

Joost Snijder

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

2,964
citations

26
h-index

54
g-index

55
ext. papers

3,840
ext. citations

12.7
avg, IF

5.3
L-index

#	Paper	IF	Citations
46	Fluoxetine targets an allosteric site in the enterovirus 2C AAA+ ATPase and stabilizes a ring-shaped hexameric complex.. <i>Science Advances</i> , 2022 , 8, eabj7615	14.3	1
45	Assessment of genome packaging in AAVs using Orbitrap-based charge-detection mass spectrometry.. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022 , 24, 40-47	6.4	2
44	Adeno-associated virus capsid assembly is divergent and stochastic. <i>Nature Communications</i> , 2021 , 12, 1642	17.4	22
43	Mass Spectrometry-Based Sequencing of Monoclonal Antibodies Using Multiple Proteases and a Dual Fragmentation Scheme. <i>Journal of Proteome Research</i> , 2021 , 20, 3559-3566	5.6	4
42	Mass Spectrometry-Based Structural Virology. <i>Analytical Chemistry</i> , 2021 , 93, 620-640	7.8	9
41	Multimerization- and glycosylation-dependent receptor binding of SARS-CoV-2 spike proteins. <i>PLoS Pathogens</i> , 2021 , 17, e1009282	7.6	23
40	Human plasma IgG1 repertoires are simple, unique, and dynamic. <i>Cell Systems</i> , 2021 ,	10.6	5
39	Resolving heterogeneous macromolecular assemblies by Orbitrap-based single-particle charge detection mass spectrometry. <i>Nature Methods</i> , 2020 , 17, 395-398	21.6	47
38	Cryo-EM structure of coronavirus-HKU1 haemagglutinin esterase reveals architectural changes arising from prolonged circulation in humans. <i>Nature Communications</i> , 2020 , 11, 4646	17.4	16
37	Unexpected Receptor Functional Mimicry Elucidates Activation of Coronavirus Fusion. <i>Cell</i> , 2019 , 176, 1026-1039.e15	56.2	416
36	Induction of Potent Neutralizing Antibody Responses by a Designed Protein Nanoparticle Vaccine for Respiratory Syncytial Virus. <i>Cell</i> , 2019 , 176, 1420-1431.e17	56.2	190
35	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019 , 16, 595-602	21.6	216
34	Structural Studies of Coronavirus Fusion Proteins. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1300-1301	0.5	3
33	The Kai-Protein Clock-Keeping Track of Cyanobacteria's Daily Life. <i>Sub-Cellular Biochemistry</i> , 2019 , 93, 359-391	5.5	0
32	An antibody against the F glycoprotein inhibits Nipah and Hendra virus infections. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 980-987	17.6	28
31	An Antibody Targeting the Fusion Machinery Neutralizes Dual-Tropic Infection and Defines a Site of Vulnerability on Epstein-Barr Virus. <i>Immunity</i> , 2018 , 48, 799-811.e9	32.3	72
30	Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. <i>ELife</i> , 2018 , 7,	8.9	19

29	Glycan Shield and Fusion Activation of a Deltacoronavirus Spike Glycoprotein Fine-Tuned for Enteric Infections. <i>Journal of Virology</i> , 2018 , 92,	6.6	92
28	Bacterial encapsulins as orthogonal compartments for mammalian cell engineering. <i>Nature Communications</i> , 2018 , 9, 1990	17.4	51
27	Vitrification after multiple rounds of sample application and blotting improves particle density on cryo-electron microscopy grids. <i>Journal of Structural Biology</i> , 2017 , 198, 38-42	3.4	43
26	Structural Analysis of a Temperature-Induced Transition in a Viral Capsid Probed by HDX-MS. <i>Biophysical Journal</i> , 2017 , 112, 1157-1165	2.9	18
25	Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. <i>Science</i> , 2017 , 355, 1181-1184	33.3	77
24	Tectonic conformational changes of a coronavirus spike glycoprotein promote membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11157-11162	11.5	351
23	Glycan shield and epitope masking of a coronavirus spike protein observed by cryo-electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 899-905	17.6	252
22	Fluctuating Nonlinear Spring Model of Mechanical Deformation of Biological Particles. <i>PLoS Computational Biology</i> , 2016 , 12, e1004729	5	16
21	Assembly and Mechanical Properties of the Cargo-Free and Cargo-Loaded Bacterial Nanocompartment Encapsulin. <i>Biomacromolecules</i> , 2016 , 17, 2522-9	6.9	50
20	Structural basis of myelin-associated glycoprotein adhesion and signalling. <i>Nature Communications</i> , 2016 , 7, 13584	17.4	68
19	Examining the Heterogeneous Genome Content of Multipartite Viruses BMV and CCMV by Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 1000-9	3.5	32
18	Conformational landscape and pathway of disulfide bond reduction of human alpha defensin. <i>Protein Science</i> , 2015 , 24, 1264-71	6.3	6
17	Boundaries of mass resolution in native mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 906-17	3.5	92
16	Defining the stoichiometry and cargo load of viral and bacterial nanoparticles by Orbitrap mass spectrometry. <i>Journal of the American Chemical Society</i> , 2014 , 136, 7295-9	16.4	108
15	Architecture of a dsDNA viral capsid in complex with its maturation protease. <i>Structure</i> , 2014 , 22, 230-7	5.2	30
14	Self-assembly and characterization of small and monodisperse dye nanospheres in a protein cage. <i>Chemical Science</i> , 2014 , 5, 575-581	9.4	44
13	Analytical approaches for size and mass analysis of large protein assemblies. <i>Annual Review of Analytical Chemistry</i> , 2014 , 7, 43-64	12.5	59
12	Self-sorting of foreign proteins in a bacterial nanocompartment. <i>Journal of the American Chemical Society</i> , 2014 , 136, 3828-32	16.4	75

11	Adenovirus composition, proteolysis, and disassembly studied by in-depth qualitative and quantitative proteomics. <i>Journal of Biological Chemistry</i> , 2014 , 289, 11421-11430	5.4	67
10	The cleaved N-terminus of pVI binds peripentonal hexons in mature adenovirus. <i>Journal of Molecular Biology</i> , 2014 , 426, 1971-9	6.5	23
9	Insight into cyanobacterial circadian timing from structural details of the KaiB-KaiC interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 1379-84	11.5	49
8	Studying 18 MDa virus assemblies with native mass spectrometry. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 4020-3	16.4	140
7	Integrin and defensin modulate the mechanical properties of adenovirus. <i>Journal of Virology</i> , 2013 , 87, 2756-66	6.6	66
6	Structural transitions and energy landscape for Cowpea Chlorotic Mottle Virus capsid mechanics from nanomanipulation in vitro and in silico. <i>Biophysical Journal</i> , 2013 , 105, 1893-903	2.9	40
5	Human Plasma IgG1 Repertoires are Simple, Unique, and Dynamic. <i>SSRN Electronic Journal</i> ,	1	3
4	Adeno-associated virus capsid assembly is divergent and stochastic		1
3	Structure-based design of a highly stable, covalently-linked SARS-CoV-2 spike trimer with improved structural properties and immunogenicity		9
2	Travel-driven emergence and spread of SARS-CoV-2 lineage B.1.620 with multiple VOC-like mutations and deletions in Europe		11
1	Mass spectrometry-based de novo sequencing of the anti-FLAG-M2 antibody using multiple proteases and a dual fragmentation scheme		1