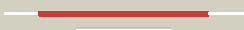
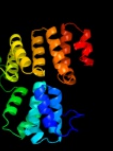
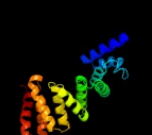


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yhca_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
2	c3qkyA_	 Alignment		99.9	25	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
3	c2vq2A_	 Alignment		99.9	14	PDB header: structural protein Chain: A: PDB Molecule: putative fimbrial biogenesis and twitching PDBTitle: crystal structure of pilw, widely conserved type iv pilus2 biogenesis factor
4	c2ho1B_	 Alignment		99.9	11	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
5	c1fchB_	 Alignment		99.9	12	PDB header: signaling protein Chain: B: PDB Molecule: peroxisomal targeting signal 1 receptor; PDBTitle: crystal structure of the pts1 complexed to the tpr region2 of human pex5
6	c3cypA_	 Alignment		99.9	13	PDB header: transport protein Chain: A: PDB Molecule: peroxisome targeting signal 1 receptor pex5; PDBTitle: structure of peroxisomal targeting signal 1 (pts1) binding2 domain of trypanosoma brucei peroxin 5 (tbpex5)complexed3 to pts1 peptide (10-skl)
7	c2v4tA_	 Alignment		99.9	17	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
8	c3hymB_	 Alignment		99.9	10	PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
9	c3iegB_	 Alignment		99.9	17	PDB header: chaperone Chain: B: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of p58(ipk) tpr domain at 2.5 a
10	c3pe3D_	 Alignment		99.9	19	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnaac transferase and its complex with a peptide2 substrate
11	c2xpiA_	 Alignment		99.8	12	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1

12	d1fcha_	Alignment		99.8	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
13	d1w3ba_	Alignment		99.8	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
14	c3urzB_	Alignment		99.8	9	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (bacova_03105) from bacteroides ovatus atcc 8483 at 2.19 a resolution
15	c2q7fA_	Alignment		99.8	10	PDB header: protein binding Chain: A: PDB Molecule: yrrb protein; PDBTitle: crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
16	d1xnfa_	Alignment		99.8	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
17	c2gw1A_	Alignment		99.8	24	PDB header: protein transport Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor; PDBTitle: crystal structure of the yeast tom70
18	c2pl2A_	Alignment		99.8	13	PDB header: protein binding Chain: A: PDB Molecule: hypothetical conserved protein ttc0263; PDBTitle: crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27
19	c3as5A_	Alignment		99.7	14	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
20	c2r5sB_	Alignment		99.7	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp0806; PDBTitle: the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
21	c3q75A_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvm peptide
22	c3mkrA_	Alignment	not modelled	99.7	10	PDB header: transport protein Chain: A: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the cop12 vesicular coat
23	c2xevB_	Alignment	not modelled	99.7	26	PDB header: metal binding Chain: B: PDB Molecule: ybgf; PDBTitle: crystal structure of the tpr domain of xanthomonas2 campestris ybgf
24	c3fp4A_	Alignment	not modelled	99.7	12	PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
25	c3draA_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
26	d1dcea1	Alignment	not modelled	99.7	8	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
27	c3mv3B_	Alignment	not modelled	99.7	13	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
28	c3q15A_	Alignment	not modelled	99.6	11	PDB header: hydrolase/kinase Chain: A: PDB Molecule: response regulator aspartate phosphatase h; PDBTitle: crystal structure of raph complexed with spo0f
						Fold: alpha-alpha superhelix

29	d2h6fa1	Alignment	not modelled	99.6	12	Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
30	c2ifuA	Alignment	not modelled	99.6	8	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
31	d2o0ea1	Alignment	not modelled	99.6	6	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
32	c3ulqA	Alignment	not modelled	99.6	8	PDB header: gene regulation/transcription activator Chain: A: PDB Molecule: response regulator aspartate phosphatase f; PDBTitle: crystal structure of the anti-activator rapf complexed with the2 response regulator coma dna binding domain
33	c1tnol	Alignment	not modelled	99.6	12	PDB header: transferase Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a gppp analog and a kksktkcvim peptide derived from k-3 ras4b
34	c3sf4B	Alignment	not modelled	99.6	21	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
35	d1qsaa1	Alignment	not modelled	99.6	9	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
36	d1hz4a	Alignment	not modelled	99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
37	d1hh8a	Alignment	not modelled	99.6	18	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
38	c2hyzA	Alignment	not modelled	99.6	20	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix2 (orthorhombic crystal form)
39	c3gw4B	Alignment	not modelled	99.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
40	c2e2eA	Alignment	not modelled	99.5	9	PDB header: lyase Chain: A: PDB Molecule: formate-dependent nitrite reductase complex nrfg subunit; PDBTitle: tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
41	c1wao4	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
42	c2uy1A	Alignment	not modelled	99.5	11	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
43	d1d8da	Alignment	not modelled	99.5	13	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
44	d2c2la1	Alignment	not modelled	99.5	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
45	c2dbaA	Alignment	not modelled	99.4	14	PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1, isoform PDBTitle: the solution structure of the tetratricopeptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
46	d1a17a	Alignment	not modelled	99.4	20	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
47	c3nf1A	Alignment	not modelled	99.4	10	PDB header: motor protein, transport protein Chain: A: PDB Molecule: kinesin light chain 1; PDBTitle: crystal structure of the tpr domain of kinesin light chain 1
48	d1p5qa1	Alignment	not modelled	99.4	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
49	c3qdnA	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
50	c2vyiA	Alignment	not modelled	99.4	17	PDB header: chaperone Chain: A: PDB Molecule: sgta protein; PDBTitle: crystal structure of the tpr domain of human sgt
51	c3q49B	Alignment	not modelled	99.4	15	PDB header: ligase/chaperone Chain: B: PDB Molecule: stip1 homology and u box-containing protein 1; PDBTitle: crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide
52	c3gyzB	Alignment	not modelled	99.4	6	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein ipgc; PDBTitle: crystal structure of ipgc from shigella flexneri
53	c2c21D	Alignment	not modelled	99.4	10	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase

54	d1zu2a1	Alignment	not modelled	99.4	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
55	d1kt1a1	Alignment	not modelled	99.3	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
56	d1elwa	Alignment	not modelled	99.3	20	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
57	c3rkva	Alignment	not modelled	99.3	14	PDB header: isomerase Chain: A: PDB Molecule: putative peptidylprolyl isomerase; PDBTitle: c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans
58	c2xcba	Alignment	not modelled	99.3	9	PDB header: protein binding Chain: A: PDB Molecule: regulatory protein pcrh; PDBTitle: crystal structure of pcrh in complex with the chaperone2 binding region of popd
59	d1qqea	Alignment	not modelled	99.3	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
60	c1ihga	Alignment	not modelled	99.3	17	PDB header: isomerase Chain: A: PDB Molecule: cyclophilin 40; PDBTitle: bovine cyclophilin 40, monoclinic form
61	c3ceqb	Alignment	not modelled	99.3	13	PDB header: motor protein, transport protein Chain: B: PDB Molecule: kinesin light chain 2; PDBTitle: the tpr domain of human kinesin light chain 2 (hklc2)
62	d1elra	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
63	d2buga1	Alignment	not modelled	99.3	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
64	d1hxia	Alignment	not modelled	99.2	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
65	d1tjca	Alignment	not modelled	99.2	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
66	c1kt0A	Alignment	not modelled	99.2	12	PDB header: isomerase Chain: A: PDB Molecule: 51 kda fk506-binding protein; PDBTitle: structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
67	c2kcka	Alignment	not modelled	99.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tpr repeat; PDBTitle: nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
68	c1slyA	Alignment	not modelled	99.2	7	PDB header: glycosyltransferase Chain: A: PDB Molecule: 70-kda soluble lytic transglycosylase; PDBTitle: complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
69	d1ihga1	Alignment	not modelled	99.2	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
70	c1na3A	Alignment	not modelled	99.2	18	PDB header: de novo protein Chain: A: PDB Molecule: designed protein ctrp2; PDBTitle: design of stable alpha-helical arrays from an idealized tpr2 motif
71	c1qz2B	Alignment	not modelled	99.2	15	PDB header: isomerase/chaperone Chain: B: PDB Molecule: fk506-binding protein 4; PDBTitle: crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
72	c3n71A	Alignment	not modelled	99.1	11	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
73	c2kc7A	Alignment	not modelled	99.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bfr218_protein; PDBTitle: solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
74	d2hr2a1	Alignment	not modelled	99.1	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
75	d2fbna1	Alignment	not modelled	99.1	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
76	c2fbaA	Alignment	not modelled	99.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 70 kda peptidylprolyl isomerase, putative; PDBTitle: plasmodium falciparum putative fk506-binding protein2 pfl2275c, c-terminal tpr-containing domain
77	c3sz7A	Alignment	not modelled	99.1	12	PDB header: chaperone regulator Chain: A: PDB Molecule: hsc70 cochaperone (sgt); PDBTitle: crystal structure of the sgt2 tpr domain from aspergillus fumigatus
78	c3ly8A	Alignment	not modelled	99.1	10	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
79	c3k9iA	Alignment	not modelled	99.1	12	PDB header: protein binding Chain: A: PDB Molecule: bh0479 protein; PDBTitle: crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
						PDB header: transferase Chain: B: PDB Molecule: xcogt;

80	c2vsnB_	Alignment	not modelled	99.0	15	PDBTitle: structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
81	c2avpA_	Alignment	not modelled	99.0	21	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix
82	c2l6jA_	Alignment	not modelled	99.0	15	PDB header: protein binding Chain: A: PDB Molecule: tpr repeat-containing protein associated with hsp90; PDBTitle: tah1 complexed by meevd
83	dliyga_	Alignment	not modelled	99.0	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
84	c2katA_	Alignment	not modelled	99.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
85	d2onda1	Alignment	not modelled	99.0	9	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
86	c2kcvA_	Alignment	not modelled	99.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat domain protein; PDBTitle: solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
87	c3fflC_	Alignment	not modelled	99.0	19	PDB header: cell cycle Chain: C: PDB Molecule: anaphase-promoting complex subunit 7; PDBTitle: crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7
88	c1xi4D_	Alignment	not modelled	99.0	18	PDB header: endocytosis/exocytosis Chain: D: PDB Molecule: clathrin heavy chain; PDBTitle: clathrin d6 coat
89	c2if4A_	Alignment	not modelled	98.9	8	PDB header: signaling protein Chain: A: PDB Molecule: atfkbp42; PDBTitle: crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
90	d1nzna_	Alignment	not modelled	98.9	7	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
91	d1zbpa1	Alignment	not modelled	98.8	11	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
92	d1pc2a_	Alignment	not modelled	98.8	8	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
93	c2vgxA_	Alignment	not modelled	98.7	6	PDB header: chaperone Chain: A: PDB Molecule: chaperone sycd; PDBTitle: structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
94	c3beeB_	Alignment	not modelled	98.7	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 parahaemolyticus
95	d1y8ma1	Alignment	not modelled	98.7	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
96	d2pqrbl	Alignment	not modelled	98.6	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
97	d2ff4a2	Alignment	not modelled	98.5	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
98	d1ouva_	Alignment	not modelled	98.4	8	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
99	c1ltxA_	Alignment	not modelled	98.4	10	PDB header: transferase/protein binding Chain: A: PDB Molecule: rab geranylgeranyltransferase alpha subunit; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
100	c3mekA_	Alignment	not modelled	97.9	9	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 3; PDBTitle: crystal structure of human histone-lysine n-2 methyltransferase smyd3 in complex with s-adenosyl-l-3 methionine
101	c3oxgA_	Alignment	not modelled	97.9	15	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 3; PDBTitle: human lysine methyltransferase smyd3 in complex with adohcy (form iii)
102	c3e4bD_	Alignment	not modelled	97.9	10	PDB header: protein binding Chain: D: PDB Molecule: algk; PDBTitle: crystal structure of algk from pseudomonas fluorescens wcs374r
103	c3q3hA_	Alignment	not modelled	97.8	7	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
104	c3qvvA_	Alignment	not modelled	97.6	10	PDB header: transferase Chain: A: PDB Molecule: set and mynd domain-containing protein 2; PDBTitle: crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy

105	c2qfcB_	Alignment	not modelled	97.4	9	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
106	d1iipa1	Alignment	not modelled	97.3	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
107	c3bxA_	Alignment	not modelled	96.0	7	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: 26s proteasome regulatory complex subunit p42b; PDBTitle: crystal structure of rpn6 from drosophila melanogaster, gd(3+) complex
108	c2ff4B_	Alignment	not modelled	93.8	12	PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
109	c3mkqA_	Alignment	not modelled	90.2	12	PDB header: transport protein Chain: A: PDB Molecule: coatomer beta'-subunit; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
110	c2xm6A_	Alignment	not modelled	84.6	7	PDB header: unknown function Chain: A: PDB Molecule: protein corresponding to locus c5321 from cft073 e.coli PDBTitle: crystal structure of the protein corresponding to locus c5321 from2 cft073 e.coli strain
111	d2cfua2	Alignment	not modelled	83.8	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
112	c2cfuA_	Alignment	not modelled	80.7	12	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
113	c3rvA_	Alignment	not modelled	77.7	10	PDB header: protein binding Chain: A: PDB Molecule: putative sel1 repeat protein; PDBTitle: crystal structure of a putative sel1 repeat protein (kpn_04481) from2 klebsiella pneumoniae subsp. pneumoniae at 1.65 a resolution
114	d1wfdA_	Alignment		76.2	9	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
115	d2ijqa1	Alignment	not modelled	68.8	10	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
116	c3lvhA_	Alignment	not modelled	62.4	6	PDB header: structural protein Chain: A: PDB Molecule: clathrin heavy chain 1; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
117	c3nqpB_	Alignment	not modelled	59.5	9	PDB header: sugar binding protein Chain: B: PDB Molecule: susd superfamily protein; PDBTitle: crystal structure of a susd superfamily protein (bf1802) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
118	c3mkqB_	Alignment	not modelled	58.4	20	PDB header: transport protein Chain: B: PDB Molecule: coatomer subunit alpha; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the cop12 vesicular coat
119	c2w2uA_	Alignment	not modelled	55.0	10	PDB header: hydrolase/transport Chain: A: PDB Molecule: hypothetical p60 katanin; PDBTitle: structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase
120	c3eslA_	Alignment	not modelled	52.8	8	PDB header: cell cycle Chain: A: PDB Molecule: checkpoint serine/threonine-protein kinase bub1; PDBTitle: crystal structure of the conserved n-terminal domain of the2 mitotic checkpoint component bub1