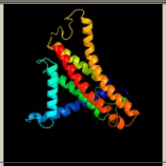
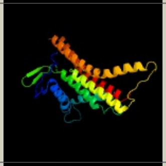
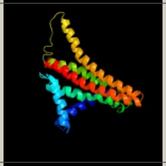
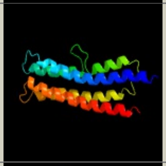
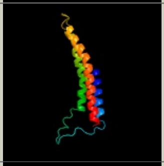
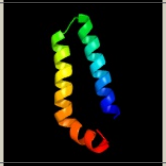
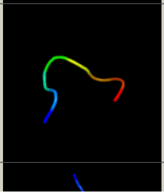
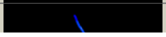
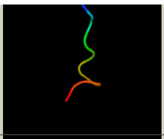
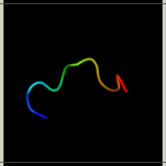
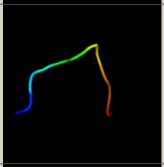
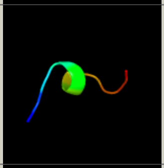
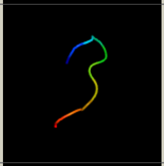
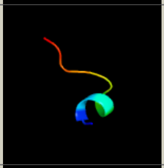
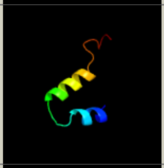
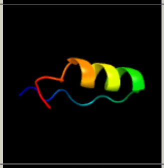
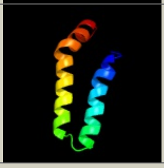
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1304_(atpB)_1460250_1461002
Date	Wed Jul 31 22:05:40 BST 2019
Unique Job ID	4fbcaa65146ea89b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkia_	Alignment		100.0	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp synthase subunit alpha, chloroplastic; **PDBTitle:** chloroplast f1fo conformation 3
2	c6b2za_	Alignment		100.0	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp synthase protein 8; **PDBTitle:** cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
3	c5t4pK_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**atp synthase subunit a; **PDBTitle:** autoinhibited e. coli atp synthase state 2
4	c5fikW_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** W: **PDB Molecule:**atp synthase subunit beta, mitochondrial; **PDBTitle:** bovine mitochondrial atp synthase state 3a
5	c5filW_	Alignment		100.0	22	**PDB header:**atp synthase **Chain:** W: **PDB Molecule:**atp synthase subunit beta, mitochondrial; **PDBTitle:** bovine mitochondrial atp synthase state 3b
6	c6f36M_	Alignment		100.0	17	**PDB header:**proton transport **Chain:** M: **PDB Molecule:**mitochondrial atp synthase subunit 6; **PDBTitle:** polytomella fo model
7	d1c17m_	Alignment		100.0	34	**Fold:**F1F0 ATP synthase subunit A **Superfamily:**F1F0 ATP synthase subunit A **Family:**F1F0 ATP synthase subunit A
8	c5lqxY_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** Y: **PDB Molecule:**atp synthase subunit a; **PDBTitle:** structure of f-atpase from pichia angusta, state3
9	c5dn6X_	Alignment		99.8	36	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atp synthase subunit a,atp synthase subunit a; **PDBTitle:** atp synthase from paracoccus denitrificans
10	c3qbrA_	Alignment		30.8	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**sjchgc06286 protein; **PDBTitle:** bakbh3 in complex with sja
11	c6eioA_	Alignment		25.0	38	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**antifreeze protein; **PDBTitle:** crystal structure of an ice binding protein from an antarctic2 biological consortium
						

12	c2n2uA_	Alignment		22.1	27	**PDB header:**unknown function, structural genomics **Chain:** A: **PDB Molecule:**or358; **PDBTitle:** solution nmr structure of de novo designed ferredoxin fold protein2 sfr3, northeast structural genomics consortium (nesg) target or358
13	c2k3iA_	Alignment		21.3	45	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yiis; **PDBTitle:** solution nmr structure of protein yiis from shigella flexneri.2 northeast structural genomics consortium target sfr90
14	c2dw3A_	Alignment		20.7	33	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**intrinsic membrane protein pufx; **PDBTitle:** solution structure of the rhodobacter sphaeroides pufx2 membrane protein
15	c2k2eA_	Alignment		20.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bp2786; **PDBTitle:** solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
16	c2kpoA_	Alignment		19.6	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x2 fold protein; **PDBTitle:** solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
17	c5vfkA_	Alignment		19.5	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an archaeal duf61 family protein sso0941
18	c2kjgA_	Alignment		18.9	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**archaeal protein sso6904; **PDBTitle:** solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus
19	c6eyyB_	Alignment		18.8	25	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**acriia6; **PDBTitle:** anti-crispr acriia6 cubic form
20	d1o0la_	Alignment		18.6	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
21	c2mr6A_	Alignment	not modelled	17.9	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein or462; **PDBTitle:** solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or462
22	c5kpeA_	Alignment	not modelled	16.6	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo beta sheet design protein or664; **PDBTitle:** solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664
23	c2o2fA_	Alignment	not modelled	16.4	6	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
24	c2xa0A_	Alignment	not modelled	16.3	6	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
25	c5wddA_	Alignment	not modelled	16.2	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related ovarian killer protein; **PDBTitle:** crystal structure of chicken bok
26	c2lciA_	Alignment	not modelled	15.6	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein or36; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or36 (casd3 target)
27	d1f16a_	Alignment	not modelled	15.4	16	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
28	c5twaA_	Alignment	not modelled	15.3	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-x homologous protein, bhp2; **PDBTitle:** crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2

29	c2lndA_	Alignment	not modelled	15.1	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein, pfk fold; **PDBTitle:** solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
30	d1bxla_	Alignment	not modelled	15.1	8	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
31	d1pq1a_	Alignment	not modelled	14.8	8	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
32	c2krxA_	Alignment	not modelled	14.6	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asl3597 protein; **PDBTitle:** solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
33	c2n3zA_	Alignment	not modelled	14.5	27	**PDB header:**structural genomics, de novo protein **Chain:** A: **PDB Molecule:**or446; **PDBTitle:** solution nmr structure of de novo designed protein, rossmann2x2 fold,2 northeast structural genomics consortium (nesg) target or446
34	d1zy3a1	Alignment	not modelled	14.3	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
35	c2mdtA_	Alignment	not modelled	14.2	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** a pilt n-terminus domain protein sso1118 from hyperthemophilic2 archaeon sulfolobus solfataricus p2
36	c3pk1A_	Alignment	not modelled	13.8	8	**PDB header:**apoptosis/apoptosis regulator **Chain:** A: **PDB Molecule:**induced myeloid leukemia cell differentiation protein mcl- **PDBTitle:** crystal structure of mcl-1 in complex with the baxbh3 domain
37	d1g5ma_	Alignment	not modelled	13.8	6	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
38	c3rq9B_	Alignment	not modelled	13.8	30	**PDB header:**tse2-binding protein **Chain:** B: **PDB Molecule:**type vi secretion immunity protein; **PDBTitle:** structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
39	c3gaeA_	Alignment	not modelled	13.7	36	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul
40	c2l5qA_	Alignment	not modelled	13.7	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bvu_3817 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr159
41	c2kvsA_	Alignment	not modelled	13.5	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mw0776; **PDBTitle:** nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
42	c2l82A_	Alignment	not modelled	13.5	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
43	c2ln3A_	Alignment	not modelled	13.0	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein or135; **PDBTitle:** solution nmr structure of de novo designed protein, if3-like fold,2 northeast structural genomics consortium target or135 (casd target)
44	d1ysga1	Alignment	not modelled	12.9	8	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
45	c2l69A_	Alignment	not modelled	12.8	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
46	c2kl0A_	Alignment	not modelled	12.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
47	c2mblA_	Alignment	not modelled	12.6	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7 fold protein top7m13; **PDBTitle:** solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
48	c4hhuA_	Alignment	not modelled	12.6	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**or280; **PDBTitle:** crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
49	c2k5iA_	Alignment	not modelled	12.4	40	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron transport protein; **PDBTitle:** solution structure of iron(ii) transport protein a from2 clostridium thermocellum , northeast structural genomics3 consortium (nesg) target vr131
50	c2l9uA_	Alignment	not modelled	12.3	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
51	c6hyhA_	Alignment	not modelled	12.2	33	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
						PDB header:ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3;

52	c2kt9A_	Alignment	not modelled	12.2	20	**PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
53	c3ebbD_	Alignment	not modelled	12.0	55	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**phospholipase a2-activating protein; **PDBTitle:** plap/p97 complex
54	c2n2tA_	Alignment	not modelled	11.9	30	**PDB header:**unknown function, structural genomics **Chain:** A: **PDB Molecule:**or303; **PDBTitle:** solution nmr structure of de novo designed protein (fda_60), northeast2 structural genomics consortium (nesg) target or303
55	c2kptA_	Alignment	not modelled	11.9	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative secreted protein; **PDBTitle:** solution nmr structure of the n-terminal domain of cg24962 protein from corynebacterium glutamicum. northeast3 structural genomics consortium target cgr26a
56	d2ponb1	Alignment	not modelled	11.9	8	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
57	c2w50B_	Alignment	not modelled	11.7	29	**PDB header:**hormone **Chain:** B: **PDB Molecule:**armet-like protein 1; **PDBTitle:** n-terminal domain of human conserved dopamine neurotrophic factor2 (cdnf)
58	d2jm6b1	Alignment	not modelled	11.7	10	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
59	c2k9qB_	Alignment	not modelled	11.6	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
60	c2ltaA_	Alignment	not modelled	11.5	28	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein; **PDBTitle:** solution nmr structure of de novo designed protein, rossmann 3x1 fold,2 northeast structural genomics consortium target or157
61	c2k3dA_	Alignment	not modelled	11.5	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0334 protein; **PDBTitle:** solution nmr structure of the folded 79 residue fragment of2 lin0334 from listeria innocua. northeast structural3 genomics consortium target lkr15
62	c2kcuA_	Alignment	not modelled	11.2	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ctr107; **PDBTitle:** nmr solution structure of an uncharacterized protein from chlorobium2 tepidum. northeast structural genomics target ctr107
63	c6c2uA_	Alignment	not modelled	11.1	36	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**phosphate-loop protein; **PDBTitle:** solution structure of a phosphate-loop protein
64	c2kvoA_	Alignment	not modelled	11.1	23	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
65	c2mq8A_	Alignment	not modelled	11.1	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein lfr1; **PDBTitle:** solution nmr structure of de novo designed protein lfr1 1 with2 ferredoxin fold, northeast structural genomics consortium (nesg)3 target or414
66	c2k5rA_	Alignment	not modelled	11.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
67	c2jrpA_	Alignment	not modelled	11.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
68	c4rmbB_	Alignment	not modelled	11.0	30	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**serine rich repeat protein-1 (srr-1); **PDBTitle:** crystal structure of keratin 4 binding domain of surface adhesin srr-12 of s.agalactiae
69	d1gwma_	Alignment	not modelled	10.8	38	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 29 carbohydrate binding module, CBM29
70	c2kt7A_	Alignment	not modelled	10.7	38	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**putative peptidoglycan bound protein (lpxtg **PDBTitle:** solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
71	c2k4nA_	Alignment	not modelled	10.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein pf0246; **PDBTitle:** nmr structure of protein pf0246 from pyrococcus furiosus:2 target pfr75 from the northeast structural genomics3 consortium
72	c5xbcB_	Alignment	not modelled	10.6	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nsp1 protein; **PDBTitle:** crystal structure basis for pedv nsp1
73	d1kn0a_	Alignment	not modelled	10.5	50	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
74	d1m3va2	Alignment	not modelled	10.4	83	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
75	d1pc2a_	Alignment	not modelled	10.4	33	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like

						Family: Tetratricopeptide repeat (TPR)
76	c2yv6A_	Alignment	not modelled	10.2	10	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2 homologous antagonist/killer; **PDBTitle:** crystal structure of human bcl-2 family protein bak
77	c2muyA_	Alignment	not modelled	10.1	27	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**atp-dependent zinc metalloprotease ftsh; **PDBTitle:** the solution structure of the ftsh periplasmic n-domain
78	c2l01A_	Alignment	not modelled	10.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
79	c2kcyA_	Alignment	not modelled	10.1	23	**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
80	c2jwyA_	Alignment	not modelled	10.0	38	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yajj; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein yajj from2 escherichia coli. northeast structural genomics target er540
81	c5wosA_	Alignment	not modelled	10.0	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**cnpv058 bcl-2 like protein; **PDBTitle:** structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
82	c5gasN_	Alignment	not modelled	9.7	17	**PDB header:**hydrolase **Chain:** N: **PDB Molecule:**archaeal/vacuolar-type h+-atpase subunit i; **PDBTitle:** thermus thermophilus v/a-atpase, conformation 2
83	c4s1hA_	Alignment	not modelled	9.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** pyridoxal kinase of entamoeba histolytica with adp
84	c6gboG_	Alignment	not modelled	9.7	38	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** crystal structure of the oligomerization domain of vp35 from ebola2 virus
85	c5w63A_	Alignment	not modelled	9.6	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bax; **PDBTitle:** crystal structure of channel catfish bax
86	c2kpsA_	Alignment	not modelled	9.4	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of domain iv from the ybbr family protein of2 desulfitobacterium hafniense
87	c2khdA_	Alignment	not modelled	9.4	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vc_a0919; **PDBTitle:** solution nmr structure of vc_a0919 from vibrio cholerae.2 northeast structural genomics consortium target vcr52
88	c3pddA_	Alignment	not modelled	9.3	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**glycoside hydrolase, family 9; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
89	c3pstA_	Alignment	not modelled	9.3	36	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**protein doa1; **PDBTitle:** crystal structure of pul and pfu(mutate) domain
90	c2jwxA_	Alignment	not modelled	9.2	38	**PDB header:**apoptosis, isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of the n-terminal domain of human fkbp382 (fkbp38ntd)
91	c2gm2A_	Alignment	not modelled	9.1	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
92	c4ediC_	Alignment	not modelled	9.1	38	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein; **PDBTitle:** disulfide bonded eutl from clostridium perfringens
93	c2jmrA_	Alignment	not modelled	9.0	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf
94	d1mzga_	Alignment	not modelled	8.8	33	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
95	c4ix5B_	Alignment	not modelled	8.8	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**msstt7d protein; **PDBTitle:** crystal structure of a stt7 homolog from micromonas algae in complex2 with amp-pnp
96	c2mraA_	Alignment	not modelled	8.8	38	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein or459; **PDBTitle:** solution nmr structure of de novo designed protein, northeast2 structural genomics consortium (nesg) target or459
97	c2kl8A_	Alignment	not modelled	8.7	38	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
98	c4ux3B_	Alignment	not modelled	8.4	31	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**mitotic chromosome determinant-related protein; **PDBTitle:** cohesin smc3-hd:scc1-n complex from yeast
99	c2jz2A_	Alignment	not modelled	8.3	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42