

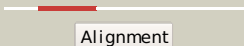

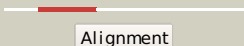



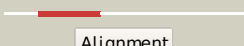

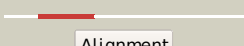

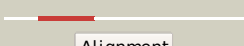

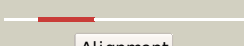









Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O95081
Date	Wed May 9 18:00:30 BST 2012
Unique Job ID	dd03a86d26de46f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d9lA_	 Alignment		100.0	68	PDB header: gene regulation Chain: A: PDB Molecule: nucleoporin-like protein rip; PDBTitle: solution structure of the arfgap domain of human rip
2	c3lvrE_	 Alignment		100.0	19	PDB header: protein transport Chain: E: PDB Molecule: arf-gap with sh3 domain, ank repeat and ph domain- PDBTitle: the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
3	c2iqjB_	 Alignment		100.0	22	PDB header: protein transport Chain: B: PDB Molecule: stromal membrane-associated protein 1-like; PDBTitle: crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
4	d1dcqa2	 Alignment		100.0	20	Fold: ArfGap/RecO-like zinc finger Superfamily: ArfGap/RecO-like zinc finger Family: Pyk2-associated protein beta ARF-GAP domain
5	c3fehA_	 Alignment		100.0	22	PDB header: hydrolase activator Chain: A: PDB Molecule: centaurin-alpha-1; PDBTitle: crystal structure of full length centaurin alpha-1
6	c3jueA_	 Alignment		100.0	22	PDB header: protein transport/endocytosis Chain: A: PDB Molecule: arfgap with coiled-coil, ank repeat and ph domain- PDBTitle: crystal structure of arfgap and ank repeat domain of acap1
7	c1dcqa_	 Alignment		100.0	20	PDB header: metal binding protein Chain: A: PDB Molecule: pyk2-associated protein beta; PDBTitle: crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
8	c2b0oF_	 Alignment		100.0	18	PDB header: metal binding protein Chain: F: PDB Molecule: uplc1; PDBTitle: crystal structure of uplc1 gap domain
9	c2owaB_	 Alignment		100.0	21	PDB header: protein transport Chain: B: PDB Molecule: arfgap-like finger domain containing protein; PDBTitle: crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
10	c2p57A_	 Alignment		100.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: gtpase-activating protein znf289; PDBTitle: gap domain of znf289, an id1-regulated zinc finger protein
11	c3o47A_	 Alignment		100.0	24	PDB header: hydrolase, hydrolase activator Chain: A: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1, adp- PDBTitle: crystal structure of arfgap1-arf1 fusion protein

12	c3dwdB_	Alignment		100.0	24	PDB header: transport protein Chain: B: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1; PDBTitle: crystal structure of the arfgap domain of human arfgap1
13	d1u5ka2	Alignment		96.4	16	Fold: ArfGap/RecO-like zinc finger Superfamily: ArfGap/RecO-like zinc finger Family: RecO C-terminal domain-like
14	c1u5kA_	Alignment		95.7	16	PDB header: recombination,replication Chain: A: PDB Molecule: hypothetical protein; PDBTitle: recombinational repair protein reco
15	c3bjia_	Alignment		93.9	14	PDB header: signaling protein Chain: A: PDB Molecule: proto-oncogene vav; PDBTitle: structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
16	c1kxuA_	Alignment		82.7	19	PDB header: regulatory protein Chain: A: PDB Molecule: cyclin h; PDBTitle: cyclin h, a positive regulatory subunit of cdk activating kinase
17	c3ihpB_	Alignment		81.1	18	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: covalent ubiquitin-usp5 complex
18	d2ba0d2	Alignment		80.4	14	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
19	d1cjya2	Alignment		78.4	29	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
20	d2br2b2	Alignment		77.8	18	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
21	d2g45a1	Alignment	not modelled	77.5	20	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
22	c2dvkA_	Alignment	not modelled	76.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0130 protein ape0816; PDBTitle: crystal structure of hypothetical protein from aeropyrum pernix
23	d1y0ja1	Alignment	not modelled	76.1	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
24	c2qg3B_	Alignment	not modelled	75.5	13	PDB header: unknown function Chain: B: PDB Molecule: upf0130 protein af_2059; PDBTitle: crystal structure of a tyw3 methyltransferase-like protein (af_2059)2 from archaeoglobus fulgidus dsm 4304 at 1.95 a resolution
25	d2je6b2	Alignment	not modelled	74.9	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
26	d2djaa1	Alignment	not modelled	74.7	20	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
27	c3c5kA_	Alignment	not modelled	74.5	13	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase 6; PDBTitle: crystal structure of human hdac6 zinc finger domain
28	c2junA_	Alignment	not modelled	70.9	27	PDB header: ligase Chain: A: PDB Molecule: midline-1; PDBTitle: structure of the mid1 tandem b-boxes reveals an interaction2 reminiscent of intermolecular ring heterodimers

29	d2dq5a1	Alignment	not modelled	70.8	27	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
30	c2egmA	Alignment	not modelled	70.7	19	PDB header: transcription/metal binding protein Chain: A: PDB Molecule: tripartite motif-containing protein 41; PDBTitle: solution structure of the zf-b_box domain from human2 tripartite motif protein 41
31	c2d8uA	Alignment	not modelled	70.1	19	PDB header: ligase Chain: A: PDB Molecule: ubiquitin ligase trim63; PDBTitle: solution structure of the b-box domain of the human2 tripartite motif-containing 63 protein
32	d1jkwa1	Alignment	not modelled	67.0	19	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
33	d5gata	Alignment	not modelled	64.3	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
34	c2yrgA	Alignment	not modelled	64.1	25	PDB header: ligase Chain: A: PDB Molecule: tripartite motif-containing protein 5; PDBTitle: solution structure of the b-box domain from tripartite2 motif-containing protein 5
35	d1gnfa	Alignment	not modelled	59.1	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
36	c2it3B	Alignment	not modelled	58.2	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0130 protein ph1069; PDBTitle: structure of ph1069 protein from pyrococcus horikoshii
37	c2vrwB	Alignment	not modelled	57.1	15	PDB header: signaling protein Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: critical structural role for the ph and c1 domains of the2 vav1 exchange factor
38	c2gb5B	Alignment	not modelled	56.1	21	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
39	d2nn6b2	Alignment	not modelled	55.8	6	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
40	d2a1ja1	Alignment	not modelled	54.9	20	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
41	c3mhsA	Alignment	not modelled	54.4	15	PDB header: hydrolase/transcription regulator/protei Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 8; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
42	c1y1yS	Alignment	not modelled	54.4	20	PDB header: transferase/transcription/dna-rna hybrid Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
43	c2i6yA	Alignment	not modelled	53.2	5	PDB header: lyase Chain: A: PDB Molecule: anthranilate synthase component i, putative; PDBTitle: structure and mechanism of mycobacterium tuberculosis salicylate2 synthase, mbti
44	c2kgoA	Alignment	not modelled	52.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ybil; PDBTitle: solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, oscp target ec0402
45	d2crga1	Alignment	not modelled	52.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
46	c2zetD	Alignment	not modelled	52.2	19	PDB header: signaling protein Chain: D: PDB Molecule: melanophilin; PDBTitle: crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
47	d2dida1	Alignment	not modelled	51.8	19	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
48	d2uzga1	Alignment	not modelled	51.4	15	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
49	d2d8ua1	Alignment	not modelled	51.2	18	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
50	c2riqA	Alignment	not modelled	50.9	19	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: crystal structure of the thir d zinc-binding domain of human parp-1
51	d3gata	Alignment	not modelled	50.8	15	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
52	c1nltA	Alignment	not modelled	50.4	26	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial protein import protein mas5; PDBTitle: the crystal structure of hsp40 ydj1
53	d2idaa1	Alignment	not modelled	49.9	17	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
54	c3ky9B	Alignment	not modelled	49.8	13	PDB header: apoptosis Chain: B: PDB Molecule: proto-oncogene vav; PDBTitle: autoinhibited vav1
55	d2a2pa1	Alignment	not modelled	49.8	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related

56	d1hkya_	Alignment	not modelled	49.7	54	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Pan module (APPLE domain)
57	d2vuti1	Alignment	not modelled	49.7	23	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
58	c1d4uA_	Alignment	not modelled	49.2	25	PDB header: dna binding protein Chain: A: PDB Molecule: nucleotide excision repair protein xpa (xpa-mbd); PDBTitle: interactions of human nucleotide excision repair protein2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
59	d1pjua1	Alignment	not modelled	49.1	31	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
60	c2kdxA_	Alignment	not modelled	47.5	20	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
61	d2dipa1	Alignment	not modelled	47.3	18	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
62	c1x68A_	Alignment	not modelled	47.1	20	PDB header: protein binding Chain: A: PDB Molecule: fhl5 protein; PDBTitle: solution structures of the c-terminal lim domain of human2 fhl5 protein
63	d2g5fa1	Alignment	not modelled	46.6	5	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
64	c1x79C_	Alignment	not modelled	46.4	28	PDB header: protein transport Chain: C: PDB Molecule: rab gtpase binding effector protein 1; PDBTitle: crystal structure of human gga1 gat domain complexed with2 the gat-binding domain of rabaptin5
65	d1cvra2	Alignment	not modelled	46.2	14	Fold: Caspase-like Superfamily: Caspase-like Family: Gingipain R (RgpB), N-terminal domain
66	c2eqrA_	Alignment	not modelled	46.1	17	PDB header: transcription Chain: A: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: solution structure of the first sant domain from human2 nuclear receptor corepressor 1
67	d2bkra1	Alignment	not modelled	46.1	8	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
68	d1y0pa1	Alignment	not modelled	45.8	15	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
69	c1pqvS_	Alignment	not modelled	43.2	30	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
70	c2jvnA_	Alignment	not modelled	42.2	19	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: domain c of human parp-1
71	d1zbdb_	Alignment	not modelled	41.9	17	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: FYVE, a phosphatidylinositol-3-phosphate binding domain
72	d1k0ga_	Alignment	not modelled	40.6	25	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
73	d1v6za2	Alignment	not modelled	40.5	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
74	c2j83B_	Alignment	not modelled	40.1	20	PDB header: hydrolase Chain: B: PDB Molecule: ulilysin; PDBTitle: ulilysin metalloprotease in complex with batimastat.
75	c2yusA_	Alignment	not modelled	39.8	16	PDB header: transcription Chain: A: PDB Molecule: swi/snf-related matrix-associated actin- PDBTitle: solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
76	d1ffya1	Alignment	not modelled	39.0	12	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
77	d1qdlA_	Alignment	not modelled	38.8	5	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
78	d2nn6d2	Alignment	not modelled	38.8	20	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
79	d1cota_	Alignment	not modelled	38.5	20	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
80	d2nl1b_	Alignment	not modelled	38.1	24	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
81	c3r07A_	Alignment	not modelled	37.3	17	PDB header: transferase Chain: A: PDB Molecule: lipoate-protein ligase a subunit 1; PDBTitle: structural analysis of an archaeal lipoylation system. a

						bi-partite2 lipoate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
82	d1fyba1	Alignment	not modelled	36.8	39	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
83	c2hyxA	Alignment	not modelled	36.7	16	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
84	d1tja	Alignment	not modelled	36.3	14	Fold: SSo0622-like Superfamily: SSo0622-like Family: SSo0622-like
85	c1tjA	Alignment	not modelled	36.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0130 protein sso0622; PDBTitle: crystal structure of conserved protein of unknown function2 sso0622 from sulfolobus solfataricus
86	c2cszA	Alignment	not modelled	36.0	29	PDB header: signaling protein Chain: A: PDB Molecule: synaptotagmin-like protein 4; PDBTitle: solution structure of the ring domain of the synaptotagmin-2 like protein 4
87	d2fn0a1	Alignment	not modelled	35.2	5	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
88	d1wkqa	Alignment	not modelled	34.9	13	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: Deoxycytidylate deaminase-like
89	c2eblA	Alignment	not modelled	34.8	23	PDB header: transcription Chain: A: PDB Molecule: coup transcription factor 1; PDBTitle: solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1
90	d1pfta	Alignment	not modelled	34.1	32	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
91	c1x64A	Alignment	not modelled	33.7	19	PDB header: contractile protein Chain: A: PDB Molecule: alpha-actinin-2 associated lim protein; PDBTitle: solution structure of the lim domain of alpha-actinin-22 associated lim protein
92	d2cora1	Alignment	not modelled	33.6	17	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
93	d2csva1	Alignment	not modelled	33.3	18	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
94	d1lc5a	Alignment	not modelled	33.1	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
95	c3h9mA	Alignment	not modelled	32.9	12	PDB header: lyase Chain: A: PDB Molecule: p-aminobenzoate synthetase, component i; PDBTitle: crystal structure of para-aminobenzoate synthetase,2 component i from cytophaga hutchinsonii
96	c2difA	Alignment	not modelled	32.1	17	PDB header: protein binding Chain: A: PDB Molecule: tripartite motif protein 39; PDBTitle: one sequence two fold ? : miss fold of the zf-b-box domain2 from human tripartite motif protein 39
97	d1qypa	Alignment	not modelled	32.1	20	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
98	c1xt5A	Alignment	not modelled	32.0	16	PDB header: immune system Chain: A: PDB Molecule: variable region-containing chitin-binding PDBTitle: crystal structure of vcbp3, domain 1, from branchiostoma2 floridae
99	d1dl6a	Alignment	not modelled	31.6	21	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
100	c3tsuA	Alignment	not modelled	31.5	26	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
101	d1unld	Alignment	not modelled	30.9	38	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
102	c1l4aE	Alignment	not modelled	30.8	20	PDB header: endocytosis/exocytosis Chain: E: PDB Molecule: synaphin a; PDBTitle: x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
103	c1unhD	Alignment	not modelled	30.3	38	PDB header: cell cycle Chain: D: PDB Molecule: cyclin-dependent kinase 5 activator 1; PDBTitle: structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
104	d1tiha	Alignment	not modelled	30.1	39	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
105	d1ynwa1	Alignment	not modelled	29.8	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
106	c3pkiF	Alignment	not modelled	29.7	40	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
107	c3jyvN	Alignment	not modelled	29.6	22	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29(a); PDBTitle: structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces

						lanuginosus ribosome at 3.8.9a resolution
108	d2fc7a1	Alignment	not modelled	29.6	26	Fold: RING/U-box Superfamily: RING/U-box Family: ZZ domain
109	c2darA	Alignment	not modelled	29.6	25	PDB header: metal binding protein Chain: A: PDB Molecule: pdz and lim domain protein 5; PDBTitle: solution structure of first lim domain of enigma-like pdz2 and lim domains protein
110	c1cvrA	Alignment	not modelled	29.5	13	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: gingipain r; PDBTitle: crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
111	d1hcqa	Alignment	not modelled	29.3	24	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
112	c1oahA	Alignment	not modelled	29.2	19	PDB header: reductase Chain: A: PDB Molecule: cytochrome c nitrite reductase; PDBTitle: cytochrome c nitrite reductase from desulfovibrio2 desulfuricans atcc 27774: the relevance of the two3 calcium sites in the structure of the catalytic subunit4 (nrfa).
113	d1oaha	Alignment	not modelled	29.2	19	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
114	c2gamA	Alignment	not modelled	28.6	16	PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-1) in complex3 with galb1,3galnac
115	d1ce3a	Alignment	not modelled	28.3	35	Fold: Plant proteinase inhibitors Superfamily: Plant proteinase inhibitors Family: Plant proteinase inhibitors
116	d1i7qa	Alignment	not modelled	27.8	19	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
117	c1qh2B	Alignment	not modelled	27.5	36	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: protein (trypsin inhibitor c2); PDBTitle: chymotrypsin inhibitor (c2) from nicotiana alata
118	c2d8xA	Alignment	not modelled	27.4	25	PDB header: structural protein, cell cycle Chain: A: PDB Molecule: protein pinch; PDBTitle: solution structure of the second lim domain of particularly2 interesting new cys-his protein (pinch)
119	d2o9ca1	Alignment	not modelled	27.4	13	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
120	c3bvoA	Alignment	not modelled	27.3	50	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb