



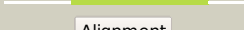

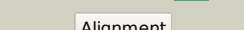
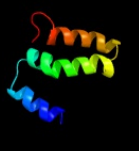
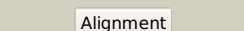
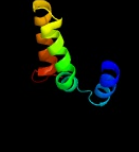


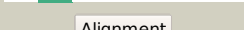

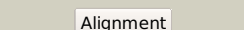


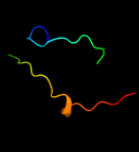
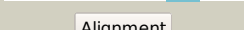
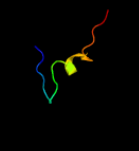
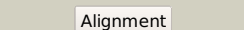
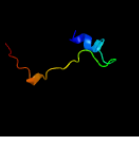
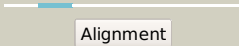
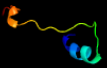

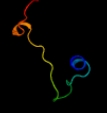


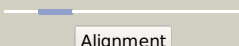

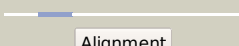
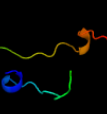
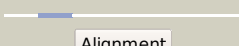
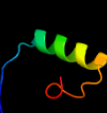
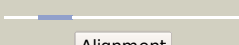






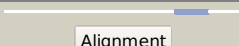
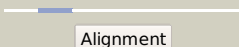
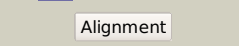
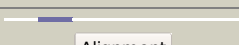


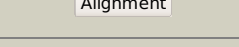


# Phyre2

Email	rachel.harding@utoronto.ca
Description	2401-3144
Date	Wed Mar 2 01:08:25 GMT 2016
Unique Job ID	541df811f7c63f48

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2jkrL_</a>	 Alignment		82.5	14	<b>PDB header:</b> endocytosis <b>Chain:</b> L: <b>PDB Molecule:</b> ap-2 complex subunit alpha-2; <b>PDBTitle:</b> ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
2	<a href="#">c4cr2Z_</a>	 Alignment		70.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> Z: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn1; <b>PDBTitle:</b> deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
3	<a href="#">d1wa5c_</a>	 Alignment		61.5	10	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Armadillo repeat
4	<a href="#">c1htjF_</a>	 Alignment		46.3	18	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> kiaa0380; <b>PDBTitle:</b> structure of the rgs-like domain from pdz-rhogef
5	<a href="#">d1htjF_</a>	 Alignment		46.3	18	<b>Fold:</b> Regulator of G-protein signaling, RGS <b>Superfamily:</b> Regulator of G-protein signaling, RGS <b>Family:</b> Regulator of G-protein signaling, RGS
6	<a href="#">c3rgbG_</a>	 Alignment		42.5	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> methane monooxygenase subunit c2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
7	<a href="#">c3rfrK_</a>	 Alignment		40.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> pmoc; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
8	<a href="#">c1yewC_</a>	 Alignment		39.3	36	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> particulate methane monooxygenase subunit c2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
9	<a href="#">d3e7ma1</a>	 Alignment		37.9	35	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
10	<a href="#">d7odca1</a>	 Alignment		37.5	30	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
11	<a href="#">d3e7ga1</a>	 Alignment		35.5	35	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain

12	<a href="#">d1m9ma_</a>	 Alignment		33.3	29	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
13	<a href="#">d1nosa_</a>	 Alignment		32.3	35	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
14	<a href="#">c3ngvA_</a>	 Alignment		30.3	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d7 protein; <b>PDBTitle:</b> crystal structure of anst-d711
15	<a href="#">d1q2oa_</a>	 Alignment		29.7	29	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
16	<a href="#">d1om4a_</a>	 Alignment		28.2	29	<b>Fold:</b> Nitric oxide (NO) synthase oxygenase domain <b>Superfamily:</b> Nitric oxide (NO) synthase oxygenase domain <b>Family:</b> Nitric oxide (NO) synthase oxygenase domain
17	<a href="#">c1q5vB_</a>	 Alignment		26.1	7	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
18	<a href="#">c2ca9B_</a>	 Alignment		24.2	28	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
19	<a href="#">c1fooA_</a>	 Alignment		24.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase; <b>PDBTitle:</b> bovine endothelial nitric oxide synthase heme domain complexed with l-2 arg and no(h4b-free)
20	<a href="#">c2rmrA_</a>	 Alignment		24.0	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> paired amphipathic helix protein sin3a; <b>PDBTitle:</b> solution structure of msin3a pah1 domain
21	<a href="#">d1b3ua_</a>	 Alignment	not modelled	22.9	16	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> HEAT repeat
22	<a href="#">d1iapa_</a>	 Alignment	not modelled	22.7	22	<b>Fold:</b> Regulator of G-protein signaling, RGS <b>Superfamily:</b> Regulator of G-protein signaling, RGS <b>Family:</b> Regulator of G-protein signaling, RGS
23	<a href="#">c4fmoB_</a>	 Alignment	not modelled	22.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein pms1; <b>PDBTitle:</b> structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1
24	<a href="#">c2flqA_</a>	 Alignment	not modelled	19.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric oxide synthase; <b>PDBTitle:</b> crystal structure of nitric oxide synthase from geobacillus2 stearrowthermophilus (atcc 12980) complexed with l-arginine
25	<a href="#">d2hzab1</a>	 Alignment	not modelled	18.3	6	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
26	<a href="#">c3pvlA_</a>	 Alignment	not modelled	18.2	22	<b>PDB header:</b> motor protein/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> myosin viia isoform 1; <b>PDBTitle:</b> structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
27	<a href="#">c3wozA_</a>	 Alignment	not modelled	17.5	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> clip-associating protein 2; <b>PDBTitle:</b> crystal structure of clasp2 tog domain (tog3)
28	<a href="#">d1dgfa_</a>	 Alignment	not modelled	16.8	18	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases

29	<a href="#">c2bj3D_</a>	Alignment	not modelled	16.6	24	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
30	<a href="#">c2keba_</a>	Alignment	not modelled	16.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase subunit alpha b; <b>PDBTitle:</b> nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
31	<a href="#">c3p9a1_</a>	Alignment	not modelled	16.3	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> dna-packaging protein gp3; <b>PDBTitle:</b> an atomic view of the nonameric small terminase subunit of2 bacteriophage p22
32	<a href="#">c5a31A_</a>	Alignment	not modelled	16.1	16	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> anaphase-promoting complex subunit 1; <b>PDBTitle:</b> structure of the human apc-cdh1-hsl1-ubch10 complex.
33	<a href="#">c4e2i3_</a>	Alignment	not modelled	15.6	17	<b>PDB header:</b> hydrolase/dna binding protein <b>Chain:</b> 3: <b>PDB Molecule:</b> dna polymerase alpha subunit b; <b>PDBTitle:</b> the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase
34	<a href="#">d2hzaa1</a>	Alignment	not modelled	14.8	6	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
35	<a href="#">c4fmoA_</a>	Alignment	not modelled	13.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein mlh1; <b>PDBTitle:</b> structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1
36	<a href="#">c3chxG_</a>	Alignment	not modelled	13.4	27	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> pmoc; <b>PDBTitle:</b> crystal structure of methyloinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)
37	<a href="#">d1adta3</a>	Alignment	not modelled	13.3	13	<b>Fold:</b> Zn-binding domains of ADDBP <b>Superfamily:</b> Zn-binding domains of ADDBP <b>Family:</b> Zn-binding domains of ADDBP
38	<a href="#">c3dztA_</a>	Alignment	not modelled	13.1	12	<b>PDB header:</b> odorant-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> d7 protein; <b>PDBTitle:</b> aed7-leukotriene e4 complex
39	<a href="#">c1f4jC_</a>	Alignment	not modelled	13.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> structure of tetragonal crystals of human erythrocyte2 catalase
40	<a href="#">c2y35A_</a>	Alignment	not modelled	12.8	34	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ld22664p; <b>PDBTitle:</b> crystal structure of xrn1-substrate complex
41	<a href="#">d2bj7a1</a>	Alignment	not modelled	12.8	24	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
42	<a href="#">c4nncA_</a>	Alignment	not modelled	12.5	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> obca, oxalate biosynthetic component a; <b>PDBTitle:</b> ternary complex of obca with c4-coa adduct and oxalate
43	<a href="#">c4nknF_</a>	Alignment	not modelled	12.1	18	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> comm domain-containing protein 9; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of commd9
44	<a href="#">c2mfjA_</a>	Alignment	not modelled	12.0	27	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> blo t 19; <b>PDBTitle:</b> solution structure of blo t 19, a minor dust mite allergen from blomia2 tropicalis
45	<a href="#">d4blca_</a>	Alignment	not modelled	11.4	18	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
46	<a href="#">c1w63A_</a>	Alignment	not modelled	11.2	15	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> adapter-related protein complex 1 gamma 1 <b>PDBTitle:</b> ap1 clathrin adaptor core
47	<a href="#">c4kxdA_</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl aminopeptidase; <b>PDBTitle:</b> crystal structure of human aminopeptidase a complexed with glutamate2 and calcium
48	<a href="#">c2of3A_</a>	Alignment	not modelled	10.9	11	<b>PDB header:</b> structural protein, cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> zyg-9; <b>PDBTitle:</b> tog domain structure from c.elegans zyg9
49	<a href="#">d2f05a1</a>	Alignment	not modelled	10.6	10	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
50	<a href="#">c4b7hb_</a>	Alignment	not modelled	10.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase; <b>PDBTitle:</b> structure of a highdose liganded bacterial catalase
51	<a href="#">c4lqxB_</a>	Alignment	not modelled	9.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tena/thi-4 domain-containing protein; <b>PDBTitle:</b> crystal structure of a tena/thi-4 domain-containing protein (sso2700)2 from sulfobolus solfataricus p2 at 2.34 a resolution
52	<a href="#">c2pq1A_</a>	Alignment	not modelled	9.3	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d7r4 protein; <b>PDBTitle:</b> crystal structure of anopheles gambiae d7r4-tryptamine complex
53	<a href="#">c1x31D_</a>	Alignment	not modelled	9.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> sarcosine oxidase delta subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
54	<a href="#">c4k2ba_</a>	Alignment	not modelled	9.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ntd biosynthesis operon protein ntda; <b>PDBTitle:</b> crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
55	<a href="#">d2ds5a1</a>	Alignment	not modelled	9.1	27	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain)

						<b>Family:</b> ClpX chaperone zinc binding domain
56	<a href="#">c2qk1A</a>	Alignment	not modelled	9.0	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein stu2; <b>PDBTitle:</b> structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
57	<a href="#">c1ovxB</a>	Alignment	not modelled	8.9	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpX; <b>PDBTitle:</b> nmr structure of the e. coli clpX chaperone zinc binding domain dimer
58	<a href="#">c3oc3B</a>	Alignment	not modelled	8.7	15	<b>PDB header:</b> hydrolase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> helicase mot1; <b>PDBTitle:</b> crystal structure of the mot1 n-terminal domain in complex with tbp
59	<a href="#">d1oeva</a>	Alignment	not modelled	8.6	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> PB1 domain
60	<a href="#">c3vh5D</a>	Alignment	not modelled	8.2	41	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> cenp-x; <b>PDBTitle:</b> crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
61	<a href="#">c3f5cC</a>	Alignment	not modelled	8.1	12	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> nuclear receptor subfamily 0 group b member 1; <b>PDBTitle:</b> structure of dax-1:lrx-1 complex
62	<a href="#">c3v5yC</a>	Alignment	not modelled	8.0	10	<b>PDB header:</b> gene regulation <b>Chain:</b> C: <b>PDB Molecule:</b> f-box/lrr-repeat protein 5; <b>PDBTitle:</b> structure of fbx15 hemerythrin domain, p2(1) cell
63	<a href="#">c5a1vV</a>	Alignment	not modelled	7.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> V: <b>PDB Molecule:</b> coatomer subunit gamma-1; <b>PDBTitle:</b> the structure of the copi coat linkage i
64	<a href="#">d1ug3a2</a>	Alignment	not modelled	7.8	21	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
65	<a href="#">c2opdA</a>	Alignment	not modelled	7.6	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> pilx; <b>PDBTitle:</b> structure of the neisseria meningitidis minor type iv pilin,2 pilx
66	<a href="#">d3b7sa3</a>	Alignment	not modelled	7.4	10	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Leukotriene A4 hydrolase catalytic domain
67	<a href="#">c3pifD</a>	Alignment	not modelled	7.3	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'->3' exoribonuclease (xrn1); <b>PDBTitle:</b> crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
68	<a href="#">c3zj31</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> 1: <b>PDB Molecule:</b> claudin-2; <b>PDB Fragment:</b> residues 38-319; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
69	<a href="#">c3zj35</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> 5: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
70	<a href="#">c3zj35</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> S: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
71	<a href="#">c3zj3T</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> T: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
72	<a href="#">c3zj3P</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> P: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
73	<a href="#">c3zj3Y</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> Y: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
74	<a href="#">c3zj3Z</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> Z: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
75	<a href="#">c3zj3U</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> U: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
76	<a href="#">c3zj33</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> 3: <b>PDB Molecule:</b> claudin-2; <b>PDB Fragment:</b> residues 38-319; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
77	<a href="#">c3zj32</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> 2: <b>PDB Molecule:</b> claudin-2; <b>PDB Fragment:</b> ecl2, residues 141-160; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
78	<a href="#">c3zj3X</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> X: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
79	<a href="#">c3zj3R</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> R: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
80	<a href="#">c3zj3Q</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> Q: <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a

						peptide2 derived from a modified version of ecl-2 of claudin 2 <b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> V; <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
81	<a href="#">c3zj3V_</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> V; <b>PDB Molecule:</b> claudin-2; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
82	<a href="#">c3zj34_</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> toxin/cell adhesion <b>Chain:</b> 4; <b>PDB Molecule:</b> claudin-2; <b>PDB Fragment:</b> ecl2, residues 141-160; <b>PDBTitle:</b> structure of clostridium perfringens enterotoxin with a peptide2 derived from a modified version of ecl-2 of claudin 2
83	<a href="#">c2fs1A_</a>	Alignment	not modelled	7.2	33	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> psd-1; <b>PDBTitle:</b> solution structure of psd-1
84	<a href="#">d1gjsa_</a>	Alignment	not modelled	7.2	33	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Bacterial immunoglobulin/albumin-binding domains <b>Family:</b> GA module, an albumin-binding domain
85	<a href="#">c3rkIA_</a>	Alignment	not modelled	7.0	43	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> stiv-a81; <b>PDBTitle:</b> the crystal structure of a81 from sulfobolus turreted icosahedral2 virus
86	<a href="#">d1gwea_</a>	Alignment	not modelled	7.0	14	<b>Fold:</b> Heme-dependent catalase-like <b>Superfamily:</b> Heme-dependent catalase-like <b>Family:</b> Heme-dependent catalases
87	<a href="#">c3fhgA_</a>	Alignment	not modelled	7.0	11	<b>PDB header:</b> dna repair, hydrolase, lyase <b>Chain:</b> A; <b>PDB Molecule:</b> n-glycosylase/dna lyase; <b>PDBTitle:</b> crystal structure of sulfobolus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
88	<a href="#">c3nicA_</a>	Alignment	not modelled	7.0	28	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A; <b>PDB Molecule:</b> eco29kir; <b>PDBTitle:</b> dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
89	<a href="#">c1ygmA_</a>	Alignment	not modelled	6.7	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein bsu31320; <b>PDBTitle:</b> nmr structure of mistic
90	<a href="#">c2jmkA_</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ta0956; <b>PDBTitle:</b> solution structure of ta0956
91	<a href="#">d1glxc_</a>	Alignment	not modelled	6.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein S18 <b>Family:</b> Ribosomal protein S18
92	<a href="#">c3mguA_</a>	Alignment	not modelled	6.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> pkhd-type hydroxylase tpa1; <b>PDBTitle:</b> saccharomyces cerevisiae tpa1
93	<a href="#">c3p8cB_</a>	Alignment	not modelled	6.4	19	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> nck-associated protein 1; <b>PDBTitle:</b> structure and control of the actin regulatory wave complex
94	<a href="#">c4juyB_</a>	Alignment	not modelled	6.4	16	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf31; <b>PDBTitle:</b> crystal structure of the pub domain of e3 ubiquitin ligase rnf31
95	<a href="#">c3su8X_</a>	Alignment	not modelled	6.3	21	<b>PDB header:</b> apoptosis/signaling protein <b>Chain:</b> X; <b>PDB Molecule:</b> plexin-b1; <b>PDBTitle:</b> crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
96	<a href="#">d1librb_</a>	Alignment	not modelled	6.3	11	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Armadillo repeat
97	<a href="#">d2dsya1</a>	Alignment	not modelled	6.3	21	<b>Fold:</b> TTHA1013/TTHA0281-like <b>Superfamily:</b> TTHA1013/TTHA0281-like <b>Family:</b> TTHA0281-like
98	<a href="#">c2p5tA_</a>	Alignment	not modelled	6.2	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A; <b>PDB Molecule:</b> putative transcriptional regulator peza; <b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
99	<a href="#">d1x7fa2</a>	Alignment	not modelled	6.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Outer surface protein, N-terminal domain