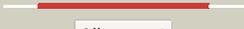
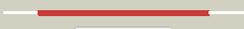
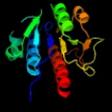


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0380c (-)_456269_456820
Date	Tue Jul 23 14:50:45 BST 2019
Unique Job ID	232309bc984912ce

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gz0H_	Alignment 		100.0	21	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase r1mb
2	c1zjrA_	Alignment 		100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
3	d1v2xa_	Alignment 		100.0	25	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
4	c3gyqB_	Alignment 		100.0	24	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
5	c1ipaA_	Alignment 		100.0	20	PDB header: transferase Chain: A: PDB Molecule: rrna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase
6	d1gz0a1	Alignment 		100.0	22	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
7	c1gz0G_	Alignment 		100.0	22	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase r1mb
8	c5kzkA_	Alignment 		100.0	22	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rrna methyltransferase from sinorhizobium2 meliloti
9	c2i6dA_	Alignment 		100.0	17	PDB header: transferase Chain: A: PDB Molecule: rrna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
10	c1x7pB_	Alignment 		100.0	26	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spo methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
11	c4x3mB_	Alignment 		100.0	19	PDB header: transferase Chain: B: PDB Molecule: rrna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121

12	c2ha8A	Alignment		100.0	22	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
13	d1ipaa1	Alignment		100.0	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
14	c5co4A	Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
15	c4pzka	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
16	d1mxia	Alignment		100.0	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
17	c3onpA	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trmh/rrna methyltransferase spou from rhodobacter2 sphaeroides
18	c5gm8A	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
19	c3e5yB	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
20	c3ic6A	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
21	c4cndB	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
22	c4cngB	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
23	c3l8uA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
24	c4xboA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
25	c3ilkB	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rrna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
26	c5graA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of trmj from z. mobilis zm4
27	c3ktyA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
						PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570;

28	c3dcmX_	Alignment	not modelled	99.9	16	PDBTitle: crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-l-3 methionine
29	c6ahwB_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: B: PDB Molecule: circular-permuted trna (cytidine(34)-2'-o)- PDBTitle: crystal structure of circular-permuted yibk methyltransferase from2 haemophilus influenzae
30	c2yy8B_	Alignment	not modelled	97.5	13	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
31	d1vhka2	Alignment	not modelled	97.1	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
32	c1vhkA_	Alignment	not modelled	96.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
33	d2o3aa1	Alignment	not modelled	96.9	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
34	c3kw2A_	Alignment	not modelled	96.4	13	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
35	c2egwB_	Alignment	not modelled	96.1	11	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rna methyltransferase with sah ligand
36	c4j3cB_	Alignment	not modelled	95.4	15	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
37	c5o96F_	Alignment	not modelled	95.2	12	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
38	c1vhyB_	Alignment	not modelled	95.0	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
39	d1nxza2	Alignment	not modelled	94.7	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
40	c5vm8A_	Alignment	not modelled	94.3	14	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
41	c4l69A_	Alignment	not modelled	94.2	17	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
42	c4e8bA_	Alignment	not modelled	94.1	15	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
43	c3ai9X_	Alignment	not modelled	93.9	12	PDB header: transferase Chain: X: PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
44	d1v6za2	Alignment	not modelled	92.0	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
45	c2cx8B_	Alignment	not modelled	91.3	17	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
46	c2cx8A_	Alignment	not modelled	90.6	15	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
47	d2qwva1	Alignment	not modelled	86.0	10	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
48	d2qmma1	Alignment	not modelled	72.9	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
49	c1z85B_	Alignment	not modelled	72.7	11	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
50	d1k3ra2	Alignment	not modelled	66.0	24	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
51	c1k3rA_	Alignment	not modelled	55.1	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
52	c4rg1A_	Alignment	not modelled	49.9	19	PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114

53	d2c42a3	Alignment	not modelled	40.7	16	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
54	c2v3jA	Alignment	not modelled	40.4	15	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
55	c2x3yA	Alignment	not modelled	31.9	16	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
56	d2ivya1	Alignment	not modelled	31.2	10	Fold: Ferredoxin-like Superfamily: TTP0101/SSO1404-like Family: TTP0101/SSO1404-like
57	c3o7bA	Alignment	not modelled	28.1	12	PDB header: transferase Chain: A: PDB Molecule: ribosome biogenesis nep1 rna methyltransferase; PDBTitle: crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
58	d1a9xa3	Alignment	not modelled	25.7	10	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
59	d2f06a1	Alignment	not modelled	25.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
60	c5ol2E	Alignment	not modelled	23.1	10	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
61	c3lyhB	Alignment	not modelled	22.5	16	PDB header: lyase Chain: B: PDB Molecule: cobalamin (vitamin b12) biosynthesis cbix protein; PDBTitle: crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
62	c1z0eF	Alignment	not modelled	22.2	10	PDB header: hydrolase Chain: F: PDB Molecule: putative protease la homolog type; PDBTitle: crystal structure of a. fulgidus lon proteolytic domain
63	c3excX	Alignment	not modelled	21.9	4	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: structure of the rna'se sso8090 from sulfolobus solfataricus
64	c4kpuB	Alignment	not modelled	21.4	18	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
65	d1o94c	Alignment	not modelled	19.7	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
66	c2n9rA	Alignment	not modelled	18.3	45	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide padbs1r1; PDBTitle: novel antimicrobial peptide padbs1r1 designed from the ribosomal2 protein l39e from pyrobaculum aerophilum using bioinformatics
67	d1jvna2	Alignment	not modelled	16.9	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
68	c4lyaA	Alignment	not modelled	16.4	12	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
69	c2iswB	Alignment	not modelled	16.2	13	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
70	c3j1rS	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: S: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
71	c3j1rK	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: K: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
72	c3j1rL	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: L: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
73	c3j1rU	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: U: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
74	c3j1rR	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: R: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
75	c3j1rQ	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: Q: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
76	c3j1rH	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: H: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
						PDB header: cell adhesion, structural protein

77	c3j1rC_	Alignment	not modelled	14.3	31	Chain: C: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
78	c3j1rD_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: D: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
79	c3j1rJ_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: J: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
80	c3j1rA_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: A: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
81	c3j1rO_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: O: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
82	c3j1rT_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: T: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
83	c3j1rN_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: N: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
84	c3j1rE_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: E: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
85	c3j1rI_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: I: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
86	c3j1rB_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
87	c3j1rF_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: F: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
88	c3j1rP_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: P: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
89	c3j1rG_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: G: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
90	c3j1rM_	Alignment	not modelled	14.3	31	PDB header: cell adhesion, structural protein Chain: M: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from iginicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
91	c2y0fD_	Alignment	not modelled	14.2	11	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispq) from thermus thermophilus hb27
92	d2v3ka1	Alignment	not modelled	12.9	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: EMG1/NEP1-like
93	d1u7za_	Alignment	not modelled	12.8	14	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
94	c5douC_	Alignment	not modelled	12.2	12	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
95	c4s1aB_	Alignment	not modelled	12.0	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein cthe_0052 from2 ruminiclostridium thermocellum atcc 27405
96	c6fahB_	Alignment	not modelled	11.8	12	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
97	c3lmaC_	Alignment	not modelled	11.7	21	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
98	d1ulza2	Alignment	not modelled	11.2	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
99	c3ajfA_	Alignment	not modelled	10.9	15	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: structural insighths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus