Sek-Man Wong

List of Publications by Year
in descending order

93	2,023	236925 25	289244 40
papers	citations	h-index	g-index

94	94	94	1893
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Strong host resistance targeted against a viral suppressor of the plant gene silencing defence mechanism. EMBO Journal, 1999, 18, 2683-2691.	7.8	206
2	Detection of two orchid viruses using quartz crystal microbalance (QCM) immunosensors. Journal of Virological Methods, 2002, 99, 71-79.	2.1	106
3	Salicylic Acid-Induced Resistance to Cucumber mosaic virus in Squash and Arabidopsis thaliana: Contrasting Mechanisms of Induction and Antiviral Action. Molecular Plant-Microbe Interactions, 2005, 18, 428-434.	2.6	101
4	Simultaneous quantitation of two orchid viruses by the TaqManÂ® real-time RT-PCR. Journal of Virological Methods, 2000, 87, 151-160.	2.1	70
5	In vitro-reassembled plant virus-like particles for loading of polyacids. Journal of General Virology, 2006, 87, 2749-2754.	2.9	67
6	Transcriptome analysis of genes responding to NNV infection in Asian seabass epithelial cells. Fish and Shellfish Immunology, 2016, 54, 342-352.	3.6	62
7	Simultaneous TD/RT-PCR detection of cymbidium mosaic potexvirus and odontoglossum ringspot tobamovirus with a single pair of primers. Journal of Virological Methods, 1998, 72, 197-204.	2.1	61
8	Molecular Beacons: A New Approach to Plant Virus Detection. Phytopathology, 2000, 90, 269-275.	2.2	60
9	Complete Nucleotide Sequence and Genome Organization of Hibiscus Chlorotic Ringspot Virus, a New Member of the Genus Carmovirus: Evidence for the Presence and Expression of Two Novel Open Reading Frames. Journal of Virology, 2000, 74, 3149-3155.	3.4	55
10	Mapping QTL for Resistance Against Viral Nervous Necrosis Disease in Asian Seabass. Marine Biotechnology, 2016, 18, 107-116.	2.4	49
11	The Rate of Cell-to-Cell Movement in Squash of Cucumber Mosaic Virus Is Affected by Sequences of the Capsid Protein. Molecular Plant-Microbe Interactions, 1999, 12, 628-632.	2.6	44
12	Detection of Two Orchid Viruses Using Quartz Crystal Microbalance-Based DNA Biosensors. Phytopathology, 2002, 92, 654-658.	2.2	38
13	The complete sequence of a Singapore isolate of odontoglossum ringspot virus and comparison with other tobamoviruses. Gene, 1996, 171, 155-161.	2.2	37
14	The use of DIG-labelled cRNA probes for the detection of cymbidium mosaic potexvirus (CymMV) and odontoglossum ringspot tobamovirus (ORSV) in orchids. Journal of Virological Methods, 1998, 70, 193-199.	2.1	35
15	Covariation in the Capsid Protein of Hibiscus Chlorotic Ringspot Virus Induced by Serial Passaging in a Host That Restricts Movement Leads to Avirulence in Its Systemic Host. Journal of Virology, 2002, 76, 12320-12324.	3.4	33
16	Fine mapping QTL for resistance to VNN disease using a high-density linkage map in Asian seabass. Scientific Reports, 2016, 6, 32122.	3.3	33
17	A Six-Nucleotide Segment within the 3â€² Untranslated Region of Hibiscus Chlorotic Ringspot Virus Plays an Essential Role in Translational Enhancement. Journal of Virology, 2002, 76, 1144-1153.	3.4	32
18	Synergism of the 3â€²-Untranslated Region and an Internal Ribosome Entry Site Differentially Enhances the Translation of a Plant Virus Coat Protein. Journal of Biological Chemistry, 2003, 278, 20565-20573.	3.4	32

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19	Determination of Suitable RT-qPCR Reference Genes for Studies of Gene Functions in Laodelphax striatellus (FallÃ©n). Genes, 2019, 10, 887.	2.4	30
20	Comparative proteomics of Tobacco mosaic virus-infected Nicotiana tabacum plants identified major host proteins involved in photosystems and plant defence. Journal of Proteomics, 2019, 194, 191-199.	2.4	30
21	Detection of Cymbidium Mosaic Potexvirus and Odontoglossum Ringspot Tobamovirus Using Immuno-Capillary Zone Electrophoresis. Phytopathology, 1999, 89, 522-528.	2.2	29
22	Host-induced avirulence of hibiscus chlorotic ringspot virus mutants correlates with reduced gene-silencing suppression activity. Journal of General Virology, 2006, 87, 451-459.	2.9	29
23	Rapid simultaneous detection of two orchid viruses using LC- and/or MALDI-mass spectrometry. Journal of Virological Methods, 2000, 85, 93-99.	2.1	27
24	Identification of a Plant Viral RNA Genome in the Nucleus. PLoS ONE, 2012, 7, e48736.	2.5	27
25	Expression and purification of a neuropeptide nocistatin using two related plant viral vectors. Gene, 2002, 289, 69-79.	2.2	26
26	Hibiscus chlorotic ringspot virus Coat Protein Upregulates Sulfur Metabolism Genes for Enhanced Pathogen Defense. Molecular Plant-Microbe Interactions, 2012, 25, 1574-1583.	2.6	25
27	Upregulation of LINC-AP2 is negatively correlated with AP2 gene expression with Turnip crinkle virus infection in Arabidopsis thaliana. Plant Cell Reports, 2016, 35, 2257-2267.	5.6	25
28	iTRAQ-based quantitative proteomics reveals a ferroptosis-like programmed cell death in plants infected by a highly virulent tobacco mosaic virus mutant 24A+UPD. Phytopathology Research, 2020, 2, .	2.4	25
29	Genome-wide transcriptomic analysis reveals correlation between higher WRKY61 expression and reduced symptom severity in Turnip crinkle virus infected Arabidopsis thaliana. Scientific Reports, 2016, 6, 24604.	3.3	24
30	Three-dimensional reconstruction of hibiscus chlorotic ringspot virus. Journal of Structural Biology, 2003, 144, 253-261.	2.8	23
31	Resistance to CymMV and ORSV in artificial microRNA transgenic Nicotiana benthamiana plants. Scientific Reports, 2018, 8, 9958.	3.3	23
32	Phylogenetic analysis of triple gene block viruses based on the TGB 1 homolog gene indicates a convergent evolution. Virus Genes, 1998, 16, 295-302.	1.6	22
33	In planta proximity-dependent biotin identification (BioID) identifies a TMV replication co-chaperone NbSGT1 in the vicinity of 126â€‰kDa replicase. Journal of Proteomics, 2019, 204, 103402.	2.4	22
34	Characterization of a novel disease resistance gene rtp3 and its association with VNN disease resistance in Asian seabass. Fish and Shellfish Immunology, 2017, 61, 61-67.	3.6	21
35	Reciprocal function of movement proteins and complementation of long-distance movement of Cymbidium mosaic virus RNA by Odontoglossum ringspot virus coat protein. Journal of General Virology, 2005, 86, 1543-1553.	2.9	20
36	The p23 Protein of Hibiscus Chlorotic Ringspot Virus Is Indispensable for Host-Specific Replication. Journal of Virology, 2002, 76, 12312-12319.	3.4	19

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37	Proximity-dependent biotinylation screening identifies NbHYPK as a novel interacting partner of ATG8 in plants. BMC Plant Biology, 2019, 19, 326.	3.6	19
38	Variability of P1 Protein of Zucchini Yellow Mosaic Virus for Strain Differentiation and. Phylogenetic Analysis with Other Potyviruses. DNA Sequence, 1998, 9, 275-293.	0.7	18
39	The length of an internal poly(A) tract of hibiscus latent Singapore virus is crucial for its replication. Virology, 2015, 474, 52-64.	2.4	18
40	iTRAQ-based analysis of leaf proteome identifies important proteins in secondary metabolite biosynthesis and defence pathways crucial to cross-protection against TMV. Journal of Proteomics, 2019, 196, 42-56.	2.4	18
41	In Vitro and In Vivo Inhibition of the Infectivity of Human Enterovirus 71 by a Sulfonated Food Azo Dye, Brilliant Black BN. Journal of Virology, 2019, 93, .	3.4	17
42	Plant Growth Retardation and Conserved miRNAs Are Correlated to Hibiscus Chlorotic Ringspot Virus Infection. PLoS ONE, 2013, 8, e85476.	2.5	17
43	Hibiscus chlorotic ringspot virus upregulates plant sulfite oxidase transcripts and increases sulfate levels in kenaf (Hibiscus cannabinus L.). Journal of General Virology, 2009, 90, 3042-3050.	2.9	16
44	Analyses of RNA-Seq and sRNA-Seq data reveal a complex network of anti-viral defense in TCV-infected Arabidopsis thaliana. Scientific Reports, 2016, 6, 36007.	3.3	16
45	Hibiscus chlorotic ringspot virus coat protein inhibits trans-acting small interfering RNA biogenesis in Arabidopsis. Journal of General Virology, 2008, 89, 2349-2358.	2.9	15
46	VNN disease and status of breeding for resistance to NNV in aquaculture. Aquaculture and Fisheries, 2022, 7, 147-157.	2.2	15
47	Analyses of Subgenomic Promoters of Hibiscus Chlorotic Ringspot Virus and Demonstration of 5â€² Untranslated Region and 3â€²-Terminal Sequences Functioning as Subgenomic Promoters. Journal of Virology, 2006, 80, 3395-3405.	3.4	14
48	Purification and Characterization of an Isolate of Apple Mosaic Virus from Rose in the USA. Journal of Phytopathology, 1993, 139, 33-47.	1.0	13
49	Nucleotide sequence of a Singapore isolate of zucchini yellow mosaic virus coat protein gene revealed an altered DAG motif. Virus Genes, 1993, 7, 381-387.	1.6	13
50	Nucleotide sequence and in vitro translation of the coat protein gene of cymbidium mosaic virus. Virus Genes, 1993, 7, 157-170.	1.6	11
51	Cucurbit protoplast isolation for the study of plant virus replication. Journal of Virological Methods, 2001, 91, 21-27.	2.1	11
52	Complete cDNA sequence of chitin deacetylase from Gongronella butleri and its phylogenetic analysis revealed clusters corresponding to taxonomic classification of fungi. Journal of Bioscience and Bioengineering, 2002, 93, 376-381.	2.2	11
53	Host-specific encapsidation of a defective RNA 3 of Cucumber mosaic virus. Journal of General Virology, 2004, 85, 3757-3763.	2.9	11
54	Hibiscus Chlorotic Ringspot Virus Coat Protein Is Essential for Cell-to-Cell and Long-Distance Movement but Not for Viral RNA Replication. PLoS ONE, 2014, 9, e113347.	2.5	11

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55	Sequence and phylogenetic analysis of the cytoplasmic inclusion protein gene of zucchini yellow mosaic potyvirus: its role in classification of the Potyviridae. Virus Genes, 1997, 14, 41-53.	1.6	9
56	Cloning of cDNAs encoding the three subunits of oxygen evolving complex in Nicotiana benthamiana and gene expression changes in tobacco leaves infected with Tobacco mosaic virus. Physiological and Molecular Plant Pathology, 2006, 68, 61-68.	2.5	9
57	TMV mutants with poly(A) tracts of different lengths demonstrate structural variations in 3â€²UTR affecting viral RNAs accumulation and symptom expression. Scientific Reports, 2015, 5, 18412.	3.3	9
58	Significance of the 3â€²-terminal region in minus-strand RNA synthesis of Hibiscus chlorotic ringspot virus. Journal of General Virology, 2004, 85, 1763-1776.	2.9	9
59	Nucleotide sequence of the 3â€² half of zucchini yellow mosaic virus (Singapore isolate) genome encoding the 4K protein, protease, polymerase and coat protein. Nucleic Acids Research, 1993, 21, 1317-1317.	14.5	8
60	Purification, crystallization and X-ray analysis of Hibiscus chlorotic ringspot virus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1481-1483.	2.5	8
61	Structure of Hibiscus Latent Singapore Virus by Fiber Diffraction: A Nonconserved His122 Contributes to Coat Protein Stability. Journal of Molecular Biology, 2011, 406, 516-526.	4.2	8
62	A Game-Theoretic Model of Interactions between Hibiscus Latent Singapore Virus and Tobacco Mosaic Virus. PLoS ONE, 2012, 7, e37007.	2.5	8
63	Selection of DNA Aptamers for Subcellular Localization of RBSDV P10 Protein in the Midgut of Small Brown Planthoppers by Emulsion PCR-Based SELEX. Viruses, 2020, 12, 1239.	3.3	8
64	Translation initiation at an upstream CUG codon regulates the expression of Hibiscus chlorotic ringspot virus coat protein. Virus Research, 2006, 122, 35-44.	2.2	7
65	Profiling of Genes Related to Cross Protection and Competition for NbTOM1 by HLSV and TMV. PLoS ONE, 2013, 8, e73725.	2.5	7
66	Yeast expression and characterization of SARS-CoV N protein. Journal of Virological Methods, 2005, 130, 83-88.	2.1	6
67	Identification of Hepta- and Octo-Uridine stretches as sole signals for programmed +1 and -1 ribosomal frameshifting during translation of SARS-CoV ORF 3a variants. Nucleic Acids Research, 2006, 34, 1250-1260.	14.5	6
68	Host-dependent effects of the 3â€² untranslated region of turnip crinkle virus RNA on accumulation in Hibiscus and Arabidopsis. Journal of General Virology, 2007, 88, 680-687.	2.9	6
69	Identification of Plant Virus IRES. Methods in Molecular Biology, 2008, 451, 125-133.	0.9	6
70	Preliminary X-ray data analysis of crystalline hibiscus chlorotic ringspot virus. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 589-593.	0.7	6
71	Hibiscus latent Fort Pierce virus in Brazil and synthesis of its biologically active full-length cDNA clone. Virus Genes, 2016, 52, 754-757.	1.6	6
72	Disruption of a stem-loop structure located upstream of pseudoknot domain in Tobacco mosaic virus enhanced its infectivity and viral RNA accumulation. Virology, 2018, 519, 170-179.	2.4	6

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73	Nucleotide sequences of the two ORFs upstream to the coat protein gene of cymbidium mosaic virus. Plant Molecular Biology, 1992, 18, 1027-1029.	3.9	5
74	Deep sequencing analysis reveals a TMV mutant with a poly(A) tract reduces host defense responses in Nicotiana benthamiana. Virus Research, 2017, 239, 126-135.	2.2	5
75	Differential expression of novel microRNAs in response to the infection of a TMV mutant with an internal poly(A) tract in N . benthamiana. Virus Research, 2017, 239, 143-171.	2.2	5
76	Basic Amino Acid Mutations in the Nuclear Localization Signal of Hibiscus Chlorotic Ringspot Virus p23 Inhibit Virus Long Distance Movement. PLoS ONE, 2013, 8, e74000.	2.5	5
77	YKE2, a yeast nuclear gene encoding a protein showing homology to mouse KE2 and containing a putative leucine-zipper motif. Gene, 1994, 151, 197-201.	2.2	4
78	An infectious RNA with a hepta-adenosine stretch responsible for programmed â^'1 ribosomal frameshift derived from a full-length cDNA clone of Hibiscus latent Singapore virus. Virology, 2014, 449, 229-234.	2.4	4
79	Small RNA derived from Tobacco mosaic virus targets a host C2-domain abscisic acid-related (CAR) 7-like protein gene. Phytopathology Research, 2020, 2, .	2.4	4
80	iTRAQ-based quantitative proteomics suggests mitophagy involvement after Rice black-streaked dwarf virus acquisition in insect vector small brown planthopper Laodelphax striatellus FallÃ©n. Journal of Proteomics, 2021, 246, 104314.	2.4	4
81	Poly(A) introduced upstream of the upstream pseudoknot domain of Tobacco mosaic virus led to sequence deletion after serial passaging in host plants. Phytopathology Research, 2019, 1, .	2.4	3
82	iTRAQ-based protein analysis provides insight into heterologous superinfection exclusion with TMV-43A against CMV in tobacco (Nicotiana benthamiana) plants. Journal of Proteomics, 2020, 229, 103948.	2.4	3
83	Mutation of Phe50 to Ser50 in the 126/183-kDa proteins of Odontoglossum ringspot virus abolishes virus replication but can be complemented and restored by exact reversion. Journal of General Virology, 2004, 85, 2447-2457.	2.9	3
84	Identification of putative binding interface of PI(3,5)P2 lipid on rice black-streaked dwarf virus (RBSDV) P10 protein. Virology, 2022, 570, 81-95.	2.4	3
85	Development of a cell sorting procedure to increase the sensitivity of detection of proteinâ€“protein interactions in plant protoplasts. Journal of Virological Methods, 2011, 173, 347-352.	2.1	2
86	Molecular modeling and interaction between Arabidopsis sulfite oxidase and the GW motif of Turnip crinkle virus coat protein. Virology, 2020, 551, 64-74.	2.4	2
87	A Novel Attenuated Enterovirus A71 Mutant with VP1-V238A,K244R Exhibits Reduced Efficiency of Cell Entry/Exit and Augmented Binding Affinity to Sulfated Glycans. Journal of Virology, 2021, 95, e0105521.	3.4	2
88	Virology. , 2009, , 251-277.		2
89	In Vitro-Reassembled Plant Virus-Like Particles of Hibiscus Chlorotic Ringspot Virus (HCRSV) as Nano-Protein Cages for Drugs. Methods in Molecular Biology, 2018, 1776, 229-236.	0.9	1
90	Sulfonated azo dyes enhance the genome release of enterovirus A71 VP1â€“98K variants by preventing the virions from being trapped by sulfated glycosaminoglycans at acidic pH. Virology, 2021, 555, 19-34.	2.4	1

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91	A novel method employing polymerase chain reaction to disrupt genes lacking convenient restriction enzyme sites in yeast. Molecular Biotechnology, 1995, 3, 72-74.	2.4	0
92	Discovery, Identification, and Functional Characterization of Plant Long Intergenic Noncoding RNAs After Virus Infection. Methods in Molecular Biology, 2019, 1933, 187-194.	0.9	0
93	Effects of deletion at the TTTSTTT motif of Hibiscus latent Singapore virus coat protein on viral replication and long-distance movement. Virology, 2019, 526, 13-21.	2.4	0