Phyre^2

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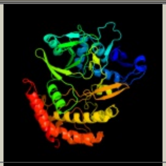
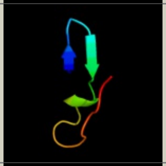
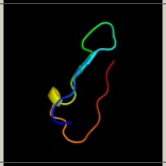
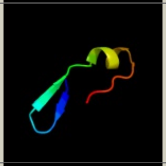
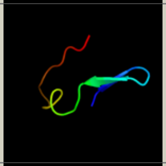
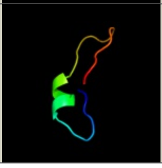
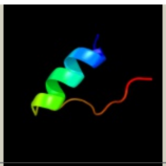
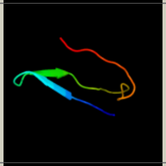
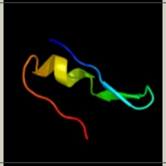
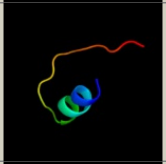
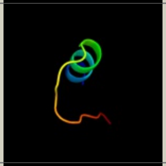
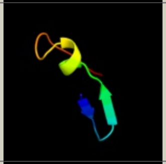
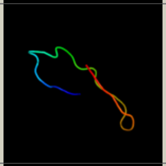
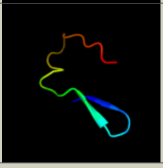
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dntB_	Alignment		100.0	98	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein hipa; **PDBTitle:** structures of mdt proteins
2	c3akjB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctka; **PDBTitle:** crystal structure of a helicobacter pylori proinflammatory kinase ctka
3	d1cjaa_	Alignment		95.1	14	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Actin-fragmin kinase, catalytic domain
4	c3attA_	Alignment		35.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv3168 with atp
5	d2je8a4	Alignment		33.7	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
6	d1bhga2	Alignment		31.4	19	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
7	d1jz8a3	Alignment		30.8	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
8	d1yq2a3	Alignment		29.2	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
9	c3fn9B_	Alignment		26.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
10	d2vzsa4	Alignment		25.0	12	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
11	c3bgaB_	Alignment		23.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482

12	d1eucb2	Alignment		23.1	23	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
13	c3gm8A_	Alignment		23.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
14	c3cmgA_	Alignment		22.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
15	d1iowa2	Alignment		22.0	24	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
16	d1uc8a2	Alignment		20.1	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Lysine biosynthesis enzyme LysX ATP-binding domain
17	d2nu7b2	Alignment		19.2	27	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
18	c3obaA_	Alignment		19.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
19	c3lpgA_	Alignment		18.8	36	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
20	c2vzvB_	Alignment		18.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
21	c3ln7A_	Alignment	not modelled	18.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
22	c1jz6C_	Alignment	not modelled	17.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
23	d1e4ea2	Alignment	not modelled	16.9	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
24	c3mv14_	Alignment	not modelled	16.1	18	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
25	c3oq9C_	Alignment	not modelled	15.2	17	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly
26	c1yq2C_	Alignment	not modelled	14.6	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1)
27	d1ddfa_	Alignment	not modelled	14.5	12	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
28	c3cqbB_	Alignment	not modelled	14.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable protease htpx homolog; **PDBTitle:** crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633

29	c3ln6A_	Alignment	not modelled	13.6	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
30	d1kjqa3	Alignment	not modelled	13.4	27	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
31	c1bhgB_	Alignment	not modelled	12.3	23	**PDB header:**glycosidase **Chain:** B: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** human beta-glucuronidase at 2.6 a resolution
32	c3tqtB_	Alignment	not modelled	11.8	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
33	c2ddcA_	Alignment	not modelled	11.8	14	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**photoconvertible fluorescent protein; **PDBTitle:** unique behavior of a histidine responsible for an2 engineered green-to-red photoconversion process
34	d1ehia2	Alignment	not modelled	11.6	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
35	d3etja3	Alignment	not modelled	11.6	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
36	c1ehiB_	Alignment	not modelled	11.4	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine:d-lactate ligase; **PDBTitle:** d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
37	c1wr2A_	Alignment	not modelled	10.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1789; **PDBTitle:** crystal structure of ph1788 from pyrococcus horikoshii ot3
38	c2otbB_	Alignment	not modelled	10.9	16	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**gfp-like fluorescent chromoprotein cfp484; **PDBTitle:** crystal structure of a monomeric cyan fluorescent protein2 in the fluorescent state
39	d1tg7a2	Alignment	not modelled	10.5	27	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Beta-galactosidase LacA, domains 4 and 5
40	d1moua_	Alignment	not modelled	10.4	14	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
41	c3da4B_	Alignment	not modelled	10.2	39	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
42	d1ggxa_	Alignment	not modelled	10.2	12	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
43	d1icha_	Alignment	not modelled	10.1	8	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
44	c1ichA_	Alignment	not modelled	10.1	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
45	c2rcyB_	Alignment	not modelled	10.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase; **PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
46	c3cglE_	Alignment	not modelled	9.7	13	**PDB header:**fluorescent protein **Chain:** E: **PDB Molecule:**gfp-like fluorescent chromoprotein dsfp483; **PDBTitle:** crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
47	d2cg4a1	Alignment	not modelled	9.7	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
48	c3i12A_	Alignment	not modelled	9.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
49	c3riwA_	Alignment	not modelled	9.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ascorbate peroxidase; **PDBTitle:** the crystal structure of leishmania major peroxidase mutant c197t
50	c2z04A_	Alignment	not modelled	8.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
51	c2z6zA_	Alignment	not modelled	8.8	15	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**fluorescent protein dronpa; **PDBTitle:** crystal structure of a photoswitchable gfp-like protein2 dronpa in the bright-state
52	c3ls1A_	Alignment	not modelled	8.5	15	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
53	c2je8B_	Alignment	not modelled	8.5	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
						PDB header:ligase

54	c3r23B_	Alignment	not modelled	8.3	11	**Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
55	d1uisa_	Alignment	not modelled	8.2	14	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
56	c2nu9E_	Alignment	not modelled	8.1	29	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
57	c3se7A_	Alignment	not modelled	8.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
58	c3lwbA_	Alignment	not modelled	7.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
59	d1zyla1	Alignment	not modelled	7.8	9	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**APH phosphotransferases
60	d1h5wa_	Alignment	not modelled	7.7	13	**Fold:**Upper collar protein gp10 (connector protein) **Superfamily:**Upper collar protein gp10 (connector protein) **Family:**Upper collar protein gp10 (connector protein)
61	d3buxb2	Alignment	not modelled	7.7	30	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
62	c1ijgE_	Alignment	not modelled	7.6	13	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**upper collar protein; **PDBTitle:** structure of the bacteriophage phi29 head-tail connector2 protein
63	d2cyya1	Alignment	not modelled	7.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
64	d1z67a1	Alignment	not modelled	7.5	9	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
65	c2icrD_	Alignment	not modelled	7.4	17	**PDB header:**fluorescent protein **Chain:** D: **PDB Molecule:**red fluorescent protein zoanrfp; **PDBTitle:** red fluorescent protein zrfp574 from zoanthus sp.
66	d1i1ga1	Alignment	not modelled	7.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
67	c2pvpB_	Alignment	not modelled	7.3	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
68	c2i80B_	Alignment	not modelled	7.2	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
69	c2c9iG_	Alignment	not modelled	7.0	18	**PDB header:**luminescent protein **Chain:** G: **PDB Molecule:**green fluorescent protein asfp499; **PDBTitle:** structure of the fluorescent protein asfp499 from anemonia2 sulcata
70	c1e4eB_	Alignment	not modelled	6.9	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
71	c3nezB_	Alignment	not modelled	6.9	12	**PDB header:**fluorescent protein **Chain:** B: **PDB Molecule:**mrojoa; **PDBTitle:** mrojoa
72	d1re0b_	Alignment	not modelled	6.6	19	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
73	d1e0ea_	Alignment	not modelled	6.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
74	d2rh7a1	Alignment	not modelled	6.3	8	**Fold:**GFP-like **Superfamily:**GFP-like **Family:**Fluorescent proteins
75	c1rr7A_	Alignment	not modelled	6.2	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
76	d1rr7a_	Alignment	not modelled	6.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
77	c2w48D_	Alignment	not modelled	6.2	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
78	d1bc9a_	Alignment	not modelled	6.2	25	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
79	c1eucB_	Alignment	not modelled	6.1	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
80	d2ahra1	Alignment	not modelled	6.1	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like

81	c2zo7A_	Alignment	not modelled	6.1	18	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**cyan/green-emitting gfp-like protein, kusabira-cyan mutant **PDBTitle:** crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
82	c2l4aA_	Alignment	not modelled	6.1	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
83	c3op0B_	Alignment	not modelled	6.0	14	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide
84	c2a8vA_	Alignment	not modelled	6.0	24	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
85	d2j9ga3	Alignment	not modelled	5.9	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
86	d1uptd_	Alignment	not modelled	5.9	14	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
87	c2zdqA_	Alignment	not modelled	5.8	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophius hb8
88	c2dlnA_	Alignment	not modelled	5.8	19	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
89	d1xsza1	Alignment	not modelled	5.8	31	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
90	d1ojra_	Alignment	not modelled	5.7	18	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
91	c2ib5H_	Alignment	not modelled	5.7	10	**PDB header:**luminescent protein **Chain:** H: **PDB Molecule:**chromo protein; **PDBTitle:** structural characterization of a blue chromoprotein and its yellow2 mutant from the sea anemone cnidopus japonicus
92	c3jr1A_	Alignment	not modelled	5.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase2 (yp_719053.1) from haemophilus somnus 129pt at 2.32 a3 resolution
93	d1p1ma1	Alignment	not modelled	5.6	10	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
94	c2jpmA_	Alignment	not modelled	5.6	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**bacteriocin lactococcin-g subunit beta; **PDBTitle:** lactococcin g-b in tfe
95	c2vbzA_	Alignment	not modelled	5.6	4	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
96	d1dwka1	Alignment	not modelled	5.6	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
97	d1ku1a_	Alignment	not modelled	5.6	19	**Fold:**alpha-alpha superhelix **Superfamily:**Sec7 domain **Family:**Sec7 domain
98	c2iifA_	Alignment	not modelled	5.5	17	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
99	c3ls8A_	Alignment	not modelled	5.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit **PDBTitle:** crystal structure of human pik3c3 in complex with 3-[4-(4-2 morpholinyl)thieno[3,2-d]pyrimidin-2-yl]-phenol