












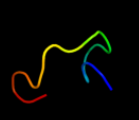



















# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76162
Date	Thu Jan 5 12:19:57 GMT 2012
Unique Job ID	6bcd13fd902e966

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qgpA_</a>	 Alignment		88.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease; <b>PDBTitle:</b> x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
2	<a href="#">c3plwA_</a>	 Alignment		64.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> recombination enhancement function protein; <b>PDBTitle:</b> ref protein from p1 bacteriophage
3	<a href="#">c3dzuD_</a>	 Alignment		63.0	28	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> peroxisome proliferator-activated receptor gamma; <b>PDBTitle:</b> intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
4	<a href="#">c3g27A_</a>	 Alignment		45.6	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> 82 prophage-derived uncharacterized protein ybco; <b>PDBTitle:</b> structure of a putative bacteriophage protein from escherichia coli2 str. k-12 substr. mg1655
5	<a href="#">c3alrA_</a>	 Alignment		42.8	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nanos protein; <b>PDBTitle:</b> crystal structure of nanos
6	<a href="#">d1dsza_</a>	 Alignment		39.0	25	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
7	<a href="#">d1r4ra_</a>	 Alignment		38.0	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
8	<a href="#">d1lata_</a>	 Alignment		37.8	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
9	<a href="#">c2o2kA_</a>	 Alignment		36.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
10	<a href="#">d1hraa_</a>	 Alignment		36.4	27	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
11	<a href="#">d1glua_</a>	 Alignment		36.2	31	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor

12	<a href="#">d1hcqa_</a>	Alignment		35.4	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
13	<a href="#">c1xx6B_</a>	Alignment		34.8	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
14	<a href="#">d2b8ta2</a>	Alignment		31.1	26	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Type II thymidine kinase zinc finger
15	<a href="#">d1r0oa_</a>	Alignment		30.3	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
16	<a href="#">c1w4rC_</a>	Alignment		29.4	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> structure of a type ii thymidine kinase with bound dtp
17	<a href="#">c3ds8A_</a>	Alignment		29.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
18	<a href="#">d2nllb_</a>	Alignment		28.7	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
19	<a href="#">d1ji3a_</a>	Alignment		28.4	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
20	<a href="#">d1ei9a_</a>	Alignment		27.7	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
21	<a href="#">c2hihB_</a>	Alignment	not modelled	27.3	47	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase 46 kda form; <b>PDBTitle:</b> crystal structure of a macpf/perforin-like protein
22	<a href="#">d1cita_</a>	Alignment	not modelled	26.6	38	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
23	<a href="#">d1ku0a_</a>	Alignment	not modelled	26.6	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
24	<a href="#">c2qp2A_</a>	Alignment	not modelled	24.8	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> unknown protein; <b>PDBTitle:</b> structure of a macpf/perforin-like protein
25	<a href="#">c2zkqn_</a>	Alignment	not modelled	23.2	36	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> N: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
26	<a href="#">d1xbta2</a>	Alignment	not modelled	23.2	28	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Type II thymidine kinase zinc finger
27	<a href="#">d1jmkc_</a>	Alignment	not modelled	23.2	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
28	<a href="#">c2eblA_</a>	Alignment	not modelled	22.5	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> coup transcription factor 1; <b>PDBTitle:</b> solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1

29	<a href="#">c3e2iA_</a>	Alignment	not modelled	22.3	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> crystal structure of thymidine kinase from s. aureus
30	<a href="#">c2b8tA_</a>	Alignment	not modelled	21.7	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> crystal structure of thymidine kinase from u.urealyticum in2 complex with thymidine
31	<a href="#">c2p0pA_</a>	Alignment	not modelled	21.1	33	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alr1010 protein; <b>PDBTitle:</b> calcium binding protein in the free form
32	<a href="#">c3dzyA_</a>	Alignment	not modelled	20.7	33	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor rxr-alpha; <b>PDBTitle:</b> intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with rosiglitazone, 9-cis retinoic acid and ncoa2 peptide
33	<a href="#">d1mo2a_</a>	Alignment	not modelled	20.0	29	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
34	<a href="#">c1mo2A_</a>	Alignment	not modelled	20.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> erythronolide synthase, modules 5 and 6; <b>PDBTitle:</b> thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
35	<a href="#">c2xznN_</a>	Alignment	not modelled	20.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> rps29e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
36	<a href="#">d1x3za1</a>	Alignment	not modelled	19.8	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
37	<a href="#">d1cvla_</a>	Alignment	not modelled	19.6	47	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
38	<a href="#">d1kb2a_</a>	Alignment	not modelled	19.5	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
39	<a href="#">c2envA_</a>	Alignment	not modelled	19.3	31	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisome proliferator-activated receptor delta; <b>PDBTitle:</b> solution sturcture of the c4-type zinc finger domain from2 human peroxisome proliferator-activated receptor delta
40	<a href="#">d1xkta_</a>	Alignment	not modelled	19.3	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
41	<a href="#">c3jyvN_</a>	Alignment	not modelled	19.1	27	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s29(a); <b>PDBTitle:</b> structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
42	<a href="#">c1bomB_</a>	Alignment	not modelled	19.1	31	<b>PDB header:</b> insulin-like brain-secretory peptide <b>Chain:</b> B: <b>PDB Molecule:</b> bombyxin-ii,bombyxin a-6; <b>PDBTitle:</b> three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkmoth bombyx3 mori: comparison with insulin and relaxin
43	<a href="#">d1ynwa1</a>	Alignment	not modelled	19.0	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
44	<a href="#">c3lcrA_</a>	Alignment	not modelled	18.8	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycetin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycetin biosynthetic pathway
45	<a href="#">d2f4ma1</a>	Alignment	not modelled	18.4	36	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core
46	<a href="#">d1r0na_</a>	Alignment	not modelled	18.1	33	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
47	<a href="#">d1r4ia_</a>	Alignment	not modelled	18.1	29	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
48	<a href="#">c1r4iA_</a>	Alignment	not modelled	18.1	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> androgen receptor; <b>PDBTitle:</b> crystal structure of androgen receptor dna-binding domain2 bound to a direct repeat response element
49	<a href="#">d2h8pc1</a>	Alignment	not modelled	17.9	27	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
50	<a href="#">d1weoa_</a>	Alignment	not modelled	17.6	33	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
51	<a href="#">d1tcaa_</a>	Alignment	not modelled	17.3	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
52	<a href="#">c2dIIA_</a>	Alignment	not modelled	17.1	19	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interferon regulatory factor 4; <b>PDBTitle:</b> solution structure of the irf domain of human interferon2 regulator factors 4
53	<a href="#">d1dszb_</a>	Alignment	not modelled	16.9	31	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
54	<a href="#">d1uxoa_</a>	Alignment	not modelled	16.7	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases

						<b>Family:</b> YdeN-like
55	<a href="#">c2yqpA</a>	Alignment	not modelled	16.0	33	<b>PDB header:</b> gene regulation, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx59; <b>PDBTitle:</b> solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
56	<a href="#">d1lo1a</a>	Alignment	not modelled	15.7	31	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
57	<a href="#">d1bdsa</a>	Alignment	not modelled	15.6	46	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
58	<a href="#">d1kb6b</a>	Alignment	not modelled	15.5	31	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
59	<a href="#">d1jbsa</a>	Alignment	not modelled	14.9	44	<b>Fold:</b> Microbial ribonucleases <b>Superfamily:</b> Microbial ribonucleases <b>Family:</b> Ribotoxin
60	<a href="#">d4lipd</a>	Alignment	not modelled	14.4	60	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
61	<a href="#">c3ahpA</a>	Alignment	not modelled	13.8	25	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cuta1; <b>PDBTitle:</b> crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
62	<a href="#">d1xx6a2</a>	Alignment	not modelled	13.7	63	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Type II thymidine kinase zinc finger
63	<a href="#">c2ja1A</a>	Alignment	not modelled	13.6	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
64	<a href="#">d1ex9a</a>	Alignment	not modelled	13.2	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
65	<a href="#">d2ccya</a>	Alignment	not modelled	13.2	36	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome c'-like
66	<a href="#">c2j0eA</a>	Alignment	not modelled	13.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconolactonase; <b>PDBTitle:</b> three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
67	<a href="#">d1mqva</a>	Alignment	not modelled	12.9	25	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome c'-like
68	<a href="#">d2hfha</a>	Alignment	not modelled	12.7	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Forkhead DNA-binding domain
69	<a href="#">d2bv3a4</a>	Alignment	not modelled	12.7	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
70	<a href="#">c3bdvB</a>	Alignment	not modelled	12.3	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf1234; <b>PDBTitle:</b> crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
71	<a href="#">c2orvB</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> human thymidine kinase 1 in complex with tp4a
72	<a href="#">d1jw2a</a>	Alignment	not modelled	12.1	47	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Hemolysin expression modulating protein HHA <b>Family:</b> Hemolysin expression modulating protein HHA
73	<a href="#">c1pjaA</a>	Alignment	not modelled	11.9	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> palmitoyl-protein thioesterase 2 precursor; <b>PDBTitle:</b> the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
74	<a href="#">d1pjaa</a>	Alignment	not modelled	11.9	60	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
75	<a href="#">d1kbha</a>	Alignment	not modelled	11.8	70	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
76	<a href="#">c2zyiB</a>	Alignment	not modelled	11.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
77	<a href="#">c3cbbA</a>	Alignment	not modelled	11.6	46	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte nuclear factor 4-alpha, dna binding <b>PDBTitle:</b> crystal structure of hepatocyte nuclear factor 4alpha in2 complex with dna: diabetes gene product
78	<a href="#">c1l7qA</a>	Alignment	not modelled	11.6	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cocaine esterase; <b>PDBTitle:</b> ser117ala mutant of bacterial cocaine esterase coce
79	<a href="#">d2nlla</a>	Alignment	not modelled	11.6	38	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
80	<a href="#">d1nj1a2</a>	Alignment	not modelled	11.4	36	<b>Fold:</b> IF3-like <b>Superfamily:</b> C-terminal domain of ProRS

					<b>Family:</b> C-terminal domain of ProRS
81	<a href="#">c3mplA</a>	Alignment	not modelled	11.4	17 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence sensor protein bvgs; <b>PDBTitle:</b> crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
82	<a href="#">c1qgeD</a>	Alignment	not modelled	11.4	47 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (triacylglycerol hydrolase); <b>PDBTitle:</b> new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
83	<a href="#">d2hana1</a>	Alignment	not modelled	11.3	38 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
84	<a href="#">c2ri0B</a>	Alignment	not modelled	11.1	19 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
85	<a href="#">c2rauA</a>	Alignment	not modelled	11.1	27 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
86	<a href="#">c1dtaA</a>	Alignment	not modelled	11.0	36 <b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
87	<a href="#">c2dtbA</a>	Alignment	not modelled	11.0	36 <b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-toxin; <b>PDBTitle:</b> delta-toxin and analogues as peptide models for protein ion2 channels
88	<a href="#">c2kamA</a>	Alignment	not modelled	11.0	36 <b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> delta-hemolysin; <b>PDBTitle:</b> nmr structure of delta-toxin from staphylococcus aureus in2 cd3oh
89	<a href="#">c3lp5A</a>	Alignment	not modelled	10.9	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
90	<a href="#">c3eswA</a>	Alignment	not modelled	10.9	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine <b>PDBTitle:</b> complex of yeast pngase with glcnac2-iac.
91	<a href="#">c1r0nB</a>	Alignment	not modelled	10.6	33 <b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysone receptor; <b>PDBTitle:</b> crystal structure of heterodimeric ecdysone receptor dna2 binding complex
92	<a href="#">c2d8zA</a>	Alignment	not modelled	10.5	16 <b>PDB header:</b> signaling protein, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> four and a half lim domains 2; <b>PDBTitle:</b> solution structure of the third lim domain of four and a2 half lim domains protein 2 (fhl-2)
93	<a href="#">d1gqaa</a>	Alignment	not modelled	10.5	25 <b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome c'-like
94	<a href="#">d1bbha</a>	Alignment	not modelled	10.3	25 <b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Cytochromes <b>Family:</b> Cytochrome c'-like
95	<a href="#">d2c52b1</a>	Alignment	not modelled	10.2	71 <b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
96	<a href="#">c1t98B</a>	Alignment	not modelled	10.2	18 <b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein mukf; <b>PDBTitle:</b> crystal structure of mukf(1-287)
97	<a href="#">c2h7xA</a>	Alignment	not modelled	10.2	40 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i polyketide synthase pikaiv; <b>PDBTitle:</b> pikromycin thioesterase adduct with reduced triketide2 affinity label
98	<a href="#">d2hanb1</a>	Alignment	not modelled	10.0	33 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Nuclear receptor
99	<a href="#">d1lpbb2</a>	Alignment	not modelled	9.9	56 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain