Phyre^2

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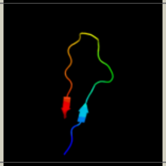
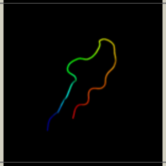
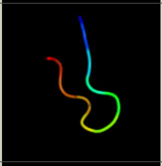
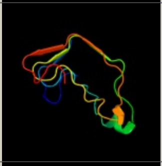
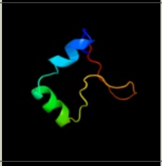
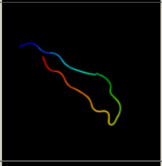
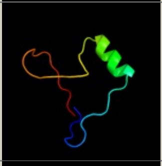
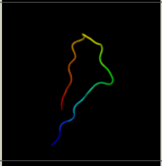
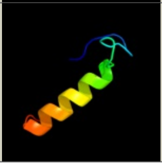
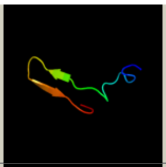
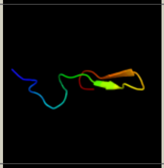
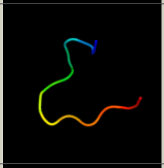
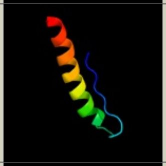
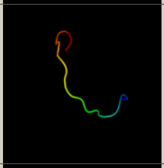
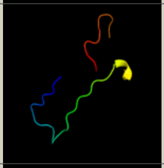
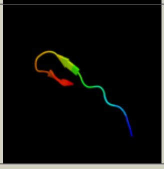
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3idwA_	Alignment		52.4	20	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
2	c2a74B_	Alignment		51.9	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement component c3c; **PDBTitle:** human complement component c3c
3	c3hs0B_	Alignment		45.5	5	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b
4	d2fhzb1	Alignment		26.8	64	**Fold:**Colicin D/E5 nuclease domain **Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin E5 nuclease domain
5	d1h80a_	Alignment		24.7	33	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**iota-carrageenase
6	c2gm2A_	Alignment		22.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
7	d3es6b1	Alignment		22.8	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**SVA-like
8	d2fvta1	Alignment		22.3	25	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
9	c3g6jB_	Alignment		21.1	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3 alpha chain; **PDBTitle:** c3b in complex with a c3b specific fab
10	c2of5A_	Alignment		19.9	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
11	c2i1vB_	Alignment		19.9	24	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate

12	d2ckaa1	Alignment		19.6	21	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
13	c2ckaA_	Alignment		19.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
14	d1ueba3	Alignment		19.2	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
15	c1h2iG_	Alignment		18.8	26	**PDB header:**dna-binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog; **PDBTitle:** human rad52 protein, n-terminal domain
16	d2nn6i1	Alignment		17.7	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	c3f59A_	Alignment		17.1	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** crystal structure of zu5-ank, the spectrin binding region of human2 erythroid ankyrin
18	c1yfzA_	Alignment		16.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
19	d1yfza1	Alignment		16.9	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	d2i8ga1	Alignment		16.8	36	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**DIP2269-like
21	d2dy1a4	Alignment	not modelled	15.2	16	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
22	c2a73B_	Alignment	not modelled	14.8	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**complement c3; **PDBTitle:** human complement component c3
23	c2j37W_	Alignment	not modelled	14.5	39	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
24	d1kn0a_	Alignment	not modelled	14.5	23	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
25	d2bm0a4	Alignment	not modelled	13.8	16	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
26	c1wm9D_	Alignment	not modelled	13.7	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase i; **PDBTitle:** structure of gtp cyclohydrolase i from thermus thermophilus hb8
27	c3e4fB_	Alignment	not modelled	13.5	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
28	d1m1ha1	Alignment	not modelled	13.3	42	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
						PDB header:transcription/dna

29	c2o8kA_	Alignment	not modelled	13.2	27	**Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
30	d1wura1	Alignment	not modelled	13.1	23	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
31	c2j9wB_	Alignment	not modelled	12.8	24	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vps28-prov protein; **PDBTitle:** structural insight into the escrt-i-ii link and its role in2 mvb trafficking
32	d2ckca1	Alignment	not modelled	12.8	29	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
33	c2ckcA_	Alignment	not modelled	12.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
34	c1dpuA_	Alignment	not modelled	12.7	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
35	d1dpua_	Alignment	not modelled	12.7	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
36	d1ge9a_	Alignment	not modelled	12.5	18	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
37	d1sv6a_	Alignment	not modelled	12.5	23	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
38	c3gmgB_	Alignment	not modelled	12.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
39	c1bifA_	Alignment	not modelled	11.9	24	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
40	d1iv0a_	Alignment	not modelled	11.6	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
41	c2wl8D_	Alignment	not modelled	11.2	26	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
42	d2v0ea1	Alignment	not modelled	11.2	29	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
43	c3fsyC_	Alignment	not modelled	11.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase; **PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
44	c3r6oA_	Alignment	not modelled	11.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
45	c3ouvA_	Alignment	not modelled	10.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase; **PDBTitle:** semet derivative of l512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
46	c2zf9D_	Alignment	not modelled	10.6	31	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**scae cell-surface anchored scaffoldin protein; **PDBTitle:** crystal structure of a type iii cohesin module from the cellulosomal2 scae cell-surface anchoring scaffoldin of ruminococcus flavefaciens
47	c2lf3A_	Alignment	not modelled	10.5	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab3; **PDBTitle:** solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
48	c3i7tA_	Alignment	not modelled	10.4	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
49	c2jvfA_	Alignment	not modelled	10.4	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
50	d1k6ma1	Alignment	not modelled	10.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
51	d2q4qa1	Alignment	not modelled	10.2	25	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
						Fold: Obg GTP-binding protein C-terminal domain

52	d1udxa3	Alignment	not modelled	10.1	17	**Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
53	d2k8ea1	Alignment	not modelled	10.0	22	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
54	c1i7oC_	Alignment	not modelled	9.8	12	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
55	c3gtzA_	Alignment	not modelled	9.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative translation initiation inhibitor; **PDBTitle:** crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
56	c1d2fB_	Alignment	not modelled	9.7	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maly protein; **PDBTitle:** x-ray structure of maly from escherichia coli: a pyridoxal-5'-2 phosphate-dependent enzyme acting as a modulator in mal gene3 expression
57	c2v3cC_	Alignment	not modelled	9.6	39	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
58	c2ig8C_	Alignment	not modelled	9.6	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pa3499; **PDBTitle:** crystal structure of a protein of unknown function pa3499 from2 pseudomonas aeruginosa
59	c3pisA_	Alignment	not modelled	9.6	40	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kazal-type serine protease inhibitor spi-1; **PDBTitle:** crystal structure of carcinoscorpius rotundicauda serine protease2 inhibitor domain 1
60	c2b39B_	Alignment	not modelled	9.5	9	**PDB header:**immune system **Chain:** B: **PDB Molecule:**c3; **PDBTitle:** structure of mammalian c3 with an intact thioester at 3a resolution
61	d2dl6a1	Alignment	not modelled	9.4	29	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
62	c2hfuB_	Alignment	not modelled	9.3	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mevalonate kinase, putative; **PDBTitle:** crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
63	c3ez4B_	Alignment	not modelled	9.2	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
64	c2eb5D_	Alignment	not modelled	9.2	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2-oxo-hept-3-ene-1,7-dioate hydratase; **PDBTitle:** crystal structure of hpcg complexed with oxalate
65	c3gdwA_	Alignment	not modelled	9.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
66	c1vpzB_	Alignment	not modelled	9.1	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**carbon storage regulator homolog; **PDBTitle:** crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
67	c2kmmA_	Alignment	not modelled	9.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
68	d1t3da_	Alignment	not modelled	9.0	12	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
69	d1vk2a_	Alignment	not modelled	8.9	34	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
70	d2od5a1	Alignment	not modelled	8.9	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Marine metagenome family WH1
71	c2od5A_	Alignment	not modelled	8.9	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative nucleic acid binding protein2 (jcvi_pep_1096688149193) from uncultured marine organism at 1.79 a3 resolution
72	d1r17a1	Alignment	not modelled	8.8	16	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Fibrinogen-binding domain
73	c2jppB_	Alignment	not modelled	8.8	16	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**translational repressor; **PDBTitle:** structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
74	d1cuka1	Alignment	not modelled	8.7	38	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
75	c3l7qD_	Alignment	not modelled	8.6	16	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
76	c2x7iA_	Alignment	not modelled	8.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
						PDB header:rna-binding

77	c2iy3A_	Alignment	not modelled	8.6	39	**Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
78	c2f1rA_	Alignment	not modelled	8.4	32	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
79	d1ssqa_	Alignment	not modelled	8.4	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
80	d1x6va3	Alignment	not modelled	8.3	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
81	c3dm5A_	Alignment	not modelled	8.3	43	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
82	c1t3oA_	Alignment	not modelled	8.2	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**carbon storage regulator; **PDBTitle:** solution structure of csra, a bacterial carbon storage2 regulatory protein
83	d1stza1	Alignment	not modelled	8.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
84	d1a8ra_	Alignment	not modelled	8.0	21	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
85	c2bpsA_	Alignment	not modelled	8.0	16	**PDB header:**ubiquitin **Chain:** A: **PDB Molecule:**yukd protein; **PDBTitle:** ubiquitin-like protein yukd of bacillus subtilis
86	d1vpza_	Alignment	not modelled	7.9	19	**Fold:**CsrA-like **Superfamily:**CsrA-like **Family:**CsrA-like
87	c3cu7A_	Alignment	not modelled	7.9	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
88	c2kxsA_	Alignment	not modelled	7.8	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1, linker, peptide of myocardium- **PDBTitle:** zo1 zu5 domain in complex with grinl1a peptide
89	c2xdyA_	Alignment	not modelled	7.8	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**post-transcriptional gene silencing protein qde-2; **PDBTitle:** crystal structure of the n. crassa qde-2 ago mid domain
90	d1y76b1	Alignment	not modelled	7.6	25	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
91	c2ea3A_	Alignment	not modelled	7.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chymotrypsin; **PDBTitle:** crystal structure of cellulomonas bogoriensis chymotrypsin
92	c1qzwC_	Alignment	not modelled	7.4	39	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
93	c3k0tA_	Alignment	not modelled	7.3	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**endoribonuclease l-psp, putative; **PDBTitle:** crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
94	c3gr1A_	Alignment	not modelled	7.3	46	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
95	c3a3eB_	Alignment	not modelled	7.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin-binding protein 4; **PDBTitle:** crystal structure of penicillin binding protein 4 (dacb)2 from haemophilus influenzae, complexed with novel beta-3 lactam (cmv)
96	d2k8ea2	Alignment	not modelled	7.3	23	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
97	c3oyyA_	Alignment	not modelled	7.2	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
98	c1gqqA_	Alignment	not modelled	7.1	21	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
99	c1dlyA_	Alignment	not modelled	7.0	25	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin; **PDBTitle:** x-ray crystal structure of hemoglobin from the green2 unicellular alga chlamydomonas eugametos