

Christiane Berger-Schaffitzel

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,746
citations

257450

24
h-index

214800

47
g-index

63
all docs

63
docs citations

63
times ranked

4213
citing authors

#	ARTICLE	IF	CITATIONS
1	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> , 2022, 20, 139-147.	4.1	19
2	Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2. <i>Nature Communications</i> , 2022, 13, 222.	12.8	23
3	Synthetic virions reveal fatty acid-coupled adaptive immunogenicity of SARS-CoV-2 spike glycoprotein. <i>Nature Communications</i> , 2022, 13, 868.	12.8	20
4	Structures of nonsense-mediated mRNA decay factors UPF3B and UPF3A in complex with UPF2 reveal molecular basis for competitive binding and for neurodevelopmental disorder-causing mutation. <i>Nucleic Acids Research</i> , 2022, 50, 5934-5947.	14.5	8
5	No-nonsense: insights into the functional interplay of nonsense-mediated mRNA decay factors. <i>Biochemical Journal</i> , 2022, 479, 973-993.	3.7	9
6	Pathogen-sugar interactions revealed by universal saturation transfer analysis. <i>Science</i> , 2022, 377, .	12.6	24
7	Highly efficient CRISPR-mediated large DNA docking and multiplexed prime editing using a single baculovirus. <i>Nucleic Acids Research</i> , 2022, 50, 7783-7799.	14.5	15
8	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.	13.8	77
9	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.	2.0	6
10	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, .	2.0	7
11	Frontispiece: 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, .	13.8	0
12	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.	2.9	9
13	Blasticidin S inhibits mammalian translation and enhances production of protein encoded by nonsense mRNA. <i>Nucleic Acids Research</i> , 2021, 49, 7665-7679.	14.5	13
14	Identification and Phenotypic Characterization of Hsp90 Phosphorylation Sites That Modulate Virulence Traits in the Major Human Fungal Pathogen <i>Candida albicans</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 637836.	3.9	9
15	Structural biology in the fight against COVID-19. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 2-7.	8.2	20
16	Production of Multi-subunit Membrane Protein Complexes. <i>Methods in Molecular Biology</i> , 2021, 2247, 3-16.	0.9	1
17	New insights into no-go, non-stop and nonsense-mediated mRNA decay complexes. <i>Current Opinion in Structural Biology</i> , 2020, 65, 110-118.	5.7	40
18	Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein. <i>Science</i> , 2020, 370, 725-730.	12.6	348

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19	The SARS-CoV-2 spike protein: balancing stability and infectivity. <i>Cell Research</i> , 2020, 30, 1059-1060.	12.0	82
20	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.	0.9	7
21	Synthetic self-assembling ADDomer platform for highly efficient vaccination by genetically encoded multipeptide display. <i>Science Advances</i> , 2019, 5, eaaw2853.	10.3	29
22	Structure and Dynamics of the Central Lipid Pool and Proteins of the Bacterial Holo-Translocon. <i>Biophysical Journal</i> , 2019, 116, 1931-1940.	0.5	22
23	MultiBac: Baculovirus-Mediated Multigene DNA Cargo Delivery in Insect and Mammalian Cells. <i>Viruses</i> , 2019, 11, 198.	3.3	25
24	Cloning, expression, and purification of intact polyketide synthase modules. <i>Methods in Enzymology</i> , 2019, 617, 63-82.	1.0	3
25	New insights into the interplay between the translation machinery and nonsense-mediated mRNA decay factors. <i>Biochemical Society Transactions</i> , 2018, 46, 503-512.	3.4	38
26	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018, 46, 2678-2689.	14.5	76
27	Efficient production of a mature and functional gamma secretase protease. <i>Scientific Reports</i> , 2018, 8, 12834.	3.3	5
28	Multiprotein Complex Production in <i>E. coli</i> : The SecYEG-SecDFYajC-YidC Holotranslocon. <i>Methods in Molecular Biology</i> , 2017, 1586, 279-290.	0.9	2
29	Dual function of UPF3B in early and late translation termination. <i>EMBO Journal</i> , 2017, 36, 2968-2986.	7.8	89
30	Cryo-EM structure of <i>Saccharomyces cerevisiae</i> target of rapamycin complex 2. <i>Nature Communications</i> , 2017, 8, 1729.	12.8	46
31	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016, 6, 38399.	3.3	54
32	Membrane protein insertion and assembly by the bacterial holo-translocon SecYEG-SecDFYajC-YidC. <i>Biochemical Journal</i> , 2016, 473, 3341-3354.	3.7	61
33	Cell-Free Synthesis of Macromolecular Complexes. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 79-95.	1.6	0
34	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.	1.6	17
35	PABP enhances release factor recruitment and stop codon recognition during translation termination. <i>Nucleic Acids Research</i> , 2016, 44, 7766-7776.	14.5	99
36	MCM2-7 conformational changes in the presence of DNA. <i>Cell Cycle</i> , 2016, 15, 2391-2392.	2.6	0

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37	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015, 58, 977-988.	9.7	120
38	Cytoplasmic TAF2â€“TAF8â€“TAF10 complex provides evidence for nuclear holoâ€“TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015, 6, 6011.	12.8	77
39	ACEMBLing a Multiprotein Transmembrane Complex. <i>Methods in Enzymology</i> , 2015, 556, 23-49.	1.0	9
40	Advances and challenges of membraneâ€“protein complex production. <i>Current Opinion in Structural Biology</i> , 2015, 32, 123-130.	5.7	32
41	Ribosomeâ€“SRPâ€“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, 3943-3948.	7.1	26
42	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, 7600-7611.	14.5	51
43	Structural and functional analysis of the three MIF4G domains of nonsense-mediated decay factor UPF2. <i>Nucleic Acids Research</i> , 2014, 42, 2673-2686.	14.5	43
44	Membrane protein insertion and proton-motive-force-dependent secretion through the bacterial holo-translocon SecYEGâ€“SecDFâ€“YajCâ€“YidC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4844-4849.	7.1	124
45	Continuous fluorescence-based measurement of redox-driven sodium ion translocation. <i>Analytical Biochemistry</i> , 2014, 459, 53-55.	2.4	2
46	The architecture of human general transcription factor TFIID core complex. <i>Nature</i> , 2013, 493, 699-702.	27.8	142
47	Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011, 175, 198-208.	2.8	92
48	Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009, 6, 447-450.	19.0	98
49	Multiprotein Expression Strategy for Structural Biology of Eukaryotic Complexes. <i>Structure</i> , 2007, 15, 275-279.	3.3	50
50	Protein complex expression by using multigene baculoviral vectors. <i>Nature Methods</i> , 2006, 3, 1021-1032.	19.0	330
51	Ribosome display: an in vitro method for selection and evolution of antibodies from libraries. <i>Journal of Immunological Methods</i> , 1999, 231, 119-135.	1.4	202