












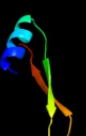












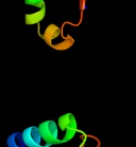
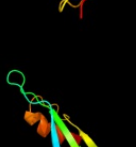
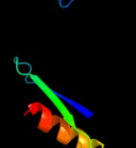
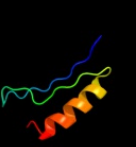
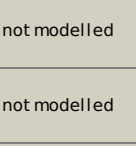


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sr9a3	 Alignment		60.5	17	Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
2	c3beeB_	 Alignment		59.1	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative yfre protein; PDBTitle: crystal structure of putative yfre protein from vibrio2 paraaemolyticus
3	c2hfvA_	 Alignment		45.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
4	c2q5cA_	 Alignment		43.3	21	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
5	d2hfva1	 Alignment		41.2	27	Fold: Ferredoxin-like Superfamily: GlnB-like Family: RPA1041-like
6	c3pmdA_	 Alignment		32.9	21	PDB header: lipid binding protein Chain: A: PDB Molecule: conserved domain protein; PDBTitle: crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
7	d1ewqa4	 Alignment		29.6	32	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
8	c2katA_	 Alignment		29.3	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
9	d2uube2	 Alignment		28.7	17	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
10	d1fcha_	 Alignment		27.5	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
11	c2e2eA_	 Alignment		25.1	22	PDB header: lyase Chain: A: PDB Molecule: formate-dependent nitrite reductase complex nrfg subunit; PDBTitle: tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7

12	d1pkpa2	Alignment		24.9	14	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
13	c1ykuB_	Alignment		22.8	18	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein pxo2-61; PDBTitle: crystal structure of a sensor domain homolog
14	d2cp9a1	Alignment		22.3	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
15	d2id1a1	Alignment		20.9	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
16	d1o98a1	Alignment		20.4	26	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
17	d2pju1	Alignment		19.6	18	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
18	d1t41b_	Alignment		19.5	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
19	c2zkqe_	Alignment		19.4	11	PDB header: ribosomal protein/rna Chain: E: PDB Molecule: rna expansion segment es6 part ii; 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
20	c2khxA_	Alignment		19.1	22	PDB header: gene regulation,nuclear protein Chain: A: PDB Molecule: ribonuclease 3; PDBTitle: drosha double-stranded rna binding motif
21	d2qale2	Alignment	not modelled	18.7	11	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Ribosomal S5 protein, N-terminal domain
22	d1aipc1	Alignment	not modelled	18.6	26	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
23	c2xzmE_	Alignment	not modelled	18.5	14	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein s5 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
24	d1efub3	Alignment	not modelled	18.0	26	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
25	c2pjuD_	Alignment	not modelled	17.7	18	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
26	d1xb2b1	Alignment	not modelled	16.9	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: TS-N domain
27	c1s1hE_	Alignment	not modelled	16.6	14	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s2; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
						Fold: Ferredoxin-like

28	d1vk8a_	Alignment	not modelled	15.9	14	Superfamily: MTH1187/YkoF-like Family: MTH1187-like
29	d1lxja_	Alignment	not modelled	15.7	7	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
30	c1t4oA_	Alignment	not modelled	15.0	15	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of rnt1p dsrbd
31	d1t4oa_	Alignment	not modelled	15.0	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
32	d2o5aa1	Alignment	not modelled	14.3	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
33	d1ekza_	Alignment	not modelled	14.3	13	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
34	c2kckA_	Alignment	not modelled	14.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tpr repeat; PDBTitle: nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
35	c3urzB_	Alignment	not modelled	14.0	19	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution
36	d2iboa1	Alignment	not modelled	14.0	9	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
37	d1yqha1	Alignment	not modelled	13.8	18	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
38	c3pm7A_	Alignment	not modelled	13.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
39	d1zxoal	Alignment	not modelled	13.4	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
40	c3fflC_	Alignment	not modelled	13.3	8	PDB header: cell cycle Chain: C: PDB Molecule: anaphase-promoting complex subunit 7; PDBTitle: crystal structure of the n-terminal domain of anaphase-2 promoting complex subunit 7
41	d1qu6a1	Alignment	not modelled	13.1	18	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
42	c2pokB_	Alignment	not modelled	13.0	11	PDB header: hydrolase Chain: B: PDB Molecule: peptidase, m20/m25/m40 family; PDBTitle: crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
43	d1qu6a2	Alignment	not modelled	12.9	12	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
44	c3upsA_	Alignment	not modelled	12.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
45	d1t0ba_	Alignment	not modelled	12.5	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
46	c3k9iA_	Alignment	not modelled	11.9	12	PDB header: protein binding Chain: A: PDB Molecule: bh0479 protein; PDBTitle: crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
47	c3c6cA_	Alignment	not modelled	11.9	13	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
48	d1g94a2	Alignment	not modelled	11.8	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
49	c3lotC_	Alignment	not modelled	11.8	19	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
50	d1ckqa_	Alignment	not modelled	11.8	19	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoRI
51	d2hr2a1	Alignment	not modelled	11.7	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
52	c3ramC_	Alignment	not modelled	11.6	18	PDB header: hydrolase Chain: C: PDB Molecule: hmra protein; PDBTitle: crystal structure of hmra
53	c3chvA_	Alignment	not modelled	11.4	13	PDB header: metal binding protein Chain: A: PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi

					dss-3 at 1.45 a3 resolution
54	c1wr1B_	Alignment	not modelled	11.4	38 PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like protein dsk2; PDBTitle: the complex sturcture of dsk2p uba with ubiquitin
55	c1y7eA_	Alignment	not modelled	11.3	22 PDB header: hydrolase Chain: A: PDB Molecule: probable m18-family aminopeptidase 1; PDBTitle: the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
56	d1u9pa1	Alignment	not modelled	11.1	14 Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
57	c1bplA_	Alignment	not modelled	11.0	20 PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
58	c2dbaA_	Alignment	not modelled	10.9	15 PDB header: structural protein Chain: A: PDB Molecule: smooth muscle cell associated protein-1, isoform PDBTitle: the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
59	c2x4bA_	Alignment	not modelled	10.7	12 PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
60	c1eg0B_	Alignment	not modelled	10.5	15 PDB header: ribosome PDB COMPND:
61	d1hx0a2	Alignment	not modelled	10.5	25 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	c1p6gE_	Alignment	not modelled	10.5	11 PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s5; PDBTitle: real space refined coordinates of the 30s subunit fitted2 into the low resolution cryo-em map of the ef-g.gtp state3 of e. coli 70s ribosome
63	c1o0wB_	Alignment	not modelled	10.4	23 PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease iii; PDBTitle: crystal structure of ribonuclease iii (tm1102) from2 thermotoga maritima at 2.0 a resolution
64	c2ow8f_	Alignment	not modelled	10.4	17 PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
65	c3nj2B_	Alignment	not modelled	10.1	21 PDB header: unknown function Chain: B: PDB Molecule: duf269-containing protein; PDBTitle: crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
66	d1jaea2	Alignment	not modelled	9.9	20 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
67	d1hz4a_	Alignment	not modelled	9.8	17 Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
68	c1ysjB_	Alignment	not modelled	9.8	16 PDB header: hydrolase Chain: B: PDB Molecule: protein yxep; PDBTitle: crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
69	d1ua7a2	Alignment	not modelled	9.7	25 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	c3faxA_	Alignment	not modelled	9.7	18 PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
71	d1b74a1	Alignment	not modelled	9.7	13 Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
72	c3bbnE_	Alignment	not modelled	9.4	11 PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein s5; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
73	c3e02A_	Alignment	not modelled	9.4	13 PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
74	c1sp8A_	Alignment	not modelled	9.3	25 PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: 4-hydroxyphenylpyruvate dioxygenase
75	d1zbsa2	Alignment	not modelled	9.1	18 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
76	c3e49A_	Alignment	not modelled	9.1	16 PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
77	c3draA_	Alignment	not modelled	9.0	11 PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
78	d1ddga2	Alignment	not modelled	8.9	15 Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain

					Family: NADPH-cytochrome p450 reductase-like PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hopj type iii effector protein; PDBTitle: putative hopj type iii effector protein from vibrio parahaemolyticus
79	c2qm2B_	Alignment	not modelled	8.8	38
80	d1eeja2	Alignment	not modelled	8.8	22
81	d1oqya1	Alignment	not modelled	8.6	21
82	c2xeVB_	Alignment	not modelled	8.6	11
83	d3dhpa2	Alignment	not modelled	8.6	25
84	c1sr9A_	Alignment	not modelled	8.5	19
85	d1sp8a2	Alignment	not modelled	8.5	25
86	c2cwBA_	Alignment	not modelled	8.4	28
87	c3obhA_	Alignment	not modelled	8.3	19
88	c2dnaA_	Alignment	not modelled	8.2	19
89	d1e43a2	Alignment	not modelled	8.2	15
90	c3g7pA_	Alignment	not modelled	8.2	21
91	d1myka_	Alignment	not modelled	8.1	14
92	d2fi0a1	Alignment	not modelled	8.1	15
93	d1ud2a2	Alignment	not modelled	8.0	15
94	d1baza_	Alignment	not modelled	8.0	14
95	c2vvyC_	Alignment	not modelled	7.7	16
96	d1gja2	Alignment	not modelled	7.6	14
97	c2dskA_	Alignment	not modelled	7.6	25
98	c2zfdB_	Alignment	not modelled	7.6	12
99	c2epiA_	Alignment	not modelled	7.5	14