

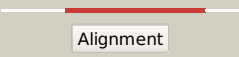

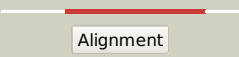

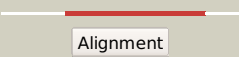

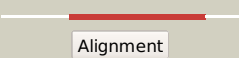

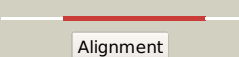

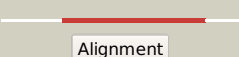







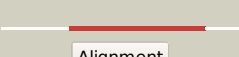



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2921c_(ftsY)_3232881_3234149
Date	Thu Aug 8 16:20:07 BST 2019
Unique Job ID	fa36f807cc5ade5b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yhsA_	 Alignment		100.0	40	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
2	c5gafi_	 Alignment		100.0	32	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
3	c2iy3A_	 Alignment		100.0	36	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
4	c3dm5A_	 Alignment		100.0	32	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.
5	c2j37W_	 Alignment		100.0	30	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
6	c2qy9A_	 Alignment		100.0	41	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
7	c6cy1B_	 Alignment		100.0	42	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
8	c3b9qA_	 Alignment		100.0	42	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsY from arabidopsis thaliana
9	c2og2A_	 Alignment		100.0	41	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
10	c2j289_	 Alignment		100.0	32	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
11	c1qzwC_	 Alignment		100.0	30	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

12	c1vmaA_	Alignment		100.0	48	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from <i>M. thermotoga maritima</i> at 1.60 Å resolution
13	c2v3cC_	Alignment		100.0	33	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 <i>M. jannaschii</i>
14	c1zu4A_	Alignment		100.0	35	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from <i>Mycoplasma mycoides</i> -space2 group p21212
15	c3dmdA_	Alignment		100.0	38	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 <i>Pyrococcus furiosus</i>
16	c1j8yF_	Alignment		100.0	31	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from <i>A.2 ambivalens t112a</i> mutant
17	c4ak9A_	Alignment		100.0	41	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from <i>Physcomitrella patens</i>
18	c2j7pA_	Alignment		100.0	36	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
19	c2q9cA_	Alignment		100.0	45	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
20	c5l3sF_	Alignment		100.0	37	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
21	c5l3rC_	Alignment	not modelled	100.0	35	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 ftsy from <i>A.2 arabidopsis thaliana</i>
22	c2cnwF_	Alignment	not modelled	100.0	50	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
23	c5l3qB_	Alignment	not modelled	100.0	32	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
24	c2px0D_	Alignment	not modelled	100.0	24	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
25	d1j8yf2	Alignment	not modelled	100.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
26	d1vmaa2	Alignment	not modelled	100.0	59	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
27	d2qy9a2	Alignment	not modelled	100.0	48	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
28	d1qzxa3	Alignment	not modelled	100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

29	d1ls1a2	Alignment	not modelled	100.0	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	d1okkd2	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
31	d1nija1	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
32	d2qm8a1	Alignment	not modelled	99.4	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
33	c3cioA_	Alignment	not modelled	99.2	18	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
34	d2p67a1	Alignment	not modelled	99.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	c2wwwB_	Alignment	not modelled	99.1	21	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
36	c2vedA_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
37	c3nxsA_	Alignment	not modelled	99.1	25	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
38	d2qy9a1	Alignment	not modelled	99.1	23	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
39	c3of5A_	Alignment	not modelled	99.1	14	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
40	d1vmaa1	Alignment	not modelled	99.0	19	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
41	c3la6P_	Alignment	not modelled	98.9	22	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	c3zq6D_	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
43	c4nkrB_	Alignment	not modelled	98.9	18	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
44	c3ibgF_	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
45	d2afhe1	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
46	c3k9gA_	Alignment	not modelled	98.8	18	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
47	d1ihua2	Alignment	not modelled	98.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
48	c5zmfA_	Alignment	not modelled	98.8	16	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
49	c4dzzB_	Alignment	not modelled	98.7	21	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
50	c6bs3A_	Alignment	not modelled	98.7	22	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
51	d1cp2a_	Alignment	not modelled	98.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
52	c4pfsA_	Alignment	not modelled	98.7	28	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
53	c2f1rA_	Alignment	not modelled	98.7	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
54	c6g2gA_	Alignment	not modelled	98.7	17	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
						PDB header: chaperone

55	c3io3A_	Alignment	not modelled	98.7	17	Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
56	c2ozeA_	Alignment	not modelled	98.7	16	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
57	c6bs5B_	Alignment	not modelled	98.7	30	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
58	c5hcnA_	Alignment	not modelled	98.7	16	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
59	c2wooC_	Alignment	not modelled	98.7	18	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
60	c3ug7D_	Alignment	not modelled	98.7	24	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
61	c4rz3B_	Alignment	not modelled	98.6	16	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase filhg
62	c3fkqA_	Alignment	not modelled	98.6	13	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
63	c3fmfA_	Alignment	not modelled	98.6	20	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
64	c5j1jA_	Alignment	not modelled	98.6	25	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
65	c2ph1A_	Alignment	not modelled	98.6	20	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
66	c3endA_	Alignment	not modelled	98.6	18	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
67	c2qmoA_	Alignment	not modelled	98.6	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
68	c4v02B_	Alignment	not modelled	98.6	16	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
69	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
70	d1byia_	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
71	c1ii0A_	Alignment	not modelled	98.6	20	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
72	d1iona_	Alignment	not modelled	98.6	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
73	d1g3qa_	Alignment	not modelled	98.6	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	c3igfB_	Alignment	not modelled	98.6	20	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
75	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
76	c2xj9B_	Alignment	not modelled	98.6	25	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
77	c3md0A_	Alignment	not modelled	98.5	24	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)
78	d1hyqa_	Alignment	not modelled	98.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	c1hyqA_	Alignment	not modelled	98.5	21	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
						PDB header: hydrolase, metal binding protein

80	c3kjgB	Alignment	not modelled	98.5	20	Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
81	c3ez6B	Alignment	not modelled	98.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
82	c2wojD	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
83	c2p5tD	Alignment	not modelled	98.4	21	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
84	c3cwqB	Alignment	not modelled	98.4	21	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
85	c6b8vA	Alignment	not modelled	98.3	10	PDB header: transferase Chain: A: PDB Molecule: adenylsulfate kinase; PDBTitle: crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
86	c3vx3A	Alignment	not modelled	98.3	22	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
87	c3q9lB	Alignment	not modelled	98.3	16	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
88	c5bwkA	Alignment	not modelled	98.3	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
89	c5xktA	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel
90	d1ihua1	Alignment	not modelled	98.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
91	c2bekB	Alignment	not modelled	98.3	23	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
92	d1bifa1	Alignment	not modelled	98.3	22	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
93	c1xp8A	Alignment	not modelled	98.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
94	c3pg5A	Alignment	not modelled	98.3	25	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
95	c1bifa	Alignment	not modelled	98.2	20	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
96	c1k6mA	Alignment	not modelled	98.2	17	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
97	c6iuuC	Alignment	not modelled	98.2	19	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
98	d1tf7a2	Alignment	not modelled	98.2	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
99	c5jlSA	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
100	c2ilvB	Alignment	not modelled	98.2	17	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
101	c1xzqA	Alignment	not modelled	98.2	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
102	c4wiaA	Alignment	not modelled	98.2	12	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
103	d1xp8a1	Alignment	not modelled	98.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
104	c2recB	Alignment	not modelled	98.2	14	PDB header: helicase PDB COMPND:

105	c4ydsA_	Alignment	not modelled	98.2	11	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfobolbus acidocaldarius with atp and mg-ion
106	c4lpsA_	Alignment	not modelled	98.1	18	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein hypb; PDBTitle: crystal structure of hypb from helicobacter pylori in complex with2 nickel
107	d1mo6a1	Alignment	not modelled	98.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
108	d1ls1a1	Alignment	not modelled	98.1	19	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
109	d1cr2a_	Alignment	not modelled	98.1	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
110	c2e87A_	Alignment	not modelled	98.1	21	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
111	d1k6ma1	Alignment	not modelled	98.1	13	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
112	c6hegA_	Alignment	not modelled	98.1	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rha helicase hrpb
113	c1nijA_	Alignment	not modelled	98.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
114	c2j3eA_	Alignment	not modelled	98.1	21	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
115	d1tq4a_	Alignment	not modelled	98.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
116	c1u9iA_	Alignment	not modelled	98.0	22	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
117	d1h65a_	Alignment	not modelled	98.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
118	d1wgwa_	Alignment	not modelled	98.0	14	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
119	c4hi0F_	Alignment	not modelled	98.0	18	PDB header: metal binding protein Chain: F: PDB Molecule: urease accessory protein ureg; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h/g complex
120	c3hr8A_	Alignment	not modelled	98.0	12	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca