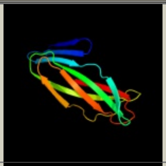
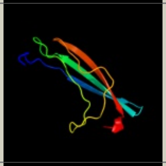
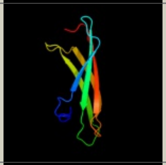
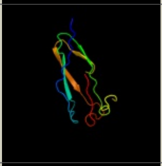
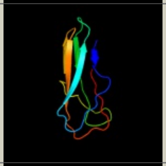
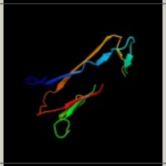
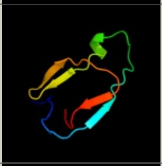
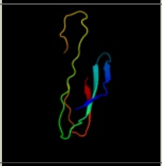
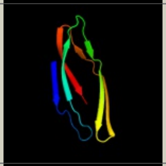
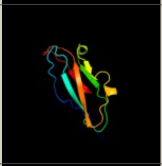
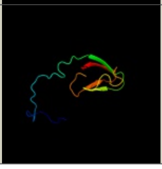
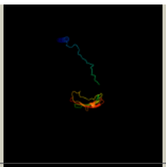
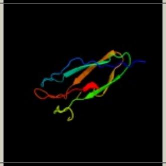
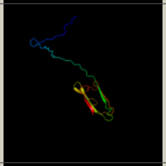
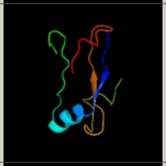
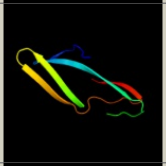
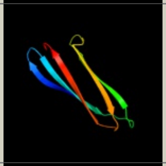
Email	l.a.kelley@imperial.ac.uk
Description	P75946
Date	Thu Jan 5 12:16:17 GMT 2012
Unique Job ID	127f737c8d731093

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o0lB_	Alignment		100.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
2	d2vzsa2	Alignment		91.2	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
3	c3fn9B_	Alignment		85.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
4	d2co7b1	Alignment		85.1	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
5	d3bwuc1	Alignment		82.8	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
6	c3isyA_	Alignment		77.8	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
7	d1lm8v_	Alignment		77.5	20	**Fold:**Prealbumin-like **Superfamily:**VHL **Family:**VHL
8	c2x41A_	Alignment		76.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
9	c3butA_	Alignment		71.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_0446; **PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus
10	d1p5va1	Alignment		62.4	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
11	c1e9zA_	Alignment		59.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease

12	c3rgbA_	Alignment		59.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase subunit b2; **PDBTitle:** crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
13	c2co7B_	Alignment		59.4	11	**PDB header:**fibril protein **Chain:** B: **PDB Molecule:**putative fimbriae assembly chaperone; **PDBTitle:** salmonella enterica safa pilin in complex with the safb2 chaperone (type ii)
14	c1s3rA_	Alignment		57.7	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**intermedilysin; **PDBTitle:** crystal structure of the human-specific toxin intermedilysin
15	c3cfuA_	Alignment		56.7	13	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha; **PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562
16	c1yycA_	Alignment		54.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein; **PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
17	d2je8a1	Alignment		53.1	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
18	c3ac0B_	Alignment		52.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
19	c2kl6A_	Alignment		51.3	12	**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
20	c1z9sA_	Alignment		50.7	11	**PDB header:**chaperone/immune system **Chain:** A: **PDB Molecule:**chaperone protein caf1m; **PDBTitle:** crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
21	c2xfgB_	Alignment	not modelled	47.7	11	**PDB header:**hydrolase/sugar binding protein **Chain:** B: **PDB Molecule:**endoglucanase 1; **PDBTitle:** reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
22	c2xbtA_	Alignment	not modelled	46.1	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin; **PDBTitle:** structure of a scaffoldin carbohydrate-binding module family 3b from2 the cellulosome of bacteroides cellulosolvens: structural diversity3 and implications for carbohydrate binding
23	d2j2za1	Alignment	not modelled	45.2	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
24	c3qgaD_	Alignment	not modelled	43.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
25	d1pfoa_	Alignment	not modelled	42.3	19	**Fold:**Perfringolysin **Superfamily:**Perfringolysin **Family:**Perfringolysin
26	c1pfoA_	Alignment	not modelled	42.3	19	**PDB header:**toxin **Chain:** A: **PDB Molecule:**perfringolysin o; **PDBTitle:** perfringolysin o
27	d1xo8a_	Alignment	not modelled	42.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**LEA14-like **Family:**LEA14-like
28	c3q48B_	Alignment	not modelled	41.7	9	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone cupb2; **PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2

						chaperone
29	d1jz8a2	Alignment	not modelled	38.3	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
30	c3hs0B_	Alignment	not modelled	33.5	19	**PDB header:**immune system **Chain:** B: **PDB Molecule:**cobra venom factor; **PDBTitle:** cobra venom factor (cvf) in complex with human factor b
31	c3cu7A_	Alignment	not modelled	33.0	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**complement c5; **PDBTitle:** human complement component 5
32	c2ys4A_	Alignment	not modelled	32.8	10	**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
33	c3hvnA_	Alignment	not modelled	32.7	16	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of cytotoxin protein suilysin from2 streptococcus suis
34	d1cyga2	Alignment	not modelled	32.0	17	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
35	d1qhoa2	Alignment	not modelled	31.9	17	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
36	d1yq2a1	Alignment	not modelled	31.1	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
37	d1i5pa1	Alignment	not modelled	31.0	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
38	c1skhA_	Alignment	not modelled	30.6	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**major prion protein 2; **PDBTitle:** n-terminal (1-30) of bovine prion protein
39	c2c3wB_	Alignment	not modelled	30.4	22	**PDB header:**sugar-binding protein **Chain:** B: **PDB Molecule:**alpha-amylase g-6; **PDBTitle:** structure of cbm25 from bacillus halodurans amylase in2 complex with maltotetraose
40	d1l4ia1	Alignment	not modelled	29.4	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**Pilus chaperone
41	d1ejxb_	Alignment	not modelled	28.4	7	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
42	c2f3xA_	Alignment	not modelled	28.4	9	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcription factor fapr; **PDBTitle:** crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
43	d4ubpb_	Alignment	not modelled	28.1	4	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
44	d1nbca_	Alignment	not modelled	27.5	14	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
45	c2e6jA_	Alignment	not modelled	27.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hydin protein; **PDBTitle:** solution structure of the c-terminal papd-like domain from2 human hydin protein
46	c2je8B_	Alignment	not modelled	25.3	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron
47	c2l8aA_	Alignment	not modelled	24.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** structure of a novel cbm3 lacking the calcium-binding site
48	c1l4iA_	Alignment	not modelled	23.5	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sfae protein; **PDBTitle:** crystal structure of the periplasmic chaperone sfae
49	d2j5wa3	Alignment	not modelled	23.1	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
50	c2w5fB_	Alignment	not modelled	23.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-1,4-beta-xylanase y; **PDBTitle:** high resolution crystallographic structure of the2 clostridium thermocellum n-terminal endo-1,4-beta-d-3 xylanase 10b (xyn10b) cbm22-1-gh10 modules complexed with4 xylohexaose
51	d2q0zx2	Alignment	not modelled	22.8	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Sec63 C-terminal domain-like
52	c2q0zX_	Alignment	not modelled	22.4	16	**PDB header:**protein transport **Chain:** X: **PDB Molecule:**protein pro2281; **PDBTitle:** crystal structure of q9p172/sec63 from homo sapiens.2 northeast structural genomics target hr1979.
53	d1e9ya1	Alignment	not modelled	22.4	10	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
54	c3hftA_	Alignment	not modelled	19.8	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide

						deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
55	c1qunA_	Alignment	not modelled	19.2	11	**PDB header:**chaperone/structural protein **Chain:** A: **PDB Molecule:**papd-like chaperone fimc; **PDBTitle:** x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli
56	d1lgta2	Alignment	not modelled	19.1	29	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
57	d1aoza2	Alignment	not modelled	19.1	9	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
58	c1sddA_	Alignment	not modelled	17.0	11	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
59	d2je8a3	Alignment	not modelled	16.4	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
60	c3qbtH_	Alignment	not modelled	15.6	18	**PDB header:**protein transport/hydrolase **Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp
61	d1kula_	Alignment	not modelled	15.0	16	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**Starch-binding domain
62	c2x3bB_	Alignment	not modelled	14.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**toxic extracellular endopeptidase; **PDBTitle:** asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
63	c2wo4A_	Alignment	not modelled	13.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** 3b' carbohydrate-binding module from the cel9v glycoside2 hydrolase from clostridium thermocellum, in-house data
64	d1nqjb_	Alignment	not modelled	13.6	11	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
65	d1f1ua2	Alignment	not modelled	13.5	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
66	c2l0dA_	Alignment	not modelled	13.1	9	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell surface protein; **PDBTitle:** solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
67	c3zx1A_	Alignment	not modelled	12.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** multicopper oxidase from campylobacter jejuni: a metallo-oxidase
68	d1m1sa_	Alignment	not modelled	12.7	8	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PapD-like **Family:**MSP-like
69	d2vzsa1	Alignment	not modelled	12.5	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
70	d1uura2	Alignment	not modelled	12.0	6	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**STAT DNA-binding domain
71	c1yewI_	Alignment	not modelled	11.6	16	**PDB header:**oxidoreductase, membrane protein **Chain:** I: **PDB Molecule:**particulate methane monooxygenase, b subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
72	d1f1xa2	Alignment	not modelled	11.6	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
73	d1ex0a2	Alignment	not modelled	11.5	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
74	d2je8a2	Alignment	not modelled	11.4	0	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
75	d1jzga_	Alignment	not modelled	11.1	3	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
76	d1e42a1	Alignment	not modelled	11.0	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Clathrin adaptor appendage domain **Family:**Alpha-adaptin ear subdomain-like
77	d2k5qa1	Alignment	not modelled	10.7	23	**Fold:**OB-fold **Superfamily:**BC4932-like **Family:**BC4932-like
78	d1ifra_	Alignment	not modelled	10.6	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Lamin A/C globular tail domain **Family:**Lamin A/C globular tail domain
79	d1nwpa_	Alignment	not modelled	10.4	12	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like

80	d1mpya1	Alignment	not modelled	10.3	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
81	c3gekA_	Alignment	not modelled	10.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioesterase yhda; **PDBTitle:** crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
82	c2lllA_	Alignment	not modelled	10.1	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-b2; **PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
83	c2h47C_	Alignment	not modelled	9.9	3	**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)
84	d1h6ya_	Alignment	not modelled	9.4	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**CBM22
85	d1azca_	Alignment	not modelled	9.4	3	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
86	c2r39A_	Alignment	not modelled	9.3	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fixg-related protein; **PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus
87	d2j5wa1	Alignment	not modelled	9.2	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
88	c2opkC_	Alignment	not modelled	9.2	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
89	c1qpxA_	Alignment	not modelled	9.2	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**papd chaperone; **PDBTitle:** crystal structures of self-capping papd chaperone homodimers
90	d3eipa_	Alignment	not modelled	8.9	13	**Fold:**FKBP-like **Superfamily:**Colicin E3 immunity protein **Family:**Colicin E3 immunity protein
91	d1q38a_	Alignment	not modelled	8.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
92	c2h7fX_	Alignment	not modelled	8.9	9	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
93	d1f53a_	Alignment	not modelled	8.7	33	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Killer toxin-like protein SKLP
94	d1cc3a_	Alignment	not modelled	8.6	7	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
95	c3qhtD_	Alignment	not modelled	8.6	21	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**monobody ysmb-1; **PDBTitle:** crystal structure of the monobody ysmb-1 bound to yeast sumo
96	c1cyxA_	Alignment	not modelled	8.6	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cyoa; **PDBTitle:** quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
97	d1cyxa_	Alignment	not modelled	8.6	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Periplasmic domain of cytochrome c oxidase subunit II
98	d2ccwa1	Alignment	not modelled	8.5	4	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
99	c2rk0B_	Alignment	not modelled	8.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase domain; **PDBTitle:** crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec