

# Stan J J Brouns

## List of Publications by Year in descending order

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Version: 2024-02-01

95  
papers

16,580  
citations

57631

44  
h-index

45213

90  
g-index

112  
all docs

112  
docs citations

112  
times ranked

11643  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms and clinical importance of bacteriophage resistance. FEMS Microbiology Reviews, 2022, 46, .	3.9	92
2	Short prokaryotic Argonaute systems trigger cell death upon detection of invading DNA. Cell, 2022, 185, 1471-1486.e19.	13.5	85
3	Single cell variability of CRISPR-Cas interference and adaptation. Molecular Systems Biology, 2022, 18, e10680.	3.2	3
4	Structural basis for broad anti-phage immunity by DISARM. Nature Communications, 2022, 13, .	5.8	10
5	Iron can be microbially extracted from Lunar and Martian regolith simulants and 3D printed into tough structural materials. PLoS ONE, 2021, 16, e0249962.	1.1	12
6	SCOPE enables type III CRISPR-Cas diagnostics using flexible targeting and stringent CARF ribonuclease activation. Nature Communications, 2021, 12, 5033.	5.8	57
7	Cas4-Cas1 Is a Protospacer Adjacent Motif-Processing Factor Mediating Half-Site Spacer Integration During CRISPR Adaptation. CRISPR Journal, 2021, 4, 536-548.	1.4	9
8	PAM-repeat associations and spacer selection preferences in single and co-occurring CRISPR-Cas systems. Genome Biology, 2021, 22, 281.	3.8	26
9	The gRAMP CRISPR-Cas effector is an RNA endonuclease complexed with a caspase-like peptidase. Science, 2021, 373, 1349-1353.	6.0	76
10	Mechanism for Cas4-assisted directional spacer acquisition in CRISPR-Cas. Nature, 2021, 598, 515-520.	13.7	29
11	RNA   Small RNAs in Bacteria. , 2021, , 580-586.		0
12	Direct Visualization of Native CRISPR Target Search in Live Bacteria Reveals Cascade DNA Surveillance Mechanism. Molecular Cell, 2020, 77, 39-50.e10.	4.5	43
13	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
14	Extracting Transition Rates in Particle Tracking Using Analytical Diffusion Distribution Analysis. Biophysical Journal, 2020, 119, 1970-1983.	0.2	19
15	Adsorption Sequencing as a Rapid Method to Link Environmental Bacteriophages to Hosts. IScience, 2020, 23, 101439.	1.9	23
16	Prophages are associated with extensive CRISPR-Cas auto-immunity. Nucleic Acids Research, 2020, 48, 12074-12084.	6.5	35
17	Development of Styrene Maleic Acid Lipid Particles as a Tool for Studies of Phage-Host Interactions. Journal of Virology, 2020, 94, .	1.5	3
18	An educational guide for nanopore sequencing in the classroom. PLoS Computational Biology, 2020, 16, e1007314.	1.5	20

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19	Selective loading and processing of prespacers for precise CRISPR adaptation. <i>Nature</i> , 2020, 579, 141-145.	13.7	46
20	Visualisation of dCas9 target search in vivo using an open-microscopy framework. <i>Nature Communications</i> , 2019, 10, 3552.	5.8	70
21	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
22	Creation of Conductive Graphene Materials by Bacterial Reduction Using <i>Shewanella Oneidensis</i> . <i>ChemistryOpen</i> , 2019, 8, 888-895.	0.9	20
23	Conserved motifs in the CRISPR leader sequence control spacer acquisition levels in Type I-D CRISPR-Cas systems. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	16
24	Addiction systems antagonize bacterial adaptive immunity. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	5
25	Systematic analysis of Type I <i>Escherichia coli</i> CRISPR-Cas PAM sequences ability to promote interference and primed adaptation. <i>Molecular Microbiology</i> , 2019, 111, 1558-1570.	1.2	27
26	Cas4-Cas1 fusions drive efficient PAM selection and control CRISPR adaptation. <i>Nucleic Acids Research</i> , 2019, 47, 5223-5230.	6.5	34
27	Using CAPTURE to detect spacer acquisition in native CRISPR arrays. <i>Nature Protocols</i> , 2019, 14, 976-990.	5.5	14
28	CRISPR-Cas Systems Reduced to a Minimum. <i>Molecular Cell</i> , 2019, 73, 641-642.	4.5	0
29	Harnessing type I CRISPR-Cas systems for genome engineering in human cells. <i>Nature Biotechnology</i> , 2019, 37, 1471-1477.	9.4	91
30	Evolution of BACON Domain Tandem Repeats in crAssphage and Novel Gut Bacteriophage Lineages. <i>Viruses</i> , 2019, 11, 1085.	1.5	20
31	Molecular and Evolutionary Determinants of Bacteriophage Host Range. <i>Trends in Microbiology</i> , 2019, 27, 51-63.	3.5	277
32	Complete Genome Sequence of the <i>Escherichia coli</i> Phage Ayreon. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
33	Bacteriophage DNA glucosylation impairs target DNA binding by type I and II but not by type V CRISPR-Cas effector complexes. <i>Nucleic Acids Research</i> , 2018, 46, 873-885.	6.5	57
34	Repetitive DNA Reeling by the Cascade-Cas3 Complex in Nucleotide Unwinding Steps. <i>Molecular Cell</i> , 2018, 70, 385-394.e3.	4.5	54
35	Cas4 Facilitates PAM-Compatible Spacer Selection during CRISPR Adaptation. <i>Cell Reports</i> , 2018, 22, 3377-3384.	2.9	102
36	Complete Genome Sequences of Two T4-Like <i>Escherichia coli</i> Bacteriophages. <i>Genome Announcements</i> , 2018, 6, .	0.8	1

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37	Targeting mechanisms of tailed bacteriophages. <i>Nature Reviews Microbiology</i> , 2018, 16, 760-773.	13.6	310
38	Role of nucleotide identity in effective CRISPR target escape mutations. <i>Nucleic Acids Research</i> , 2018, 46, 10395-10404.	6.5	10
39	CRISPR-Cas: Adapting to change. <i>Science</i> , 2017, 356, .	6.0	323
40	Cas3-Derived Target DNA Degradation Fragments Fuel Primed CRISPR Adaptation. <i>Molecular Cell</i> , 2016, 63, 852-864.	4.5	111
41	Interference-driven spacer acquisition is dominant over naive and primed adaptation in a native CRISPR-Cas system. <i>Nature Communications</i> , 2016, 7, 12853.	5.8	125
42	CRISPR interference and priming varies with individual spacer sequences. <i>Nucleic Acids Research</i> , 2015, 43, 10831-10847.	6.5	95
43	CRISPR sabotage. <i>Genome Biology</i> , 2015, 16, 248.	3.8	3
44	Two Distinct DNA Binding Modes Guide Dual Roles of a CRISPR-Cas Protein Complex. <i>Molecular Cell</i> , 2015, 58, 60-70.	4.5	100
45	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	13.6	2,081
46	Electrophoretic Mobility Shift Assay of DNA and CRISPR-Cas Ribonucleoprotein Complexes. <i>Methods in Molecular Biology</i> , 2015, 1311, 171-184.	0.4	4
47	Archaeal MBF1 binds to 30S and 70S ribosomes via its helix-turn-helix domain. <i>Biochemical Journal</i> , 2014, 462, 373-384.	1.7	16
48	DNA-guided DNA interference by a prokaryotic Argonaute. <i>Nature</i> , 2014, 507, 258-261.	13.7	373
49	Planting the seed: target recognition of short guide RNAs. <i>Trends in Microbiology</i> , 2014, 22, 74-83.	3.5	70
50	Crystal structure of the CRISPR RNA-guided surveillance complex from <i>Escherichia coli</i> . <i>Science</i> , 2014, 345, 1473-1479.	6.0	226
51	Degenerate target sites mediate rapid primed CRISPR adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1629-38.	3.3	239
52	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	2.9	64
53	Distribution and Mechanism of the Type I CRISPR-Cas Systems. , 2013, , 145-169.		5
54	CRISPR-Cas systems preferentially target the leading regions of MOB <sub>F</sub> conjugative plasmids. <i>RNA Biology</i> , 2013, 10, 749-761.	1.5	32

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55	Comparative Genomic and Functional Analysis of 100 <i>Lactobacillus rhamnosus</i> Strains and Their Comparison with Strain GC. <i>PLoS Genetics</i> , 2013, 9, e1003683.	1.5	180
56	Type I-E CRISPR-Cas Systems Discriminate Target from Non-Target DNA through Base Pairing-Independent PAM Recognition. <i>PLoS Genetics</i> , 2013, 9, e1003742.	1.5	187
57	A capture approach for supercoiled plasmid DNA using a triplex-forming oligonucleotide. <i>Nucleic Acids Research</i> , 2013, 41, e111-e111.	6.5	1
58	CRISPRTarget. <i>RNA Biology</i> , 2013, 10, 817-827.	1.5	272
59	Distribution and Mechanism of the Type I CRISPR-Cas Systems. , 2013, , 145-169.		7
60	Native Tandem and Ion Mobility Mass Spectrometry Highlight Structural and Modular Similarities in Clustered-Regularly-Interspaced Shot-Palindromic-Repeats (CRISPR)-associated Protein Complexes From <i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1430-1441.	2.5	74
61	A Swiss Army Knife of Immunity. <i>Science</i> , 2012, 337, 808-809.	6.0	8
62	Cascade-mediated binding and bending of negatively supercoiled DNA. <i>RNA Biology</i> , 2012, 9, 1134-1138.	1.5	37
63	CRISPR Immunity Relies on the Consecutive Binding and Degradation of Negatively Supercoiled Invader DNA by Cascade and Cas3. <i>Molecular Cell</i> , 2012, 46, 595-605.	4.5	475
64	The CRISPRs, They Are A-Changin': How Prokaryotes Generate Adaptive Immunity. <i>Annual Review of Genetics</i> , 2012, 46, 311-339.	3.2	260
65	RNA in Defense: CRISPRs Protect Prokaryotes against Mobile Genetic Elements. <i>Cold Spring Harbor Perspectives in Biology</i> , 2012, 4, a003657-a003657.	2.3	76
66	The rise and fall of CRISPRs – dynamics of spacer acquisition and loss. <i>Molecular Microbiology</i> , 2012, 85, 1021-1025.	1.2	26
67	CRISPR Interference Directs Strand Specific Spacer Acquisition. <i>PLoS ONE</i> , 2012, 7, e35888.	1.1	335
68	Clustered regularly interspaced short palindromic repeats (CRISPRs): the hallmark of an ingenious antiviral defense mechanism in prokaryotes. <i>Biological Chemistry</i> , 2011, 392, 277-89.	1.2	145
69	Structures of the RNA-guided surveillance complex from a bacterial immune system. <i>Nature</i> , 2011, 477, 486-489.	13.7	355
70	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011, 9, 467-477.	13.6	2,078
71	Assembling the archaeal ribosome: roles for translation-factor-related GTPases. <i>Biochemical Society Transactions</i> , 2011, 39, 45-50.	1.6	16
72	Structural basis for CRISPR RNA-guided DNA recognition by Cascade. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 529-536.	3.6	498

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73	Interference by clustered regularly interspaced short palindromic repeat (CRISPR) RNA is governed by a seed sequence. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10098-10103.	3.3	665
74	Structure of the ribosome associating GTPase HflX. Proteins: Structure, Function and Bioinformatics, 2010, 78, 705-713.	1.5	19
75	H $\sigma$ -mediated repression of CRISPR-based immunity in <i>Escherichia coli</i> K12 can be relieved by the transcription activator LeuO. Molecular Microbiology, 2010, 77, 1380-1393.	1.2	220
76	Fidelity in Archaeal Information Processing. Archaea, 2010, 2010, 1-15.	2.3	4
77	CRISPR-based adaptive and heritable immunity in prokaryotes. Trends in Biochemical Sciences, 2009, 34, 401-407.	3.7	453
78	RNAi: Prokaryotes Get in on the Act. Cell, 2009, 139, 863-865.	13.5	22
79	Role of multiprotein bridging factor 1 in archaea: bridging the domains?. Biochemical Society Transactions, 2009, 37, 52-57.	1.6	21
80	Laboratory evolution of <i>Pyrococcus furiosus</i> alcohol dehydrogenase to improve the production of (2S,5S)-hexanediol at moderate temperatures. Extremophiles, 2008, 12, 587-594.	0.9	37
81	Structural Insight into Substrate Binding and Catalysis of a Novel 2-Keto-3-deoxy-d-arabinonate Dehydratase Illustrates Common Mechanistic Features of the FAH Superfamily. Journal of Molecular Biology, 2008, 379, 357-371.	2.0	34
82	Small CRISPR RNAs Guide Antiviral Defense in Prokaryotes. Science, 2008, 321, 960-964.	6.0	2,138
83	Transcriptome Analysis of Infection of the Archaeon <i>Sulfolobus solfataricus</i> with <i>Sulfolobus</i> Turreted Icosahedral Virus. Journal of Virology, 2008, 82, 4874-4883.	1.5	84
84	Crystal Structure and Biochemical Properties of the d-Arabinose Dehydrogenase from <i>Sulfolobus solfataricus</i> . Journal of Molecular Biology, 2007, 371, 1249-1260.	2.0	16
85	Purification, crystallization and preliminary crystallographic analysis of a GTP-binding protein from the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> . Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 239-241.	0.7	3
86	Improving the Performance of a Quadrupole Time-of-Flight Instrument for Macromolecular Mass Spectrometry. Analytical Chemistry, 2006, 78, 7473-7483.	3.2	240
87	Identification of a Novel $\beta$ -Galactosidase from the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> . Journal of Bacteriology, 2006, 188, 2392-2399.	1.0	51
88	Identification of the Missing Links in Prokaryotic Pentose Oxidation Pathways. Journal of Biological Chemistry, 2006, 281, 27378-27388.	1.6	102
89	Evidence Supporting a cis-enediol-based Mechanism for <i>Pyrococcus furiosus</i> Phosphoglucose Isomerase. Journal of Molecular Biology, 2006, 358, 1353-1366.	2.0	29
90	9 Functional Genomics of the Thermo-Acidophilic Archaeon <i>Sulfolobus solfataricus</i> . Methods in Microbiology, 2006, 35, 201-231.	0.4	0

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91	Reconstruction of central carbon metabolism in <i>Sulfolobus solfataricus</i> using a two-dimensional gel electrophoresis map, stable isotope labelling and DNA microarray analysis. <i>Proteomics</i> , 2006, 6, 1518-1529.	1.3	52
92	Engineering a Selectable Marker for Hyperthermophiles. <i>Journal of Biological Chemistry</i> , 2005, 280, 11422-11431.	1.6	78
93	Cloning and Expression of Islandisin, a New Thermostable Subtilisin from <i>Fervidobacterium islandicum</i> , in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 3951-3958.	1.4	28
94	DNA family shuffling of hyperthermostable $\beta$ -glycosidases. <i>Biochemical Journal</i> , 2002, 368, 461-470.	1.7	38
95	Adaptation by Type V-A and V-B CRISPR-Cas Systems Demonstrates Conserved Protospacer Selection Mechanisms Between Diverse CRISPR-Cas Types. <i>CRISPR Journal</i> , 0, , .	1.4	1