Phyre^2

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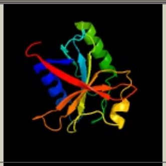
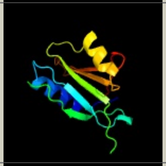
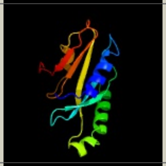
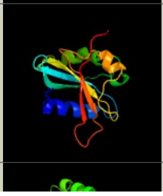
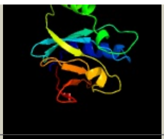
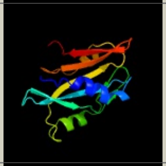
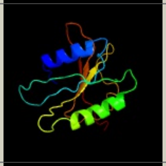
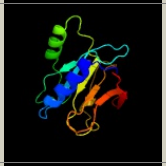
Description	RVBD1334_(-)_1502647_1503087
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	f70b03e7a0504096

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kksA_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein dsy2949 from desulfitobacterium2 hafniense. northeast structural genomics consortium target dhr27
2	c2kcqA_	Alignment		100.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mov34/mpn/pad-1 family; **PDBTitle:** solution structure of protein sru_2040 from salinibacter2 ruber (strain dsm 13855) . northeast structural genomics3 consortium target srr106
3	c5ld9B_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**jamm1; **PDBTitle:** structure of deubiquitinating enzyme homolog, pyrococcus furiosus2 jamm1.
4	c5cw6A_	Alignment		100.0	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**drbrcc36; **PDBTitle:** structure of metal dependent enzyme drbrcc36
5	d1oi0a_	Alignment		99.9	24	**Fold:**Cytidine deaminase-like **Superfamily:**JAB1/MPN domain **Family:**JAB1/MPN domain
6	c6fnnB_	Alignment		99.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**26s proteasome regulatory subunit n11-like protein; **PDBTitle:** caldiarchaeum subterraneum ubiquitin:rpn11-homolog complex
7	c6r8fA_	Alignment		99.9	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lys-63-specific deubiquitinase brcc36; **PDBTitle:** cryo-em structure of the human brisc-shmt2 complex
8	c6fjuA_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit n11-like protein; **PDBTitle:** rpn11 homolog from caldiarchaeum subterraneum
9	c5cw4C_	Alignment		99.9	16	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**brca1/brca2-containing complex subunit 3; **PDBTitle:** structure of cfbrcc36-cfkiaa0157 complex (selenium edge)
10	c4b4tV_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** V: **PDB Molecule:**26s proteasome regulatory subunit rpn11; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
11	c4d18E_	Alignment		99.9	19	**PDB header:**signaling protein **Chain:** E: **PDB Molecule:**cop9 signalosome complex subunit 5; **PDBTitle:** crystal structure of the cop9 signalosome
						

12	c5gjqV_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** V: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 14; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal
13	c2znrA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amsh-like protease; **PDBTitle:** crystal structure of the dub domain of human amsh-lp
14	c4k1rA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amsh-like protease sst2; **PDBTitle:** crystal structure of schizosaccharomyces pombe sst2 catalytic domain2 and ubiquitin
15	c4f7oB_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cop9 signalosome complex subunit 5; **PDBTitle:** crystal structure of csn5
16	c3j7kH_	Alignment		99.7	18	**PDB header:**translation **Chain:** H: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit h; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s em map
17	c3j7jH_	Alignment		99.7	18	**PDB header:**translation **Chain:** H: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit h; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
18	c3j8cH_	Alignment		99.7	18	**PDB header:**translation **Chain:** H: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit h; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s em map
19	c3j8bH_	Alignment		99.7	18	**PDB header:**translation **Chain:** H: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit h; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
20	c5a5tH_	Alignment		99.6	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit h; **PDBTitle:** structure of mammalian eif3 in the context of the 43s preinitiation2 complex
21	c2p87A_	Alignment	not modelled	99.4	17	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor prp8; **PDBTitle:** crystal structure of the c-terminal domain of c. elegans2 pre-mrna splicing factor prp8
22	c4kitC_	Alignment	not modelled	99.4	15	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**pre-mrna-processing-splicing factor 8; **PDBTitle:** crystal structure of human brr2 in complex with the prp8 jab1/mpn2 domain
23	c2og4A_	Alignment	not modelled	99.4	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** structure of an expanded jab1-mpn-like domain of splicing factor prp8p2 from yeast
24	c2o95A_	Alignment	not modelled	99.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 7; **PDBTitle:** crystal structure of the metal-free dimeric human mov34 mpn domain2 (residues 1-186)
25	c5m59F_	Alignment	not modelled	99.3	15	**PDB header:**splicing **Chain:** F: **PDB Molecule:**putative pre-mrna splicing factor; **PDBTitle:** crystal structure of chaetomium thermophilum brr2 helicase core in2 complex with prp8 jab1 domain
26	c3sbgA_	Alignment	not modelled	99.3	12	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** crystal structure of a prp8 c-terminal fragment
27	c4cr4U_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** U: **PDB Molecule:**26s proteasome regulatory subunit rpn8; **PDBTitle:** deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
28	c4b4tU_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** U: **PDB Molecule:**26s proteasome regulatory subunit rpn8; **PDBTitle:** near-atomic resolution structural model of the yeast 26s proteasome
						PDB header:signaling protein

29	c4d18F_	Alignment	not modelled	99.2	10	**Chain:** F: **PDB Molecule:**cop9 signalosome complex subunit 6; **PDBTitle:** crystal structure of the cop9 signalosome
30	c5a5tF_	Alignment	not modelled	99.1	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit f; **PDBTitle:** structure of mammalian eif3 in the context of the 43s preinitiation2 complex
31	c5gjqU_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** U: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 7; **PDBTitle:** structure of the human 26s proteasome bound to usp14-ubal
32	c3j8bF_	Alignment	not modelled	98.9	14	**PDB header:**translation **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit f; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
33	c3j7kF_	Alignment	not modelled	98.9	14	**PDB header:**translation **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit f; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s em map
34	c3j8cF_	Alignment	not modelled	98.9	14	**PDB header:**translation **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit f; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s em map
35	c3j7jF_	Alignment	not modelled	98.9	14	**PDB header:**translation **Chain:** F: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit f; **PDBTitle:** model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
36	c4e0qB_	Alignment	not modelled	98.9	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cop9 signalosome complex subunit 6; **PDBTitle:** crystal structure of mpn domain from cop9 signalosome
37	c5m32n_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**proteasome subunit beta type-6; **PDBTitle:** human 26s proteasome in complex with oprozomib
38	c6cddB_	Alignment	not modelled	97.6	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**npl4 zinc finger; **PDBTitle:** npl4 zinc finger and mpn domains (chaetomium thermophilum)
39	c4i43B_	Alignment	not modelled	97.4	13	**PDB header:**splicing **Chain:** B: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** crystal structure of prp8:aar2 complex
40	c5z58A_	Alignment	not modelled	97.4	18	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-processing-splicing factor 8; **PDBTitle:** cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
41	c6oa9G_	Alignment	not modelled	97.4	13	**PDB header:**motor protein **Chain:** G: **PDB Molecule:**nuclear protein localization protein 4; **PDBTitle:** cdc48-npl4 complex processing poly-ubiquitinated substrate in the2 presence of atp
42	c3jcrA_	Alignment	not modelled	97.4	17	**PDB header:**splicing **Chain:** A: **PDB Molecule:**hprp8; **PDBTitle:** 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
43	c6oaaG_	Alignment	not modelled	97.3	14	**PDB header:**motor protein **Chain:** G: **PDB Molecule:**nuclear protein localization protein 4; **PDBTitle:** cdc48-npl4 complex processing poly-ubiquitinated substrate in the2 presence of adp-befx, state 1
44	c5lj5A_	Alignment	not modelled	97.0	15	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** overall structure of the yeast spliceosome immediately after2 branching.
45	c6gvwF_	Alignment	not modelled	96.9	16	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**brca1-a complex subunit abraxas 1; **PDBTitle:** crystal structure of the brca1-a complex
46	c5ganA_	Alignment	not modelled	96.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
47	c5lqwA_	Alignment	not modelled	96.4	15	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 8; **PDBTitle:** yeast activated spliceosome
48	c6r8fD_	Alignment	not modelled	96.4	15	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**brisc complex subunit abraxas 2; **PDBTitle:** cryo-em structure of the human brisc-shmt2 complex
49	c5cw5D_	Alignment	not modelled	95.9	11	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**protein fam175b; **PDBTitle:** structure of cfbrcc36-cfkiaa0157 complex (qsq mutant)
50	c2qlcC_	Alignment	not modelled	95.4	13	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein radc homolog; **PDBTitle:** the crystal structure of dna repair protein radc from chlorobium2 tepidum tls
51	d1knwa2	Alignment	not modelled	53.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
52	c5bwaA_	Alignment	not modelled	39.6	7	**PDB header:**lyase/lyase inhibitor **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure of odc-plp-az1 ternary complex
53	c1knwA_	Alignment	not modelled	25.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
						PDB header:plp-binding protein

54	c1w8gA_	Alignment	not modelled	22.8	11	**Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
55	c5nm8A_	Alignment	not modelled	21.5	7	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**pipy; **PDBTitle:** structure of pipy, the cog0325 family member of synechococcus2 elongatus pcc7942, with plp bound
56	d1gska1	Alignment	not modelled	20.0	38	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
57	c2qghA_	Alignment	not modelled	19.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
58	d1x87a_	Alignment	not modelled	19.0	10	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
59	c6hbeA_	Alignment	not modelled	17.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper-containing nitrite reductase; **PDBTitle:** cu-containing nitrite reductase (nirk) from thermus scotoductus sa-01
60	c3aw5A_	Alignment	not modelled	17.3	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**multicopper oxidase; **PDBTitle:** structure of a multicopper oxidase from the hyperthermophilic archaeon2 pyrobaculum aerophilum
61	c1njjC_	Alignment	not modelled	17.2	6	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine decarboxylase2 bound to d-ornithine and to g418
62	c6evgA_	Alignment	not modelled	16.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**multi-copper oxidase cueo; **PDBTitle:** structural and functional characterisation of a bacterial laccase-like2 multi-copper oxidase cueo from lignin-degrading bacterium3 ochrobactrum sp. with oxidase activity towards lignin model compounds4 and lignosulfonate
63	d7odca2	Alignment	not modelled	16.8	3	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
64	c2fknC_	Alignment	not modelled	16.4	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
65	c3zx1A_	Alignment	not modelled	16.2	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** multicopper oxidase from campylobacter jejuni: a metallo-oxidase
66	d2isya2	Alignment	not modelled	16.0	8	**Fold:**Iron-dependent repressor protein, dimerization domain **Superfamily:**Iron-dependent repressor protein, dimerization domain **Family:**Iron-dependent repressor protein, dimerization domain
67	c3cdzA_	Alignment	not modelled	15.5	60	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
68	d1uwka_	Alignment	not modelled	15.5	17	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
69	d2j5wa4	Alignment	not modelled	14.0	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
70	d1g01a_	Alignment	not modelled	14.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
71	c5zl1A_	Alignment	not modelled	13.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper-type nitrite reductase; **PDBTitle:** hexameric structure of copper-containing nitrite reductase of an2 anammox organism ksu-1
72	c4xg1C_	Alignment	not modelled	13.8	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** psychromonas ingrahamii diaminopimelate decarboxylase with llp
73	c5gjmB_	Alignment	not modelled	13.7	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal strcuture of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
74	d1sddb1	Alignment	not modelled	13.5	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
75	c4kbxA_	Alignment	not modelled	13.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yhfx; **PDBTitle:** crystal structure of the pyridoxal-5'-phosphate dependent protein yhfx2 from escherichia coli
76	c4eyzB_	Alignment	not modelled	13.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cellulosome-related protein module from ruminococcus **PDBTitle:** crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
77	c3abgA_	Alignment	not modelled	13.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bilirubin oxidase; **PDBTitle:** x-ray crystal analysis of bilirubin oxidase from myrothecium2 verrucaria at 2.3 angstrom resolution using a twin crystal
78	c4eclA_	Alignment	not modelled	12.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**serine racemase; **PDBTitle:** crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
79	c2fqeA_	Alignment	not modelled	12.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**blue copper oxidase cueo;

79		Alignment	not modelled			**PDBTitle:** crystal structures of e. coli laccase cueo under different copper2 binding situations
80	d1mzya1	Alignment	not modelled	12.4	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
81	d1kv7a1	Alignment	not modelled	12.4	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
82	c2g23G_	Alignment	not modelled	12.3	60	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**phenoxazinone synthase; **PDBTitle:** the crystal structure of hexameric phenoxazinone synthase
83	c3n2bD_	Alignment	not modelled	12.0	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
84	c5l20A_	Alignment	not modelled	11.4	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**clostripain-related protein; **PDBTitle:** crystal structure of a clostripain (bt_0727) from bacteroides2 thetaiotaomicron atcc 29148 in complex with peptide inhibitor btn-3 vltk-aomk
85	c1zpuE_	Alignment	not modelled	11.2	80	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3; **PDBTitle:** crystal structure of fet3p, a multicopper oxidase that functions in2 iron import
86	c3ppsD_	Alignment	not modelled	11.2	80	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of an ascomycete fungal laccase from thielavia2 arenaria
87	c1wa1X_	Alignment	not modelled	11.1	22	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite reductase; **PDBTitle:** crystal structure of h313q mutant of alcaligenes xylosoxidans nitrite2 reductase
88	c2xllC_	Alignment	not modelled	11.0	38	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**bilirubin oxidase; **PDBTitle:** the crystal structure of bilirubin oxidase from myrothecium2 verrucaria
89	d2v94a1	Alignment	not modelled	10.9	57	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
90	c2q9oA_	Alignment	not modelled	10.7	80	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase-1; **PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase
91	c3izbU_	Alignment	not modelled	10.5	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
92	c5lwxA_	Alignment	not modelled	9.4	80	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**multicopper oxidase; **PDBTitle:** crystal structure of the h253d mutant of mcog from aspergillus niger
93	d1sdda1	Alignment	not modelled	8.9	38	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
94	d2q9oa1	Alignment	not modelled	8.9	80	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
95	d1hfua1	Alignment	not modelled	8.8	80	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
96	c1mzzC_	Alignment	not modelled	8.7	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper-containing nitrite reductase; **PDBTitle:** crystal structure of mutant (m182t)of nitrite reductase
97	c5dynA_	Alignment	not modelled	8.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** b. fragilis cysteine protease
98	c1gycA_	Alignment	not modelled	8.6	80	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase 2; **PDBTitle:** crystal structure determination at room temperature of a laccase from2 trametes versicolor in its oxidised form containing a full complement3 of copper ions
99	d1aoza1	Alignment	not modelled	8.5	60	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins