








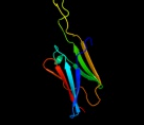

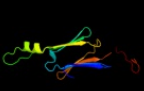












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlgmea_	 Alignment		99.9	19	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: HSP20
2	dlgmeb_	 Alignment		99.9	22	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: HSP20
3	dlshsa_	 Alignment		99.9	19	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: HSP20
4	c1shsD_	 Alignment		99.9	19	PDB header: heat shock protein Chain: D: PDB Molecule: small heat shock protein; PDBTitle: small heat shock protein from methanococcus jannaschii
5	c3glaA_	 Alignment		99.8	18	PDB header: chaperone Chain: A: PDB Molecule: low molecular weight heat shock protein; PDBTitle: crystal structure of the hspa from xanthomonas axonopodis
6	c3l1eA_	 Alignment		99.8	20	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin a chain; PDBTitle: bovine alphaa crystallin zinc bound
7	c2bolA_	 Alignment		99.8	20	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
8	c2wj5A_	 Alignment		99.8	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein beta-6; PDBTitle: rat alpha crystallin domain
9	c3aabA_	 Alignment		99.7	16	PDB header: chaperone Chain: A: PDB Molecule: putative uncharacterized protein st1653; PDBTitle: small heat shock protein hsp14.0 with the mutations of i120f and i122f2 in the form i crystal
10	d2h50a1	 Alignment		99.7	18	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: HSP20
11	c2klrA_	 Alignment		99.7	22	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers

12	c3q9qB_	Alignment		99.6	27	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
13	c2wj7D_	Alignment		99.5	24	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
14	c3igfB_	Alignment		97.9	21	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
15	d1rl1a_	Alignment		97.7	8	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: GS domain
16	c2jkiS_	Alignment		97.6	10	PDB header: chaperone Chain: S: PDB Molecule: sgt1-like protein; PDBTitle: complex of hsp90 n-terminal and sgt1 cs domain
17	c3eudE_	Alignment		96.5	16	PDB header: nuclear protein Chain: E: PDB Molecule: protein shq1; PDBTitle: structure of the cs domain of the essential h/aca rnp2 assembly protein shq1p
18	d1wfia_	Alignment		96.3	13	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: Nuclear movement domain
19	d1ejfa_	Alignment		96.2	7	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: Co-chaperone p23-like
20	c1x5mA_	Alignment		96.0	4	PDB header: apoptosis, signaling protein Chain: A: PDB Molecule: calcyclin-binding protein; PDBTitle: solution structure of the core domain of calcyclin binding2 protein; siah-interacting protein (sip)
21	d1wh0a_	Alignment	not modelled	95.6	7	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: GS domain
22	c2o30A_	Alignment	not modelled	95.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nuclear movement protein; PDBTitle: nuclear movement protein from e. cuniculi gb-m1
23	c2k8qA_	Alignment	not modelled	95.1	16	PDB header: structural protein Chain: A: PDB Molecule: protein shq1; PDBTitle: nmr structure of shq1p n-terminal domain
24	d1wgva_	Alignment	not modelled	94.0	14	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: Nuclear movement domain
25	d1xo9a_	Alignment	not modelled	93.8	9	Fold: HSP20-like chaperones Superfamily: HSP20-like chaperones Family: Co-chaperone p23-like
26	c2rh0B_	Alignment	not modelled	92.0	13	PDB header: nuclear protein Chain: B: PDB Molecule: nucd domain-containing protein 2; PDBTitle: crystal structure of nucd domain-containing protein 22 (13542905) from mus musculus at 1.95 a resolution
27	c2cg9Y_	Alignment	not modelled	84.6	16	PDB header: chaperone Chain: Y: PDB Molecule: co-chaperone protein sba1; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
28	d2c7fa1	Alignment	not modelled	43.2	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
						Fold: Ribosomal protein L6

29	d2cqla1	Alignment	not modelled	33.6	24	Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
30	d2ga5a1	Alignment	not modelled	33.0	13	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
31	c2leza_	Alignment	not modelled	31.6	16	PDB header: signaling protein Chain: A: PDB Molecule: secreted effector protein pipb2; PDBTitle: solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a
32	d2fqla1	Alignment	not modelled	31.2	13	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
33	dlekga_	Alignment	not modelled	28.0	20	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
34	c2wvsD_	Alignment	not modelled	23.1	5	PDB header: hydrolase Chain: D: PDB Molecule: alpha-l-fucosidase; PDBTitle: crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
35	dlew4a_	Alignment	not modelled	23.1	27	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
36	d1rl6a1	Alignment	not modelled	22.3	19	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
37	d1h8la1	Alignment	not modelled	21.7	8	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
38	d1vqoe1	Alignment	not modelled	19.3	12	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
39	c2xxsA_	Alignment	not modelled	18.8	24	PDB header: protein binding Chain: A: PDB Molecule: protein mxig; PDBTitle: solution structure of the n-terminal domain of the shigella2 type iii secretion protein mxig
40	d2j01h1	Alignment	not modelled	16.9	18	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
41	d1sm3h2	Alignment	not modelled	16.5	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
42	d2fath2	Alignment	not modelled	15.2	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
43	d1c12b2	Alignment	not modelled	14.9	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
44	d1mexh2	Alignment	not modelled	13.8	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
45	c487dj_	Alignment	not modelled	12.2	19	PDB header: ribosome Chain: J: PDB Molecule: protein (50s 16 ribosomal protein); PDBTitle: seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
46	d1teth2	Alignment	not modelled	12.2	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
47	d1osph2	Alignment	not modelled	11.7	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
48	d1hxmb2	Alignment	not modelled	11.5	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
49	c2qjha_	Alignment	not modelled	11.2	16	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
50	c3muwU_	Alignment	not modelled	10.1	10	PDB header: virus Chain: U: PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
51	d1pz5b2	Alignment	not modelled	10.1	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
52	d1fe8h2	Alignment	not modelled	10.0	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
53	d2pcpb2	Alignment	not modelled	10.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
54	d1uwya1	Alignment	not modelled	9.8	17	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
55	d1clzh2	Alignment	not modelled	9.7	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)

56	d1mjuh2	Alignment	not modelled	9.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
57	d1a5fh2	Alignment	not modelled	9.3	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
58	d1q72h2	Alignment	not modelled	9.3	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
59	d1qw9a1	Alignment	not modelled	9.3	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
60	d1zs8a1	Alignment	not modelled	9.3	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
61	d1q0yh2	Alignment	not modelled	9.0	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
62	d1q0xh2	Alignment	not modelled	9.0	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
63	d1kcvh2	Alignment	not modelled	8.9	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
64	d2g60h1	Alignment	not modelled	8.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
65	c4a1eE	Alignment	not modelled	7.9	35	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein l9; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
66	c2xfbl	Alignment	not modelled	7.9	15	PDB header: virus Chain: I: PDB Molecule: e2 envelope glycoprotein; PDBTitle: the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
67	c3n43B	Alignment	not modelled	7.8	15	PDB header: viral protein Chain: B: PDB Molecule: e2 envelope glycoprotein; PDBTitle: crystal structures of the mature envelope glycoprotein complex2 (trypsin cleavage) of chikungunya virus.
68	c2hguH	Alignment	not modelled	7.8	14	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein l6; PDBTitle: 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
69	c2zkre	Alignment	not modelled	7.7	29	PDB header: ribosomal protein/rna Chain: E: PDB Molecule: rna expansion segment es7 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
70	d2jelh2	Alignment	not modelled	7.7	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
71	c2nsmA	Alignment	not modelled	7.7	11	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase n catalytic chain; PDBTitle: crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
72	d2nwtal	Alignment	not modelled	7.6	27	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: AF2212-like
73	c3iz5F	Alignment	not modelled	7.3	12	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l9 (l6p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
74	d1ji1a2	Alignment	not modelled	7.1	14	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
75	c3n40P	Alignment	not modelled	7.1	15	PDB header: viral protein Chain: P: PDB Molecule: p62 envelope glycoprotein; PDBTitle: crystal structure of the immature envelope glycoprotein complex of2 chikungunya virus.
76	d1u8ib2	Alignment	not modelled	7.0	5	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
77	d1eapb2	Alignment	not modelled	6.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
78	d3c2ah2	Alignment	not modelled	6.7	4	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
79	d1r3ha1	Alignment	not modelled	6.6	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
80	d1nldh2	Alignment	not modelled	6.6	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
81	c3j0cH	Alignment	not modelled	6.5	10	PDB header: virus Chain: H: PDB Molecule: e2 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map

82	d1lk3h2	Alignment	not modelled	6.5	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
83	d1pg7x2	Alignment	not modelled	6.4	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
84	d1s21a	Alignment	not modelled	6.3	29	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector
85	c1s21A	Alignment	not modelled	6.3	29	PDB header: chaperone Chain: A: PDB Molecule: orf2; PDBTitle: crystal structure of avrpvh orf2, a type iii effector from2 p. syringae
86	d1bfob2	Alignment	not modelled	6.3	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
87	d1je6a1	Alignment	not modelled	6.1	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
88	c3ccmE	Alignment	not modelled	6.0	12	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l6p; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
89	d1a6tb2	Alignment	not modelled	6.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
90	c2e0gA	Alignment	not modelled	6.0	22	PDB header: replication Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: dnaa n-terminal domain
91	c2x89G	Alignment	not modelled	5.7	12	PDB header: immune system Chain: G: PDB Molecule: beta-2-microglobulin; PDBTitle: structure of the beta2_microglobulin involved in2 amyloidogenesis
92	c1h8lA	Alignment	not modelled	5.6	11	PDB header: carboxypeptidase Chain: A: PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gensa
93	d1t66d2	Alignment	not modelled	5.5	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
94	d1kfah2	Alignment	not modelled	5.5	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
95	c3bbol	Alignment	not modelled	5.4	35	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein l6; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
96	d1h0db2	Alignment	not modelled	5.4	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
97	d1nvpc	Alignment	not modelled	5.2	18	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
98	c1nvpc	Alignment	not modelled	5.2	18	PDB header: transcription/dna Chain: C: PDB Molecule: transcription initiation factor iia beta chain; PDBTitle: human tfiia/tbp/dna complex
99	d1a3rh2	Alignment	not modelled	5.1	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)