

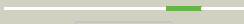
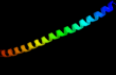



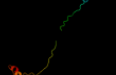



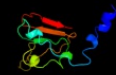





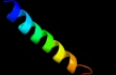








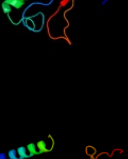
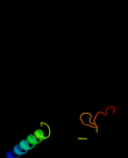


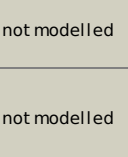


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dljmxal	 Alignment		55.4	12	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
2	cleboE_	 Alignment		51.9	13	PDB header: viral protein Chain: E: PDB Molecule: ebola virus envelope protein chimera consisting PDBTitle: crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
3	dlpbyal	 Alignment		51.6	24	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
4	c3ifqD_	 Alignment		50.0	28	PDB header: cell adhesion Chain: D: PDB Molecule: e-cadherin; PDBTitle: interaction of plakoglobin and beta-catenin with desmosomal2 cadherins
5	d2q09a1	 Alignment		43.3	89	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
6	c3k5bE_	 Alignment		42.0	19	PDB header: hydrolase Chain: E: PDB Molecule: v-type atp synthase subunit e; PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
7	c2jo1A_	 Alignment		41.8	28	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
8	d2isba1	 Alignment		31.2	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: FumA C-terminal domain-like Family: FumA C-terminal domain-like
9	c3mk7F_	 Alignment		31.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
10	d1y0na_	 Alignment		28.2	30	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
11	c3c6eC_	 Alignment		24.2	33	PDB header: viral protein Chain: C: PDB Molecule: prm; PDBTitle: crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the dengue 2 virus at neutral ph

12	c3c6rE_	Alignment		24.1	33	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: low ph immature dengue virus
13	d1ny722	Alignment		23.1	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
14	d1pgl22	Alignment		23.1	24	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
15	c3rfrl_	Alignment		22.7	24	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
16	c3i24B_	Alignment		21.7	19	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
17	d1v54k_	Alignment		21.6	17	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIb Family: Mitochondrial cytochrome c oxidase subunit VIIb
18	c2y69X_	Alignment		21.6	17	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 7b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
19	c3nohA_	Alignment		20.2	26	PDB header: peptide binding protein Chain: A: PDB Molecule: putative peptide binding protein; PDBTitle: crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
20	c2bpbB_	Alignment		19.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
21	d1u61a_	Alignment	not modelled	18.9	24	Fold: RNase III domain-like Superfamily: RNase III domain-like Family: RNase III catalytic domain-like
22	c3heiF_	Alignment	not modelled	18.6	25	PDB header: transferase/signaling protein Chain: F: PDB Molecule: ephrin-a1; PDBTitle: ligand recognition by a-class eph receptors: crystal structures of the2 epha2 ligand-binding domain and the epha2/ephrin-a1 complex
23	d1dgsa2	Alignment	not modelled	18.5	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
24	c3ikmD_	Alignment	not modelled	17.6	26	PDB header: transferase Chain: D: PDB Molecule: dna polymerase subunit gamma-1; PDBTitle: crystal structure of human mitochondrial dna polymerase2 holoenzyme
25	c2q04C_	Alignment	not modelled	17.2	19	PDB header: transferase Chain: C: PDB Molecule: acetoin utilization protein; PDBTitle: crystal structure of acetoin utilization protein (zp_00540088.1) from2 exiguobacterium sibiricum 255-15 at 2.33 a resolution
26	c2x11B_	Alignment	not modelled	16.7	25	PDB header: receptor/signaling protein Chain: B: PDB Molecule: ephrin-a5; PDBTitle: crystal structure of the complete epha2 ectodomain in2 complex with ephrin a5 receptor binding domain
27	d1shxa1	Alignment	not modelled	16.7	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Ephrin ectodomain
28	d2o6ka1	Alignment	not modelled	16.7	19	Fold: SAM domain-like Superfamily: YozE-like Family: YozE-like

29	c3czuB	Alignment	not modelled	16.6	25	PDB header: transferase/signaling protein Chain: B: PDB Molecule: ephrin-a1; PDBTitle: crystal structure of the human ephrin a2- ephrin a1 complex
30	c2wo3B	Alignment	not modelled	16.5	25	PDB header: transferase/signaling protein Chain: B: PDB Molecule: ephrin-a2; PDBTitle: crystal structure of the epha4-ephrina2 complex
31	d2j5wa3	Alignment	not modelled	16.3	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
32	d1ngka	Alignment	not modelled	15.9	26	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
33	d1v33a	Alignment	not modelled	15.8	19	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
34	d2cqaa1	Alignment	not modelled	15.7	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
35	c3uowB	Alignment	not modelled	15.5	19	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
36	d2ctda1	Alignment	not modelled	14.6	14	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
37	d1g71a	Alignment	not modelled	14.0	15	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
38	c3d12E	Alignment	not modelled	13.9	29	PDB header: hydrolase/membrane protein Chain: E: PDB Molecule: ephrin-b3; PDBTitle: crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
39	d1h1oa1	Alignment	not modelled	13.9	12	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
40	c3p87H	Alignment	not modelled	13.8	60	PDB header: hydrolase/dna binding protein Chain: H: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
41	c3p87I	Alignment	not modelled	13.8	60	PDB header: hydrolase/dna binding protein Chain: I: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
42	c3p87K	Alignment	not modelled	13.8	60	PDB header: hydrolase/dna binding protein Chain: K: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
43	c3p87G	Alignment	not modelled	13.4	60	PDB header: hydrolase/dna binding protein Chain: G: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
44	c3p87J	Alignment	not modelled	13.4	60	PDB header: hydrolase/dna binding protein Chain: J: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
45	c3p87L	Alignment	not modelled	13.4	60	PDB header: hydrolase/dna binding protein Chain: L: PDB Molecule: ribonuclease h2 subunit b; PDBTitle: structure of human pcna bound to rnaseh2b pip box peptide
46	d2nwua1	Alignment	not modelled	13.3	12	Fold: RL5-like Superfamily: RL5-like Family: SSO1042-like
47	d1zsoa1	Alignment	not modelled	13.1	25	Fold: MAL13P1.257-like Superfamily: MAL13P1.257-like Family: MAL13P1.257-like
48	c2p2vA	Alignment	not modelled	13.0	19	PDB header: transferase Chain: A: PDB Molecule: alpha-2,3-sialyltransferase; PDBTitle: crystal structure analysis of monofunctional alpha-2,3-2 sialyltransferase cst-i from campylobacter jejuni
49	c3ktbD	Alignment	not modelled	12.1	10	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
50	c3pdsA	Alignment	not modelled	12.0	14	PDB header: membrane protein/hydrolase Chain: A: PDB Molecule: fusion protein beta-2 adrenergic receptor/lysozyme; PDBTitle: irreversible agonist-beta2 adrenoceptor complex
51	c3kgkA	Alignment	not modelled	12.0	29	PDB header: chaperone Chain: A: PDB Molecule: arsenical resistance operon trans-acting repressor arsd; PDBTitle: crystal structure of arsd
52	d1likop	Alignment	not modelled	11.9	47	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Ephrin ectodomain
53	clikoP	Alignment	not modelled	11.9	47	PDB header: signaling protein Chain: P: PDB Molecule: ephrin-b2; PDBTitle: crystal structure of the murine ephrin-b2 ectodomain
54	c2f8mB	Alignment	not modelled	11.5	13	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
						Fold: SAM domain-like

55	d1v38a_	Alignment	not modelled	11.4	30	Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
56	c2j5dA_	Alignment	not modelled	11.4	40	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: nmr structure of bnip3 transmembrane domain in lipid2 bicelles
57	d1o0la_	Alignment	not modelled	11.4	17	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
58	c2w2hD_	Alignment	not modelled	11.3	23	PDB header: rna-binding protein Chain: D: PDB Molecule: protein tat; PDBTitle: structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiaV
59	c2fl8N_	Alignment	not modelled	11.3	23	PDB header: virus/viral protein Chain: N: PDB Molecule: baseplate structural protein gp10; PDBTitle: fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.
60	c3lgoA_	Alignment	not modelled	11.2	19	PDB header: protein binding Chain: A: PDB Molecule: protein sIm4; PDBTitle: structure of gse1p, member of the gse/ego complex
61	c2lmaA_	Alignment	not modelled	11.0	38	PDB header: immune system Chain: A: PDB Molecule: thp5 peptide; PDBTitle: solution structure of cd4+ t cell derived peptide thp5
62	c2jwaA_	Alignment	not modelled	10.9	18	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
63	d1fcdc1	Alignment	not modelled	10.7	5	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
64	d2fj6a1	Alignment	not modelled	10.5	25	Fold: SAM domain-like Superfamily: YozE-like Family: YozE-like
65	d1lira_	Alignment	not modelled	10.5	30	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
66	c3cp5A_	Alignment	not modelled	10.4	20	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: cytochrome c from rhodothermus marinus
67	d2evra2	Alignment	not modelled	10.4	60	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NIpC/P60
68	c3oa8A_	Alignment	not modelled	10.3	19	PDB header: heme-binding protein/heme-binding protei Chain: A: PDB Molecule: soxa; PDBTitle: diheme soxax
69	c2l4dA_	Alignment	not modelled	10.3	38	PDB header: electron transport Chain: A: PDB Molecule: sco1/senc family protein/cytochrome c; PDBTitle: cytochrome c domain of pp3183 protein from pseudomonas putida
70	d1mida_	Alignment	not modelled	10.0	42	Fold: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Superfamily: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin Family: Plant lipid-transfer and hydrophobic proteins
71	c3ixxE_	Alignment	not modelled	10.0	33	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: the pseudo-atomic structure of west nile immature virus in2 complex with fab fragments of the anti-fusion loop antibody3 e53
72	d2bmta_	Alignment	not modelled	9.8	45	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
73	c1pbyA_	Alignment	not modelled	9.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: quinoxinohemoprotein amine dehydrogenase 60 kda PDBTitle: structure of the phenylhydrazine adduct of the2 quinoxinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
74	c1sddA_	Alignment	not modelled	9.6	11	PDB header: blood clotting Chain: A: PDB Molecule: coagulation factor v; PDBTitle: crystal structure of bovine factor vai
75	c2vofA_	Alignment	not modelled	9.6	20	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
76	c2ehwD_	Alignment	not modelled	9.3	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein tthb059; PDBTitle: conserved hypothetical protein (tthb059) from thermo thermophilus hb8
77	d1g3wa3	Alignment	not modelled	9.3	32	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
78	d1m70a2	Alignment	not modelled	9.0	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
79	d1y88a1	Alignment	not modelled	8.9	43	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: Hypothetical protein AF1548, C-terminal domain
80	d1kpfa_	Alignment	not modelled	8.9	17	Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins

81	dlwejf_	Alignment	not modelled	8.7	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
82	c3qrqA_	Alignment	not modelled	8.7	24	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of the ryr domain of the rabbit ryanodine receptor
83	c2ka2A_	Alignment	not modelled	8.5	40	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
84	c2ka1B_	Alignment	not modelled	8.5	40	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
85	d1hlca_	Alignment	not modelled	8.4	28	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
86	c2zkqg_	Alignment	not modelled	8.3	19	PDB header: ribosomal protein/rna Chain: G: PDB Molecule: rna helix; PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
87	c1bmw2_	Alignment	not modelled	8.1	24	PDB header: virus/rna Chain: 2: PDB Molecule: protein (icosahedral virus - b and c domain); PDBTitle: protein-rna interactions in an icosahedral virus at 3.02 angstroms resolution
88	c2fg0B_	Alignment	not modelled	8.1	60	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
89	c2axkA_	Alignment	not modelled	8.1	36	PDB header: toxin Chain: A: PDB Molecule: discrepin; PDBTitle: solution structure of discrepin, a scorpion venom toxin2 blocking k+ channels.
90	c3arcl_	Alignment	not modelled	8.0	35	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein l; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
91	c2ka2B_	Alignment	not modelled	8.0	42	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
92	c2ka1A_	Alignment	not modelled	8.0	42	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
93	c2p57A_	Alignment	not modelled	8.0	32	PDB header: metal binding protein Chain: A: PDB Molecule: gtpase-activating protein znf289; PDBTitle: gap domain of znf289, an id1-regulated zinc finger protein
94	c2xivA_	Alignment	not modelled	8.0	80	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
95	c3o47A_	Alignment	not modelled	7.9	18	PDB header: hydrolase, hydrolase activator Chain: A: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1, adp- PDBTitle: crystal structure of arfgap1-arf1 fusion protein
96	c2k8iA_	Alignment	not modelled	7.9	38	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
97	c1oheA_	Alignment	not modelled	7.9	20	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
98	c3gt2A_	Alignment	not modelled	7.9	60	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
99	d1xrda1	Alignment	not modelled	7.8	23	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits