



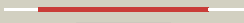



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iy3A_	 Alignment		100.0	43	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein ffh; PDBTitle: structure of the e. coli signal recognition particle2 bound to a translating ribosome
2	c3dm5A_	 Alignment		100.0	36	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
3	c2j289_	 Alignment		100.0	100	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
4	c2j37W_	 Alignment		100.0	31	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
5	c1qzWC_	 Alignment		100.0	34	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
6	c2v3cC_	 Alignment		100.0	37	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
7	c3dmdA_	 Alignment		100.0	35	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
8	c2j7pA_	 Alignment		100.0	48	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and tsy
9	c1j8yF_	 Alignment		100.0	36	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
10	c2yhsA_	 Alignment		100.0	32	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
11	c2qy9A_	 Alignment		100.0	32	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy

12	c3b9qA_	Alignment		100.0	33	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
13	c1zu4A_	Alignment		100.0	30	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
14	c2og2A_	Alignment		100.0	33	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsyt from arabidopsis2 thaliana
15	c1vmaA_	Alignment		100.0	38	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: crystal structure of cell division protein ftsyt (tm0570) from2 thermotoga maritima at 1.60 a resolution
16	c2cnwF_	Alignment		100.0	38	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyt; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyt
17	c2px0D_	Alignment		100.0	21	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
18	d1j8yf2	Alignment		100.0	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
19	d1qzxa2	Alignment		100.0	32	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
20	d1qzxa3	Alignment		100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
21	d1vmaa2	Alignment	not modelled	100.0	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
22	c2jqeA_	Alignment	not modelled	100.0	37	PDB header: signaling protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: soutuion structure of af54 m-domain
23	d1ls1a2	Alignment	not modelled	100.0	50	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
24	d2ffha2	Alignment	not modelled	100.0	44	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
25	d2qy9a2	Alignment	not modelled	100.0	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
26	d1qb2a_	Alignment	not modelled	100.0	28	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
27	d1okkd2	Alignment	not modelled	99.9	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
28	d1hq1a_	Alignment	not modelled	99.9	100	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
						Fold: Signal peptide-binding domain

29	d1dula_	Alignment	not modelled	99.8	76	Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
30	d1ls1a1	Alignment	not modelled	99.6	45	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
31	d1j8yf1	Alignment	not modelled	99.5	27	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
32	d1wgwa_	Alignment	not modelled	99.5	26	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
33	d1qzxa1	Alignment	not modelled	99.5	18	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
34	d2qm8a1	Alignment	not modelled	99.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	d1rj9b1	Alignment	not modelled	99.4	47	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
36	d1nija1	Alignment	not modelled	99.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
37	c2wwwB_	Alignment	not modelled	99.2	16	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
38	c3nxsA_	Alignment	not modelled	99.2	19	PDB header: transport protein Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
39	c3cioA_	Alignment	not modelled	99.1	23	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
40	c2vedA_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
41	c3la6P_	Alignment	not modelled	98.9	23	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
42	c3of5A_	Alignment	not modelled	98.9	10	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
43	d2afhe1	Alignment	not modelled	98.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
44	d2p67a1	Alignment	not modelled	98.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
45	c3zq6D_	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
46	c3io3A_	Alignment	not modelled	98.7	13	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
47	c3k9gA_	Alignment	not modelled	98.7	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
48	c3ibgF_	Alignment	not modelled	98.7	25	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
49	d1ihua2	Alignment	not modelled	98.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
50	d1cp2a_	Alignment	not modelled	98.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
51	cliioA_	Alignment	not modelled	98.6	23	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
52	c3ea0B_	Alignment	not modelled	98.6	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
53	c2hf9A_	Alignment	not modelled	98.6	21	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hybp from methanocaldococcus2 jannaschii in the triphosphate form
54	c2ozeA_	Alignment	not modelled	98.6	20	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes PDB header: hydrolase

55	c3ug7D_	Alignment	not modelled	98.6	23	Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
56	c2qmoA_	Alignment	not modelled	98.5	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
57	d1bifa1_	Alignment	not modelled	98.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
58	c2wooC_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
59	d1g3qa_	Alignment	not modelled	98.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
60	c3fmfA_	Alignment	not modelled	98.5	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
61	d1byia_	Alignment	not modelled	98.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
62	c2xj9B_	Alignment	not modelled	98.5	22	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
63	c3igfB_	Alignment	not modelled	98.5	23	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
64	c2ph1A_	Alignment	not modelled	98.5	21	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
65	c1k6mA_	Alignment	not modelled	98.4	22	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
66	c3kjgB_	Alignment	not modelled	98.4	19	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
67	c3endA_	Alignment	not modelled	98.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
68	d1ihua1_	Alignment	not modelled	98.4	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
69	c2f1rA_	Alignment	not modelled	98.4	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
70	c3fkqA_	Alignment	not modelled	98.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
71	d1iona_	Alignment	not modelled	98.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
72	c2wojD_	Alignment	not modelled	98.4	16	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
73	c1hyqA_	Alignment	not modelled	98.4	25	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
74	d1hyqa_	Alignment	not modelled	98.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	d1tq4a_	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
76	c1bifA_	Alignment	not modelled	98.3	21	PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
77	c1nijA_	Alignment	not modelled	98.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
78	c2i1vB_	Alignment	not modelled	98.3	21	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
						PDB header: cell cycle, hydrolase

79	c3q9lB_	Alignment	not modelled	98.3	16	Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
80	c2vyeA_	Alignment	not modelled	98.2	12	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnaC-ssdna complex
81	c3ez6B_	Alignment	not modelled	98.2	21	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
82	c3kx2A_	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna PDBTitle: crystal structure of prp43p in complex with adp
83	c3cwqB_	Alignment	not modelled	98.2	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: para family chromosome partitioning protein; PDBTitle: crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
84	c2e87A_	Alignment	not modelled	98.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1320; PDBTitle: crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp
85	c3pg5A_	Alignment	not modelled	98.2	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
86	c2p5tD_	Alignment	not modelled	98.1	18	PDB header: transcription regulator Chain: D: PDB Molecule: pez2; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
87	c2xzlA_	Alignment	not modelled	98.1	22	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
88	c2q6tB_	Alignment	not modelled	98.1	12	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
89	c3md0A_	Alignment	not modelled	98.1	19	PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein)
90	d1tf7a2_	Alignment	not modelled	98.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
91	c2wjyA_	Alignment	not modelled	98.1	25	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
92	c1a1vA_	Alignment	not modelled	98.0	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (ns3 protein); PDBTitle: hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
93	c2bekB_	Alignment	not modelled	98.0	26	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein2 soj
94	c2j3eA_	Alignment	not modelled	98.0	23	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
95	d1yrba1_	Alignment	not modelled	98.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
96	c1xzqA_	Alignment	not modelled	98.0	24	PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
97	c1cu1B_	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: B: PDB Molecule: protein (protease/helicase ns3); PDBTitle: crystal structure of an enzyme complex from hepatitis c2 virus
98	c3ec2A_	Alignment	not modelled	98.0	17	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnaC; PDBTitle: crystal structure of the dnaC helicase loader
99	d1cr2a_	Alignment	not modelled	97.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
100	c3i8sC_	Alignment	not modelled	97.9	20	PDB header: transport protein Chain: C: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
101	c3cr8C_	Alignment	not modelled	97.9	15	PDB header: transferase Chain: C: PDB Molecule: sulfate adenyllyltransferase, adenyllysulfate PDBTitle: hexameric aps kinase from thiobacillus denitrificans
102	c2recB_	Alignment	not modelled	97.9	21	PDB header: helicase PDB COMPND:
103	d1h65a_	Alignment	not modelled	97.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

					Family: G proteins
104	d1mo6a1	Alignment	not modelled	97.9	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
105	c2qgzA	Alignment	not modelled	97.9	21 PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
106	c1xp8A	Alignment	not modelled	97.9	16 PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
107	c3gehA	Alignment	not modelled	97.9	15 PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
108	c3ldaA	Alignment	not modelled	97.9	16 PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
109	d1xp8a1	Alignment	not modelled	97.8	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
110	c2ztsB	Alignment	not modelled	97.8	18 PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
111	d1qvra3	Alignment	not modelled	97.8	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
112	d1x6va3	Alignment	not modelled	97.8	23 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5' phosphosulfate kinase (APS kinase)
113	c1d2eA	Alignment	not modelled	97.8	31 PDB header: rna binding protein Chain: A: PDB Molecule: elongation factor tu (ef-tu); PDBTitle: crystal structure of mitochondrial ef-tu in complex with gdp
114	c2hjaA	Alignment	not modelled	97.8	17 PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein enga; PDBTitle: the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
115	c2w58B	Alignment	not modelled	97.8	23 PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dna1
116	c3d8bB	Alignment	not modelled	97.8	16 PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
117	d1xjca	Alignment	not modelled	97.8	24 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
118	c1szpC	Alignment	not modelled	97.8	14 PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
119	d1odfa	Alignment	not modelled	97.7	18 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
120	d1knqa	Alignment	not modelled	97.7	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Gluconate kinase