18	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
68	<a href="#">d2q3za2</a>	Alignment	not modelled	61.0	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
69	<a href="#">d1vjja2</a>	Alignment	not modelled	57.4	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
70	<a href="#">d1hfua2</a>	Alignment	not modelled	54.6	11	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
71	<a href="#">c2xbtA</a>	Alignment	not modelled	53.8	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cellulosomal scaffoldin; <b>PDBTitle:</b> structure of a scaffoldin carbohydrate-binding module family 3b from2 the cellulosome of bacteroides cellulosolvans: structural diversity3 and implications for carbohydrate binding
72	<a href="#">c4u48A</a>	Alignment	not modelled	53.1	13	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> putative inner membrane lipoprotein; <b>PDBTitle:</b> crystal structure of salmonella alpha-2-macroglobulin
73	<a href="#">c5vhvB</a>	Alignment	not modelled	51.3	9	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> alkylpurine dna glycosylase alk; <b>PDBTitle:</b> pseudomonas fluorescens alkylpurine dna glycosylase alk bound to dna2 containing an oxocarbenium-intermediate analog
74	<a href="#">d1jv2a2</a>	Alignment	not modelled	49.7	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Integrin domains <b>Family:</b> Integrin domains
75	<a href="#">c4gucA</a>	Alignment	not modelled	49.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ba_2500; <b>PDBTitle:</b> 1.4 angstrom resolution crystal structure of uncharacterized protein2 ba_2500 from bacillus anthracis str. ames
76	<a href="#">c2qkiA</a>	Alignment	not modelled	48.9	11	<b>PDB header:</b> immune system/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> complement c3; <b>PDBTitle:</b> human c3c in complex with the inhibitor compstatin
77	<a href="#">c2f1eA</a>	Alignment	not modelled	45.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein apag; <b>PDBTitle:</b> solution structure of apag protein
78	<a href="#">c3gdcC</a>	Alignment	not modelled	45.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> multicopper oxidase; <b>PDBTitle:</b> crystal structure of multicopper oxidase
79	<a href="#">c3ppsD</a>	Alignment	not modelled	44.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> laccase; <b>PDBTitle:</b> crystal structure of an ascomycete fungal laccase from thielavia2 arenaria
80	<a href="#">d2q9oa2</a>	Alignment	not modelled	42.0	12	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
						<b>Fold:</b> Immunoglobulin-like beta-sandwich

81	<a href="#">d1xvsa_</a>	Alignment	not modelled	41.5	10	<b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
82	<a href="#">c1pjeA_</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpvu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpvu) from hiv-1
83	<a href="#">c2gohA_</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpvu protein; <b>PDBTitle:</b> three-dimensional structure of the trans-membrane domain of2 vpvu from hiv-1 in aligned phospholipid bicelles
84	<a href="#">c2gofA_</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpvu protein; <b>PDBTitle:</b> three-dimensional structure of the trans-membrane domain of2 vpvu from hiv-1 in aligned phospholipid bicelles
85	<a href="#">c1pi7A_</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpvu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpvu) from hiv-1
86	<a href="#">c1pi8A_</a>	Alignment	not modelled	41.1	28	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> vpvu protein; <b>PDBTitle:</b> structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpvu) from hiv-1
87	<a href="#">d1tzaa_</a>	Alignment	not modelled	40.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
88	<a href="#">d1b2pa_</a>	Alignment	not modelled	40.0	20	<b>Fold:</b> beta-Prism II <b>Superfamily:</b> alpha-D-mannose-specific plant lectins <b>Family:</b> alpha-D-mannose-specific plant lectins
89	<a href="#">c6f0kA_</a>	Alignment	not modelled	39.1	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
90	<a href="#">c4umgA_</a>	Alignment	not modelled	38.9	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein lin-41; <b>PDBTitle:</b> crystal structure of the lin-41 filamin domain
91	<a href="#">d1v10a2</a>	Alignment	not modelled	38.7	12	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
92	<a href="#">c1kv3F_</a>	Alignment	not modelled	38.6	9	<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
93	<a href="#">c6mitC_</a>	Alignment	not modelled	38.3	17	<b>PDB header:</b> lipid transport <b>Chain:</b> C: <b>PDB Molecule:</b> lipopolysaccharide export system protein lptc; <b>PDBTitle:</b> lptbfgc from enterobacter cloacae
94	<a href="#">c5khnB_</a>	Alignment	not modelled	37.1	8	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
95	<a href="#">c4xydB_</a>	Alignment	not modelled	36.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> norc-like protein; <b>PDBTitle:</b> nitric oxide reductase from roseobacter denitrificans (rdnor)
96	<a href="#">c2e6jA_</a>	Alignment	not modelled	35.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydin protein; <b>PDBTitle:</b> solution structure of the c-terminal papd-like domain from2 human hydin protein
97	<a href="#">c2l8sA_</a>	Alignment	not modelled	35.4	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
98	<a href="#">d1k3ia1</a>	Alignment	not modelled	35.1	23	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
99	<a href="#">d1nqja_</a>	Alignment	not modelled	33.8	21	<b>Fold:</b> CUB-like <b>Superfamily:</b> Collagen-binding domain <b>Family:</b> Collagen-binding domain
100	<a href="#">d1fftb2</a>	Alignment	not modelled	33.1	17	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
101	<a href="#">c2kogA_</a>	Alignment	not modelled	33.1	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
102	<a href="#">d1xq4a_</a>	Alignment	not modelled	32.3	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
103	<a href="#">c5hnoC_</a>	Alignment	not modelled	32.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> abc type transport system putative atp binding protein; <b>PDBTitle:</b> the structure of the kdo-capped saccharide binding subunit of the o-122 specific abc transporter, wzt
104	<a href="#">d1wlha1</a>	Alignment	not modelled	31.5	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
105	<a href="#">c1qfhB_</a>	Alignment	not modelled	29.5	21	<b>PDB header:</b> actin binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gelation factor); <b>PDBTitle:</b> dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
106	<a href="#">c3g7mA_</a>	Alignment	not modelled	29.5	9	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> xylanase inhibitor tl-xi; <b>PDBTitle:</b> structure of the thaumatin-like xylanase inhibitor tlxi
107	<a href="#">c2jwaA_</a>	Alignment	not modelled	28.5	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-2;

						<b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
108	<a href="#">c2ks1A_</a>	Alignment	not modelled	28.5	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
109	<a href="#">c3sqrA_</a>	Alignment	not modelled	28.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> laccase; <b>PDBTitle:</b> crystal structure of laccase from botrytis aclada at 1.67 a resolution
110	<a href="#">c3wmmY_</a>	Alignment	not modelled	27.6	22	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> lh1 alpha polypeptide; <b>PDBTitle:</b> crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
111	<a href="#">c5daoA_</a>	Alignment	not modelled	26.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> laccase; <b>PDBTitle:</b> laccase from antrodiella faginea
112	<a href="#">c3hd7A_</a>	Alignment	not modelled	26.1	26	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
113	<a href="#">c6d5bL_</a>	Alignment	not modelled	26.1	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> L: <b>PDB Molecule:</b> glycoside hydrolase wp_045175321; <b>PDBTitle:</b> structure of caldicellulosiruptor danielii cbm3 module of glycoside2 hydrolase wp_045175321
114	<a href="#">c5sv5A_</a>	Alignment	not modelled	26.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> microbial collagenase; <b>PDBTitle:</b> 1.0 angstrom crystal structure of pre-peptidase c-terminal domain of2 collagenase from bacillus anthracis.
115	<a href="#">c3rghA_</a>	Alignment	not modelled	25.3	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
116	<a href="#">c2n28A_</a>	Alignment	not modelled	24.8	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu
117	<a href="#">c6hrbD_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e2 inward-facing state2 (state 2)
118	<a href="#">c5mrwH_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
119	<a href="#">c5mrwD_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
120	<a href="#">c6hraD_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> potassium-transporting atpase kdpf subunit; <b>PDBTitle:</b> cryo-em structure of the kdpfabc complex in an e1 outward-facing state2 (state 1)