

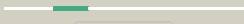



















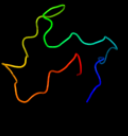
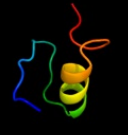






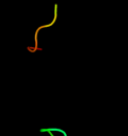


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PJX4
Date	Fri May 25 09:46:33 BST 2012
Unique Job ID	7e12dc0df08ceb1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m4fA_	 Alignment		48.3	42	PDB header: antimicrobial protein Chain: A: PDB Molecule: hepcidin; PDBTitle: solution structure of hepcidin-25
2	c3h0tC_	 Alignment		47.0	42	PDB header: immune system/antimicrobial protein Chain: C: PDB Molecule: hepcidin; PDBTitle: hepcidin-fab complex
3	c2kefA_	 Alignment		46.9	42	PDB header: antibiotic, hormone Chain: A: PDB Molecule: hepcidin; PDBTitle: solution nmr structures of human hepcidin at 325k
4	c1m4eA_	 Alignment		46.0	42	PDB header: antimicrobial protein Chain: A: PDB Molecule: hepcidin; PDBTitle: solution structure of hepcidin-20
5	d2dlqa2	 Alignment		34.2	54	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
6	c2xrgA_	 Alignment		33.0	24	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
7	d1kg1a_	 Alignment		28.0	38	Fold: Necrosis inducing protein 1, NIP1 Superfamily: Necrosis inducing protein 1, NIP1 Family: Necrosis inducing protein 1, NIP1
8	d1i71a_	 Alignment		27.6	18	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
9	c3hh7A_	 Alignment		25.0	32	PDB header: toxin Chain: A: PDB Molecule: muscarinic toxin-like protein 3 homolog; PDBTitle: structural and functional characterization of a novel2 homodimeric three-finger neurotoxin from the venom of3 ophiophagus hannah (king cobra)
10	d1sfkb_	 Alignment		20.5	27	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
11	d2hppp_	 Alignment		15.8	23	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules

12	c2pf2A_	Alignment		15.1	20	PDB header: hydrolase(serine protease) Chain: A: PDB Molecule: prothrombin fragment 1; PDBTitle: the ca+2 ion and membrane binding structure of the gla domain of ca-2 prothrombin fragment 1
13	c2fqhA_	Alignment		14.7	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0938; PDBTitle: nmr structure of hypothetical protein ta0938 from2 termoplasma acidophilum
14	c1x4sA_	Alignment		14.6	22	PDB header: metal binding protein Chain: A: PDB Molecule: zinc finger hit domain containing protein 2; PDBTitle: solution structure of zinc finger hit domain in protein fon
15	d1tv0a_	Alignment		14.5	50	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
16	d2pf1a1	Alignment		14.4	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
17	d1ki0a3	Alignment		11.9	25	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
18	c2xr9A_	Alignment		11.9	24	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
19	c2lewA_	Alignment		11.8	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: alpha-defensin 4; PDBTitle: structural plasticity of paneth cell alpha-defensins: characterization2 of salt-bridge deficient analogues of mouse cryptdin-4
20	d1zu1a2	Alignment		11.6	32	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
21	d2hpgp_	Alignment	not modelled	11.2	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
22	c2fwtA_	Alignment	not modelled	11.0	38	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
23	c1zpzA_	Alignment	not modelled	10.8	24	PDB header: transferase Chain: A: PDB Molecule: proto-oncogene tyrosine-protein kinase abl1; PDBTitle: solution structure of the f-actin binding domain of bcr-2 abl/c-abl
24	d1e4ta_	Alignment	not modelled	10.1	37	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
25	d1wiia_	Alignment	not modelled	10.0	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
26	d1jgka_	Alignment	not modelled	9.8	24	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
27	d1sfka_	Alignment	not modelled	9.5	29	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
28	d1ki0a2	Alignment	not modelled	9.5	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
						PDB header: hormone

29	c1gmoC_	Alignment	not modelled	9.4	20	Chain: C: PDB Molecule: hepatocyte growth factor; PDBTitle: crystal structures of nk1-heparin complexes reveal the basis for nk12 activity and enable engineering of potent agonists of the met3 receptor
30	c1znmA_	Alignment	not modelled	8.9	88	PDB header: zinc finger Chain: A: PDB Molecule: yy1; PDBTitle: a zinc finger with an artificial beta-turn, original2 sequence taken from the third zinc finger domain of the3 human transcriptional repressor protein yy1 (ying and yang4 1, a delta transcription factor), nmr, 34 structures
31	c1r6rA_	Alignment	not modelled	8.9	24	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
32	d1r6ra_	Alignment	not modelled	8.9	24	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
33	d1nl1a1	Alignment	not modelled	8.8	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
34	c2e72A_	Alignment	not modelled	8.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pogo transposable element with znf domain; PDBTitle: solution structure of the zinc finger domain of human2 kiaa0461
35	d1wffa_	Alignment	not modelled	8.7	36	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
36	c2leyA_	Alignment	not modelled	8.5	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: alpha-defensin 4; PDBTitle: solution structure of (r7g)-crp4
37	d1wfla_	Alignment	not modelled	8.5	21	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
38	c2kk1A_	Alignment	not modelled	8.3	35	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase abl2; PDBTitle: solution structure of c-terminal domain of tyrosine-protein2 kinase abl2 from homo sapiens, northeast structural3 genomics consortium (nesg) target hr5537a
39	d1jfna_	Alignment	not modelled	8.2	18	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
40	d1krna_	Alignment	not modelled	8.1	18	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
41	c1zmmD_	Alignment	not modelled	7.5	40	PDB header: antimicrobial protein Chain: D: PDB Molecule: neutrophil defensin 4; PDBTitle: crystal structure of human alpha-defensin-4
42	d1i5ka_	Alignment	not modelled	7.3	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
43	d1e4ua_	Alignment	not modelled	7.3	21	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
44	d1e4qa_	Alignment	not modelled	7.1	41	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
45	c3kv1A_	Alignment	not modelled	6.9	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional repressor; PDBTitle: crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
46	d2qj2a2	Alignment	not modelled	6.9	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
47	d1atxa_	Alignment	not modelled	6.7	38	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
48	d1a0ha1	Alignment	not modelled	6.7	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules
49	c1zmmA_	Alignment	not modelled	6.6	46	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 4; PDBTitle: crystal structure of human alpha-defensin-4
50	c3qteA_	Alignment	not modelled	5.5	28	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-6; PDBTitle: crystal structure of human alpha-defensin 6 (h27w mutant)
51	d1xpa2	Alignment	not modelled	5.4	19	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
52	c1v5aA_	Alignment	not modelled	5.3	60	PDB header: toxin Chain: A: PDB Molecule: covalitoxin-i; PDBTitle: solution structure of covalitoxin i
53	d3kiva_	Alignment	not modelled	5.2	20	Fold: Kringle-like Superfamily: Kringle-like Family: Kringle modules