Phyre2

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Description	P0A6S0
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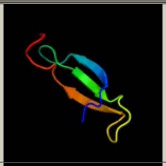
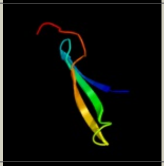
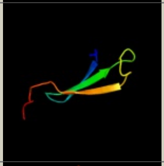
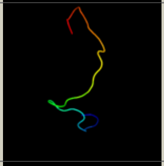
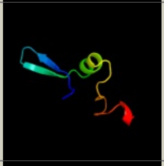
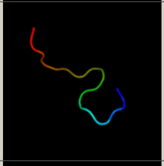
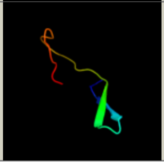
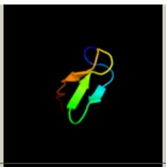
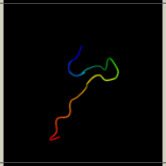
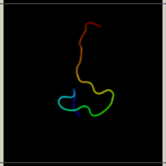
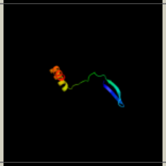
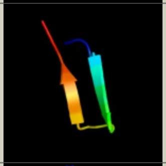
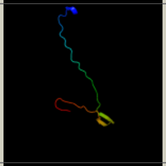
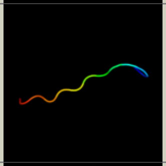
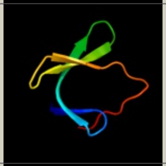
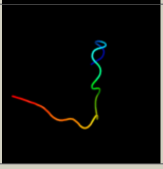
Unique Job ID	395ac949a8a281a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ah9a_	Alignment		61.4	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
2	c3i4oA_	Alignment		57.8	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
3	d1m9sa4	Alignment		51.1	19	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**GW domain
4	d1tt2a_	Alignment		49.4	12	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
5	c3bdlA_	Alignment		48.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
6	d2ix0a3	Alignment		35.4	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
7	d2ijra1	Alignment		32.7	27	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
8	d1snoa_	Alignment		29.7	12	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
9	c3etcB_	Alignment		29.6	32	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
10	d1khca_	Alignment		26.7	24	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
11	c2yyjA_	Alignment		24.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylacetate-3-hydroxylase; **PDBTitle:** crystal structure of the oxygenase component (hpab) of 4-2 hydroxyphenylacetate 3-monooxygenase complexed with fad and 4-3 hydroxyphenylacetate

12	c3pzvB_	Alignment		24.3	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
13	d1vlba3	Alignment		23.2	22	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
14	d1dgja3	Alignment		22.4	30	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
15	c3f8tA_	Alignment		22.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
16	c3izcG_	Alignment		22.0	25	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein rpl6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	d1nbwa2	Alignment		21.9	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
18	c2l66B_	Alignment		21.8	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
19	c2dzcA_	Alignment		21.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin--[acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
20	c3llrA_	Alignment		20.4	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a; **PDBTitle:** crystal structure of the pwwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
21	d1hr0w_	Alignment	not modelled	20.2	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d1qupa2	Alignment	not modelled	18.8	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1n62b1	Alignment	not modelled	18.7	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
24	d1fvia1	Alignment	not modelled	18.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
25	c2wctC_	Alignment	not modelled	18.0	25	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**non-structural protein 3; **PDBTitle:** human sars coronavirus unique domain (triclinic form)
26	d1m9sa2	Alignment	not modelled	17.0	13	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**GW domain
27	d1rkna_	Alignment	not modelled	16.3	12	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
28	d2k0bx1	Alignment	not modelled	15.7	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
29	d1ng2a2	Alignment	not modelled	13.2	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain

						Family:SH3-domain
30	d1ffvb1	Alignment	not modelled	12.8	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
31	c2wj7D_	Alignment	not modelled	12.8	14	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin
32	d1kj1a_	Alignment	not modelled	12.6	27	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
33	c2b9kA_	Alignment	not modelled	12.3	46	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**antimicrobial peptide lci; **PDBTitle:** solution structure of lci, an amp from bacillus subtilis
34	d2essa1	Alignment	not modelled	12.0	7	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
35	d1t3qb1	Alignment	not modelled	12.0	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
36	d2hlja1	Alignment	not modelled	11.9	9	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
37	d2soba_	Alignment	not modelled	11.7	10	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
38	c2crlA_	Alignment	not modelled	11.5	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
39	d1tdja3	Alignment	not modelled	11.2	31	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
40	c3r0eD_	Alignment	not modelled	11.1	15	**PDB header:**sugar binding protein **Chain:** D: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
41	c3mezB_	Alignment	not modelled	10.6	36	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**mannose-specific lectin 3 chain 2; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
42	c2oi3A_	Alignment	not modelled	10.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase hck; **PDBTitle:** nmr structure analysis of the hematopoetic cell kinase sh32 domain complexed with an artificial high affinity ligand3 (pd1)
43	d1cc8a_	Alignment	not modelled	10.3	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
44	d1g2913	Alignment	not modelled	10.2	17	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
45	c2ewnA_	Alignment	not modelled	10.1	12	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
46	c3ipfA_	Alignment	not modelled	9.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q251q8_deshy protein from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr8c.
47	d1bwud_	Alignment	not modelled	9.5	21	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
48	d1hnga1	Alignment	not modelled	9.4	40	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
49	c2wgnB_	Alignment	not modelled	9.4	25	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**inhibitor of cysteine peptidase compnd 3; **PDBTitle:** pseudomonas aeruginosa icp
50	d7a3ha_	Alignment	not modelled	9.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
51	c2kctA_	Alignment	not modelled	9.1	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccme; **PDBTitle:** solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g.
52	d1b2pa_	Alignment	not modelled	9.1	12	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
53	d1vqoq1	Alignment	not modelled	8.6	7	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
54	c2dpfB_	Alignment	not modelled	8.6	14	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**curculin; **PDBTitle:** crystal structure of curculin1 homodimer
55	d1v25a_	Alignment	not modelled	8.5	12	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like

						Family: Acetyl-CoA synthetase-like
56	c2zkrq_	Alignment	not modelled	8.4	30	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
57	c4a1dE_	Alignment	not modelled	8.4	38	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**rpl6; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
58	d1kj1d_	Alignment	not modelled	8.2	29	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
59	c1s1iQ_	Alignment	not modelled	8.2	22	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
60	c3r0eC_	Alignment	not modelled	8.2	36	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
61	c2eayB_	Alignment	not modelled	8.2	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
62	c1w3gA_	Alignment	not modelled	8.0	16	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.
63	d1jrob1	Alignment	not modelled	7.9	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
64	c3iz5U_	Alignment	not modelled	7.9	26	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
65	c2cghB_	Alignment	not modelled	7.8	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin ligase; **PDBTitle:** crystal structure of biotin ligase from mycobacterium2 tuberculosis
66	c4a1aP_	Alignment	not modelled	7.7	13	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
67	d1npla_	Alignment	not modelled	7.7	20	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
68	d1kafa_	Alignment	not modelled	7.7	29	**Fold:**MotA C-terminal domain-like **Superfamily:**DNA-binding C-terminal domain of the transcription factor MotA **Family:**DNA-binding C-terminal domain of the transcription factor MotA
69	d1khda2	Alignment	not modelled	7.6	19	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
70	c3elqA_	Alignment	not modelled	7.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfate sulfotransferase; **PDBTitle:** crystal structure of a bacterial arylsulfate2 sulfotransferase
71	d1hnfa1	Alignment	not modelled	7.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
72	c3m86B_	Alignment	not modelled	7.4	31	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**amoebiasin-2; **PDBTitle:** crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
73	d1bwua_	Alignment	not modelled	7.4	21	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
74	d2joya1	Alignment	not modelled	7.4	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
75	c2w54F_	Alignment	not modelled	7.4	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
76	c3izcU_	Alignment	not modelled	7.4	22	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
77	d1d7qa_	Alignment	not modelled	7.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
78	d2elca2	Alignment	not modelled	7.3	19	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase

						catalytic domain
79	c2imzA_	Alignment	not modelled	7.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
80	c3ij3A_	Alignment	not modelled	7.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
81	d1jpca_	Alignment	not modelled	7.1	20	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
82	c2oqkA_	Alignment	not modelled	7.1	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
83	c2dbkA_	Alignment	not modelled	7.0	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**crk-like protein; **PDBTitle:** solution structures of the sh3 domain of human crk-like2 protein
84	d1oxxk1	Alignment	not modelled	7.0	22	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
85	c2klrA_	Alignment	not modelled	6.9	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
86	d1l4zb_	Alignment	not modelled	6.9	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
87	c2k5hA_	Alignment	not modelled	6.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
88	d2zjrm1	Alignment	not modelled	6.8	27	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
89	c1u8vA_	Alignment	not modelled	6.7	20	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**gamma-aminobutyrate metabolism **PDBTitle:** crystal structure of 4-hydroxybutyryl-coa dehydratase from2 clostridium aminobutyricum: radical catalysis involving a3 [4fe-4s] cluster and flavin
90	d2exda1	Alignment	not modelled	6.7	20	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
91	c1qupA_	Alignment	not modelled	6.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
92	c3iuwA_	Alignment	not modelled	6.7	36	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**activating signal cointegrator; **PDBTitle:** crystal structure of activating signal cointegrator (np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
93	c3iz5G_	Alignment	not modelled	6.6	31	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein l6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
94	d1jt8a_	Alignment	not modelled	6.5	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
95	c3h8gC_	Alignment	not modelled	6.4	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
96	c2zs6B_	Alignment	not modelled	6.4	22	**PDB header:**toxin **Chain:** B: **PDB Molecule:**hemagglutinin components ha3; **PDBTitle:** ha3 subcomponent of botulinum type c progenitor toxin
97	c2e4mC_	Alignment	not modelled	6.3	44	**PDB header:**toxin **Chain:** C: **PDB Molecule:**ha-17; **PDBTitle:** crystal structure of hemagglutinin subcomponent complex (ha-2 33/ha-17) from clostridium botulinum serotype d strain 4947
98	d1v97a3	Alignment	not modelled	6.3	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
99	d3b9jc1	Alignment	not modelled	6.1	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like