

Christiane Berger-Schaffitzel

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.

52
papers

1,841
citations

22
h-index

42
g-index

63
ext. papers

2,377
ext. citations

11.7
avg, IF

4.77
L-index

#	Paper	IF	Citations
52	Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2.. <i>Nature Communications</i> , 2022 , 13, 222	17.4	2
51	Synthetic virions reveal fatty acid-coupled adaptive immunogenicity of SARS-CoV-2 spike glycoprotein.. <i>Nature Communications</i> , 2022 , 13, 868	17.4	5
50	No-nonsense: insights into the functional interplay of nonsense-mediated mRNA decay factors.. <i>Biochemical Journal</i> , 2022 , 479, 973-993	3.8	1
49	The fatty acid site is coupled to functional motifs in the SARS-CoV-2 spike protein and modulates spike allosteric behaviour.. <i>Computational and Structural Biotechnology Journal</i> , 2021 ,	6.8	2
48	Production of Multi-subunit Membrane Protein Complexes. <i>Methods in Molecular Biology</i> , 2021 , 2247, 3-16	1.4	
47	Frontispiz: Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARS-CoV-2 Spike Protein. <i>Angewandte Chemie</i> , 2021 , 133,	3.6	3
46	VLP-factory and ADDomer : Self-assembling Virus-Like Particle (VLP) Technologies for Multiple Protein and Peptide Epitope Display. <i>Current Protocols</i> , 2021 , 1, e55		1
45	Blasticidin S inhibits mammalian translation and enhances production of protein encoded by nonsense mRNA. <i>Nucleic Acids Research</i> , 2021 , 49, 7665-7679	20.1	2
44	Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARS-CoV-2 Spike Protein*. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 7098-7110	16.4	37
43	Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARS-CoV-2 Spike Protein**. <i>Angewandte Chemie</i> , 2021 , 133, 7174-7186	3.6	4
42	Identification and Phenotypic Characterization of Hsp90 Phosphorylation Sites That Modulate Virulence Traits in the Major Human Fungal Pathogen. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 637836	5.9	4
41	The SARS-CoV-2 spike protein: balancing stability and infectivity. <i>Cell Research</i> , 2020 , 30, 1059-1060	24.7	36
40	New insights into no-go, non-stop and nonsense-mediated mRNA decay complexes. <i>Current Opinion in Structural Biology</i> , 2020 , 65, 110-118	8.1	17
39	Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein. <i>Science</i> , 2020 , 370, 725-730	33.3	182
38	Synthetic self-assembling ADDomer platform for highly efficient vaccination by genetically encoded multiepitope display. <i>Science Advances</i> , 2019 , 5, eaaw2853	14.3	13
37	Structure and Dynamics of the Central Lipid Pool and Proteins of the Bacterial Holo-Translocon. <i>Biophysical Journal</i> , 2019 , 116, 1931-1940	2.9	14
36	MultiBac: Baculovirus-Mediated Multigene DNA Cargo Delivery in Insect and Mammalian Cells. <i>Viruses</i> , 2019 , 11,	6.2	19

35	High-Throughput Production of Influenza Virus-Like Particle (VLP) Array by Using VLP-factory, a MultiBac Baculoviral Genome Customized for Enveloped VLP Expression. <i>Methods in Molecular Biology</i> , 2019 , 2025, 213-226	1.4	7
34	Cloning, expression, and purification of intact polyketide synthase modules. <i>Methods in Enzymology</i> , 2019 , 617, 63-82	1.7	1
33	New insights into the interplay between the translation machinery and nonsense-mediated mRNA decay factors. <i>Biochemical Society Transactions</i> , 2018 , 46, 503-512	5.1	24
32	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018 , 46, 2678-2689	20.1	47
31	Efficient production of a mature and functional gamma secretase protease. <i>Scientific Reports</i> , 2018 , 8, 12834	4.9	3
30	Multiprotein Complex Production in E. coli: The SecYEG-SecDFYajC-YidC Holotranslocon. <i>Methods in Molecular Biology</i> , 2017 , 1586, 279-290	1.4	2
29	Dual function of UPF3B in early and late translation termination. <i>EMBO Journal</i> , 2017 , 36, 2968-2986	13	60
28	Cryo-EM structure of <i>Saccharomyces cerevisiae</i> target of rapamycin complex 2. <i>Nature Communications</i> , 2017 , 8, 1729	17.4	38
27	PABP enhances release factor recruitment and stop codon recognition during translation termination. <i>Nucleic Acids Research</i> , 2016 , 44, 7766-76	20.1	67
26	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016 , 6, 38399	4.9	38
25	Membrane protein insertion and assembly by the bacterial holo-translocon SecYEG-SecDF-YajC-YidC. <i>Biochemical Journal</i> , 2016 , 473, 3341-54	3.8	40
24	Cell-Free Synthesis of Macromolecular Complexes. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 896, 79-95	3.6	
23	ACEMBL Tool-Kits for High-Throughput Multigene Delivery and Expression in Prokaryotic and Eukaryotic Hosts. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 896, 27-42	3.6	10
22	ACEMBLing a multiprotein transmembrane complex: the functional SecYEG-SecDF-YajC-YidC Holotranslocon protein secretase/insertase. <i>Methods in Enzymology</i> , 2015 , 556, 23-49	1.7	8
21	Advances and challenges of membrane-protein complex production. <i>Current Opinion in Structural Biology</i> , 2015 , 32, 123-30	8.1	24
20	Ribosome-SRP-FtsY cotranslational targeting complex in the closed state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 3943-8	11.5	19
19	A network of SMG-8, SMG-9 and SMG-1 C-terminal insertion domain regulates UPF1 substrate recruitment and phosphorylation. <i>Nucleic Acids Research</i> , 2015 , 43, 7600-11	20.1	35
18	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015 , 58, 977-88	17.6	101

17	Cytoplasmic TAF2-TAF8-TAF10 complex provides evidence for nuclear holo-TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015 , 6, 6011	17.4	57
16	Membrane protein insertion and proton-motive-force-dependent secretion through the bacterial holo-translocon SecYEG-SecDF-YajC-YidC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4844-9	11.5	93
15	Continuous fluorescence-based measurement of redox-driven sodium ion translocation. <i>Analytical Biochemistry</i> , 2014 , 459, 53-5	3.1	2
14	Structural and functional analysis of the three MIF4G domains of nonsense-mediated decay factor UPF2. <i>Nucleic Acids Research</i> , 2014 , 42, 2673-86	20.1	32
13	The architecture of human general transcription factor TFIID core complex. <i>Nature</i> , 2013 , 493, 699-702	50.4	116
12	Robots, pipelines, polyproteins: enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011 , 175, 198-208	3.4	80
11	Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009 , 6, 447-50	21.6	84
10	Multiprotein expression strategy for structural biology of eukaryotic complexes. <i>Structure</i> , 2007 , 15, 275-9	5.2	45
9	Protein complex expression by using multigene baculoviral vectors. <i>Nature Methods</i> , 2006 , 3, 1021-32	21.6	262
8	Ribosome display: an in vitro method for selection and evolution of antibodies from libraries. <i>Journal of Immunological Methods</i> , 1999 , 231, 119-35	2.5	166
7	Live-cell 3D single-molecule tracking reveals how NuRD modulates enhancer dynamics		4
6	Unexpected free fatty acid binding pocket in the cryo-EM structure of SARS-CoV-2 spike protein		8
5	Cryptic pathogen-sugar interactions revealed by universal saturation transfer analysis		5
4	Structural basis for cell-type specific evolution of viral fitness by SARS-CoV-2		2
3	The fatty acid site is coupled to functional motifs in the SARS-CoV-2 spike protein and modulates spike allosteric behaviour		3
2	Escherichia coli Cotranslational Targeting and Translocation		1
1	Molecular basis of neurodevelopmental disorder-causing mutation in nonsense-mediated mRNA decay factor UPF3B		1