



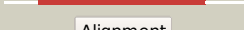

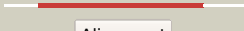









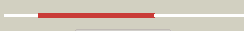







Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2916c_ffh_3224718_3226295
 Date Thu Aug 8 16:20:07 BST 2019
 Unique Job ID 088725bf7b49cf82

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j37W_	 Alignment		100.0	31	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
2	c2iy3A_	 Alignment		100.0	46	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
3	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 assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
4	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
5	c2j289_	 Alignment		100.0	52	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
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	c5gafi_	 Alignment		100.0	53	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
8	c3dmdA_	 Alignment		100.0	37	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
9	c2j7pA_	 Alignment		100.0	53	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
10	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
11	c2yhsA_	 Alignment		100.0	37	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy

12	c2q9cA_	Alignment		100.0	31	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
13	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
14	c1zu4A_	Alignment		100.0	27	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
15	c2qy9A_	Alignment		100.0	37	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsyt
16	c6cy1B_	Alignment		100.0	34	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsyt; PDBTitle: crystal structure of signal recognition particle receptor ftsyt from2 elizabethkingia anophelis
17	c2og2A_	Alignment		100.0	32	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsyt from arabidopsis2 thaliana
18	c5l3sF_	Alignment		100.0	30	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsyt; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsyt
19	c5l3qB_	Alignment		100.0	29	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
20	c1vmaA_	Alignment		100.0	37	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
21	c5l3rC_	Alignment	not modelled	100.0	52	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsyt from2 arabidopsis thaliana
22	c4ak9A_	Alignment	not modelled	100.0	31	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsyt from physcomitrella patens
23	c2cnwF_	Alignment	not modelled	100.0	35	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyt; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyt
24	d1j8yf2	Alignment	not modelled	100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
25	c2px0D_	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnp/mg(2+)
26	d1qzxa2	Alignment	not modelled	100.0	31	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
27	c4xcoC_	Alignment	not modelled	100.0	30	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle 54 kda protein,signal sequence; PDBTitle: signal-sequence induced conformational changes in the signal2 recognition particle
28	d1qzxa3	Alignment	not modelled	100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

29	d1vmaa2	Alignment	not modelled	100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	c2jqeA_	Alignment	not modelled	100.0	32	PDB header: signaling protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: soutuion structure of af54 m-domain
31	d2ffha2	Alignment	not modelled	100.0	49	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
32	d1ls1a2	Alignment	not modelled	100.0	55	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
33	d2qy9a2	Alignment	not modelled	100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
34	d1qb2a_	Alignment	not modelled	100.0	30	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
35	c4ue4C_	Alignment	not modelled	100.0	56	PDB header: translation Chain: C: PDB Molecule: signal recognition particle protein; PDBTitle: structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
36	d1okkd2	Alignment	not modelled	99.9	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
37	d1hq1a_	Alignment	not modelled	99.8	57	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
38	d1dula_	Alignment	not modelled	99.8	40	Fold: Signal peptide-binding domain Superfamily: Signal peptide-binding domain Family: Signal peptide-binding domain
39	d1ls1a1	Alignment	not modelled	99.6	48	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
40	d2qm8a1	Alignment	not modelled	99.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
41	d1j8yf1	Alignment	not modelled	99.5	25	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
42	d1wgwa_	Alignment	not modelled	99.5	25	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
43	d1qzxa1	Alignment	not modelled	99.4	21	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
44	d1nija1	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
45	d1rj9b1	Alignment	not modelled	99.4	49	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
46	c2wwwB_	Alignment	not modelled	99.3	18	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
47	c3cioA_	Alignment	not modelled	99.3	24	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
48	c3nxsA_	Alignment	not modelled	99.2	18	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
49	c2vedA_	Alignment	not modelled	99.2	21	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
50	c3la6P_	Alignment	not modelled	99.1	24	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
51	c3of5A_	Alignment	not modelled	99.0	10	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
52	c5zmfA_	Alignment	not modelled	99.0	19	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
53	d2afhe1	Alignment	not modelled	98.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
54	c1ii0A_	Alignment	not modelled	98.9	26	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
55	d1ihua2	Alignment	not modelled	98.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

56	d1cp2a_	Alignment	not modelled	98.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
57	c4rz3B_	Alignment	not modelled	98.9	15	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
58	c5j1jA_	Alignment	not modelled	98.9	22	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
59	c3zq6D_	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
60	d2p67a1	Alignment	not modelled	98.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
61	c2wooc_	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
62	c6g2gA_	Alignment	not modelled	98.8	19	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
63	c3io3A_	Alignment	not modelled	98.8	14	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
64	c6bs3A_	Alignment	not modelled	98.8	20	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
65	c4nkrB_	Alignment	not modelled	98.8	12	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
66	c3k9gA_	Alignment	not modelled	98.8	20	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
67	c3fkqA_	Alignment	not modelled	98.8	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
68	d1ihua1	Alignment	not modelled	98.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
69	c3ibgF_	Alignment	not modelled	98.8	20	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
70	c3ea0B_	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
71	c2ph1A_	Alignment	not modelled	98.8	18	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
72	c6bs5B_	Alignment	not modelled	98.8	29	PDB header: unknown function Chain: B: PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
73	d1iona_	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
74	c3ug7D_	Alignment	not modelled	98.7	21	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
75	c3endA_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
76	c3fmfA_	Alignment	not modelled	98.7	17	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
77	d1g3qa_	Alignment	not modelled	98.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
78	c3kjgB_	Alignment	not modelled	98.7	19	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
79	c2wojD_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
80	c4pfsA_	Alignment	not modelled	98.7	25	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
81	c2qmoA_	Alignment	not modelled	98.7	17	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from

				98.7	25	helicobacter2 pylori PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
82	c4dzzB	Alignment	not modelled	98.7	25	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
83	c2ozeA	Alignment	not modelled	98.7	22	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
84	c3ez6B	Alignment	not modelled	98.7	16	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
85	d1byia	Alignment	not modelled	98.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	c2xj9B	Alignment	not modelled	98.7	15	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
87	d1hyqa	Alignment	not modelled	98.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
88	c1hyqA	Alignment	not modelled	98.6	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
89	c3iqfB	Alignment	not modelled	98.6	18	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
90	c2hf9A	Alignment	not modelled	98.6	18	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
91	c4ru8C	Alignment	not modelled	98.6	22	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
92	c4v02B	Alignment	not modelled	98.6	17	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: mind:mind cell division protein complex, aquifex aeolicus
93	c5hcnA	Alignment	not modelled	98.6	20	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
94	c3q9lB	Alignment	not modelled	98.5	17	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
95	c2f1rA	Alignment	not modelled	98.5	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
96	c3pg5A	Alignment	not modelled	98.5	21	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
97	d1bifa1	Alignment	not modelled	98.5	19	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
98	c6iucC	Alignment	not modelled	98.4	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spoj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
99	c3vx3A	Alignment	not modelled	98.4	18	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
100	c3cwqB	Alignment	not modelled	98.4	23	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
101	c5bwkA	Alignment	not modelled	98.4	20	PDB header: hydrolase/transport Chain: A: PDB Molecule: atpase get3; PDBTitle: 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae
102	c1xzqA	Alignment	not modelled	98.3	22	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
103	c1nijA	Alignment	not modelled	98.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
104	c5xktA	Alignment	not modelled	98.3	21	PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel
105	c2bekB	Alignment	not modelled	98.3	25	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
106	c2p5tD	Alignment	not modelled	98.3	13	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
107	d1tq4a_	Alignment	not modelled	98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
108	c4b4tI_	Alignment	not modelled	98.2	18	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
109	c5e7pA_	Alignment	not modelled	98.2	23	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
110	c3md0A_	Alignment	not modelled	98.2	20	PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
111	c2wjyA_	Alignment	not modelled	98.2	19	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
112	c6epdM_	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
113	c5eaxB_	Alignment	not modelled	98.1	23	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
114	c3ezfA_	Alignment	not modelled	98.1	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
115	c6hegA_	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rha helicase hrpb
116	c2xzlA_	Alignment	not modelled	98.1	26	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
117	c4wiaA_	Alignment	not modelled	98.1	13	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
118	c5j1sA_	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: A: PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
119	c5gjqL_	Alignment	not modelled	98.1	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
120	c3kx2A_	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp43; PDBTitle: crystal structure of prp43p in complex with adp