
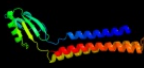





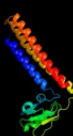

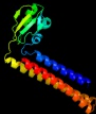

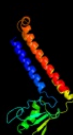



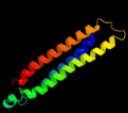







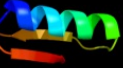


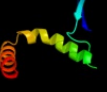


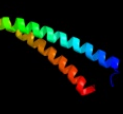



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlek8a_	 Alignment		100.0	100	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
2	dlodd5a_	 Alignment		100.0	40	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
3	dlis1a_	 Alignment		100.0	70	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
4	dlwqga1	 Alignment		100.0	40	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
5	dleh1a_	 Alignment		100.0	45	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
6	dlge9a_	 Alignment		100.0	46	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
7	c3lf9A_	 Alignment		100.0	63	PDB header: immune system Chain: A: PDB Molecule: 4e10_d0_lis1a_001_c (t161); PDBTitle: crystal structure of hiv epitope-scaffold 4e10_d0_lis1a_001_c
8	c1y698_	 Alignment		100.0	74	PDB header: ribosome Chain: 8: PDB Molecule: ribosome recycling factor; PDBTitle: rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
9	dlwiha_	 Alignment		99.9	31	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
10	c2rrnA_	 Alignment		69.8	17	PDB header: protein transport Chain: A: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
11	c2c1nA_	 Alignment		66.2	15	PDB header: signaling protein Chain: A: PDB Molecule: 14-3-3 protein zeta/delta; PDBTitle: molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3

12	dlin0a2	Alignment		65.5	19	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
13	clin0B_	Alignment		58.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
14	dlo9da_	Alignment		56.7	16	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
15	c2npmB_	Alignment		56.2	11	PDB header: protein binding Chain: B: PDB Molecule: 14-3-3 domain containing protein; PDBTitle: crystal structure of cryptosporidium parvum 14-3-3 protein2 in complex with peptide
16	c3gasA_	Alignment		52.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
17	d2o8pa1	Alignment		48.5	13	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
18	dliwga5	Alignment		47.9	23	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
19	d2o02a1	Alignment		47.8	15	Fold: alpha-alpha superhelix Superfamily: 14-3-3 protein Family: 14-3-3 protein
20	dliwga6	Alignment		46.9	22	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
21	c3ff5B_	Alignment	not modelled	46.5	23	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
22	c3m20A_	Alignment	not modelled	43.5	14	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
23	c3htkA_	Alignment	not modelled	41.2	23	PDB header: recombination/replication/ligase Chain: A: PDB Molecule: structural maintenance of chromosomes protein 5; PDBTitle: crystal structure of mms21 and smc5 complex
24	c2kl8A_	Alignment	not modelled	36.1	15	PDB header: de novo protein Chain: A: PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
25	clj1dF_	Alignment	not modelled	34.0	14	PDB header: contractile protein Chain: F: PDB Molecule: troponin i; PDBTitle: crystal structure of the 46kda domain of human cardiac2 troponin in the ca2+ saturated form
26	dlzj8a1	Alignment	not modelled	32.7	9	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
27	dltz9a_	Alignment	not modelled	30.0	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
28	dlzh5a1	Alignment	not modelled	27.3	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: La domain

29	c3mafB_	Alignment	not modelled	27.2	16	PDB header: lyase Chain: B: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (asymmetric form)
30	d1lp1b_	Alignment	not modelled	26.0	30	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
31	c2k14A_	Alignment	not modelled	25.9	10	PDB header: unknown function Chain: A: PDB Molecule: yuaf protein; PDBTitle: solution structure of the soluble domain of the nfd2 protein yuaf from bacillus subtilis
32	c3mc6C_	Alignment	not modelled	25.6	7	PDB header: lyase Chain: C: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of scdpl1
33	d1fc2c_	Alignment	not modelled	25.4	30	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
34	c3bdkB_	Alignment	not modelled	25.3	20	PDB header: lyase Chain: B: PDB Molecule: d-mannosate dehydratase; PDBTitle: crystal structure of streptococcus suis mannosate2 dehydratase complexed with substrate analogue
35	d1deeq_	Alignment	not modelled	24.8	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
36	c3onjA_	Alignment	not modelled	24.4	24	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
37	d2jwda1	Alignment	not modelled	24.2	21	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
38	c1zdbA_	Alignment	not modelled	21.1	35	PDB header: igg binding domain Chain: A: PDB Molecule: mini protein a domain, z38; PDBTitle: phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
39	d2arza1	Alignment	not modelled	20.8	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	d1r9ja1	Alignment	not modelled	20.8	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
41	c3b50A_	Alignment	not modelled	20.6	11	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
42	c3gyyC_	Alignment	not modelled	20.3	12	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
43	c2etnA_	Alignment	not modelled	18.4	20	PDB header: transcription Chain: A: PDB Molecule: anti-cleavage anti-grea transcription factor PDBTitle: crystal structure of thermus aquaticus gfh1
44	c1mkyA_	Alignment	not modelled	18.0	13	PDB header: ligand binding protein Chain: A: PDB Molecule: probable gtp-binding protein enga; PDBTitle: structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains
45	d2fqma1	Alignment	not modelled	17.9	23	Fold: Phosphoprotein oligomerization domain-like Superfamily: Phosphoprotein oligomerization domain-like Family: Phosphoprotein oligomerization domain-like
46	d1b64a_	Alignment	not modelled	17.7	18	Fold: Ferredoxin-like Superfamily: eEF-1beta-like Family: eEF-1beta-like
47	d2dula1	Alignment	not modelled	17.1	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
48	d2dexx2	Alignment	not modelled	16.8	36	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Peptidylarginine deiminase Pad4, N-terminal domain
49	c2l5gB_	Alignment	not modelled	16.1	19	PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
50	c1j1eC_	Alignment	not modelled	15.6	14	PDB header: contractile protein Chain: C: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
51	d2f23a1	Alignment	not modelled	14.5	17	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
52	c3axtA_	Alignment	not modelled	14.4	18	PDB header: transferase Chain: A: PDB Molecule: probable n(2),n(2)-dimethylguanosine trna methyltransferase PDBTitle: complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
53	d1grja1	Alignment	not modelled	13.9	19	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
54	c2zzxD_	Alignment	not modelled	13.6	11	PDB header: transport protein Chain: D: PDB Molecule: abc transporter, solute-binding protein; PDBTitle: crystal structure of a periplasmic substrate binding protein in2 complex with lactate PDB header: viral protein Chain: A: PDB Molecule: factor x protein

55	c2b9bA_	Alignment	not modelled	12.8	25	Chain: A: PDB Molecule: fusion glycoprotein ru; PDBTitle: structure of the parainfluenza virus 5 f protein in its metastable, 2 pre-fusion conformation
56	d1q8ka2	Alignment	not modelled	12.6	16	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain
57	c2vpnB_	Alignment	not modelled	12.6	9	PDB header: transport Chain: B: PDB Molecule: periplasmic substrate binding protein; PDBTitle: high-resolution structure of the periplasmic ectoine-2 binding protein from teaa bc trap-transporter of halomonas3 elongata
58	c2pfyA_	Alignment	not modelled	12.4	13	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
59	d1whra_	Alignment	not modelled	12.2	21	Fold: IF3-like Superfamily: R3H domain Family: R3H domain
60	c3nqbB_	Alignment	not modelled	11.9	17	PDB header: hydrolase Chain: B: PDB Molecule: adenine deaminase 2; PDBTitle: crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58)
61	c2wxxC_	Alignment	not modelled	11.5	24	PDB header: hormone Chain: C: PDB Molecule: angiotensinogen; PDBTitle: crystal structure of mouse angiotensinogen in the oxidised form
62	c3fxbB_	Alignment	not modelled	11.4	9	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of the ectoine-binding protein ueha
63	d1scfa_	Alignment	not modelled	11.3	17	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
64	c1scfA_	Alignment	not modelled	11.3	17	PDB header: hormone/growth factor Chain: A: PDB Molecule: stem cell factor; PDBTitle: human recombinant stem cell factor
65	c3b4uB_	Alignment	not modelled	11.1	25	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
66	c1x4rA_	Alignment	not modelled	10.9	23	PDB header: apoptosis Chain: A: PDB Molecule: parp14 protein; PDBTitle: solution structure of wwe domain in parp14 protein
67	c3fkka_	Alignment	not modelled	10.9	33	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
68	c2pfzA_	Alignment	not modelled	10.8	10	PDB header: transport protein Chain: A: PDB Molecule: putative exported protein; PDBTitle: crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
69	d2i52a1	Alignment	not modelled	10.8	16	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
70	d2akja1	Alignment	not modelled	10.8	20	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SIR/NiR-like domains 1 and 3
71	c2p4vA_	Alignment	not modelled	10.7	16	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
72	c1yv0I_	Alignment	not modelled	10.7	16	PDB header: contractile protein Chain: I: PDB Molecule: troponin i, fast skeletal muscle; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-2 free state
73	d1vcsa1	Alignment	not modelled	10.7	20	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
74	c3f9tB_	Alignment	not modelled	10.4	13	PDB header: lyase Chain: B: PDB Molecule: l-tyrosine decarboxylase mfna; PDBTitle: crystal structure of l-tyrosine decarboxylase mfna (ec 4.1.1.25)2 (np_247014.1) from methanococcus jannaschii at 2.11 a resolution
75	d1s0aa_	Alignment	not modelled	10.3	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
76	d2ieca1	Alignment	not modelled	10.2	19	Fold: MK0786-like Superfamily: MK0786-like Family: MK0786-like
77	d2qsba1	Alignment	not modelled	9.7	37	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
78	d1lfup_	Alignment	not modelled	9.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
79	c3okgB_	Alignment	not modelled	9.4	24	PDB header: dna binding protein Chain: B: PDB Molecule: restriction endonuclease s subunits; PDBTitle: crystal structure of hsdS subunit from thermoanaerobacter2 tengcongensis
80	d1elua_	Alignment	not modelled	9.2	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
81	c3lciA_	Alignment	not modelled	9.0	17	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase;

						PDBTitle: the d-sialic acid aldolase mutant v251w
82	c3mb2J_	Alignment	not modelled	9.0	10	PDB header: isomerase Chain: J: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the 4 tautomerase superfamily
83	c3hz7A_	Alignment	not modelled	8.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the sira-like protein (dsy4693) from2 desulfitobacterium hafniense, northeast structural genomics3 consortium target dhr2a
84	d1edla_	Alignment	not modelled	8.5	15	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
85	d2qzga1	Alignment	not modelled	8.5	32	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
86	c2hl2A_	Alignment	not modelled	8.4	15	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
87	c3gabC_	Alignment	not modelled	8.4	12	PDB header: hydrolase Chain: C: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: c-terminal domain of bacillus subtilis mutl crystal form i
88	c3e6yB_	Alignment	not modelled	8.3	17	PDB header: signaling protein Chain: B: PDB Molecule: 14-3-3-like protein c; PDBTitle: structure of 14-3-3 in complex with the differentiation-inducing agent2 cotylenin a
89	c2ql8A_	Alignment	not modelled	8.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
90	c1q2lA_	Alignment	not modelled	8.2	41	PDB header: antitumor protein Chain: A: PDB Molecule: pnc27; PDBTitle: nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
91	d1qtwa_	Alignment	not modelled	8.2	7	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
92	c2l5qA_	Alignment	not modelled	8.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of bvu_3817 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr159
93	c1grjA_	Alignment	not modelled	8.1	18	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
94	c1kmiZ_	Alignment	not modelled	7.9	26	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
95	c2x7vA_	Alignment	not modelled	7.9	9	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
96	c2y7cA_	Alignment	not modelled	7.9	19	PDB header: transferase Chain: A: PDB Molecule: type-1 restriction enzyme ecoki specificity protein; PDBTitle: atomic model of the ocr-bound methylase complex from the2 type i restriction-modification enzyme ecoki (m2s1). based3 on fitting into em map 1534.
97	c2ogfD_	Alignment	not modelled	7.8	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
98	c3g0sA_	Alignment	not modelled	7.7	21	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
99	d1qo5b_	Alignment	not modelled	7.6	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase