Veronica Truniger

List of Publications by Year
in descending order

32 papers	1,557 citations	411340 20 h-index	466096 32 g-index
32 all docs	32 docs citations	32 times ranked	1485 citing authors

#	Article	IF	Citations
1	A Dual Interaction Between the 5â€²- and 3â€²-Ends of the Melon Necrotic Spot Virus (MNSV) RNA Genome Is Required for Efficient Cap-Independent Translation. Frontiers in Plant Science, 2018, 9, 625.	1.7	3
2	Analysis of the interacting partners eIF4F and 3â€²â€CITE required for <i>Melon necrotic spot virus</i> capâ€independent translation. Molecular Plant Pathology, 2017, 18, 635-648.	2.0	27
3	Structure of eIF4E in Complex with an eIF4G Peptide Supports a Universal Bipartite Binding Mode for Protein Translation. Plant Physiology, 2017, 174, 1476-1491.	2.3	32
4	Non-canonical Translation in Plant RNA Viruses. Frontiers in Plant Science, 2017, 8, 494.	1.7	99
5	Structural and Functional Diversity of Plant Virus 3â€²-Cap-Independent Translation Enhancers (3â€²-CITEs). Frontiers in Plant Science, 2017, 8, 2047.	1.7	48
6	Determination of the Secondary Structure of an RNA fragment in Solution: Selective 2`-Hydroxyl Acylation Analyzed by Primer Extension Assay (SHAPE). Bio-protocol, 2015, 5, .	0.2	14
7	Interfamilial recombination between viruses led to acquisition of a novel translationâ€enhancing <scp>RNA</scp> element that allows resistance breaking. New Phytologist, 2014, 202, 233-246.	3.5	73
8	Relative incidence, spatial distribution and genetic diversity of cucurbit viruses in eastern Spain. Annals of Applied Biology, 2013, 162, 362-370.	1.3	58
9	A Cost-effective Double-Stranded cDNA Synthesis for Plant Microarrays. Plant Molecular Biology Reporter, 2012, 30, 1276-1282.	1.0	1
10	Melon RNA interference (RNAi) lines silenced for <i>Cmâ€eIF4E</i> show broad virus resistance. Molecular Plant Pathology, 2012, 13, 755-763.	2.0	105
11	<i>Nicotiana benthamiana</i> resistance to nonâ€adapted <i>Melon necrotic spot virus</i> results from an incompatible interaction between virus RNA and translation initiation factor 4E. Plant Journal, 2011, 66, 492-501.	2.8	34
12	Development of expression vectors based on pepino mosaic virus. Plant Methods, 2011, 7, 6.	1.9	62
13	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	1.2	49
14	Recessive Resistance to Plant Viruses. Advances in Virus Research, 2009, 75, 119-231.	0.9	206
15	Mechanism of plant eIF4Eâ€mediated resistance against a Carmovirus (<i>Tombusviridae</i>): capâ€independent translation of a viral RNA controlled <i>inâ€ƒcis</i> by an (a)virulence determinant. Plant Journal, 2008, 56, 716-727.	2.8	76
16	Cucurbit aphid-borne yellows virus Is Prevalent in Field-Grown Cucurbit Crops of Southeastern Spain. Plant Disease, 2007, 91, 232-238.	0.7	55
17	EcoTILLING for the identification of allelic variants of melon eIF4E, a factor that controls virus susceptibility. BMC Plant Biology, 2007, 7, 34.	1.6	123
18	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	1.2	87

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19	Involvement of the â€œlinkerâ€•region between the exonuclease and polymerization domains of Ï•29 DNA polymerase in DNA and TP binding. Gene, 2005, 348, 89-99.	1.0	3
20	Function of the C-terminus of Â29 DNA polymerase in DNA and terminal protein binding. Nucleic Acids Research, 2004, 32, 361-370.	6.5	9
21	Advances in understanding recessive resistance to plant viruses. Molecular Plant Pathology, 2004, 5, 223-233.	2.0	157
22	Two Positively Charged Residues of Ï†29 DNA Polymerase, Conserved in Protein-primed DNA Polymerases, are Involved in Stabilisation of the Incoming Nucleotide. Journal of Molecular Biology, 2004, 335, 481-494.	2.0	9
23	Molecular Characterization of a Melon necrotic spot virus Strain That Overcomes the Resistance in Melon and Nonhost Plants. Molecular Plant-Microbe Interactions, 2004, 17, 668-675.	1.4	68
24	Further variability within the genus Crinivirus, as revealed by determination of the complete RNA genome sequence of Cucurbit yellow stunting disorder virus. Journal of General Virology, 2003, 84, 2555-2564.	1.3	42
25	Ï•29 DNA Polymerase Residue Leu384, Highly Conserved in Motif B of Eukaryotic Type DNA Replicases, Is Involved in Nucleotide Insertion Fidelity. Journal of Biological Chemistry, 2003, 278, 33482-33491.	1.6	4
26	A positively charged residue of phi29 DNA polymerase, highly conserved in DNA polymerases from families A and B, is involved in binding the incoming nucleotide. Nucleic Acids Research, 2002, 30, 1483-1492.	6.5	19
27	A Highly Conserved Lysine Residue in Ï†29 DNA Polymerase is Important for Correct Binding of the Templating Nucleotide during Initiation of Ï†29 DNA Replication. Journal of Molecular Biology, 2002, 318, 83-96.	2.0	7
28	The (I/Y)XGG Motif of Adenovirus DNA Polymerase Affects Template DNA Binding and the Transition from Initiation to Elongation. Journal of Biological Chemistry, 2001, 276, 29846-29853.	1.6	13
29	Analysis of Ã˜29 DNA polymerase by partial proteolysis: binding of terminal protein in the double-stranded DNA channel 1 1Edited by M. Yaniv. Journal of Molecular Biology, 2000, 295, 441-453.	2.0	8
30	Role of the â€œYxGG/Aâ€•motif of Ã¸29 DNA polymerase in protein-primed replication. Journal of Molecular Biology, 1999, 286, 57-69.	2.0	25
31	Ã¸29 DNA polymerase requires the N-terminal domain to bind terminal protein and DNA primer substrates. Journal of Molecular Biology, 1998, 278, 741-755.	2.0	20
32	Glycerol uptake in Escherichia coli is sensitive to membrane lipid composition. Research in Microbiology, 1993, 144, 565-574.	1.0	21