Phyre^2

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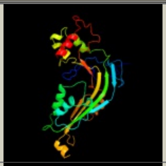
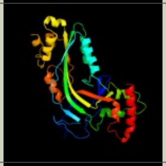
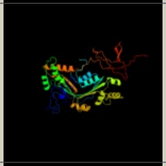
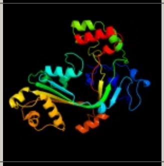
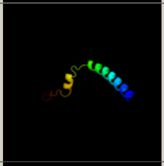
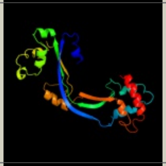
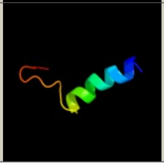
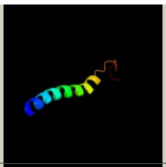
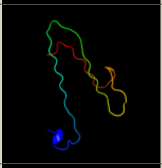
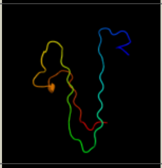
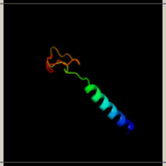
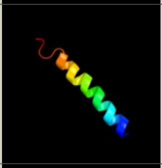
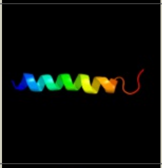
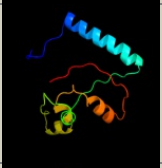
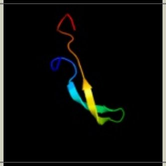
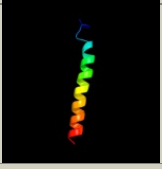
Description	A1L314
Date	Wed Jul 10 14:33:54 BST 2013
Unique Job ID	e8d85519151ae0a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qqhA_	Alignment		100.0	20	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**complement component c8 alpha chain; **PDBTitle:** structure of c8a-macpf reveals mechanism of membrane attack2 in complement immune defense
2	c2rd7A_	Alignment		100.0	20	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement component c8 alpha chain; **PDBTitle:** human complement membrane attack proteins share a common2 fold with bacterial cytolysins
3	c3nsjA_	Alignment		100.0	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**perforin-1; **PDBTitle:** the x-ray crystal structure of lymphocyte perforin
4	c2qp2A_	Alignment		99.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**unknown protein; **PDBTitle:** structure of a macpf/perforin-like protein
5	c3kk7B_	Alignment		99.2	18	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**putative cell invasion protein with mac/perforin domain; **PDBTitle:** crystal structure of putative cell invasion protein with mac/perforin2 domain (np_812351.1) from bacteriodes thetaiotaomicron vpi-5482 at3 2.46 a resolution
6	c3ojyA_	Alignment		96.4	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement component c8 alpha chain; **PDBTitle:** crystal structure of human complement component c8
7	c3t5oA_	Alignment		86.4	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement component c6; **PDBTitle:** crystal structure of human complement component c6
8	c2m20B_	Alignment		72.1	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
9	c2kncB_	Alignment		64.2	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c3ojyB_	Alignment		54.6	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement component c8 beta chain; **PDBTitle:** crystal structure of human complement component c8
11	c2kr1A_	Alignment		33.4	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin protein ligase e3a; **PDBTitle:** solution nmr structure of zinc binding n-terminal domain of ubiquitin-2 protein ligase e3a from homo sapiens. northeast structural genomics3 consortium (nesg) target hr3662

12	c2kncA_	Alignment		32.6	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
13	c1ihmC_	Alignment		27.0	18	**PDB header:**virus **Chain:** C: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure analysis of norwalk virus capsid
14	d1ihma_	Alignment		27.0	18	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Caliciviridae-like VP
15	c3floD_	Alignment		23.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
16	c2k9yB_	Alignment		23.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
17	c2k9yA_	Alignment		23.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
18	c1adyA_	Alignment		22.6	16	**PDB header:**trna synthetase **Chain:** A: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** histidyl-trna synthetase in complex with histidyl-adenylate
19	c2qbxB_	Alignment		21.2	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-b receptor 2; **PDBTitle:** ephb2/snew antagonistic peptide complex
20	c2ks1B_	Alignment		20.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
21	c2dk6A_	Alignment	not modelled	18.6	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**parp11 protein; **PDBTitle:** solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11)
22	c2auhB_	Alignment	not modelled	17.8	55	**PDB header:**transferase/signaling protein **Chain:** B: **PDB Molecule:**growth factor receptor-bound protein 14; **PDBTitle:** crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
23	d2g38b1	Alignment	not modelled	16.8	36	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
24	c2g38B_	Alignment	not modelled	16.8	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
25	c3p1iC_	Alignment	not modelled	16.2	29	**PDB header:**transferase,signaling protein **Chain:** C: **PDB Molecule:**ephrin type-b receptor 3; **PDBTitle:** ligand binding domain of human ephrin type-b receptor 3
26	c3o14B_	Alignment	not modelled	16.1	14	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**anti-ecfsigma factor, chrr; **PDBTitle:** crystal structure of an anti-ecfsigma factor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
27	c3gr0D_	Alignment	not modelled	15.9	13	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
28	c3dkbA_	Alignment	not modelled	15.7	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** crystal structure of a20, 2.5 angstrom
						PDB header:viral protein

29	c2cpbA_	Alignment	not modelled	15.4	31	**Chain:** A: **PDB Molecule:**m13 major coat protein; **PDBTitle:** solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
30	c2l2tA_	Alignment	not modelled	15.4	41	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
31	c2lcxB_	Alignment	not modelled	15.4	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** spatial structure of the erbb4 dimeric tm domain
32	c2nyuA_	Alignment	not modelled	15.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative ribosomal rna methyltransferase 2; **PDBTitle:** crystal structure of human ftsj homolog 2 (e.coli) protein2 in complex with s-adenosylmethionine
33	d1w7ja1	Alignment	not modelled	15.3	45	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
34	c2kr0A_	Alignment	not modelled	15.1	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**proteasomal ubiquitin receptor adrm1; **PDBTitle:** a proteasome protein
35	c2ko5A_	Alignment	not modelled	14.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein z; **PDBTitle:** nmr solution structure of lfv-z
36	c3gr1A_	Alignment	not modelled	14.2	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
37	d1rp4a_	Alignment	not modelled	13.7	17	**Fold:**ERO1-like **Superfamily:**ERO1-like **Family:**ERO1-like
38	d1v5ra1	Alignment	not modelled	13.6	42	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
39	c2lohA_	Alignment	not modelled	13.6	19	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**p3(42); **PDBTitle:** dimeric structure of transmembrane domain of amyloid precursor protein2 in micellar environment
40	d1c3ab_	Alignment	not modelled	13.5	23	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
41	c3h3iA_	Alignment	not modelled	13.1	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative lipid binding protein; **PDBTitle:** crystal structure of a putative lipid binding protein (bt_2261) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
42	c2l8sA_	Alignment	not modelled	13.0	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-1; **PDBTitle:** solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
43	d1v7pa_	Alignment	not modelled	12.6	36	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
44	c4bq7D_	Alignment	not modelled	11.6	40	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**rgm domain family member b; **PDBTitle:** crystal structure of the rgmb-neo1 complex form 2
45	c1ifpA_	Alignment	not modelled	11.6	20	**PDB header:**virus **Chain:** A: **PDB Molecule:**major coat protein assembly; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
46	c3douA_	Alignment	not modelled	11.1	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase j; **PDBTitle:** crystal structure of methyltransferase involved in cell2 division from thermoplasma volcanicum gss1
47	c3m8lA_	Alignment	not modelled	10.9	19	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** crystal structure analysis of the feline calicivirus capsid protein
48	c1kg1A_	Alignment	not modelled	10.8	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**necrosis inducing protein 1; **PDBTitle:** nmr structure of the nip1 elicitor protein from2 rhynchosporium secalis
49	d1kg1a_	Alignment	not modelled	10.8	33	**Fold:**Necrosis inducing protein 1, NIP1 **Superfamily:**Necrosis inducing protein 1, NIP1 **Family:**Necrosis inducing protein 1, NIP1
50	d1k1xa1	Alignment	not modelled	10.6	38	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**4-alpha-glucanotransferase, domain 2
51	c2kpeB_	Alignment	not modelled	10.5	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
52	c2kpeA_	Alignment	not modelled	10.5	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glycophorin-a; **PDBTitle:** refined structure of glycophorin a transmembrane segment dimer in dpc2 micelles
53	c1afoB_	Alignment	not modelled	10.2	31	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
54	c2xrfA_	Alignment	not modelled	10.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2

55	c1h3tB_	Alignment	not modelled	10.1	17	**PDB header:**immune system **Chain:** B: **PDB Molecule:**ig gamma-1 chain c region; **PDBTitle:** crystal structure of the human igg1 fc-fragment,glycoform2 (mn2f)2
56	c4a18P_	Alignment	not modelled	9.8	23	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**rpl38; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
57	c3k44D_	Alignment	not modelled	9.7	33	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**purine-rich binding protein-alpha, isoform b; **PDBTitle:** crystal structure of drosophila melanogaster pur-alpha
58	d1hdla_	Alignment	not modelled	9.7	16	**Fold:**Kazal-type serine protease inhibitors **Superfamily:**Kazal-type serine protease inhibitors **Family:**Serine proteinase inhibitor lekti
59	c2e2wA_	Alignment	not modelled	9.6	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** solution structure of the first brct domain of human dna2 ligase iv
60	c4g84B_	Alignment	not modelled	9.6	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidine--trna ligase, cytoplasmic; **PDBTitle:** crystal structure of human hisrs
61	c3mkuA_	Alignment	not modelled	9.6	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
62	c4esnB_	Alignment	not modelled	9.4	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a hypothetical protein (rumgna_02503) from2 ruminococcus gnavus atcc 29149 at 2.20 a resolution
63	d3bdwa1	Alignment	not modelled	9.3	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
64	c4a53A_	Alignment	not modelled	9.2	50	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**edc3; **PDBTitle:** structural basis of the dcp1:dcp2 mrna decapping complex activation2 by edc3 and scd6
65	c4djiA_	Alignment	not modelled	9.2	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable glutamate/gamma-aminobutyrate antiporter; **PDBTitle:** structure of glutamate-gaba antiporter gadc
66	c4iopB_	Alignment	not modelled	9.1	14	**PDB header:**immune system **Chain:** B: **PDB Molecule:**killer cell lectin-like receptor subfamily f member 2; **PDBTitle:** crystal structure of nkp65 bound to its ligand kacl
67	c3m9zA_	Alignment	not modelled	9.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**killer cell lectin-like receptor subfamily b member 1a; **PDBTitle:** crystal structure of extracellular domain of mouse nkr-p1a
68	c3zrhA_	Alignment	not modelled	9.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1; **PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
69	d1pfoa_	Alignment	not modelled	9.0	10	**Fold:**Perfringolysin **Superfamily:**Perfringolysin **Family:**Perfringolysin
70	c1pfoA_	Alignment	not modelled	9.0	10	**PDB header:**toxin **Chain:** A: **PDB Molecule:**perfringolysin o; **PDBTitle:** perfringolysin o
71	d1c3aa_	Alignment	not modelled	9.0	60	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
72	c2k5jB_	Alignment	not modelled	9.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
73	c2k1aA_	Alignment	not modelled	8.9	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
74	d2rgfa_	Alignment	not modelled	8.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
75	c3a9lB_	Alignment	not modelled	8.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
76	c3zf7p_	Alignment	not modelled	8.7	14	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**probable 60s ribosomal protein l14; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
77	d2zkmx4	Alignment	not modelled	8.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Mammalian PLC
78	c1b5fC_	Alignment	not modelled	8.6	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein (cardosin a); **PDBTitle:** native cardosin a from cynara cardunculus l.
79	d1dx5i2	Alignment	not modelled	8.6	29	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module

80	d1g5ga1	 Alignment	not modelled	8.5	34	**Fold:**Head and neck region of the ectodomain of NDV fusion glycoprotein **Superfamily:**Head and neck region of the ectodomain of NDV fusion glycoprotein **Family:**Head and neck region of the ectodomain of NDV fusion glycoprotein
81	c3g6nA_	 Alignment	not modelled	8.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of an efpdf complex with met-ala-ser
82	c3pilA_	 Alignment	not modelled	8.3	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
83	c1ciiA_	 Alignment	not modelled	8.2	7	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
84	c3bzjA_	 Alignment	not modelled	8.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
85	c2kppA_	 Alignment	not modelled	8.2	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
86	c3ry6A_	 Alignment	not modelled	8.2	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ig gamma-1 chain c region; **PDBTitle:** complex of fcgammariia (cd32) and the fc of human igg1
87	c3ry6B_	 Alignment	not modelled	8.2	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**ig gamma-1 chain c region; **PDBTitle:** complex of fcgammariia (cd32) and the fc of human igg1
88	d1e88a3	 Alignment	not modelled	8.1	21	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
89	c2k5lA_	 Alignment	not modelled	8.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**feoa; **PDBTitle:** solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
90	d1kshb_	 Alignment	not modelled	8.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
91	d1xdna_	 Alignment	not modelled	8.0	22	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**RNA ligase
92	d1jv2a2	 Alignment	not modelled	7.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Integrin domains **Family:**Integrin domains
93	c1no7A_	 Alignment	not modelled	7.9	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major capsid protein; **PDBTitle:** structure of the large protease resistant upper domain of2 vp5, the major capsid protein of herpes simplex virus-1
94	d1no7a_	 Alignment	not modelled	7.9	15	**Fold:**Major capsid protein VP5 **Superfamily:**Major capsid protein VP5 **Family:**Major capsid protein VP5
95	c1oqzB_	 Alignment	not modelled	7.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaryl acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 insight into autoproteolytic activation
96	d1hica_	 Alignment	not modelled	7.9	69	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
97	d1shwb_	 Alignment	not modelled	7.9	29	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Ephrin receptor ligand binding domain
98	c1rh5C_	 Alignment	not modelled	7.7	39	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**secbeta; **PDBTitle:** the structure of a protein conducting channel
99	d1rh5c_	 Alignment	not modelled	7.7	39	**Fold:**Single transmembrane helix **Superfamily:**Sec-beta subunit **Family:**Sec-beta subunit