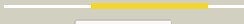

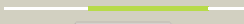
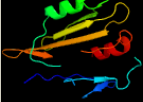



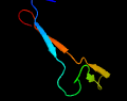

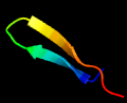

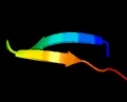

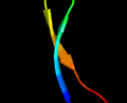

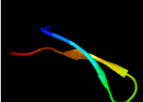



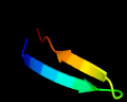

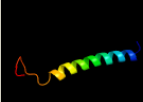











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1100_(- )_1228688_1229389
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	be61ca0d09abc7c

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tu1a_</a>	 Alignment		77.0	15	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> PA0094-like
2	<a href="#">c3lydA_</a>	 Alignment		63.4	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 putative uncharacterized protein from jonesia2 denitrificans
3	<a href="#">c2jpwA_</a>	 Alignment		53.6	54	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin i, cardiac muscle; <b>PDBTitle:</b> solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
4	<a href="#">d1ig4a_</a>	 Alignment		44.4	44	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> Methyl-CpG-binding domain, MBD
5	<a href="#">d1oa3a_</a>	 Alignment		39.0	53	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
6	<a href="#">d1oa2a_</a>	 Alignment		37.7	53	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
7	<a href="#">d2bw8a1</a>	 Alignment		34.8	29	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
8	<a href="#">c1h0bA_</a>	 Alignment		34.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> endoglucanase cel12a from rhodothermus marinus
9	<a href="#">d1oa4a_</a>	 Alignment		34.6	53	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
10	<a href="#">c5m2dB_</a>	 Alignment		34.4	41	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase-like protein; <b>PDBTitle:</b> crystal structure 4ac endoglucanase-like protein from acremonium2 chrysogenum
11	<a href="#">c3mk7F_</a>	 Alignment		34.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase

12	<a href="#">c3vlbB_</a>	Alignment		33.9	28	<b>PDB header:</b> plant protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucan-specific endo-beta-1,4-glucanase a; <b>PDBTitle:</b> crystal structure of xeg-edgp
13	<a href="#">d2nlra_</a>	Alignment		32.7	53	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
14	<a href="#">c4ol4A_</a>	Alignment		32.4	14	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
15	<a href="#">c4nprA_</a>	Alignment		32.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xyloglucan-specific endo-beta-1,4-glucanase gh12; <b>PDBTitle:</b> crystal structure of the family 12 xyloglucanase from aspergillus2 niveus
16	<a href="#">d3buxb3</a>	Alignment		32.0	20	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
17	<a href="#">c5gm5G_</a>	Alignment		30.8	29	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> endoglucanase-1; <b>PDBTitle:</b> crystal structure of fi-cmcase from aspergillus aculeatus f-50 in2 complex with cellobiose
18	<a href="#">d1olra_</a>	Alignment		29.4	24	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
19	<a href="#">d1ks5a_</a>	Alignment		29.3	41	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Xylanase/endoglucanase 11/12
20	<a href="#">d1uj4a2</a>	Alignment		28.1	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
21	<a href="#">c2k5hA_</a>	Alignment	not modelled	26.4	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein; <b>PDBTitle:</b> solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
22	<a href="#">c2jemB_</a>	Alignment	not modelled	25.6	44	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-beta-1,4-glucanase; <b>PDBTitle:</b> native family 12 xyloglucanase from bacillus licheniformis
23	<a href="#">c2ky8A_</a>	Alignment	not modelled	25.3	36	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 2; <b>PDBTitle:</b> solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
24	<a href="#">c3cp0A_</a>	Alignment	not modelled	24.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein implicated in regulation of membrane <b>PDBTitle:</b> crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
25	<a href="#">c3nctC_</a>	Alignment	not modelled	24.1	20	<b>PDB header:</b> dna binding protein, chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> protein psib; <b>PDBTitle:</b> x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
26	<a href="#">c3op0B_</a>	Alignment	not modelled	21.7	27	<b>PDB header:</b> signaling protein/signaling protein regu <b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction protein cbl-c; <b>PDBTitle:</b> crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
27	<a href="#">d2gu3a1</a>	Alignment	not modelled	20.9	24	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> PepSY-like
						<b>Fold:</b> Ferredoxin-like

28	<a href="#">d1lk5a2</a>	Alignment	not modelled	20.5	15	<b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
29	<a href="#">d1m0sa2</a>	Alignment	not modelled	20.3	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
30	<a href="#">c6eepA</a>	Alignment	not modelled	20.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
31	<a href="#">d2exda1</a>	Alignment	not modelled	20.1	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> NfeD domain-like <b>Family:</b> NfeD domain-like
32	<a href="#">c1m57H</a>	Alignment	not modelled	19.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
33	<a href="#">c5uf2A</a>	Alignment	not modelled	19.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
34	<a href="#">c6bk5A</a>	Alignment	not modelled	17.6	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin ligase cbl; <b>PDBTitle:</b> inactive choanoflagellate e3 ubiquitin ligase cbl tkb
35	<a href="#">d1o8ba2</a>	Alignment	not modelled	16.1	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), lid domain
36	<a href="#">c4x84C</a>	Alignment	not modelled	15.5	13	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
37	<a href="#">c3wwwvA</a>	Alignment	not modelled	15.4	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stomatin operon partner protein; <b>PDBTitle:</b> c-terminal domain of stomatin operon partner protein 1510-c from2 pyrococcus horikoshii
38	<a href="#">c2pjmA</a>	Alignment	not modelled	14.6	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
39	<a href="#">c3fxdD</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> protein icmr; <b>PDBTitle:</b> crystal structure of interacting domains of icmr and icmq
40	<a href="#">c1uj6A</a>	Alignment	not modelled	14.3	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
41	<a href="#">c1m0sA</a>	Alignment	not modelled	13.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> northeast structural genomics consortium (nesg id ir21)
42	<a href="#">c1lkzB</a>	Alignment	not modelled	13.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
43	<a href="#">c6g4wr</a>	Alignment	not modelled	13.3	21	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 40s ribosomal protein s17; <b>PDBTitle:</b> cryo-em structure of a late human pre-40s ribosomal subunit - state a
44	<a href="#">c4gmkB</a>	Alignment	not modelled	12.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
45	<a href="#">d2p13a1</a>	Alignment	not modelled	12.8	22	<b>Fold:</b> FAD-binding/transporter-associated domain-like <b>Superfamily:</b> FAD-binding/transporter-associated domain-like <b>Family:</b> CorC/HlyC domain-like
46	<a href="#">c3u7jA</a>	Alignment	not modelled	12.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
47	<a href="#">c2dwvB</a>	Alignment	not modelled	12.1	28	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> salvador homolog 1 protein; <b>PDBTitle:</b> solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)
48	<a href="#">c2vt8B</a>	Alignment	not modelled	11.7	20	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> proteasome inhibitor pi31 subunit; <b>PDBTitle:</b> structure of a conserved dimerisation domain within fbox7 and pi31
49	<a href="#">c6ghbB</a>	Alignment	not modelled	11.4	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> upf0413 protein gk0824; <b>PDBTitle:</b> crystal structure of spx in complex with yjhb (oxidized)
50	<a href="#">c5levA</a>	Alignment	not modelled	11.1	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--dolichyl-phosphate n- <b>PDBTitle:</b> crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpgt1) (v264g mutant)
51	<a href="#">d1v58a2</a>	Alignment	not modelled	11.0	22	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> DsbC/DsbG N-terminal domain-like <b>Family:</b> DsbC/DsbG N-terminal domain-like
52	<a href="#">c3l7oB</a>	Alignment	not modelled	10.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
53	<a href="#">d1qk9a</a>	Alignment	not modelled	10.8	30	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> Methyl-CpG-binding domain, MBD
						<b>PDB header:</b> nuclear protein

54	<a href="#">c3le4A_</a>	Alignment	not modelled	10.4	67	<b>Chain:</b> A; <b>PDB Molecule:</b> microprocessor complex subunit dgcr8; <b>PDBTitle:</b> crystal structure of the dgcr8 dimerization domain
55	<a href="#">d1nmva1</a>	Alignment	not modelled	10.3	40	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
56	<a href="#">d1pina1</a>	Alignment	not modelled	9.9	50	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
57	<a href="#">d1fftb2</a>	Alignment	not modelled	9.8	7	<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
58	<a href="#">c4p6vC_</a>	Alignment	not modelled	9.7	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit c; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
59	<a href="#">d1i8gb_</a>	Alignment	not modelled	9.0	50	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
60	<a href="#">c6gtmA_</a>	Alignment	not modelled	8.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> aldo-keto reductase family protein; <b>PDBTitle:</b> crystal structure of smba in complex with pppp.
61	<a href="#">c3kwmC_</a>	Alignment	not modelled	8.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-isomerase a
62	<a href="#">c3jcul_</a>	Alignment	not modelled	8.1	19	<b>PDB header:</b> membrane protein <b>Chain:</b> I; <b>PDB Molecule:</b> protein photosystem ii reaction center protein i; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
63	<a href="#">d1f8ab1</a>	Alignment	not modelled	7.8	44	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
64	<a href="#">c6gw6A_</a>	Alignment	not modelled	7.7	20	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> res toxin; <b>PDBTitle:</b> structure of the pseudomonas putida res-xre toxin-antitoxin complex
65	<a href="#">c2ysgA_</a>	Alignment	not modelled	7.4	50	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> syntaxin-binding protein 4; <b>PDBTitle:</b> solution structure of the ww domain from the human syntaxin-2 binding protein 4
66	<a href="#">c1wr4A_</a>	Alignment	not modelled	7.3	63	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin-protein ligase nedd4-2; <b>PDBTitle:</b> solution structure of the second ww domain of nedd4-2
67	<a href="#">d1ur3m_</a>	Alignment	not modelled	7.2	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> NAD(P)-linked oxidoreductase <b>Family:</b> Aldo-keto reductases (NADP)
68	<a href="#">c2cblA_</a>	Alignment	not modelled	7.1	12	<b>PDB header:</b> complex (proto-oncogene/peptide) <b>Chain:</b> A; <b>PDB Molecule:</b> proto-oncogene cbl; <b>PDBTitle:</b> n-terminal domain of cbl in complex with its binding site2 on zap-70
69	<a href="#">c3bunB_</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> B; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase cbl; <b>PDBTitle:</b> crystal structure of c-cbl-tkb domain complexed with its binding motif2 in sprouty4
70	<a href="#">d1cdwa2</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> TATA-box binding protein (TBP), C-terminal domain
71	<a href="#">d1rk4a2</a>	Alignment	not modelled	6.8	36	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione S-transferase (GST), N-terminal domain
72	<a href="#">c2djaA_</a>	Alignment	not modelled	6.7	42	<b>PDB header:</b> ligase/signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> smad ubiquitination regulatory factor 2; <b>PDBTitle:</b> solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
73	<a href="#">c1lk5C_</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase; <b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
74	<a href="#">c1smzA_</a>	Alignment	not modelled	6.5	67	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> transportan in bicellar solution with <b>PDBTitle:</b> structure of transportan in phospholipid bicellar solution
75	<a href="#">c4lkuA_</a>	Alignment	not modelled	6.3	38	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
76	<a href="#">c4lkuB_</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
77	<a href="#">c2n8tA_</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> ligase/peptide <b>Chain:</b> A; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase nedd4; <b>PDBTitle:</b> solution structure of the rnedd4 ww2 domain-cx43ct peptide complex by2 nmr
78	<a href="#">c2j6aA_</a>	Alignment	not modelled	5.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> protein trm112; <b>PDBTitle:</b> crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
79	<a href="#">c2zajA_</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz <b>PDBTitle:</b> solution structure of the short-isoform of the second ww2

						domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
80	<a href="#">d2axti1</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, PsbI <b>Family:</b> PsbI-like
81	<a href="#">c3a0hi</a>	Alignment	not modelled	5.8	22	<b>PDB header:</b> electron transport <b>Chain:</b> I: <b>PDB Molecule:</b> photosystem ii reaction center protein i; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
82	<a href="#">c1xmeB</a>	Alignment	not modelled	5.8	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
83	<a href="#">d2e74a1</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Transmembrane di-heme cytochromes <b>Family:</b> Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
84	<a href="#">d2ysca1</a>	Alignment	not modelled	5.7	57	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
85	<a href="#">c1h54B</a>	Alignment	not modelled	5.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose phosphorylase; <b>PDBTitle:</b> maltose phosphorylase from lactobacillus brevis
86	<a href="#">c6d0hA</a>	Alignment	not modelled	5.4	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> part: cog5654 (res domain) toxin; <b>PDBTitle:</b> part: prs adp-ribosylating toxin bound to cognate antitoxin pars
87	<a href="#">c4nooA</a>	Alignment	not modelled	5.4	30	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> vgrg protein; <b>PDBTitle:</b> molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
88	<a href="#">d3dtub2</a>	Alignment	not modelled	5.4	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
89	<a href="#">d2itka1</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> WW domain-like <b>Superfamily:</b> WW domain <b>Family:</b> WW domain
90	<a href="#">c2lb0A</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
91	<a href="#">c2lazA</a>	Alignment	not modelled	5.3	50	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
92	<a href="#">c2yshA</a>	Alignment	not modelled	5.2	44	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> growth-arrest-specific protein 7; <b>PDBTitle:</b> solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
93	<a href="#">c3gr1A</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
94	<a href="#">c1sfsA</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> 1.07 a crystal structure of an uncharacterized b. stearothermophilus2 protein
95	<a href="#">d1sfsa</a>	Alignment	not modelled	5.2	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> 1,4-beta-N-acetylmuraminidase
96	<a href="#">c2ysca</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 precursor protein-binding family <b>PDBTitle:</b> solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3