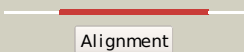

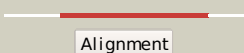

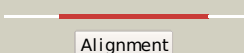
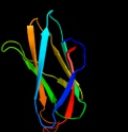
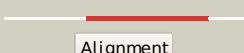


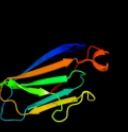
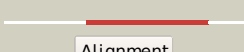
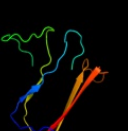
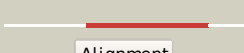

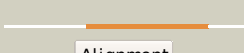


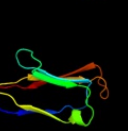
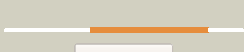






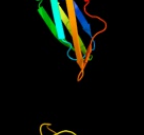





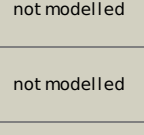


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nqjb_	 Alignment		98.3	16	Fold: CUB-like Superfamily: Collagen-binding domain Family: Collagen-binding domain
2	c3jqxA_	 Alignment		98.2	14	PDB header: cell adhesion Chain: A: PDB Molecule: colh protein; PDBTitle: crystal structure of clostridium histolyticum colh collagenase2 collagen binding domain 3 at 2.2 angstrom resolution in the presence3 of calcium and cadmium
3	d1nqja_	 Alignment		97.9	17	Fold: CUB-like Superfamily: Collagen-binding domain Family: Collagen-binding domain
4	d2c34a1	 Alignment		95.3	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: ICP-like Family: ICP-like
5	d1wm da1	 Alignment		94.8	20	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Proprotein convertase P-domain
6	c2wgnB_	 Alignment		93.3	14	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: inhibitor of cysteine peptidase compnd 3; PDBTitle: pseudomonas aeruginosa icp
7	c3m86B_	 Alignment		92.6	7	PDB header: protein binding Chain: B: PDB Molecule: amoebiasin-2; PDBTitle: crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
8	d2nqda1	 Alignment		89.9	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: ICP-like Family: ICP-like
9	c2p9rA_	 Alignment		89.5	16	PDB header: signaling protein Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: human alpha2-macroglogulin is composed of multiple domains,2 as predicted by homology with complement component c3
10	c2ds4A_	 Alignment		86.2	14	PDB header: protein binding Chain: A: PDB Molecule: tripartite motif protein 45; PDBTitle: solution structure of the filamin domain from human2 tripartite motif protein 45
11	d2ov0a1	 Alignment		86.2	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like

12	d1ld2a_	Alignment		85.6	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
13	c3c75B_	Alignment		85.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: amicyanin; PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
14	c3afgA_	Alignment		81.8	21	PDB header: hydrolase Chain: A: PDB Molecule: subtilisin-like serine protease; PDBTitle: crystal structure of pron-tk-sp from thermococcus kodakaraensis
15	d2diaa1	Alignment		79.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
16	d1bxua_	Alignment		74.7	13	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
17	d2plta_	Alignment		72.8	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
18	d2o14a1	Alignment		71.3	26	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: YxiM N-terminal domain-like
19	d1qnia1	Alignment		71.2	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
20	d2cuab_	Alignment		69.0	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
21	d2cuaa_	Alignment		67.9	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
22	d1plaa_	Alignment	not modelled	62.6	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
23	d2q0zx2	Alignment	not modelled	61.5	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Sec63 C-terminal domain-like
24	d1wlha1	Alignment	not modelled	60.6	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
25	d1v05a_	Alignment	not modelled	57.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
26	c2vzqA_	Alignment	not modelled	53.7	16	PDB header: hydrolase Chain: A: PDB Molecule: exo-beta-d-glucosaminidase; PDBTitle: c-terminal cbm35 from amycolatopsis orientalis exo-2 chitosanase csxa in complex with digalacturonic acid
27	d7pcya_	Alignment	not modelled	53.5	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
						Fold: Cupredoxin-like

28	d1paza_	Alignment	not modelled	53.2	13	Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
29	d2jxma1	Alignment	not modelled	50.9	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
30	c3eo6B_	Alignment	not modelled	50.4	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of unknown function (duf1255); PDBTitle: crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
31	c1ksrA_	Alignment	not modelled	49.2	10	PDB header: actin binding protein Chain: A: PDB Molecule: gelation factor; PDBTitle: the repeating segments of the f-actin cross-linking2 gelation factor (abp-120) have an immunoglobulin fold, nmr,3 20 structures
32	d1iuza_	Alignment	not modelled	48.4	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
33	c1xmeB_	Alignment	not modelled	47.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: structure of recombinant cytochrome ba3 oxidase from thermus2 thermophilus
34	d1g0da1	Alignment	not modelled	47.3	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
35	d2e9ia1	Alignment	not modelled	46.7	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
36	c2yetB_	Alignment	not modelled	45.8	26	PDB header: hydrolase Chain: B: PDB Molecule: gh61 isozyme a; PDBTitle: thermoascus gh61 isozyme a
37	d2d7ma1	Alignment	not modelled	45.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
38	c3hrzA_	Alignment	not modelled	45.3	15	PDB header: immune system Chain: A: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
39	c3ef4A_	Alignment	not modelled	44.3	11	PDB header: electron transport Chain: A: PDB Molecule: blue copper protein; PDBTitle: crystal structure of native pseudoazurin from2 hyphomicrobium denitrificans
40	c1kbwA_	Alignment	not modelled	44.3	20	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
41	d1kful2	Alignment	not modelled	44.0	25	Fold: Calpain large subunit, middle domain (domain III) Superfamily: Calpain large subunit, middle domain (domain III) Family: Calpain large subunit, middle domain (domain III)
42	c2e9jA_	Alignment	not modelled	43.6	11	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 14th filamin domain from human2 filamin-b
43	d1bqka_	Alignment	not modelled	43.5	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
44	d1bypa_	Alignment	not modelled	43.5	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
45	c3hqxA_	Alignment	not modelled	42.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0345 protein aciad0356; PDBTitle: crystal structure of protein of unknown function (duf1255,pf06865)2 from acinetobacter sp. adp1
46	d1qfha1	Alignment	not modelled	41.5	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
47	c2ee6A_	Alignment	not modelled	40.7	17	PDB header: structural protein Chain: A: PDB Molecule: filamin-b; PDBTitle: solution structure of the 21th filamin domain from human2 filamin-b
48	c3cu7A_	Alignment	not modelled	40.6	10	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: human complement component 5
49	d2bw4a1	Alignment	not modelled	39.3	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
50	d1libya_	Alignment	not modelled	39.2	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
51	d2dj4a1	Alignment	not modelled	38.1	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
52	c2w1wB_	Alignment	not modelled	38.0	15	PDB header: hydrolase Chain: B: PDB Molecule: lipolytic enzyme, g-d-s-l; PDBTitle: native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
53	d1pcsA_	Alignment	not modelled	37.0	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
54	d1kbva1	Alignment	not modelled	36.1	22	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins

55	c2h47C	Alignment	not modelled	35.8	14	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
56	d2d7oa1	Alignment	not modelled	33.5	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
57	d1kv7a1	Alignment	not modelled	33.2	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
58	d1fftb1	Alignment	not modelled	32.2	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
59	c3nrqB	Alignment	not modelled	31.3	19	PDB header: transport protein Chain: B: PDB Molecule: periplasmic protein-probably involved in high-affinity fe2+ PDBTitle: crystal structure of copper-reconstituted fetp from uropathogenic2 escherichia coli strain f11
60	c3rghA	Alignment	not modelled	31.3	9	PDB header: cell adhesion Chain: A: PDB Molecule: filamin-a; PDBTitle: structure of filamin a immunoglobulin-like repeat 10 from homo sapiens
61	d1qxp3	Alignment	not modelled	30.8	13	Fold: Calpain large subunit, middle domain (domain III) Superfamily: Calpain large subunit, middle domain (domain III) Family: Calpain large subunit, middle domain (domain III)
62	d1cyxa	Alignment	not modelled	30.8	9	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Periplasmic domain of cytochrome c oxidase subunit II
63	c1cyxA	Alignment	not modelled	30.8	9	PDB header: electron transport Chain: A: PDB Molecule: cyoa; PDBTitle: quinol oxidase (periplasmic fragment of subunit ii with2 engineered cu-a binding site)(cyoa)
64	d2dmca1	Alignment	not modelled	30.7	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
65	c2b39B	Alignment	not modelled	30.3	13	PDB header: immune system Chain: B: PDB Molecule: c3; PDBTitle: structure of mammalian c3 with an intact thioester at 3a resolution
66	d2jnaa1	Alignment	not modelled	30.0	33	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
67	d2diba1	Alignment	not modelled	29.9	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
68	d1kdja	Alignment	not modelled	28.5	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
69	d2dmba1	Alignment	not modelled	28.4	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
70	d1ndsaa1	Alignment	not modelled	28.2	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
71	d1ag6a	Alignment	not modelled	28.1	12	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
72	d1adwa	Alignment	not modelled	27.6	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
73	d1fwxa1	Alignment	not modelled	27.6	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
74	c1wmeA	Alignment	not modelled	27.5	23	PDB header: hydrolase Chain: A: PDB Molecule: protease; PDBTitle: crystal structure of alkaline serine protease kp-43 from bacillus sp.2 ksm-kp43 (1.50 angstrom, 293 k)
75	d2di9a1	Alignment	not modelled	26.5	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
76	d1df0a2	Alignment	not modelled	26.1	13	Fold: Calpain large subunit, middle domain (domain III) Superfamily: Calpain large subunit, middle domain (domain III) Family: Calpain large subunit, middle domain (domain III)
77	d1snra1	Alignment	not modelled	25.6	7	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
78	d1oe1a1	Alignment	not modelled	24.8	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
79	d2di8a1	Alignment	not modelled	24.7	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
80	c3zx1A	Alignment	not modelled	24.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, putative; PDBTitle: multicopper oxidase from campylobacter jejuni: a metallo-oxidase
81	d1plca	Alianment	not modelled	24.5	14	Fold: Cupredoxin-like Superfamily: Cupredoxins

					Family: Plastocyanin/azurin-like
82	d2gtol	Alignment	not modelled	24.1	20
					Fold: Streptavidin-like Superfamily: Extracellular hemoglobin linker subunit, receptor domain Family: Extracellular hemoglobin linker subunit, receptor domain
83	c1mzC	Alignment	not modelled	24.0	15
					PDB header: oxidoreductase Chain: C: PDB Molecule: copper-containing nitrite reductase; PDBTitle: crystal structure of mutant (m182t)of nitrite reductase
84	d2ccwa1	Alignment	not modelled	23.6	17
					Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
85	c3im2A	Alignment	not modelled	23.2	24
					PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: structure of the c-terminal sec63 unit of yeast brr2, p41212 form
86	c1wa1X	Alignment	not modelled	23.1	19
					PDB header: reductase Chain: X: PDB Molecule: dissimilatory copper-containing nitrite PDBTitle: crystal structure of h313q mutant of alcaligenes2 xylooxidans nitrite reductase
87	c2yrlA	Alignment	not modelled	22.9	15
					PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa1837 protein; PDBTitle: solution structure of the pkd domain from kiaa 1837 protein
88	d1pmya	Alignment	not modelled	22.6	13
					Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
89	c2w3jA	Alignment	not modelled	22.6	13
					PDB header: sugar-binding protein Chain: A: PDB Molecule: carbohydrate binding module; PDBTitle: structure of a family 35 carbohydrate binding module from2 an environmental isolate
90	d1jmx5	Alignment	not modelled	22.5	15
					Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
91	d1h8la1	Alignment	not modelled	22.5	20
					Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
92	d1vpsa	Alignment	not modelled	21.5	18
					Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
93	d1nnxa	Alignment	not modelled	21.3	20
					Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
94	c2fqeA	Alignment	not modelled	21.2	18
					PDB header: oxidoreductase Chain: A: PDB Molecule: blue copper oxidase cueo; PDBTitle: crystal structures of e. coli laccase cueo under different2 copper binding situations
95	d2oyza1	Alignment	not modelled	20.8	20
					Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: VPA0057-like
96	d2qi2a1	Alignment	not modelled	20.2	14
					Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
97	c3cnkB	Alignment	not modelled	19.0	22
					PDB header: structural protein Chain: B: PDB Molecule: filamin-a; PDBTitle: crystal structure of the dimerization domain of human2 filamin a
98	d1mzya1	Alignment	not modelled	18.9	16
					Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
99	c2w87B	Alignment	not modelled	18.5	16
					PDB header: hydrolase Chain: B: PDB Molecule: esterase d; PDBTitle: xyl-cbm35 in complex with glucuronic acid containing2 disaccharide.