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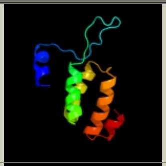
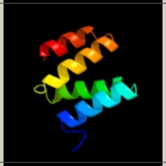
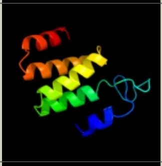
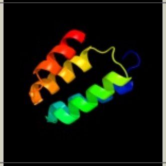
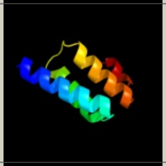
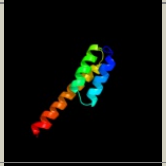
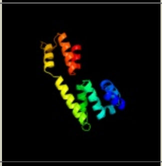
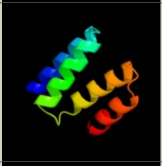
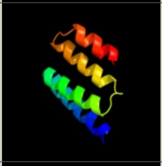
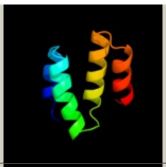
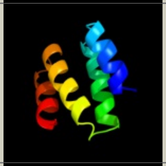
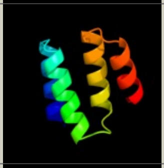
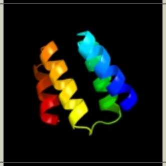
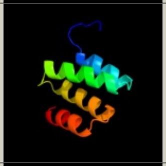
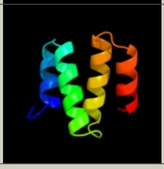
Description	P76486
Date	Thu Jan 5 12:23:32 GMT 2012
Unique Job ID	2788c30b89ac9c29

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2katA_	Alignment		93.5	24	**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
2	c3gyzB_	Alignment		90.3	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri
3	c2kcvA_	Alignment		90.2	21	**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
4	c3k9iA_	Alignment		90.0	14	**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
5	c2vyiA_	Alignment		89.4	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sgta protein; **PDBTitle:** crystal structure of the tpr domain of human sgt
6	c2xcbA_	Alignment		89.1	21	**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
7	d1hxia_	Alignment		88.5	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
8	c2r5sB_	Alignment		86.9	23	**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
9	c3pe3D_	Alignment		86.4	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
10	c3fp4A_	Alignment		83.2	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w; **PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
11	c3cvpA_	Alignment		82.1	22	**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)

12	d1w3ba_	Alignment		80.9	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
13	d1fcha_	Alignment		78.8	24	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
14	d1elwa_	Alignment		78.6	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
15	c1wao4_	Alignment		77.8	21	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
16	c2vsnB_	Alignment		77.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
17	c3hymB_	Alignment		76.8	9	**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
18	c2kc7A_	Alignment		75.8	17	**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
19	d1zbpa1	Alignment		75.5	22	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
20	c1fchB_	Alignment		74.6	23	**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
21	c3iegB_	Alignment	not modelled	73.6	21	**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
22	c3q49B_	Alignment	not modelled	72.6	21	**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
23	c2xpiA_	Alignment	not modelled	65.2	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9; **PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1
24	c2kckA_	Alignment	not modelled	64.3	15	**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
25	c2pl2A_	Alignment	not modelled	64.0	25	**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
26	c2y4tA_	Alignment	not modelled	62.3	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
27	c2vgxA_	Alignment	not modelled	61.8	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone sycd; **PDBTitle:** structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
28	c3sz7A_	Alignment	not modelled	59.9	18	**PDB header:**chaperone regulator **Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt); **PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus

29	c3qdnA_	Alignment	not modelled	59.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
30	d2c2la1	Alignment	not modelled	59.0	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
31	d2buga1	Alignment	not modelled	58.4	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
32	c2uy1A_	Alignment	not modelled	57.4	10	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 77; **PDBTitle:** crystal structure of cstf-77
33	c3mkrA_	Alignment	not modelled	54.7	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
34	c1na3A_	Alignment	not modelled	52.0	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
35	c2gw1A_	Alignment	not modelled	49.7	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor; **PDBTitle:** crystal structure of the yeast tom70
36	c2ho1B_	Alignment	not modelled	49.4	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf; **PDBTitle:** functional characterization of pseudomonas aeruginosa pilf
37	c2hyzA_	Alignment	not modelled	45.9	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix2 (orthorombic crystal form)
38	c2l6jA_	Alignment	not modelled	44.4	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90; **PDBTitle:** tah1 complexed by meevd
39	c2q7fA_	Alignment	not modelled	43.4	17	**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
40	c2e2eA_	Alignment	not modelled	42.7	16	**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	c2xevB_	Alignment	not modelled	42.1	25	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
42	c3fflC_	Alignment	not modelled	41.8	15	**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
43	c3ly8A_	Alignment	not modelled	41.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
44	d1a17a_	Alignment	not modelled	40.1	21	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
45	c3q75A_	Alignment	not modelled	40.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**farnesyltransferase alpha subunit; **PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
46	c2avpA_	Alignment	not modelled	39.9	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
47	c3thdD_	Alignment	not modelled	38.8	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
48	d2ooea1	Alignment	not modelled	38.4	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
49	c1ihgA_	Alignment	not modelled	37.6	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cyclophilin 40; **PDBTitle:** bovine cyclophilin 40, monoclinic form
50	c2vq2A_	Alignment	not modelled	37.6	17	**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
51	d2ff4a2	Alignment	not modelled	37.1	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
52	d1jr1a4	Alignment	not modelled	36.9	47	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
53	d1hh8a_	Alignment	not modelled	36.7	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
54	d1qsaa1	Alignment	not modelled	36.3	11	**Fold:**alpha-alpha superhelix **Superfamily:**Bacterial muramidases **Family:**Bacterial muramidases

55	d1iyga_	Alignment	not modelled	30.7	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
56	c2c2lD_	Alignment	not modelled	30.6	21	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
57	c3d3aA_	Alignment	not modelled	30.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
58	d1ihga1	Alignment	not modelled	29.4	26	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
59	c1xc6A_	Alignment	not modelled	27.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
60	c2fbnA_	Alignment	not modelled	27.6	17	**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
61	d2fbna1	Alignment	not modelled	27.6	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
62	c3ogrA_	Alignment	not modelled	27.2	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
63	d1pc2a_	Alignment	not modelled	26.5	23	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
64	c3urzB_	Alignment	not modelled	26.1	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution
65	d1hz4a_	Alignment	not modelled	24.5	22	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Transcription factor MalT domain III
66	c2dbaA_	Alignment	not modelled	23.0	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**smooth muscle cell associated protein-1, isoform **PDBTitle:** the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
67	c3jroC_	Alignment	not modelled	22.5	16	**PDB header:**transport protein, structural protein **Chain:** C: **PDB Molecule:**nucleoporin nup84; **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
68	c3ikoC_	Alignment	not modelled	22.4	16	**PDB header:**structural protein, protein transport **Chain:** C: **PDB Molecule:**nucleoporin nup84; **PDBTitle:** crystal structure of the heterotrimeric sec13-nup145c-nup842 nucleoporin complex
69	c3draA_	Alignment	not modelled	21.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein **PDBTitle:** candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
70	c2olvA_	Alignment	not modelled	21.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
71	d1tjca_	Alignment	not modelled	21.1	15	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
72	c1qz2B_	Alignment	not modelled	18.4	19	**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
73	c2xzeA_	Alignment	not modelled	17.7	24	**PDB header:**hydrolase/protein transport **Chain:** A: **PDB Molecule:**stam-binding protein; **PDBTitle:** structural basis for amsh-escrt-iii chmp3 interaction
74	d2onda1	Alignment	not modelled	17.5	17	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
75	c3qkyA_	Alignment	not modelled	17.3	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
76	c2xjqA_	Alignment	not modelled	16.6	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**flocculation protein flo5; **PDBTitle:** x-ray structure of the n-terminal domain of the flocculin2 flo5 from saccharomyces cerevisiae
77	d1xnfa_	Alignment	not modelled	16.2	20	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
78	d1zu2a1	Alignment	not modelled	15.2	24	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
79	d1hcca_	Alignment	not modelled	14.5	26	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
80	c1hccA_	Alignment	not modelled	14.5	26	**PDB header:**glycoprotein **Chain:** A: **PDB Molecule:**16th complement control protein; **PDBTitle:** three-dimensional structure of a complement control

						protein2 module in solution
81	c1cw5A_	Alignment	not modelled	14.2	54	**PDB header:**toxin **Chain:** A: **PDB Molecule:**type iia bacteriocin carnobacteriocin b2; **PDBTitle:** solution structure of carnobacteriocin b2
82	c3as5A_	Alignment	not modelled	12.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mama; **PDBTitle:** mama amb-1 p212121
83	c1vzjB_	Alignment	not modelled	12.4	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** structure of the tetramerization domain of2 acetylcholinesterase: four-fold interaction of a www motif3 with a left-handed polyproline helix
84	d1sisa_	Alignment	not modelled	11.1	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
85	c2yhcA_	Alignment	not modelled	10.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**upf0169 lipoprotein yfio; **PDBTitle:** structure of bamd from e. coli
86	c2zzfA_	Alignment	not modelled	10.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
87	d1p5qa1	Alignment	not modelled	10.0	16	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
88	c1ibtC_	Alignment	not modelled	9.5	26	**PDB header:**lyase **Chain:** C: **PDB Molecule:**histidine decarboxylase beta chain; **PDBTitle:** structure of the d53,54n mutant of histidine decarboxylase at-170 c
89	d1t46a_	Alignment	not modelled	9.5	18	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
90	c2ff4B_	Alignment	not modelled	9.4	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
91	d3ehbb1	Alignment	not modelled	9.1	36	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
92	d1elra_	Alignment	not modelled	9.0	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
93	c3da4B_	Alignment	not modelled	9.0	32	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
94	c3q3hA_	Alignment	not modelled	8.7	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
95	d3dtub1	Alignment	not modelled	8.7	28	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
96	c3sf4B_	Alignment	not modelled	8.7	14	**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
97	c3nf1A_	Alignment	not modelled	8.6	31	**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
98	c3h2zA_	Alignment	not modelled	8.5	52	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
99	d1lj8a4	Alignment	not modelled	8.4	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain