Phyre2

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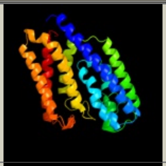
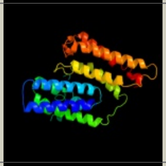
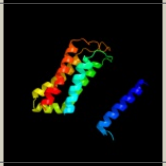
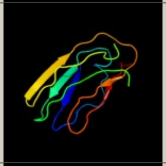
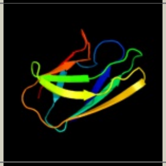
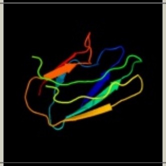
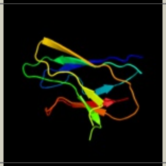
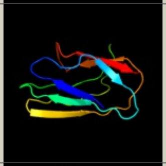
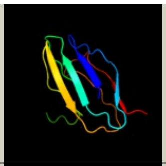
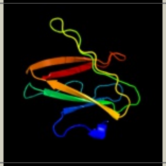
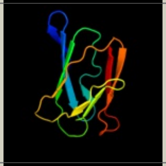
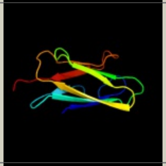
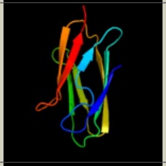
Description	P0AB24
Date	Thu Jan 5 11:14:26 GMT 2012
Unique Job ID	1f686c97f59a85cb

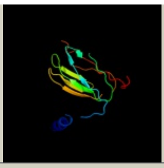
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3at7B_	Alignment		100.0	61	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**alginate-binding flagellin; **PDBTitle:** crystal structure of bacterial cell-surface alginate-binding protein2 algp7
2	c3pf0A_	Alignment		100.0	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**imelysin-like protein; **PDBTitle:** crystal structure of an imelysin-like protein (psyc_1802) from2 psychrobacter arcticum 273-4 at 2.15 a resolution
3	c3n8uB_	Alignment		99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**imelysin peptidase; **PDBTitle:** crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
4	c2h47C_	Alignment		99.2	22	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**azurin; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
5	d2ccwa1	Alignment		99.2	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
6	d1jzga_	Alignment		99.1	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
7	d1cuoa_	Alignment		99.1	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
8	d1joia_	Alignment		99.1	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
9	d1nwpa_	Alignment		99.1	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
10	d1rkra_	Alignment		99.1	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
11	d1cc3a_	Alignment		99.0	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like

12	d1azca_	Alignment		99.0	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
13	d2ov0a1	Alignment		99.0	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
14	d1id2a_	Alignment		99.0	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
15	c3c75B_	Alignment		99.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amicyanin; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
16	d2cuaa_	Alignment		98.9	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
17	d1qnia1	Alignment		98.8	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
18	c2aanA_	Alignment		98.7	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**auracyanin a; **PDBTitle:** auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium,chloroflexus aurantiacus
19	d1fwxa1	Alignment		98.7	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
20	d1qhqa_	Alignment		98.7	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
21	d1bxua_	Alignment	not modelled	98.6	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
22	d2cuab_	Alignment	not modelled	98.6	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
23	c1xmeB_	Alignment	not modelled	98.5	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
24	d2cj3a1	Alignment	not modelled	98.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
25	d1ibya_	Alignment	not modelled	98.5	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
26	d1pcsa_	Alignment	not modelled	98.4	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
27	d2q5ba1	Alignment	not modelled	98.3	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
28	d7pcya_	Alignment	not modelled	98.3	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
29	d2plta_	Alignment	not modelled	98.2	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins

						Family: Plastocyanin/azurin-like
30	d1plaa_	Alignment	not modelled	98.2	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
31	c2iwkB_	Alignment	not modelled	98.2	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** inhibitor-bound form of nitrous oxide reductase from2 achromobacter cycloclastes at 1.7 angstrom resolution
32	d1paza_	Alignment	not modelled	98.2	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
33	d2jxma1	Alignment	not modelled	98.2	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
34	d9pcya_	Alignment	not modelled	98.2	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
35	d1iuza_	Alignment	not modelled	98.1	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
36	d1plca_	Alignment	not modelled	98.1	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
37	c3sbrF_	Alignment	not modelled	98.1	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
38	d1ag6a_	Alignment	not modelled	98.1	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
39	d1bypa_	Alignment	not modelled	98.1	23	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
40	d1pmya_	Alignment	not modelled	98.1	11	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
41	d1kdja_	Alignment	not modelled	98.0	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
42	d1adwa_	Alignment	not modelled	97.9	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
43	c3ef4A_	Alignment	not modelled	97.8	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**blue copper protein; **PDBTitle:** crystal structure of native pseudoazurin from2 hyphomicrobium denitrificans
44	d1bqka_	Alignment	not modelled	97.8	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
45	c1qniE_	Alignment	not modelled	97.8	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from2 pseudomonas nautica, at 2.4a resolution
46	c1fwxB_	Alignment	not modelled	97.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrous oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from p. denitrificans
47	d1fftb1	Alignment	not modelled	96.9	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
48	d1e30a_	Alignment	not modelled	96.9	25	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
49	d3ehbb1	Alignment	not modelled	96.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
50	c1cyxA_	Alignment	not modelled	96.5	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cyoa; **PDBTitle:** quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
51	d1cyxa_	Alignment	not modelled	96.5	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
52	d1v54b1	Alignment	not modelled	96.5	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
53	c1ar1B_	Alignment	not modelled	96.2	18	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
54	d3dtub1	Alignment	not modelled	96.1	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
55	d1sddb2	Alignment	not modelled	95.9	6	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	c3gdcC_	Alignment	not modelled	95.8	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**multicopper oxidase;

						PDBTitle: crystal structure of multicopper oxidase
57	c2dv6F_	Alignment	not modelled	95.8	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from hyphomicrobium2 denitrificans
58	d2j5wa2	Alignment	not modelled	95.7	14	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
59	d1snra2	Alignment	not modelled	95.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
60	c1v55B_	Alignment	not modelled	95.6	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** bovine heart cytochrome c oxidase at the fully reduced state
61	d1kcwa2	Alignment	not modelled	95.3	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
62	c1m57H_	Alignment	not modelled	95.2	15	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
63	c1qleB_	Alignment	not modelled	95.2	18	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
64	d1kbva2	Alignment	not modelled	95.1	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
65	c1kbwA_	Alignment	not modelled	94.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**major outer membrane protein pan 1; **PDBTitle:** crystal structure of the soluble domain of ania from2 neisseria gonorrhoeae
66	c3isyA_	Alignment	not modelled	94.8	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
67	c3cdzB_	Alignment	not modelled	94.8	9	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii light chain; **PDBTitle:** crystal structure of human factor viii
68	d1ndsa2	Alignment	not modelled	94.8	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
69	d1nqjb_	Alignment	not modelled	94.4	13	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
70	c1aq8B_	Alignment	not modelled	94.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrite reductase; **PDBTitle:** structure of alcaligenes faecalis nitrite reductase reduced2 with ascorbate
71	c2x41A_	Alignment	not modelled	94.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
72	d2bw4a2	Alignment	not modelled	94.3	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
73	d2j5wa5	Alignment	not modelled	94.1	13	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
74	d1snra1	Alignment	not modelled	94.0	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
75	c1sddB_	Alignment	not modelled	93.9	5	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
76	d1w8oa1	Alignment	not modelled	93.9	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
77	c1mzzC_	Alignment	not modelled	93.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper-containing nitrite reductase; **PDBTitle:** crystal structure of mutant (m182t)of nitrite reductase
78	c3jqxA_	Alignment	not modelled	93.4	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**colh protein; **PDBTitle:** crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cadmium
79	c2r7eB_	Alignment	not modelled	93.4	9	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii; **PDBTitle:** crystal structure analysis of coagulation factor viii
80	c3rgbA_	Alignment	not modelled	92.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
81	c1yewI_	Alignment	not modelled	92.7	24	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
82	c2zooA_	Alignment	not modelled	92.6	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125

83	c1fftG_	Alignment		92.5	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
84	d1oe1a1	Alignment	not modelled	92.5	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
85	d1ndsa1	Alignment	not modelled	92.4	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
86	c3g5wC_	Alignment	not modelled	92.4	12	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**multicopper oxidase type 1; **PDBTitle:** crystal structure of blue copper oxidase from nitrosomonas europaea
87	d1v10a2	Alignment	not modelled	92.3	20	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
88	d1mzya2	Alignment	not modelled	92.1	17	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
89	d1kyaa2	Alignment	not modelled	91.9	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
90	c2kl6A_	Alignment	not modelled	91.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
91	d1kbva1	Alignment	not modelled	91.8	22	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
92	d1aoza2	Alignment	not modelled	91.7	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
93	c2xu9A_	Alignment	not modelled	91.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** crystal structure of laccase from thermus thermophilus hb27
94	d2bw4a1	Alignment	not modelled	91.7	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
95	c3cg8B_	Alignment	not modelled	91.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**laccase; **PDBTitle:** laccase from streptomyces coelicolor
96	d1mzya1	Alignment	not modelled	91.4	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
97	d1gyca2	Alignment	not modelled	91.2	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
98	c1v10A_	Alignment	not modelled	91.2	21	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**laccase; **PDBTitle:** structure of rigidoporus lignosus laccase from hemihedrally2 twinned crystals
99	d1hfua2	Alignment	not modelled	91.2	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
100	c3kw8A_	Alignment	not modelled	91.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
101	c2zwnA_	Alignment	not modelled	90.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**two-domain type laccase; **PDBTitle:** crystal structure of the novel two-domain type laccase from a2 metagenome
102	c1kcwA_	Alignment	not modelled	89.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ceruloplasmin; **PDBTitle:** x-ray crystal structure of human ceruloplasmin at 3.0 angstroms
103	d1io1a_	Alignment	not modelled	88.9	11	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
104	c2qsvA_	Alignment	not modelled	88.6	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
105	c1gycA_	Alignment	not modelled	88.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase 2; **PDBTitle:** crystal structure determination at room temperature of a2 laccase from trametes versicolor in its oxidised form3 containing a full complement of copper ions
106	c1wa1X_	Alignment	not modelled	88.0	19	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
107	d1kv7a1	Alignment	not modelled	87.7	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
						PDB header:oxidoreductase

108	c1of0A_	Alignment	not modelled	87.5	20	**Chain:** A: **PDB Molecule:**spore coat protein a; **PDBTitle:** crystal structure of bacillus subtilis cota after 1h2 soaking with ebs
109	c2uxtA_	Alignment	not modelled	87.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein sufi; **PDBTitle:** sufi protein from escherichia coli
110	d1yq2a1	Alignment	not modelled	87.4	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
111	c3ac0B_	Alignment	not modelled	86.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
112	c2ys4A_	Alignment	not modelled	84.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydrocephalus-inducing protein homolog; **PDBTitle:** solution structure of the n-terminal papd-like domain of2 hydin protein from human
113	d1m1sa_	Alignment	not modelled	83.2	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
114	c3payB_	Alignment	not modelled	82.6	13	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**putative adhesin; **PDBTitle:** crystal structure of a putative adhesin (bacova_04077) from2 bacteroides ovatus at 2.50 a resolution
115	d1x9la_	Alignment	not modelled	82.1	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
116	c3rfrI_	Alignment	not modelled	81.8	19	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**pmob; **PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
117	d1sdda1	Alignment	not modelled	81.6	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
118	d1gska3	Alignment	not modelled	81.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
119	c2q9oA_	Alignment	not modelled	81.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**laccase-1; **PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase
120	c3gf8A_	Alignment	not modelled	80.6	12	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**putative polysaccharide binding proteins (duf1812); **PDBTitle:** crystal structure of putative polysaccharide binding proteins2 (duf1812) (np_809975.1) from bacteroides thetaiotaomicron vpi-5482 at3 2.20 a resolution