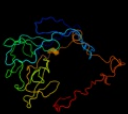
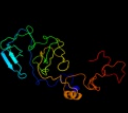
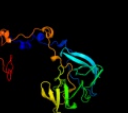
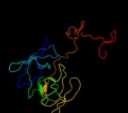
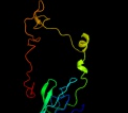
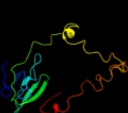
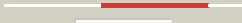
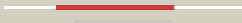
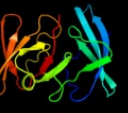
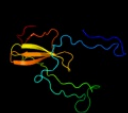
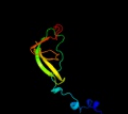
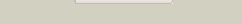
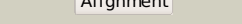
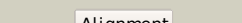
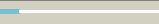
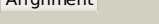
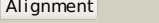
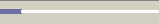
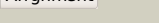
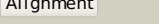
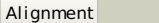
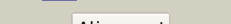
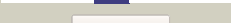
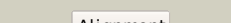
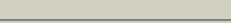
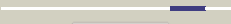


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z4lC_	 Alignment		100.0	100	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l2; PDBTitle: crystal structure of the bacterial ribosome from escherichia2 coli in complex with paromomycin and ribosome recycling3 factor (rrf). this file contains the 50s subunit of the4 first 70s ribosome, with paromomycin and rrf bound. the5 entire crystal structure contains two 70s ribosomes and is6 described in remark 400.
2	c3d5bD_	 Alignment		100.0	59	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l2; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
3	c3bboE_	 Alignment		100.0	48	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein l2; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
4	c2gyaA_	 Alignment		100.0	100	PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein l2; PDBTitle: structure of the 50s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
5	c4a1cA_	 Alignment		100.0	34	PDB header: ribosome Chain: A: PDB Molecule: rpl8; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4.
6	c2zkra_	 Alignment		100.0	32	PDB header: ribosomal protein/rna Chain: A: PDB Molecule: rna expansion segment es3; 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
7	c1kqsA_	 Alignment		100.0	40	PDB header: ribosome Chain: A: PDB Molecule: ribosomal protein l2; PDBTitle: the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
8	c2b66D_	 Alignment		100.0	60	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l2; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
9	d2qamc1	 Alignment		100.0	100	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
10	d2j0ld1	 Alignment		100.0	62	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
11	d2zjra1	 Alignment		100.0	62	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2

12	dlvqoa1	 Alignment		100.0	38	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
13	c1rl2A_	 Alignment		100.0	64	PDB header: ribosomal protein Chain: A: PDB Molecule: protein (ribosomal protein l2); PDBTitle: ribosomal protein l2 rna-binding domain from bacillus2 stearotherophilus
14	c2ftcB_	 Alignment		100.0	39	PDB header: ribosome Chain: B: PDB Molecule: mitochondrial ribosomal protein l2; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
15	d2j01d2	 Alignment		100.0	55	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
16	d2zjra2	 Alignment		100.0	62	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
17	d1rl2a1	 Alignment		99.9	60	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: C-terminal domain of ribosomal protein L2
18	dlvqoa2	 Alignment		99.9	39	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
19	d1rl2a2	 Alignment		99.9	68	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
20	d2qamc2	 Alignment		99.8	100	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
21	c3peiA_	 Alignment	not modelled	87.1	24	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from francisella2 tularensis
22	d2dy1a1	 Alignment	not modelled	65.8	21	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
23	c3ij3A_	 Alignment	not modelled	60.9	29	PDB header: hydrolase Chain: A: PDB Molecule: cytosol aminopeptidase; PDBTitle: 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
24	c1lanA_	 Alignment	not modelled	60.7	24	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase; PDBTitle: leucine aminopeptidase complex with l-leucinal
25	c3h8gC_	 Alignment	not modelled	53.3	21	PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
26	c3kzwD_	 Alignment	not modelled	45.9	22	PDB header: hydrolase Chain: D: PDB Molecule: cytosol aminopeptidase; PDBTitle: crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
27	c3d4rE_	 Alignment	not modelled	38.3	18	PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
28	c3jruB_	 Alignment	not modelled	35.7	22	PDB header: hydrolase Chain: B: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331

29	c2jmzA	 Alignment	not modelled	34.2	19	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein mj0781; PDBTitle: solution structure of a klba intein precursor from2 methanococcus jannaschii
30	d1ulva4	 Alignment	not modelled	32.4	23	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
31	d2bv3a1	 Alignment	not modelled	30.1	30	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
32	c2xzn2	 Alignment	not modelled	29.0	17	PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s8; 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 2
33	c1gytG	 Alignment	not modelled	28.8	22	PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa)
34	c1x65A	 Alignment	not modelled	22.8	18	PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
35	c3nx6A	 Alignment	not modelled	22.4	29	PDB header: chaperone Chain: A: PDB Molecule: 10kda chaperonin; PDBTitle: crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
36	d2pi2e1	 Alignment	not modelled	18.4	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
37	c2pqaB	 Alignment	not modelled	18.2	17	PDB header: replication Chain: B: PDB Molecule: replication protein a 14 kda subunit; PDBTitle: crystal structure of full-length human rpa 14/32 heterodimer
38	c3u5cl	 Alignment	not modelled	17.3	17	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution
39	d3d3ra1	 Alignment	not modelled	15.9	23	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
40	c3d3rA	 Alignment	not modelled	15.1	23	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
41	d1lama1	 Alignment	not modelled	14.6	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
42	c3flzf	 Alignment	not modelled	14.1	31	PDB header: dna binding protein Chain: F: PDB Molecule: putative nucleic acid-binding lipoprotein; PDBTitle: crystal structure of putative nucleic acid-binding lipoprotein2 (yp_001337197.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 2.46 a resolution
43	c2jz8A	 Alignment	not modelled	13.5	67	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
44	d1lf6a2	 Alignment	not modelled	13.1	20	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Bacterial glucoamylase N-terminal domain-like
45	c2dfuB	 Alignment	not modelled	11.7	25	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
46	d1gyta2	 Alignment	not modelled	11.7	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
47	d1yoxa1	 Alignment	not modelled	11.7	24	Fold: Double-stranded beta-helix Superfamily: TRAP-like Family: PA3696/SPS0176-like
48	c2kcyA	 Alignment	not modelled	11.7	22	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution structure of ribosomal protein s8e from2 methanothermobacter thermautotrophicus,3 northeaststructural genomics consortium (nesg) target tr71d
49	d1o6aa	 Alignment	not modelled	10.7	9	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
50	c2cbjA	 Alignment	not modelled	10.6	14	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase; PDBTitle: structure of the clostridium perfringens nagj family 842 glycoside hydrolase, a homologue of human o-glcnaase in3 complex with pugnac
51	d1g03a	 Alignment	not modelled	10.5	86	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
52	d2cqaa1	 Alignment	not modelled	10.4	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TIP49 domain
53	c2j5uB	 Alignment	not modelled	10.2	24	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes

54	c2kcoA	 Alignment	not modelled	10.0	24	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s8e; PDBTitle: solution nmr structure of ribosomal protein sso0164 from2 sulfobolus solfataricus. northeast structural genomics3 consortium (nesg) target sst4.
55	d1k28a3	 Alignment	not modelled	9.4	46	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
56	d1o9ya	 Alignment	not modelled	9.3	18	Fold: Surface presentation of antigens (SPOA) Superfamily: Surface presentation of antigens (SPOA) Family: Surface presentation of antigens (SPOA)
57	d1sawa	 Alignment	not modelled	9.2	24	Fold: FAH Superfamily: FAH Family: FAH
58	d1hxma2	 Alignment	not modelled	9.1	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
59	c3r6oA	 Alignment	not modelled	9.1	36	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
60	d1te7a	 Alignment	not modelled	8.5	16	Fold: PUA domain-like Superfamily: PUA domain-like Family: yqfB-like
61	d1s3sg	 Alignment	not modelled	8.5	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
62	c2kjpA	 Alignment	not modelled	8.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ylbl; PDBTitle: solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
63	c3h6qA	 Alignment	not modelled	8.1	26	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: macrocypin 1a; PDBTitle: macrocypin, a beta-trefoil cysteine protease inhibitor
64	c2qx2A	 Alignment	not modelled	8.1	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sex pheromone staph-cam373; PDBTitle: structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus
65	d1m06g	 Alignment	not modelled	7.9	26	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
66	c2hc9A	 Alignment	not modelled	7.8	29	PDB header: hydrolase Chain: A: PDB Molecule: leucine aminopeptidase 1; PDBTitle: structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
67	d1i42a	 Alignment	not modelled	7.7	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
68	d2z1ca1	 Alignment	not modelled	7.7	31	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
69	d1gtta2	 Alignment	not modelled	7.7	27	Fold: FAH Superfamily: FAH Family: FAH
70	c1wzoC	 Alignment	not modelled	7.3	18	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
71	d1gtta1	 Alignment	not modelled	7.3	24	Fold: FAH Superfamily: FAH Family: FAH
72	c1wz4A	 Alignment	not modelled	7.0	58	PDB header: gene regulation Chain: A: PDB Molecule: major surface antigen; PDBTitle: solution conformation of adr subtype hbv pre-s2 epitope
73	d1udxa1	 Alignment	not modelled	7.0	32	Fold: Obg-fold Superfamily: Obg GTP-binding protein N-terminal domain Family: Obg GTP-binding protein N-terminal domain
74	d2nvna1	 Alignment	not modelled	6.9	33	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
75	c2hbpA	 Alignment	not modelled	6.9	18	PDB header: endocytosis, protein binding Chain: A: PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
76	d2uubm1	 Alignment	not modelled	6.8	28	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
77	d2it9a1	 Alignment	not modelled	6.7	27	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: PMN2A0962/syc2379c-like
78	c2jy9A	 Alignment	not modelled	6.5	24	PDB header: hydrolase Chain: A: PDB Molecule: putative trna hydrolase domain; PDBTitle: nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
79	c2knrA	 Alignment	not modelled	6.4	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atc0905; PDBTitle: solution structure of protein atu0922 from a. tumefaciens. northeast2 structural genomics consortium target

					att13. ontario center for3 structural proteomics target atc0905
80	d2d6fa1	Alignment	not modelled	6.3	18 Fold: Sm-like fold Superfamily: GatD N-terminal domain-like Family: GatD N-terminal domain-like
81	c2dzkA	Alignment	not modelled	6.3	24 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubx domain-containing protein 2; PDBTitle: structure of the ubx domain in mouse ubx domain-containing2 protein 2
82	d2zgwa1	Alignment	not modelled	6.2	47 Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)
83	c3j0cH	Alignment	not modelled	6.1	32 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
84	c2k4yA	Alignment	not modelled	6.1	11 PDB header: metal transport Chain: A: PDB Molecule: feoa-like protein; PDBTitle: nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
85	d1q1ca2	Alignment	not modelled	6.1	12 Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
86	d2cr5a1	Alignment	not modelled	6.0	18 Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
87	d1gff2	Alignment	not modelled	6.0	30 Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
88	c2q1dX	Alignment	not modelled	5.6	20 PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
89	d2ibaa2	Alignment	not modelled	5.6	43 Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
90	c3l0xB	Alignment	not modelled	5.5	32 PDB header: replication Chain: B: PDB Molecule: proliferating cell nuclear antigen; PDBTitle: structure of split yeast pcna
91	c2xfbl	Alignment	not modelled	5.4	13 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
92	c3n43B	Alignment	not modelled	5.3	13 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.
93	d1c9ha	Alignment	not modelled	5.3	17 Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
94	d1q32a1	Alignment	not modelled	5.3	14 Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
95	d1nkqa	Alignment	not modelled	5.3	19 Fold: FAH Superfamily: FAH Family: FAH
96	d1j2ga2	Alignment	not modelled	5.2	29 Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
97	c1ponB	Alignment	not modelled	5.2	55 PDB header: calcium-binding protein Chain: B: PDB Molecule: troponin c; PDBTitle: site iii-site iv troponin c heterodimer, nmr
98	c2k5lA	Alignment	not modelled	5.1	11 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: feoa; PDBTitle: solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
99	d2znvb1	Alignment	not modelled	5.1	16 Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related