Phyre^2

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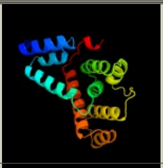
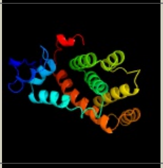
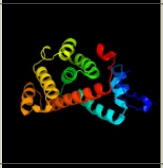
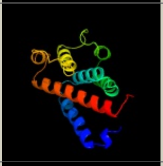
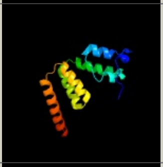
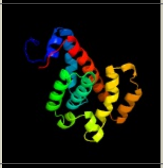
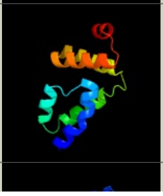
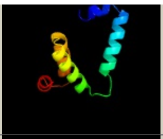
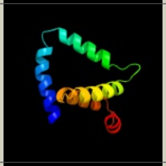
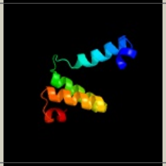
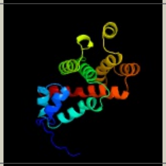
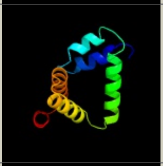
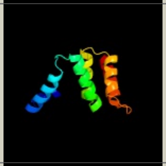
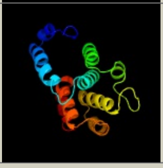
Description	RVBD1531_(-)_1732479_1733045
Date	Fri Aug 2 13:30:12 BST 2019
Unique Job ID	05b19f2eec40a38a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c1lB_	Alignment		100.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative antioxidant defense protein mlr4105; **PDBTitle:** crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
2	c3lvyB_	Alignment		100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
3	d2pfxa1	Alignment		100.0	9	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
4	d2prra1	Alignment		100.0	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
5	d2oyoa1	Alignment		100.0	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
6	c6ohiA_	Alignment		100.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**debrominase bmp8; **PDBTitle:** crystal structure of the debrominase bmp8 (apo)
7	d2gmya1	Alignment		100.0	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
8	d2o4da1	Alignment		100.0	25	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
9	d2ouwa1	Alignment		99.9	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
10	c5dj4D_	Alignment		99.8	14	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**sestrin-2; **PDBTitle:** leucine-bound sestrin2 from homo sapiens
11	c2qeuA_	Alignment		99.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution

12	c3beyC_	Alignment		99.3	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
13	c5dipB_	Alignment		99.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase ahpd; **PDBTitle:** crystal structure of lpg0406 in reduced form from legionella2 pneumophila
14	c1p8cD_	Alignment		99.3	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
15	d2q0ta1	Alignment		99.2	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
16	d2cwqa1	Alignment		99.2	20	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
17	d1vkea_	Alignment		99.2	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
18	c3d7iB_	Alignment		99.1	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
19	d1vkeb_	Alignment		98.9	21	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
20	c4g9qA_	Alignment		98.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of a 4-carboxymuconolactone decarboxylase
21	d1knca_	Alignment	not modelled	98.8	12	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
22	c5gzxD_	Alignment	not modelled	98.3	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**(r)-2-haloacid dehalogenase; **PDBTitle:** the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
23	d2af7a1	Alignment	not modelled	97.8	29	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
24	d1a9xa1	Alignment	not modelled	87.2	14	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
25	d2p7vb1	Alignment	not modelled	56.1	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
26	d1ngra_	Alignment	not modelled	47.4	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
27	c5dotA_	Alignment	not modelled	44.0	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase [ammonia], mitochondrial; **PDBTitle:** crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
28	c6ac5A_	Alignment	not modelled	43.5	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**receptor-interacting serine/threonine-protein kinase 1; **PDBTitle:** crystal structure of ripk1 death domain glcnacylated by

						epec effector2 nleb
29	c5douC_	Alignment	not modelled	38.8	9	**PDB header:**ligase **Chain:** C: **PDB Molecule:**carbamoyl-phosphate synthase [ammonia], mitochondrial; **PDBTitle:** crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
30	c4wt3A_	Alignment	not modelled	37.6	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**rubisco accumulation factor 1, isoform 2; **PDBTitle:** the n-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana
31	c1m6vE_	Alignment	not modelled	37.0	14	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
32	d1ddfa_	Alignment	not modelled	36.9	9	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
33	c4o6xA_	Alignment	not modelled	35.2	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-3; **PDBTitle:** crystal structure of human ankyrin g death domain
34	c2ib1A_	Alignment	not modelled	35.1	12	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
35	d1khda1	Alignment	not modelled	35.0	9	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
36	c1ichA_	Alignment	not modelled	26.6	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
37	d1icha_	Alignment	not modelled	26.6	13	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
38	d1fada_	Alignment	not modelled	25.3	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
39	c4n2xF_	Alignment	not modelled	25.0	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**dl-2-haloacid dehalogenase; **PDBTitle:** crystal structure of dl-2-haloacid dehalogenase
40	c1wxpA_	Alignment	not modelled	24.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
41	c2yqfA_	Alignment	not modelled	23.3	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
42	c6mtgB_	Alignment	not modelled	23.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
43	d1ttya_	Alignment	not modelled	23.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
44	d1ku3a_	Alignment	not modelled	22.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
45	c3oq9C_	Alignment	not modelled	22.0	7	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** structure of the fas/fadd death domain assembly
46	c2of5A_	Alignment	not modelled	20.2	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
47	c3k2zA_	Alignment	not modelled	18.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
48	d1p4wa_	Alignment	not modelled	18.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
49	c2k8sA_	Alignment	not modelled	17.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europea: northeast structural3 genomics target net6
50	d1ku7a_	Alignment	not modelled	17.5	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
51	c3t72o_	Alignment	not modelled	17.3	17	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
52	c3gmfA_	Alignment	not modelled	16.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
53	c3t5vC_	Alignment	not modelled	15.9	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**26s proteasome complex subunit sem1; **PDBTitle:** sac3:thp1:sem1 complex

54	c3dvwA_	Alignment	not modelled	15.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
55	c2of5K_	Alignment	not modelled	15.1	15	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing protein; **PDBTitle:** oligomeric death domain complex
56	c2k9lA_	Alignment	not modelled	15.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
57	d1brwa1	Alignment	not modelled	14.7	14	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
58	c3f4tA_	Alignment	not modelled	14.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
59	c5lc5E_	Alignment	not modelled	13.9	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nadh dehydrogenase [ubiquinone] flavoprotein 2, **PDBTitle:** structure of mammalian respiratory complex i, class2
60	c3bjxB_	Alignment	not modelled	13.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
61	c3l9vE_	Alignment	not modelled	13.8	11	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
62	d1o17a1	Alignment	not modelled	13.8	14	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
63	d1uoua1	Alignment	not modelled	13.6	7	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
64	c3bciA_	Alignment	not modelled	13.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond protein a; **PDBTitle:** crystal structure of staphylococcus aureus dsba
65	d1v8ga1	Alignment	not modelled	13.5	7	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
66	c1t3bA_	Alignment	not modelled	13.3	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
67	d1smyf2	Alignment	not modelled	13.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
68	d1t3ba1	Alignment	not modelled	12.6	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
69	d2gf5a1	Alignment	not modelled	12.5	14	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
70	c2k9mA_	Alignment	not modelled	12.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
71	c4npbA_	Alignment	not modelled	11.6	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide isomerase ii; **PDBTitle:** the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
72	c3c7mB_	Alignment	not modelled	11.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiol:disulfide interchange protein dsba-like; **PDBTitle:** crystal structure of reduced dsbl
73	c1v57A_	Alignment	not modelled	10.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
74	c4igcX_	Alignment	not modelled	10.6	23	**PDB header:**transcription, transferase **Chain:** X: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** x-ray crystal structure of escherichia coli sigma70 holoenzyme
75	c1jzdA_	Alignment	not modelled	10.3	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
76	d1x4pa1	Alignment	not modelled	10.0	13	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
77	c3hd5A_	Alignment	not modelled	9.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
78	c4k2dA_	Alignment	not modelled	9.9	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein; **PDBTitle:** crystal structure of burkholderia pseudomallei dsba
						PDB header:oxidoreductase

79	c4nxiB_	Alignment	not modelled	9.8	18	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** rv2466c mediates the activation of tp053 to kill replicating and non-2 replicating mycobacterium tuberculosis
80	c1a6bB_	Alignment	not modelled	9.7	33	**PDB header:**viral protein/dna **Chain:** B: **PDB Molecule:**zinc finger protein ncp10; **PDBTitle:** nmr structure of the complex between the zinc finger2 protein ncp10 of moloney murine leukemia virus and a3 sequence of the psi-packaging domain of hiv-1, 204 structures
81	c4ml1D_	Alignment	not modelled	9.7	8	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dsbp; **PDBTitle:** disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
82	c4xvwK_	Alignment	not modelled	9.6	17	**PDB header:**isomerase **Chain:** K: **PDB Molecule:**dsba-like protein; **PDBTitle:** crystal structure of proteus mirabilis scsc in a compact conformation
83	d2tpta1	Alignment	not modelled	9.5	7	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
84	c1x4pA_	Alignment	not modelled	9.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative splicing factor, arginine/serine-rich **PDBTitle:** solution structure of surp domain in sfrs14 protei
85	c3wodF_	Alignment	not modelled	9.1	22	**PDB header:**transferase/transcription **Chain:** F: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** rna polymerase-gp39 complex
86	c4n30A_	Alignment	not modelled	9.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein disulfide isomerase; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba2
87	c3iydF_	Alignment	not modelled	9.0	20	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
88	c5tw1F_	Alignment	not modelled	8.9	22	**PDB header:**transcription activator/transferase/dna **Chain:** F: **PDB Molecule:**rna polymerase sigma factor siga; **PDBTitle:** crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
89	c2ev2B_	Alignment	not modelled	8.8	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
90	c1vquB_	Alignment	not modelled	8.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
91	c6c05F_	Alignment	not modelled	8.8	20	**PDB header:**transcription **Chain:** F: **PDB Molecule:**rna polymerase sigma factor siga; **PDBTitle:** mycobacterium tuberculosis rnap holo/rbpa in relaxed state
92	c5hfiA_	Alignment	not modelled	8.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein, cytosolic disulfide reductase **PDBTitle:** cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
93	d1beda_	Alignment	not modelled	8.7	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
94	c3h93A_	Alignment	not modelled	8.7	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
95	c3gv1A_	Alignment	not modelled	8.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
96	c4k90A_	Alignment	not modelled	8.5	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extracellular metalloproteinase mep; **PDBTitle:** extracellular metalloproteinase from aspergillus
97	c3msuA_	Alignment	not modelled	8.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
98	d1eeja1	Alignment	not modelled	8.4	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
99	c3o0rC_	Alignment	not modelled	8.3	17	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment