Phyre2

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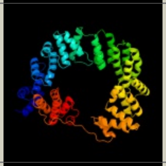
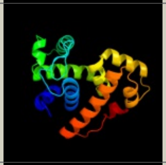
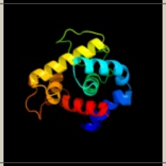
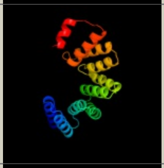
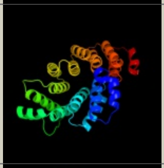
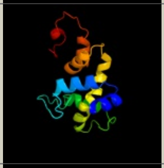
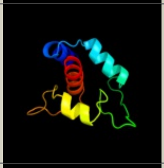
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1slyA_	Alignment		100.0	100	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
2	d1qsaa1	Alignment		100.0	100	**Fold:**alpha-alpha superhelix **Superfamily:**Bacterial muramidases **Family:**Bacterial muramidases
3	d1qsaa2	Alignment		100.0	100	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
4	c2y8pA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
5	c3mgwA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
6	c3gxkB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
7	d1gbsa_	Alignment		100.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
8	d1w3ba_	Alignment		99.4	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
9	c2xpiA_	Alignment		99.4	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cut9; **PDBTitle:** crystal structure of apc/c hetero-tetramer cut9-hcn1
10	c3hymB_	Alignment		99.0	8	**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
11	c1fchB_	Alignment		99.0	10	**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

12	c3cvpA_	Alignment		98.8	8	**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)
13	c3pe3D_	Alignment		98.8	15	**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
14	c3mkrA_	Alignment		98.8	11	**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
15	c2ho1B_	Alignment		98.7	9	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf; **PDBTitle:** functional characterization of pseudomonas aeruginosa pilf
16	d1fcha_	Alignment		98.7	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
17	c3bkhA_	Alignment		98.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
18	d1qusa_	Alignment		98.6	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
19	c2vq2A_	Alignment		98.6	12	**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
20	c3draA_	Alignment		98.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein **PDBTitle:** candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
21	c3iegB_	Alignment	not modelled	98.5	11	**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	c2r5sB_	Alignment	not modelled	98.4	12	**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
23	d2ooea1	Alignment	not modelled	98.3	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
24	c2uy1A_	Alignment	not modelled	98.3	9	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**cleavage stimulation factor 77; **PDBTitle:** crystal structure of cstf-77
25	d1hz4a_	Alignment	not modelled	98.3	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Transcription factor MalT domain III
26	c2y4tA_	Alignment	not modelled	98.3	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
27	c3urzB_	Alignment	not modelled	98.2	13	**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
28	d1xnfa_	Alignment	not modelled	98.2	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
						PDB header:transport protein

29	c3fp4A_	Alignment	not modelled	98.1	11	**Chain:** A: **PDB Molecule:**tpr repeat-containing protein yhr117w; **PDBTitle:** crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
30	c2xcbA_	Alignment	not modelled	98.1	11	**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
31	d1dcea1	Alignment	not modelled	98.1	10	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
32	c3gyzB_	Alignment	not modelled	98.0	11	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri
33	c3qdnA_	Alignment	not modelled	98.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
34	c2q7fA_	Alignment	not modelled	98.0	13	**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
35	c3ly8A_	Alignment	not modelled	97.9	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
36	c2hyzA_	Alignment	not modelled	97.8	11	**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)
37	c2katA_	Alignment	not modelled	97.6	9	**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
38	c3q75A_	Alignment	not modelled	97.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**farnesyltransferase alpha subunit; **PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
39	d1hxia_	Alignment	not modelled	97.6	7	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
40	c2pl2A_	Alignment	not modelled	97.5	14	**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
41	c2xevB_	Alignment	not modelled	97.5	15	**PDB header:**metal binding **Chain:** B: **PDB Molecule:**ybgf; **PDBTitle:** crystal structure of the tpr domain of xanthomonas2 campestris ybgf
42	c2kcvA_	Alignment	not modelled	97.5	10	**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
43	c1wao4_	Alignment	not modelled	97.5	12	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
44	c2yhcA_	Alignment	not modelled	97.4	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**upf0169 lipoprotein yfio; **PDBTitle:** structure of bamd from e. coli
45	c2c2lD_	Alignment	not modelled	97.4	13	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**carboxy terminus of hsp70-interacting protein; **PDBTitle:** crystal structure of the chip u-box e3 ubiquitin ligase
46	c3as5A_	Alignment	not modelled	97.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mama; **PDBTitle:** mama amb-1 p212121
47	c3q49B_	Alignment	not modelled	97.4	14	**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
48	d1elwa_	Alignment	not modelled	97.3	15	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
49	c3qkyA_	Alignment	not modelled	97.3	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane assembly lipoprotein yfio; **PDBTitle:** crystal structure of rhodothermus marinus bamd
50	c2e2eA_	Alignment	not modelled	97.3	12	**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
51	c2vyiA_	Alignment	not modelled	97.2	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sgta protein; **PDBTitle:** crystal structure of the tpr domain of human sgt
52	d1hh8a_	Alignment	not modelled	97.2	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
53	d2c2la1	Alignment	not modelled	97.2	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
54	d1d8da_	Alignment	not modelled	97.2	12	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase

						Family: Protein prenylyltransferase
55	c3mv3B_	Alignment	not modelled	97.1	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of a-cop in complex with e-cop
56	c2kckA_	Alignment	not modelled	97.1	9	**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
57	d2buga1	Alignment	not modelled	97.1	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
58	c2vsnB_	Alignment	not modelled	97.0	16	**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
59	c2if4A_	Alignment	not modelled	96.9	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
60	c3k9iA_	Alignment	not modelled	96.9	10	**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
61	c3nf1A_	Alignment	not modelled	96.9	12	**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
62	c2avpA_	Alignment	not modelled	96.8	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
63	c2dbaA_	Alignment	not modelled	96.8	14	**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
64	c1kt0A_	Alignment	not modelled	96.5	9	**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
65	d2ff4a2	Alignment	not modelled	96.5	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**BTAD-like
66	c2kc7A_	Alignment	not modelled	96.4	14	**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
67	d1a17a_	Alignment	not modelled	96.2	12	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
68	c2l6jA_	Alignment	not modelled	96.2	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tpr repeat-containing protein associated with hsp90; **PDBTitle:** tah1 complexed by meevd
69	d1zbpa1	Alignment	not modelled	96.1	10	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
70	c3sz7A_	Alignment	not modelled	96.0	6	**PDB header:**chaperone regulator **Chain:** A: **PDB Molecule:**hsc70 cochaperone (sgt); **PDBTitle:** crystal structure of the sgt2 tpr domain from aspergillus fumigatus
71	c1na3A_	Alignment	not modelled	96.0	6	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
72	c2gw1A_	Alignment	not modelled	96.0	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor; **PDBTitle:** crystal structure of the yeast tom70
73	c1xsfA_	Alignment	not modelled	95.9	23	**PDB header:**cell cycle, hydrolase **Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb; **PDBTitle:** solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
74	c2vgxA_	Alignment	not modelled	95.8	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone sycd; **PDBTitle:** structure of the yersinia enterocolitica type iii secretion2 translocator chaperone sycd
75	d1nzna_	Alignment	not modelled	95.8	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
76	d1tjca_	Alignment	not modelled	95.7	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
77	c1tnoI_	Alignment	not modelled	95.6	12	**PDB header:**transferase **Chain:** I: **PDB Molecule:**geranylgeranyltransferase type i alpha subunit; **PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkksktkcvim peptide derived from k-3 ras4b
78	c1ihgA_	Alignment	not modelled	95.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**cyclophilin 40; **PDBTitle:** bovine cyclophilin 40, monoclinic form
79	d1elra_	Alignment	not modelled	95.6	8	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)

80	d1xsfa1	Alignment	not modelled	95.6	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
81	d1iyga_	Alignment	not modelled	95.6	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
82	c3beeB_	Alignment	not modelled	95.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative yfre protein; **PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus
83	d2hr2a1	Alignment	not modelled	95.1	19	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**CT2138-like
84	d2h6fa1	Alignment	not modelled	95.0	12	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
85	c3ct5A_	Alignment	not modelled	94.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
86	d1y8ma1	Alignment	not modelled	94.8	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
87	c3q15A_	Alignment	not modelled	94.7	8	**PDB header:**hydrolase/kinase **Chain:** A: **PDB Molecule:**response regulator aspartate phosphatase h; **PDBTitle:** crystal structure of raph complexed with spo0f
88	c3fflC_	Alignment	not modelled	94.7	13	**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
89	d1zu2a1	Alignment	not modelled	94.6	9	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
90	d1pc2a_	Alignment	not modelled	94.3	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
91	c3gw4B_	Alignment	not modelled	93.8	13	**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.
92	c1qz2B_	Alignment	not modelled	92.4	7	**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
93	c3eo5A_	Alignment	not modelled	92.3	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
94	c2fbdB_	Alignment	not modelled	91.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme 1; **PDBTitle:** the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
95	d1gd6a_	Alignment	not modelled	91.8	14	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
96	d1iiza_	Alignment	not modelled	91.7	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
97	d1hhla_	Alignment	not modelled	91.3	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
98	d1kt1a1	Alignment	not modelled	90.9	7	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
99	d2vb1a1	Alignment	not modelled	90.9	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
100	d1ghla_	Alignment	not modelled	90.5	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
101	c2fbnA_	Alignment	not modelled	90.4	14	**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
102	d2fbna1	Alignment	not modelled	90.4	14	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
103	d2pqrb1	Alignment	not modelled	90.1	13	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
104	d1lsga1	Alignment	not modelled	89.3	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
105	c3csqC_	Alignment	not modelled	88.6	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
						Fold: Lysozyme-like

106	d1lmqa_	Alignment	not modelled	88.0	25	**Superfamily:**Lysozyme-like **Family:**C-type lysozyme
107	d1jsea_	Alignment	not modelled	88.0	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
108	c2goiC_	Alignment	not modelled	87.8	15	**PDB header:**cell adhesion, sugar binding protein **Chain:** C: **PDB Molecule:**sperm lysozyme-like protein 1; **PDBTitle:** crystal structure of mouse sperm c-type lysozyme-like2 protein 1
109	c3rkvA_	Alignment	not modelled	87.8	9	**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
110	d1juga_	Alignment	not modelled	87.3	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
111	c2z2fA_	Alignment	not modelled	86.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme c-2; **PDBTitle:** x-ray crystal structure of bovine stomach lysozyme
112	d1qqya_	Alignment	not modelled	85.9	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
113	c2ff4B_	Alignment	not modelled	85.6	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable regulatory protein embr; **PDBTitle:** mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
114	c3sf4B_	Alignment	not modelled	85.1	7	**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
115	d2eqla_	Alignment	not modelled	84.8	42	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
116	d1ivma_	Alignment	not modelled	84.4	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
117	d2onda1	Alignment	not modelled	84.0	11	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**HAT/Suf repeat
118	d1p5qa1	Alignment	not modelled	82.5	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
119	d1f6sa_	Alignment	not modelled	82.3	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
120	c3ulqA_	Alignment	not modelled	80.0	9	**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