Raoul J De Groot

List of Publications by Year
in descending order

32	4,120	218381	414034
papers	citations	26 h-index	32 g-index

35	35	35	6525
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Commentary: Middle East Respiratory Syndrome Coronavirus (MERS-CoV): Announcement of the Coronavirus Study Group. Journal of Virology, 2013, 87, 7790-7792.	1.5	1,012
2	Structural basis for human coronavirus attachment to sialic acid receptors. Nature Structural and Molecular Biology, 2019, 26, 481-489.	3.6	475
3	Human coronaviruses OC43 and HKU1 bind to 9- O -acetylated sialic acids via a conserved receptor-binding site in spike protein domain A. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2681-2690.	3.3	335
4	Identification of sialic acid-binding function for the Middle East respiratory syndrome coronavirus spike glycoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E8508-E8517.	3.3	272
5	The Genome Organization of the Nidovirales: Similarities and Differences between Arteri-, Toro-, and Coronaviruses. Seminars in Virology, 1997, 8, 33-47.	4.1	244
6	Structure of coronavirus hemagglutinin-esterase offers insight into corona and influenza virus evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9065-9069.	3.3	221
7	Small molecule ISRIB suppresses the integrated stress response within a defined window of activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2097-2102.	3.3	163
8	Middle East Respiratory Coronavirus Accessory Protein 4a Inhibits PKR-Mediated Antiviral Stress Responses. PLoS Pathogens, 2016, 12, e1005982.	2.1	161
9	Structure, function and evolution of the hemagglutinin-esterase proteins of corona- and toroviruses. Glycoconjugate Journal, 2006, 23, 59-72.	1.4	129
10	The influenza A virus hemagglutinin glycosylation state affects receptor-binding specificity. Virology, 2010, 403, 17-25.	1.1	108
11	Kinetic analysis of the influenza A virus HA/NA balance reveals contribution of NA to virus-receptor binding and NA-dependent rolling on receptor-containing surfaces. PLoS Pathogens, 2018, 14, e1007233.	2.1	101
12	9-O-Acetylation of sialic acids is catalysed by CASD1 via a covalent acetyl-enzyme intermediate. Nature Communications, 2015, 6, 7673.	5.8	90
13	Betacoronavirus Adaptation to Humans Involved Progressive Loss of Hemagglutinin-Esterase Lectin Activity. Cell Host and Microbe, 2017, 21, 356-366.	5.1	83
14	Foot-and-Mouth Disease Virus Leader Protease Cleaves G3BP1 and G3BP2 and Inhibits Stress Granule Formation. Journal of Virology, 2019, 93, .	1.5	72
15	Nidovirus Sialate-O-Acetylesterases. Journal of Biological Chemistry, 2005, 280, 6933-6941.	1.6	71
16	Complexity and Diversity of the Mammalian Sialome Revealed by Nidovirus Virolectins. Cell Reports, 2015, 11, 1966-1978.	2.9	62
17	Attachment of Mouse Hepatitis Virus to O-Acetylated Sialic Acid Is Mediated by Hemagglutinin-Esterase and Not by the Spike Protein. Journal of Virology, 2010, 84, 8970-8974.	1.5	52
18	Coronavirus hemagglutinin-esterase and spike proteins coevolve for functional balance and optimal virion avidity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25759-25770.	3.3	48

#	Article	IF	Citations
19	Essential Role of Enterovirus 2A Protease in Counteracting Stress Granule Formation and the Induction of Type I Interferon. Journal of Virology, 2019, 93, .	1.5	47
20	Structural basis for ligand and substrate recognition by torovirus hemagglutinin esterases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15897-15902.	3.3	46
21	The Murine Coronavirus Hemagglutinin-esterase Receptor-binding Site: A Major Shift in Ligand Specificity through Modest Changes in Architecture. PLoS Pathogens, 2012, 8, e1002492.	2.1	46
22	Mutation of the Second Sialic Acid-Binding Site, Resulting in Reduced Neuraminidase Activity, Preceded the Emergence of H7N9 Influenza A Virus. Journal of Virology, 2017, 91, .	1.5	44
23	Role of enhanced receptor engagement in the evolution of a pandemic acute hemorrhagic conjunctivitis virus. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 397-402.	3.3	43
24	Inhibition of the integrated stress response by viral proteins that block p-eIF2â€“eIF2B association. Nature Microbiology, 2020, 5, 1361-1373.	5.9	39
25	Coronavirus receptor switch explained from the stereochemistry of proteinâ€“carbohydrate interactions and a single mutation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3111-9.	3.3	38
26	Synthetic O-acetylated sialosides facilitate functional receptor identification for human respiratory viruses. Nature Chemistry, 2021, 13, 496-503.	6.6	31
27	Dissecting distinct proteolytic activities of FMDV Lpro implicates cleavage and degradation of RLR signaling proteins, not its deISGylase/DUB activity, in type I interferon suppression. PLoS Pathogens, 2020, 16, e1008702.	2.1	26
28	Cryo-EM structure of coronavirus-HKU1 haemagglutinin esterase reveals architectural changes arising from prolonged circulation in humans. Nature Communications, 2020, 11, 4646.	5.8	24
29	Antigenic structure of the human coronavirus OC43 spike reveals exposed and occluded neutralizing epitopes. Nature Communications, 2022, 13, .	5.8	12
30	Synthetic O-Acetylated Sialosides and their Acetamido-deoxy Analogues as Probes for Coronaviral Hemagglutinin-esterase Recognition. Journal of the American Chemical Society, 2022, 144, 424-435.	6.6	4
31	Molecular Biology and Evolution of Toroviruses. , 0, , 133-146.		3
32	Synthetic O-Acetyl-N-glycolylneuraminic Acid Oligosaccharides Reveal Host-Associated Binding Patterns of Coronaviral Glycoproteins. ACS Infectious Diseases, 2022, 8, 1041-1050.	1.8	3