

Se Hun Gu

List of Publications by Year in descending order

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29
papers

876
citations

623734

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526287

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#	ARTICLE	IF	CITATIONS
1	Reassortment Between Divergent Strains of Camp Ripley Virus (Hantaviridae) in the Northern Short-Tailed Shrew (<i>Blarina brevicauda</i>). <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 460.	3.9	6
2	ÄkrÄng virus, a novel mobatvirus (Hantaviridae) harbored by the Stoliczkaâ€™s Asian trident bat (<i>Aselliscus stoliczkanus</i>) in Vietnam. <i>Scientific Reports</i> , 2019, 9, 10239.	3.3	7
3	Highly Divergent Genetic Variants of Soricid-Borne Altai Virus (Hantaviridae) in Eurasia Suggest Ancient Host-Switching Events. <i>Viruses</i> , 2019, 11, 857.	3.3	12
4	Dynamic Circulation and Genetic Exchange of a Shrew-borne Hantavirus, Imjin virus, in the Republic of Korea. <i>Scientific Reports</i> , 2017, 7, 44369.	3.3	21
5	Isolation and partial characterization of a highly divergent lineage of hantavirus from the European mole (<i>Talpa europaea</i>). <i>Scientific Reports</i> , 2016, 6, 21119.	3.3	9
6	Genetic Diversity of Artybash Virus in the Laxmann's Shrew (<i>Sorex caecutiens</i>). <i>Vector-Borne and Zoonotic Diseases</i> , 2016, 16, 468-475.	1.5	23
7	Dahonggou Creek virus, a divergent lineage of hantavirus harbored by the long-tailed mole (<i>Scaptonyx fuscicaudus</i>). <i>Tropical Medicine and Health</i> , 2016, 44, 16.	2.8	9
8	Detection of Hantaan virus RNA from anti-Hantaan virus IgG seronegative rodents in an area of high endemicity in Republic of Korea. <i>Microbiology and Immunology</i> , 2016, 60, 268-271.	1.4	10
9	Genetic variants of Cao Bang hantavirus in the Chinese mole shrew (<i>Anourosorex squamipes</i>) and Taiwanese mole shrew (<i>Anourosorex yamashinai</i>). <i>Infection, Genetics and Evolution</i> , 2016, 40, 113-118.	2.3	10
10	Lethal disease in infant and juvenile Syrian hamsters experimentally infected with Imjin virus, a newfound crocidurine shrew-borne hantavirus. <i>Infection, Genetics and Evolution</i> , 2015, 36, 231-239.	2.3	6
11	Hokkaido genotype of Puumala virus in the grey red-backed vole (<i>Myodes rufocanus</i>) and northern red-backed vole (<i>Myodes rutilus</i>) in Siberia. <i>Infection, Genetics and Evolution</i> , 2015, 33, 304-313.	2.3	14
12	Whole-Genome Sequence of a Novel Hantavirus Isolated from the European Mole (<i>Talpa</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 302	0.8	1
13	Expanded Host Diversity and Global Distribution of Hantaviruses: Implications for Identifying and Investigating Previously Unrecognized Hantaviral Diseases. , 2015, , 161-198.		7
14	DiversitÄ© gÄ©nÄ©tique de <i>Talpa europaea</i> et de l'hantavirus Nova (NVAV) en France. <i>Bulletin De L'Academie Veterinaire De France</i> , 2014, 167, 277.	0.0	3
15	Muju Virus, Harbored by <i>Myodes regulus</i> in Korea, Might Represent a Genetic Variant of Puumala Virus, the Prototype Arvicolid Rodent-Borne Hantavirus. <i>Viruses</i> , 2014, 6, 1701-1714.	3.3	13
16	Molecular Phylogeny of Hantaviruses Harbored by Insectivorous Bats in CÃ¢te d'Ä™voire and Vietnam. <i>Viruses</i> , 2014, 6, 1897-1910.	3.3	25
17	Co-circulation of soricid- and talpid-borne hantaviruses in Poland. <i>Infection, Genetics and Evolution</i> , 2014, 28, 296-303.	2.3	27
18	Hantaviruses: Rediscovery and new beginnings. <i>Virus Research</i> , 2014, 187, 6-14.	2.2	100

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19	Prevalence and molecular characterizations of <i>Toxoplasma gondii</i> and <i>Babesia microti</i> from small mammals captured in Gyeonggi and Gangwon Provinces, Republic of Korea. <i>Veterinary Parasitology</i> , 2014, 205, 512-517.	1.8	19
20	Expanded Host Diversity and Geographic Distribution of Hantaviruses in Sub-Saharan Africa. <i>Journal of Virology</i> , 2014, 88, 7663-7667.	3.4	30
21	Reconstructing the evolutionary origins and phylogeography of hantaviruses. <i>Trends in Microbiology</i> , 2014, 22, 473-482.	7.7	75
22	Whole-Genome Sequence of Muju Virus, an Arvicolid Rodent-Borne Hantavirus. <i>Genome Announcements</i> , 2014, 2, .	0.8	0
23	Boginia virus, a newfound hantavirus harbored by the Eurasian water shrew (<i>Neomys fodiens</i>) in Poland. <i>Virology Journal</i> , 2013, 10, 160.	3.4	30
24	Complete genome sequence and molecular phylogeny of a newfound hantavirus harbored by the Doucetâ€™s musk shrew (<i>Crocidura douceti</i>) in Guinea. <i>Infection, Genetics and Evolution</i> , 2013, 20, 118-123.	2.3	58
25	Divergent ancestral lineages of newfound hantaviruses harbored by phylogenetically related crocidurine shrew species in Korea. <i>Virology</i> , 2012, 424, 99-105.	2.4	54
26	Divergent lineage of a novel hantavirus in the banana pipistrelle (<i>Neoromicia nanus</i>) in CÃˆte d'Ivoire. <i>Virology Journal</i> , 2012, 9, 34.	3.4	92
27	Genetic diversity of Imjin virus in the Ussuri white-toothed shrew (<i>Crocidura lasiura</i>) in the Republic of Korea, 2004-2010. <i>Virology Journal</i> , 2011, 8, 56.	3.4	14
28	Characterization of Imjin Virus, a Newly Isolated Hantavirus from the Ussuri White-Toothed Shrew () Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.4	97
29	Seewis virus, a genetically distinct hantavirus in the Eurasian common shrew (<i>Sorex araneus</i>). <i>Virology Journal</i> , 2007, 4, 114.	3.4	104