Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77694
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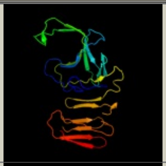
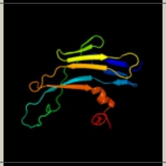
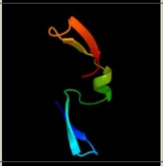
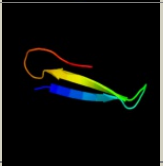
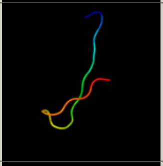
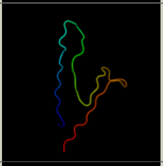
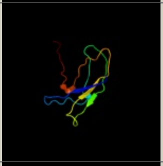
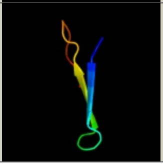
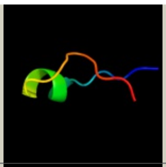
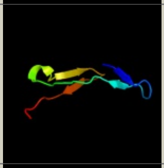
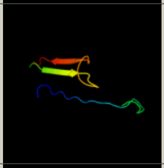
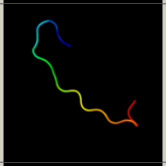
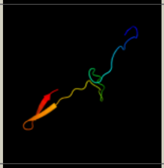
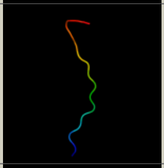
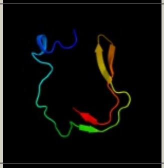
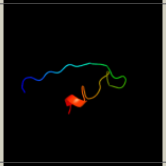
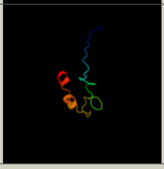
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cb8A_	Alignment		75.4	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (chondroitinase ac); **PDBTitle:** chondroitinase ac lyase from flavobacterium heparinum
2	c1o7dD_	Alignment		75.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
3	c2wdaA_	Alignment		30.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative secreted lyase; **PDBTitle:** the x-ray structure of the streptomyces coelicolor a32 chondroitin ac lyase in complex with chondroitin sulphate
4	c2wj9A_	Alignment		29.8	21	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**intergenic-region protein; **PDBTitle:** ardb
5	d2gtlm1	Alignment		28.8	24	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain
6	c2qqoB_	Alignment		23.4	33	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**neuropilin-2; **PDBTitle:** crystal structure of the a2b1b2 domains from human neuropilin-2
7	c1geaA_	Alignment		19.5	38	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** receptor-bound conformation of pacap21
8	d2nqda1	Alignment		19.4	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
9	d1ogmx1	Alignment		18.9	20	**Fold:**Dextranase, N-terminal domain **Superfamily:**Dextranase, N-terminal domain **Family:**Dextranase, N-terminal domain
10	c2b9sB_	Alignment		18.5	33	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
11	d2gtln1	Alignment		18.3	40	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain

12	d1tpna_	Alignment		16.3	41	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
13	d1hxma1	Alignment		15.1	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
14	d2c34a1	Alignment		14.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
15	c3pstA_	Alignment		14.6	18	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul and pfu(mutate) domain
16	c3biyA_	Alignment		14.5	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase p300; **PDBTitle:** crystal structure of p300 histone acetyltransferase domain in complex2 with a bisubstrate inhibitor, lys-coa
17	c3o7oB_	Alignment		14.1	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** use of synthetic symmetrization in the crystallization and structure2 determination of cela from thermotoga maritima
18	c3ts3D_	Alignment		13.5	24	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**capsid polyprotein; **PDBTitle:** crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
19	c1dgjA_	Alignment		13.1	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
20	c2janD_	Alignment		12.8	24	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
21	d2icya1	Alignment	not modelled	12.6	28	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
22	c2k89A_	Alignment	not modelled	12.1	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phospholipase a-2-activating protein; **PDBTitle:** solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
23	c2kmgA_	Alignment	not modelled	11.9	32	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
24	d1wioa2	Alignment	not modelled	11.9	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
25	c1hn0A_	Alignment	not modelled	11.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitin abc lyase i; **PDBTitle:** crystal structure of chondroitin abc lyase i from proteus2 vulgaris at 1.9 angstroms resolution
26	c3csyJ_	Alignment	not modelled	11.3	21	**PDB header:**immune system/viral protein **Chain:** J: **PDB Molecule:**envelope glycoprotein gp2; **PDBTitle:** crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
27	d2guma1	Alignment	not modelled	11.3	21	**Fold:**Viral glycoprotein ectodomain-like **Superfamily:**Viral glycoprotein ectodomain-like **Family:**Glycoprotein B-like
28	d1j8hd1	Alignment	not modelled	11.1	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)

29	d1sddb4	Alignment	not modelled	10.9	39	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
30	c3nw8B_	Alignment	not modelled	10.8	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** glycoprotein b from herpes simplex virus type 1, y179s mutant, high-ph
31	c2ol3A_	Alignment	not modelled	10.4	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**bm3.3 t-cell receptor alpha-chain; **PDBTitle:** crystal structure of bm3.3 scfv tcr in complex with pbm8-h-2kbm8 mhc2 class i molecule
32	d2gtlo1	Alignment	not modelled	10.1	37	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain
33	c1wygA_	Alignment	not modelled	9.8	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
34	c2lcyA_	Alignment	not modelled	9.7	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**virion spike glycoprotein; **PDBTitle:** nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
35	d1ehxa_	Alignment	not modelled	9.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Cellulosomal scaffoldin protein CipC, module x2.1
36	d1ks5a_	Alignment	not modelled	9.0	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
37	d1czsa_	Alignment	not modelled	9.0	39	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
38	c1bhgB_	Alignment	not modelled	8.9	33	**PDB header:**glycosidase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** human beta-glucuronidase at 2.6 a resolution
39	d1ypze1	Alignment	not modelled	8.9	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
40	c2e7mA_	Alignment	not modelled	8.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein kiaa0319; **PDBTitle:** solution structure of the pkd domain (329-428) from human2 kiaa0319
41	c2l3iA_	Alignment	not modelled	8.8	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
42	d2je8a4	Alignment	not modelled	8.6	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
43	d1fvca_	Alignment	not modelled	8.5	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
44	c1sddB_	Alignment	not modelled	8.2	39	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
45	d2phna1	Alignment	not modelled	8.2	32	**Fold:**CofE-like **Superfamily:**CofE-like **Family:**CofE-like
46	c2rqeA_	Alignment	not modelled	7.8	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta-1,3-glucan-binding protein; **PDBTitle:** solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
47	d2z15a1	Alignment	not modelled	7.8	45	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
48	d1wtla_	Alignment	not modelled	7.7	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
49	c2jemB_	Alignment	not modelled	7.6	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-beta-1,4-glucanase; **PDBTitle:** native family 12 xyloglucanase from bacillus licheniformis
50	d3e9va1	Alignment	not modelled	7.6	45	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
51	d1oa2a_	Alignment	not modelled	7.6	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
52	d1dl0a_	Alignment	not modelled	7.5	57	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
53	c1dl0A_	Alignment	not modelled	7.5	57	**PDB header:**toxin **Chain:** A: **PDB Molecule:**j-atracotoxin-hv1c; **PDBTitle:** solution structure of the insecticidal neurotoxin j-2 atracotoxin-hv1c
54	c3cdzB_	Alignment	not modelled	7.4	22	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii light chain; **PDBTitle:** crystal structure of human factor viii
55	d1sddb3	Alignment	not modelled	7.4	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like

55	d1sddb3	Alignment	not modelled	7.4	17	**Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
56	c2qqlA_	Alignment	not modelled	7.4	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neuropilin-2; **PDBTitle:** neuropilin-2 a1a2b1b2 domains in complex with a semaphorin-blocking2 fab
57	d1dc1a_	Alignment	not modelled	7.4	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BsobI
58	d2bw8a1	Alignment	not modelled	7.3	21	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
59	c1h0bA_	Alignment	not modelled	7.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulase; **PDBTitle:** endoglucanase cel12a from rhodothermus marinus
60	d1oa3a_	Alignment	not modelled	7.3	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
61	d1y4wa1	Alignment	not modelled	7.2	26	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 32 C-terminal domain
62	c3f59A_	Alignment	not modelled	7.2	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
63	d2qaln1	Alignment	not modelled	7.0	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Ribosomal protein S14
64	d1olra_	Alignment	not modelled	6.9	24	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
65	c3ie4A_	Alignment	not modelled	6.8	39	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gram-negative binding protein 3; **PDBTitle:** b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor
66	c2orxA_	Alignment	not modelled	6.7	33	**PDB header:**signaling protein, membrane protein **Chain:** A: **PDB Molecule:**neuropilin-1; **PDBTitle:** structural basis for ligand binding and heparin mediated activation of2 neuropilin
67	c1g6iA_	Alignment	not modelled	6.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class i alpha-1,2-mannosidase; **PDBTitle:** crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution
68	c3dnlG_	Alignment	not modelled	6.3	45	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state
69	d1tifa_	Alignment	not modelled	6.3	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Translation initiation factor IF3, N-terminal domain **Family:**Translation initiation factor IF3, N-terminal domain
70	c2cseB_	Alignment	not modelled	6.3	10	**PDB header:**virus **Chain:** B: **PDB Molecule:**major outer-capsid protein mu1; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
71	c1jmuD_	Alignment	not modelled	6.2	10	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**protein mu-1; **PDBTitle:** crystal structure of the reovirus mu1/sigma3 complex
72	d1sgoa_	Alignment	not modelled	6.1	20	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Hypothetical protein c14orf129, hspc210 **Family:**Hypothetical protein c14orf129, hspc210
73	d1vl4a_	Alignment	not modelled	6.1	20	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
74	c1w3gA_	Alignment	not modelled	6.0	20	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.
75	d2ijra1	Alignment	not modelled	5.9	33	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
76	d1udza_	Alignment	not modelled	5.9	55	**Fold:**ValRS/IleRS/LeuRS editing domain **Superfamily:**ValRS/IleRS/LeuRS editing domain **Family:**ValRS/IleRS/LeuRS editing domain
77	d2ae8a2	Alignment	not modelled	5.8	45	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
78	d2cu8a2	Alignment	not modelled	5.7	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
79	c2z5cB_	Alignment	not modelled	5.7	33	**PDB header:**chaperone/hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ylr021w; **PDBTitle:** crystal structure of a novel chaperone complex for yeast2 20s proteasome assembly
80	c3nttA_	Alignment	not modelled	5.6	7	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** structural insights of adeno-associated virus 5. a gene therapy vector2 for cystic fibrosis
81	c3lemA_	Alignment	not modelled	5.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructosyltransferase; **PDBTitle:** crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose

82	c3l3fX_	Alignment	not modelled	5.5	18	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
83	d2qqia2	Alignment	not modelled	5.5	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Discoidin domain (FA58C, coagulation factor 5/8 C-terminal domain)
84	c3kieF_	Alignment	not modelled	5.4	14	**PDB header:**virus **Chain:** F: **PDB Molecule:**capsid protein vp1; **PDBTitle:** crystal structure of adeno-associated virus serotype 3b
85	c2qqmA_	Alignment	not modelled	5.4	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neuropilin-1; **PDBTitle:** crystal structure of the a2b1b2 domains from human neuropilin-1
86	d2vzsa4	Alignment	not modelled	5.4	25	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
87	d1dl2a_	Alignment	not modelled	5.3	33	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
88	d1rhya2	Alignment	not modelled	5.3	32	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
89	d1vpba_	Alignment	not modelled	5.3	20	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
90	c2r7eB_	Alignment	not modelled	5.2	22	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii; **PDBTitle:** crystal structure analysis of coagulation factor viii
91	d1x9da1	Alignment	not modelled	5.2	36	**Fold:**alpha/alpha toroid **Superfamily:**Seven-hairpin glycosidases **Family:**Class I alpha-1;2-mannosidase, catalytic domain
92	c1x9dA_	Alignment	not modelled	5.2	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum mannosyl-oligosaccharide 1, **PDBTitle:** crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
93	d1ky9a1	Alignment	not modelled	5.2	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
94	d1klra_	Alignment	not modelled	5.2	56	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
95	c1klrA_	Alignment	not modelled	5.2	56	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger y-chromosomal protein; **PDBTitle:** nmr structure of the zfy-6t[y10f] zinc finger
96	d1d0da_	Alignment	not modelled	5.1	47	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Soft tick anticoagulant proteins
97	c3o0aB_	Alignment	not modelled	5.1	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**leucyl-trna synthetase subunit alpha; **PDBTitle:** crystal structure of the wild type cp1 hydrolitic domain from aquifex2 aeolicus leucyl-trna
98	c2g8gA_	Alignment	not modelled	5.0	14	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid; **PDBTitle:** structurally mapping the diverse phenotype of adeno-2 associated virus serotype 4