Phyre2

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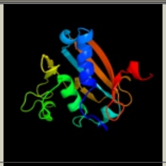
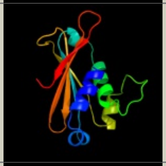
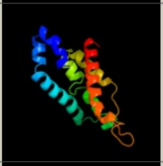
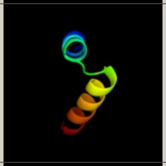
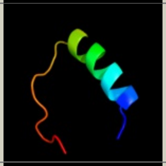
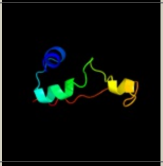
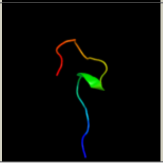
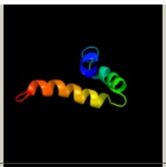
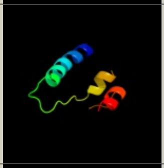
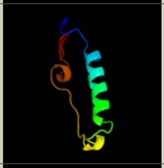
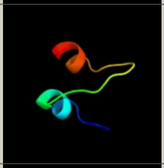
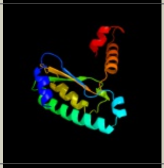
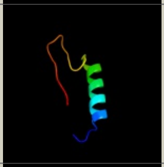
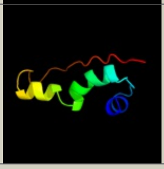
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iafa1	Alignment		100.0	43	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Serine metabolism enzymes domain **Family:**Serine dehydratase beta chain-like
2	c1ygyA_	Alignment		99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
3	d1ygya4	Alignment		99.3	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Serine metabolism enzymes domain **Family:**SerA intervening domain-like
4	d1szqa_	Alignment		97.6	17	**Fold:**2-methylcitrate dehydratase PrpD **Superfamily:**2-methylcitrate dehydratase PrpD **Family:**2-methylcitrate dehydratase PrpD
5	c2hp0A_	Alignment		97.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ids-epimerase; **PDBTitle:** crystal structure of iminodisuccinate epimerase
6	c3u4gA_	Alignment		51.7	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
7	c3s1sA_	Alignment		51.3	31	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
8	d2i7na2	Alignment		31.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
9	c2rkbE_	Alignment		29.4	24	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
10	d1rypa_	Alignment		29.3	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
11	d1no5a_	Alignment		26.0	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase

12	d1ug2a_	Alignment		24.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
13	d1g5ta_	Alignment		24.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
14	c1knyA_	Alignment		21.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kanamycin nucleotidyltransferase; **PDBTitle:** kanamycin nucleotidyltransferase
15	c2kelB_	Alignment		20.7	26	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
16	d1g64b_	Alignment		19.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
17	c3ugsB_	Alignment		19.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
18	c1yy3A_	Alignment		17.9	57	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
19	c2zfdB_	Alignment		16.4	22	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
20	d1pwha_	Alignment		15.4	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
21	d1r85a_	Alignment	not modelled	14.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
22	c2k9iB_	Alignment	not modelled	13.9	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
23	c2vfwB_	Alignment	not modelled	13.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
24	d1gg2g_	Alignment	not modelled	13.5	42	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
25	d1ylqa1	Alignment	not modelled	13.2	22	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
26	d1omwg_	Alignment	not modelled	12.2	42	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
27	d1h72c1	Alignment	not modelled	12.2	31	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
28	c2cycB_	Alignment	not modelled	12.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
29	c1us2A_	Alignment	not modelled	11.8	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-xylanase;

29	c1us2A_	Alignment	not modelled	11.8	8	**PDBTitle:** xylanase10c (mutant e385a) from cellvibrio japonicus in2 complex with xylopentaose
30	c3sz8D_	Alignment	not modelled	11.8	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
31	d1jb0l_	Alignment	not modelled	11.8	26	**Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL
32	c2rffA_	Alignment	not modelled	11.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotidyltransferase; **PDBTitle:** crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from sulfolobus solfataricus at 1.40 a3 resolution
33	c1u9pA_	Alignment	not modelled	11.2	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
34	d1j20a1	Alignment	not modelled	11.1	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
35	c1k97A_	Alignment	not modelled	11.0	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
36	d1gotg_	Alignment	not modelled	10.9	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
37	c2ddhA_	Alignment	not modelled	10.7	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
38	d1xhmb1	Alignment	not modelled	10.6	45	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
39	d1fh9a_	Alignment	not modelled	10.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
40	c1xhmB_	Alignment	not modelled	10.5	45	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein g(i)/g(s) **PDBTitle:** the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
41	d1knya2	Alignment	not modelled	10.3	26	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
42	d1tbge_	Alignment	not modelled	10.2	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
43	c2fonA_	Alignment	not modelled	10.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal acyl-coa oxidase 1a; **PDBTitle:** x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
44	c3lr6A_	Alignment	not modelled	10.0	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**major ampullate spidroin 1; **PDBTitle:** self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
45	c2dlcX_	Alignment	not modelled	10.0	18	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
46	d1ncfb3	Alignment	not modelled	9.9	40	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
47	d1b65a_	Alignment	not modelled	9.8	20	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
48	d1ng7a_	Alignment	not modelled	9.7	36	**Fold:**Soluble domain of poliovirus core protein 3a **Superfamily:**Soluble domain of poliovirus core protein 3a **Family:**Soluble domain of poliovirus core protein 3a
49	d1k61a_	Alignment	not modelled	9.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
50	d1ee8a1	Alignment	not modelled	9.2	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
51	c1kh2D_	Alignment	not modelled	9.1	25	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
52	c3bh1A_	Alignment	not modelled	9.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0371 protein dip2346; **PDBTitle:** crystal structure of protein dip2346 from corynebacterium diphtheriae
53	c2crnA_	Alignment	not modelled	9.0	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**ubash3a protein; **PDBTitle:** solution structure of the uba domain of human ubash3a2 protein
54	c2k3qA_	Alignment	not modelled	9.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tusp1; **PDBTitle:** solution structure of the n-terminal domain (tusp1-n) of the2 egg case silk from nephila antipodiana
55	d1nlna_	Alignment	not modelled	8.8	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases

						Family: Adenain-like
56	d1tuxa_	Alignment	not modelled	8.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
57	d1fi6a_	Alignment	not modelled	8.3	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
58	c1iszA_	Alignment	not modelled	8.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,4-beta-d-xylanase; **PDBTitle:** crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
59	d1wota_	Alignment	not modelled	8.0	29	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
60	c2f5xC_	Alignment	not modelled	8.0	27	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
61	d2nrha1	Alignment	not modelled	7.9	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
62	c2x3dC_	Alignment	not modelled	7.8	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
63	d2raqa1	Alignment	not modelled	7.7	11	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
64	d1bg4a_	Alignment	not modelled	7.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
65	d1k92a1	Alignment	not modelled	7.7	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
66	d1p5ja_	Alignment	not modelled	7.7	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	c1p5jA_	Alignment	not modelled	7.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
68	c2fglA_	Alignment	not modelled	7.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline thermostable endoxylanase; **PDBTitle:** an alkali thermostable f/10 xylanase from alkalophilic2 bacillus sp. ng-27
69	d1j6ua3	Alignment	not modelled	7.6	29	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
70	d1wkva1	Alignment	not modelled	7.5	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
71	d1k47a1	Alignment	not modelled	7.4	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
72	d1x2na1	Alignment	not modelled	7.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
73	d2gkea2	Alignment	not modelled	7.3	23	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
74	c2xa0A_	Alignment	not modelled	7.3	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
75	d2ar0a1	Alignment	not modelled	7.2	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
76	d1j09a1	Alignment	not modelled	7.2	25	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of glutamyl-tRNA synthetase (GluRS)
77	d1vl2a1	Alignment	not modelled	7.1	31	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
78	c1w07A_	Alignment	not modelled	7.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acyl-coa oxidase; **PDBTitle:** arabidopsis thaliana acyl-coa oxidase 1
79	c3g2bA_	Alignment	not modelled	7.0	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
80	d1vlfm2	Alignment	not modelled	6.9	16	**Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3 **Family:**Formate dehydrogenase/DMSO reductase, domains 1-3
						Fold:TNF receptor-like

81	d1exta3	Alignment	not modelled	6.9	40	**Superfamily:**TNF receptor-like **Family:**TNF receptor-like
82	d2r5yb1	Alignment	not modelled	6.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
83	c2jyaA_	Alignment	not modelled	6.9	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
84	c3ibqA_	Alignment	not modelled	6.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
85	d1uf2a_	Alignment	not modelled	6.7	36	**Fold:**Reovirus inner layer core protein p3 **Superfamily:**Reovirus inner layer core protein p3 **Family:**Phytoreovirus core
86	c1uf2A_	Alignment	not modelled	6.7	36	**PDB header:**virus **Chain:** A: **PDB Molecule:**core protein p3; **PDBTitle:** the atomic structure of rice dwarf virus (rdv)
87	d1yrnb_	Alignment	not modelled	6.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
88	c2fkkA_	Alignment	not modelled	6.6	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**baseplate structural protein gp10; **PDBTitle:** crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
89	c2j5bA_	Alignment	not modelled	6.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
90	c1qoyA_	Alignment	not modelled	6.5	12	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
91	c1pprO_	Alignment	not modelled	6.5	11	**PDB header:**light-harvesting protein **Chain:** O: **PDB Molecule:**peridinin-chlorophyll protein; **PDBTitle:** peridinin-chlorophyll-protein of amphidinium carterae
92	c2jugB_	Alignment	not modelled	6.5	39	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
93	d1us3a2	Alignment	not modelled	6.4	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
94	c2gefA_	Alignment	not modelled	6.4	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease vp4; **PDBTitle:** crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
95	d1p3da3	Alignment	not modelled	6.4	26	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
96	c3l0zC_	Alignment	not modelled	6.4	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative nicotinate-nucleotide-dimethylbenzimidazole **PDBTitle:** crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
97	c2ci8A_	Alignment	not modelled	6.3	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed
98	c3khkA_	Alignment	not modelled	6.3	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**type i restriction-modification system **PDBTitle:** crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
99	c2dagA_	Alignment	not modelled	6.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)