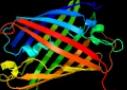
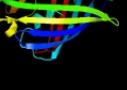
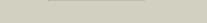
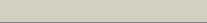
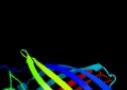
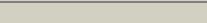
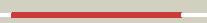
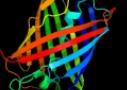
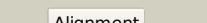
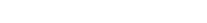
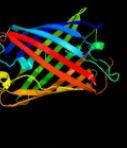
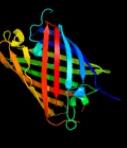


# Phyre<sup>2</sup>

Email	lhernould.t@gmail.com
Description	Undefined
Date	Tue Oct 3 16:16:01 BST 2017
Unique Job ID	77875f97c8c9be27

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1moua</a>			100.0	95	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
2	<a href="#">d1ggxa</a>			100.0	67	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
3	<a href="#">c3nezB</a>			100.0	61	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> mrojoa; <b>PDBTitle:</b> mrojoa
4	<a href="#">c3nezA</a>			100.0	61	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> mrojoa; <b>PDBTitle:</b> mrojoa
5	<a href="#">c2otbB</a>			100.0	55	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein cfp484; <b>PDBTitle:</b> crystal structure of a monomeric cyan fluorescent protein in the2 fluorescent state
6	<a href="#">c2ddcA</a>			100.0	55	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> photoconvertible fluorescent protein; <b>PDBTitle:</b> unique behavior of a histidine responsible for an engineered green-to-2 red photoconversion process
7	<a href="#">c2z6zA</a>			100.0	57	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> fluorescent protein dronpa; <b>PDBTitle:</b> crystal structure of a photoswitchable gfp-like protein2 dronpa in the bright-state
8	<a href="#">d1xqma</a>			100.0	48	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
9	<a href="#">c2ib5H</a>			100.0	50	<b>PDB header:</b> luminescent protein <b>Chain:</b> H: <b>PDB Molecule:</b> chromo protein; <b>PDBTitle:</b> structural characterization of a blue chromoprotein and its yellow2 mutant from the sea anemone cnidopus japonicus
10	<a href="#">c2c9iG</a>			100.0	49	<b>PDB header:</b> luminescent protein <b>Chain:</b> G: <b>PDB Molecule:</b> green fluorescent protein asfp499; <b>PDBTitle:</b> structure of the fluorescent protein asfp499 from anemonia2 sultata
11	<a href="#">d1uisa</a>			100.0	50	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins

12	<a href="#">c4ohsB</a>	Alignment		100.0	50	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> far-red fluorescent protein aq143; <b>PDBTitle:</b> the structure of a far-red fluorescent protein, aq143
13	<a href="#">c3cgIE</a>	Alignment		100.0	60	<b>PDB header:</b> fluorescent protein <b>Chain:</b> E: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein dsfp483; <b>PDBTitle:</b> crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
14	<a href="#">c2c9jG</a>	Alignment		100.0	39	<b>PDB header:</b> luminescent protein <b>Chain:</b> G: <b>PDB Molecule:</b> green fluorescent protein fp512; <b>PDBTitle:</b> structure of the fluorescent protein cmfp512 at 1.35a from2 cerianthus membranaceus
15	<a href="#">c2zo6A</a>	Alignment		100.0	48	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyan-emitting gfp-like protein, kusabira-cyan (kcy); <b>PDBTitle:</b> crystal structure of kusabira-cyan (kcy), a cyan-emitting gfp-like2 protein
16	<a href="#">c2zo7A</a>	Alignment		100.0	49	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyan/green-emitting gfp-like protein, kusabira-cyan mutant <b>PDBTitle:</b> crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
17	<a href="#">c2zwmwC</a>	Alignment		100.0	53	<b>PDB header:</b> luminescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> fluorescent protein; <b>PDBTitle:</b> crystal structure of monomeric kusabira-orange (mko), orange-emitting2 gfp-like protein, at ph 6.0
18	<a href="#">c1yzwB</a>	Alignment		100.0	50	<b>PDB header:</b> luminescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like non-fluorescent chromoprotein; <b>PDBTitle:</b> the 2.1a crystal structure of the far-red fluorescent2 protein hcred: inherent conformational flexibility of the3 chromophore
19	<a href="#">c2a48A</a>	Alignment		100.0	48	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein amfp486; <b>PDBTitle:</b> crystal structure of amfp486 e150q
20	<a href="#">d2rh7a1</a>	Alignment		100.0	42	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
21	<a href="#">c3gb3B</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> killerred; <b>PDBTitle:</b> x-ray structure of genetically encoded photosensitizer killerred in native form
22	<a href="#">c2icrD</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> fluorescent protein <b>Chain:</b> D: <b>PDB Molecule:</b> red fluorescent protein zoanrfp; <b>PDBTitle:</b> red fluorescent protein zrfp574 from zoanthus sp.
23	<a href="#">c4jeoB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> red fluorescent protein blfp-r5; <b>PDBTitle:</b> crystal structure of red fluorescent protein lanrfpdam exposed to2 prolonged x-ray irradiation
24	<a href="#">c5ltrA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> mneongreen; <b>PDBTitle:</b> structure of the yellow-green fluorescent protein mneongreen from2 branchiostoma lanceolatum at the near physiological ph 8.0
25	<a href="#">d1h6ra</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
26	<a href="#">c2g3oB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> luminescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> green fluorescent protein 2; <b>PDBTitle:</b> the 2.1a crystal structure of copgfp
27	<a href="#">c2dd9C</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> luminescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> a mutant of gfp-like protein from chiridius poppei
28	<a href="#">d1kp5a</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
						<b>PDB header:</b> fluorescent protein

29	<a href="#">c4dkmH</a>	Alignment	not modelled	100.0	26	<b>Chain:</b> H; <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfpcl1a; <b>PDBTitle:</b> crystal structure of amphioxus gfpcl1a <b>PDB header:</b> fluorescent protein <b>Chain:</b> A; <b>PDB Molecule:</b> yellow fluorescent protein; <b>PDBTitle:</b> crystal structure of the yellow fluorescent protein phiyfp (phialidium2 sp.)
30	<a href="#">c4he4A</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
31	<a href="#">d1oxda</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> GFP-like <b>Superfamily:</b> GFP-like <b>Family:</b> Fluorescent proteins
32	<a href="#">d1mywa</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> amphioxus green fluorescent protein, gfpal1; <b>PDBTitle:</b> crystal structure of amphioxus green fluorescent protein, gfpal1
33	<a href="#">c4dknB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> luminescent protein <b>Chain:</b> A; <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> green fluorescent protein from clytia gregaria
34	<a href="#">c2hpwA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> fluorescent protein, replication <b>Chain:</b> A; <b>PDB Molecule:</b> yeast enhanced green fluorescent protein,dna polymerase <b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein - mouse2 polymerase iota ubiquitin binding motif fusion protein
35	<a href="#">c3ai4A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> clpb protein, putative,green fluorescent protein; <b>PDBTitle:</b> structure of a malarial protein involved in proteostasis
36	<a href="#">c4xbiA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> fluorescent protein/protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> green fluorescent protein,atpase wrnp1; <b>PDBTitle:</b> crystal structure of gfp-wrnp1 ubz domain fusion protein in complex2 with ubiquitin
37	<a href="#">c3vhtB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> fluorescent protein, de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> e23p-yfp, chimeric construct,gfp-like fluorescent <b>PDBTitle:</b> crystal structure of a computational designed engrailed homeodomain2 variant fused with yfp
38	<a href="#">c4ndkA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> green fluorescent protein,hsdr; <b>PDBTitle:</b> c-terminal domain of ecor124i hsdr subunit fused with the ph-sensitive2 gfp variant ratiometric phluorin
39	<a href="#">c5j3nA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> fluorescent protein <b>Chain:</b> E; <b>PDB Molecule:</b> fluorescent protein fp480; <b>PDBTitle:</b> crystal structure of circular-permuted mkate
40	<a href="#">c3rwaE</a>	Alignment	not modelled	100.0	55	<b>PDB header:</b> motor/fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> myosin-7,green fluorescent protein; <b>PDBTitle:</b> structure of human beta-cardiac myosin motor domain:gfp chimera
41	<a href="#">c4p7hb</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of cockroach allergen bla g 1 tandem repeat as a egfp fusion
42	<a href="#">c4jrbA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> yellow fluorescent protein glutaredoxin fusion protein; <b>PDBTitle:</b> yellow fluorescent protein - glutaredoxin fusion protein
43	<a href="#">c2jadA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> crystal structure of vsfgfp-0
44	<a href="#">c4pfeB</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> metal binding, dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> green fluorescent protein,extracellular streptodornase d; <b>PDBTitle:</b> structure of sda1 nuclease apoprotein as an egfp fixed-arm fusion
45	<a href="#">c5fguA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> fluorescent protein, transcription <b>Chain:</b> A; <b>PDB Molecule:</b> yeast enhanced green fluorescent protein,ubiquitin; <b>PDBTitle:</b> crystal structure of yeast enhanced green fluorescent protein-2 ubiquitin fusion protein
46	<a href="#">c3ai5A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> green fluorescent protein, apoptosis regulator bax; <b>PDBTitle:</b> bax bh3-in-groove dimer (gfp)
47	<a href="#">c4bduC</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> motor protein/metal-bindng protein <b>Chain:</b> A; <b>PDB Molecule:</b> unconventional myosin-vi, green fluorescent protein; <b>PDBTitle:</b> myosin vi (mdinsert2-gfp fusion) pre-powerstroke state (mg.adp.alf4)
48	<a href="#">c4anjA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> calcium binding, fluorescent, transferas <b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of calmodulin, gpf-like protein eosfp, and <b>PDBTitle:</b> calcium-free campari v0.2
49	<a href="#">c4oy4A</a>	Alignment	not modelled	100.0	55	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> rgeco1; <b>PDBTitle:</b> crystal structure of the genetically encoded calcium indicator rgeco1
50	<a href="#">c4i2yB</a>	Alignment	not modelled	100.0	61	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> rgeco1; <b>PDBTitle:</b> crystal structure of the genetically encoded calcium indicator rgeco1
51	<a href="#">c3lf4B</a>	Alignment	not modelled	100.0	60	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B; <b>PDB Molecule:</b> fluorescent timer precursor blue102; <b>PDBTitle:</b> crystal structure of fluorescent timer precursor blue102
52	<a href="#">c3u0kA</a>	Alignment	not modelled	100.0	54	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A; <b>PDB Molecule:</b> ramp; <b>PDBTitle:</b> crystal structure of the genetically encoded calcium indicator ramp
53	<a href="#">c2gw4D</a>	Alignment	not modelled	100.0	53	<b>PDB header:</b> luminescent protein <b>Chain:</b> D; <b>PDB Molecule:</b> kaede; <b>PDBTitle:</b> crystal structure of stony coral fluorescent protein kaede,

						red form
54	<a href="#">c3u8pB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> fluorescent protein, electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b562 integral fusion with enhanced green <b>PDBTitle:</b> cytochrome b562 integral fusion with egfp
55	<a href="#">c3cfhB</a>	Alignment	not modelled	100.0	50	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> gfp-like photoswitchable fluorescent protein; <b>PDBTitle:</b> photoswitchable red fluorescent protein psrfp, off-state
56	<a href="#">c3akoG</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> fluorescent protein <b>Chain:</b> G: <b>PDB Molecule:</b> venus; <b>PDBTitle:</b> crystal structure of the reassembled venus
57	<a href="#">c2g3dB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> luminescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis
58	<a href="#">c3evpA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein,green fluorescent protein; <b>PDBTitle:</b> crystal structure of circular-permuted egfp
59	<a href="#">c3evrA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain kinase, green fluorescent protein, <b>PDBTitle:</b> crystal structure of calcium bound monomeric gcamp2
60	<a href="#">c3osrA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> fluorescent protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,green fluorescent <b>PDBTitle:</b> maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
61	<a href="#">c3lf4A</a>	Alignment	not modelled	100.0	69	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> fluorescent timer precursor blue102; <b>PDBTitle:</b> crystal structure of fluorescent timer precursor blue102
62	<a href="#">c2gw4C</a>	Alignment	not modelled	100.0	55	<b>PDB header:</b> luminescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> kaede; <b>PDBTitle:</b> crystal structure of stony coral fluorescent protein kaede, red form
63	<a href="#">c2a56A</a>	Alignment	not modelled	99.9	52	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> gfp-like non-fluorescent chromoprotein fp595 chain 1; <b>PDBTitle:</b> fluorescent protein asfp595, a143s, on-state, 5min irradiation
64	<a href="#">c3ek7A</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin light chain kinase, green fluorescent protein, <b>PDBTitle:</b> calcium-saturated gcamp2 dimer
65	<a href="#">c3osqA</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> fluorescent protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,green fluorescent <b>PDBTitle:</b> maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 175
66	<a href="#">c2g16A</a>	Alignment	not modelled	99.6	36	<b>PDB header:</b> luminescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein; <b>PDBTitle:</b> structure of s65a y66s gfp variant after backbone2 fragmentation
67	<a href="#">c3cgfF</a>	Alignment	not modelled	98.4	81	<b>PDB header:</b> fluorescent protein <b>Chain:</b> F: <b>PDB Molecule:</b> gfp-like fluorescent chromoprotein dsfp483; <b>PDBTitle:</b> crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
68	<a href="#">c3akoH</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> fluorescent protein <b>Chain:</b> H: <b>PDB Molecule:</b> venus; <b>PDBTitle:</b> crystal structure of the reassembled venus
69	<a href="#">c4jg9B</a>	Alignment	not modelled	74.2	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein; <b>PDBTitle:</b> x-ray crystal structure of a putative lipoprotein from bacillus2 anthracis
70	<a href="#">d1tywa</a>	Alignment	not modelled	70.4	21	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> P22 tailspike protein
71	<a href="#">c2xc1A</a>	Alignment	not modelled	67.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional tail protein; <b>PDBTitle:</b> full-length tailspike protein mutant y108w of bacteriophage p22
72	<a href="#">c3riqA</a>	Alignment	not modelled	41.4	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tailspike protein; <b>PDBTitle:</b> siphovirus 9na tailspike receptor binding domain
73	<a href="#">c4r8oB</a>	Alignment	not modelled	36.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3836 family protein (bvu_1206) from2 bacteroides vulgatus atcc 8482 at 2.50 a resolution
74	<a href="#">c4r03A</a>	Alignment	not modelled	34.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf3836 family protein (bdi_3222) from2 parabacteroides distasonis atcc 8503 at 1.50 a resolution
75	<a href="#">c2k6zA</a>	Alignment	not modelled	32.2	24	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1943; <b>PDBTitle:</b> solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
76	<a href="#">d1uisa1</a>	Alignment	not modelled	30.4	17	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Pleiotropic translational regulator Hfq
77	<a href="#">c2k4vA</a>	Alignment	not modelled	30.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1076; <b>PDBTitle:</b> solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural

						proteomics target pa1076 .
78	<a href="#">c3zk0A_</a>	Alignment	not modelled	29.3	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sco3965; <b>PDBTitle:</b> the crystal structure of a cu(i) metallochaperone from streptomyces lividans in its apo form
79	<a href="#">c3dkxA_</a>	Alignment	not modelled	26.9	30	<b>PDB header:</b> replication protein repB; <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein repB; <b>PDBTitle:</b> crystal structure of the replication initiator protein2 encoded on plasmid pmv158 (repB), trigonal form, to 2.7 ang3 resolution
80	<a href="#">c3u1wB_</a>	Alignment	not modelled	26.4	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical periplasmic protein; <b>PDBTitle:</b> crystal structure of a calcium binding protein (bdi 1975) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
81	<a href="#">c4iajC_</a>	Alignment	not modelled	25.7	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> crystal structure of a conserved domain protein (sp_1775) from2 streptococcus pneumoniae tigr4 at 1.91 a resolution
82	<a href="#">c2ldmA_</a>	Alignment	not modelled	23.1	17	<b>PDB header:</b> transcription/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
83	<a href="#">c2v5iA_</a>	Alignment	not modelled	22.9	16	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> salmonella typhimurium db7155 bacteriophage det7 <b>PDBTitle:</b> structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
84	<a href="#">d1gwma_</a>	Alignment	not modelled	22.3	30	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 29 carbohydrate binding module, CBM29
85	<a href="#">d1w36b3</a>	Alignment	not modelled	21.6	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
86	<a href="#">d1x9la_</a>	Alignment	not modelled	21.0	21	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> DR1885-like metal-binding protein <b>Family:</b> DR1885-like metal-binding protein
87	<a href="#">d1hdmb2</a>	Alignment	not modelled	17.7	11	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
88	<a href="#">c3qiiA_</a>	Alignment	not modelled	16.8	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20; <b>PDBTitle:</b> crystal structure of tudor domain 2 of human phd finger protein 20
89	<a href="#">c2kqdA_</a>	Alignment	not modelled	16.6	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aprataxin and pnk-like factor; <b>PDBTitle:</b> first pbz domain of human aplf protein in complex with2 ribofuranosyladenosine
90	<a href="#">c2xetB_</a>	Alignment	not modelled	16.2	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
91	<a href="#">d2cbra_</a>	Alignment	not modelled	16.2	7	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
92	<a href="#">c4pqxC_</a>	Alignment	not modelled	15.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a nigg-like protein (baccac_02139) from2 bacteroides caccae atcc 43185 at 2.39 a resolution
93	<a href="#">c3dvkB_</a>	Alignment	not modelled	14.3	75	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent r-type calcium channel subunit alpha-1e; <b>PDBTitle:</b> crystal structure of ca2+/cam-cav2.3 iq domain complex
94	<a href="#">c2equA_</a>	Alignment	not modelled	14.1	11	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phd finger protein 20-like 1; <b>PDBTitle:</b> solution structure of the tudor domain of phd finger2 protein 20-like 1
95	<a href="#">d1k8ib2</a>	Alignment	not modelled	13.9	11	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
96	<a href="#">c3bxIB_</a>	Alignment	not modelled	13.1	75	<b>PDB header:</b> membrane protein, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent r-type calcium channel subunit <b>PDBTitle:</b> crystal structure of the r-type calcium channel (cav2.3) iq2 domain and ca2+calmodulin complex
97	<a href="#">d2bjra2</a>	Alignment	not modelled	12.6	23	<b>Fold:</b> MFPT repeat-like <b>Superfamily:</b> MFPT repeat-like <b>Family:</b> MFPT repeat
98	<a href="#">c3mp6A_</a>	Alignment	not modelled	12.2	21	<b>PDB header:</b> histone binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,linker,saga-associated <b>PDBTitle:</b> complex structure of sgf29 and dimethylated h3k4
99	<a href="#">d1igqa_</a>	Alignment	not modelled	12.1	45	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> C-terminal domain of transcriptional repressors <b>Family:</b> Transcriptional repressor protein KorB