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Description	P32710
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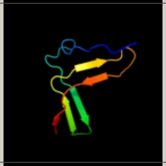
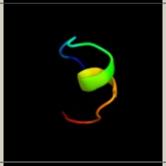
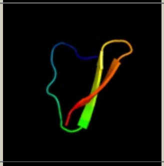
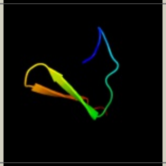
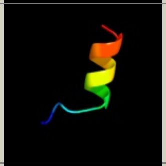
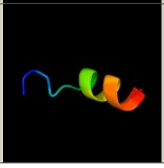
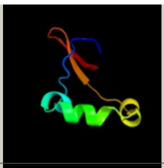
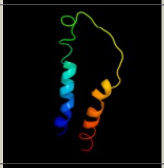
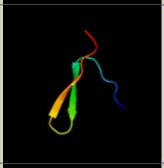
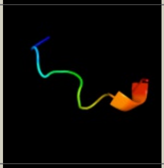
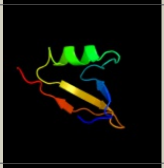
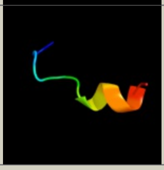
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cfuA_	Alignment		88.8	10	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
2	d2affa1	Alignment		51.8	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
3	c3lkxB_	Alignment		47.7	23	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha; **PDBTitle:** human nac dimerization domain
4	c1r21A_	Alignment		45.4	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
5	c2lezA_	Alignment		34.5	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**secreted effector protein pipb2; **PDBTitle:** solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a
6	d1udxa3	Alignment		31.4	24	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
7	c1agqB_	Alignment		27.2	42	**PDB header:**growth factor **Chain:** B: **PDB Molecule:**glial cell-derived neurotrophic factor; **PDBTitle:** glial cell-derived neurotrophic factor from rat
8	d2ff4a3	Alignment		26.0	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
9	c3gqsB_	Alignment		17.3	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
10	d3b55a1	Alignment		15.8	27	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
11	c2radB_	Alignment		15.4	27	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135

12	c2zpmA_	Alignment		13.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
13	d2f69a1	Alignment		13.2	16	**Fold:**open-sided beta-meander **Superfamily:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain **Family:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
14	d1fftb2	Alignment		13.1	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
15	c3uotB_	Alignment		12.9	21	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
16	c2l9uA_	Alignment		12.4	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
17	d1c8na_	Alignment		12.2	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
18	c1lcyA_	Alignment		12.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
19	d1dlpa1	Alignment		12.2	13	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
20	d1f2nc_	Alignment		11.9	54	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
21	c2kklA_	Alignment	not modelled	11.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
22	d4sbva_	Alignment	not modelled	11.3	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
23	d2o3ga1	Alignment	not modelled	11.2	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
24	d1smvc_	Alignment	not modelled	11.2	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
25	c2bbjB_	Alignment	not modelled	11.2	8	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
26	c3poaA_	Alignment	not modelled	10.7	14	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
27	c1bhbA_	Alignment	not modelled	10.6	30	**PDB header:**photoreceptor **Chain:** A: **PDB Molecule:**bacteriorhodopsin; **PDBTitle:** three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
28	d2gmqa1	Alignment	not modelled	10.4	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PrgU-like

29	c2r76A_	Alignment	not modelled	10.3	9	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**rare lipoprotein b; **PDBTitle:** crystal structure of the rare lipoprotein b (so_1173) from shewanella2 oneidensis, northeast structural genomics consortium target sor91a
30	c3mpbA_	Alignment	not modelled	10.2	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
31	c3ia8A_	Alignment	not modelled	10.1	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**thap domain-containing protein 4; **PDBTitle:** the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens
32	d1ng0c_	Alignment	not modelled	10.0	50	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
33	d1smva_	Alignment	not modelled	9.6	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
34	c4a0kB_	Alignment	not modelled	9.2	75	**PDB header:**ligase/dna-binding protein/dna **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rbx1; **PDBTitle:** structure of ddb1-ddb2-cul4a-rbx1 bound to a 12 bp abasic2 site containing dna-duplex
35	d1f2na_	Alignment	not modelled	9.2	54	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
36	c1f2nA_	Alignment	not modelled	9.2	54	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** rice yellow mottle virus
37	d2p13a1	Alignment	not modelled	9.2	26	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
38	c1hgvA_	Alignment	not modelled	9.2	26	**PDB header:**virus **Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein; **PDBTitle:** filamentous bacteriophage ph75
39	d1hdmb2	Alignment	not modelled	9.2	83	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
40	c2p0vA_	Alignment	not modelled	9.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
41	d2p0va1	Alignment	not modelled	9.1	28	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
42	c3lw52_	Alignment	not modelled	9.1	18	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from photosystem i; **PDB Fragment:**residues 81-246; **PDBTitle:** improved model of plant photosystem i
43	d2vq0a1	Alignment	not modelled	9.0	31	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
44	c2dfwA_	Alignment	not modelled	8.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
45	d2nvpa1	Alignment	not modelled	8.3	39	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
46	d1bwua_	Alignment	not modelled	8.3	25	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
47	c1c8nC_	Alignment	not modelled	7.9	23	**PDB header:**virus **Chain:** C: **PDB Molecule:**coat protein; **PDBTitle:** tobacco necrosis virus
48	d1c8nc_	Alignment	not modelled	7.9	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
49	c3rkoN_	Alignment	not modelled	7.7	20	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
50	d2qgma1	Alignment	not modelled	7.7	13	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
51	c2qgmA_	Alignment	not modelled	7.7	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of succinoglycan biosynthesis protein at2 the resolution 1.7 a. northeast structural genomics3 consortium target bcr136.
52	d2o1ra1	Alignment	not modelled	7.7	11	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
53	c3o0rB_	Alignment	not modelled	7.7	14	**PDB header:**immune system/oxidoreductase **Chain:** B: **PDB Molecule:**nitric oxide reductase subunit b; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
54	d1u60a_	Alignment	not modelled	7.7	29	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
						PDB header:transcription

55	c2l7eA_	Alignment	not modelled	7.6	63	**Chain:** A: **PDB Molecule:**transcription initiation factor tfiid subunit 14; **PDBTitle:** the structure of a domain from yeast
56	c2yyoA_	Alignment	not modelled	7.5	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**spry domain-containing protein 3; **PDBTitle:** crystal sturcture of human spry domain
57	d2bgca2	Alignment	not modelled	7.4	80	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**Listeriolysin regulatory protein PrfA, N-terminal domain
58	c1ng0A_	Alignment	not modelled	7.4	50	**PDB header:**virus **Chain:** A: **PDB Molecule:**coat protein; **PDBTitle:** the three-dimensional structure of cocksfoot mottle virus2 at 2.7a resolution
59	d1ng0a_	Alignment	not modelled	7.4	50	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Tombusviridae-like VP
60	c3mezA_	Alignment	not modelled	7.2	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**mannose-specific lectin 3 chain 1; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
61	c2kjpA_	Alignment	not modelled	7.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
62	c2ksfA_	Alignment	not modelled	7.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein kdpd; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpd, center for structures of3 membrane proteins (csmp) target 4312c
63	d3deda1	Alignment	not modelled	7.2	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
64	c1yj5C_	Alignment	not modelled	7.1	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
65	d1rl2a2	Alignment	not modelled	7.1	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
66	c3fm8A_	Alignment	not modelled	7.1	16	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
67	d1gh6b2	Alignment	not modelled	7.1	7	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Retinoblastoma tumor suppressor domains
68	c2yvxD_	Alignment	not modelled	7.1	21	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
69	c2jkdB_	Alignment	not modelled	7.1	21	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** structure of the yeast pml1 splicing factor and its2 integration into the res complex
70	d1bwud_	Alignment	not modelled	7.0	20	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
71	d2plia1	Alignment	not modelled	7.0	23	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
72	d2brfa1	Alignment	not modelled	7.0	28	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
73	d1kj1a_	Alignment	not modelled	7.0	25	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
74	c3m4wH_	Alignment	not modelled	7.0	26	**PDB header:**signaling protein/signaling protein **Chain:** H: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** structural basis for the negative regulation of bacterial stress2 response by rseb
75	c2vo9C_	Alignment	not modelled	6.9	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase; **PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
76	c3dedB_	Alignment	not modelled	6.9	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable hemolysin; **PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum
77	c3elsA_	Alignment	not modelled	6.9	23	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna leakage protein 1; **PDBTitle:** crystal structure of yeast pml1p, residues 51-204
78	c1gh6B_	Alignment	not modelled	6.9	13	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**retinoblastoma-associated protein; **PDBTitle:** retinoblastoma pocket complexed with sv40 large t antigen
79	d1p9ka_	Alignment	not modelled	6.8	23	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
80	d2plsa1	Alignment	not modelled	6.7	16	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like

81	d1qcsa1	Alignment	not modelled	6.7	43	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
82	d2vera1	Alignment	not modelled	6.7	40	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Dr-family adhesin
83	c3llbA_	Alignment	not modelled	6.7	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
84	c2qcqA_	Alignment	not modelled	6.6	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bone morphogenetic protein 3; **PDBTitle:** crystal structure of bone morphogenetic protein-3 (bmp-3)
85	d1uhta_	Alignment	not modelled	6.6	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
86	c2p28A_	Alignment	not modelled	6.6	38	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of the phe2 and phe3 fragments of the integrin beta2 subunit
87	c1fftG_	Alignment	not modelled	6.6	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
88	d1h3ga1	Alignment	not modelled	6.6	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
89	c2gyrB_	Alignment	not modelled	6.6	38	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**neurotrophic factor artemin, isoform 3; **PDBTitle:** crystal structure of human artemin
90	c2rf9D_	Alignment	not modelled	6.5	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**erbb receptor feedback inhibitor 1; **PDBTitle:** crystal structure of the complex between the egfr kinase2 domain and a mig6 peptide
91	d2oaia1	Alignment	not modelled	6.5	23	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
92	c3pv4A_	Alignment	not modelled	6.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
93	d1vjja2	Alignment	not modelled	6.4	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
94	c1zkzA_	Alignment	not modelled	6.4	38	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**growth/differentiation factor 2; **PDBTitle:** crystal structure of bmp9
95	c2hczX_	Alignment	not modelled	6.4	38	**PDB header:**allergen **Chain:** X: **PDB Molecule:**beta-expansin 1a; **PDBTitle:** crystal structure of expb1 (zea m 1), a beta-expansin and group-12 pollen allergen from maize
96	d2r7ga2	Alignment	not modelled	6.4	7	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Retinoblastoma tumor suppressor domains
97	d1jpca_	Alignment	not modelled	6.4	15	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
98	c2odkD_	Alignment	not modelled	6.4	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
99	c3htxA_	Alignment	not modelled	6.4	17	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1