

Christiane 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.

58

papers

3,208

citations

31

h-index

56

g-index

69

ext. papers

3,800

ext. citations

13.6

avg, IF

5

L-index

#	Paper	IF	Citations
58	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
57	Synthetic virions reveal fatty acid-coupled adaptive immunogenicity of SARS-CoV-2 spike glycoprotein.. <i>Nature Communications</i> , 2022 , 13, 868	17.4	5
56	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
55	Production of Multi-subunit Membrane Protein Complexes. <i>Methods in Molecular Biology</i> , 2021 , 2247, 3-16	1.4	
54	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
53	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
52	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
51	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
50	The SARS-CoV-2 spike protein: balancing stability and infectivity. <i>Cell Research</i> , 2020 , 30, 1059-1060	24.7	36
49	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
48	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
47	MultiBac: Baculovirus-Mediated Multigene DNA Cargo Delivery in Insect and Mammalian Cells. <i>Viruses</i> , 2019 , 11,	6.2	19
46	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
45	Structure of a human cap-dependent 48S translation pre-initiation complex. <i>Nucleic Acids Research</i> , 2018 , 46, 2678-2689	20.1	47
44	Efficient production of a mature and functional gamma secretase protease. <i>Scientific Reports</i> , 2018 , 8, 12834	4.9	3
43	Multiprotein Complex Production in E. coli: The SecYEG-SecDFYajC-YidC Holotranslocon. <i>Methods in Molecular Biology</i> , 2017 , 1586, 279-290	1.4	2
42	Dual function of UPF3B in early and late translation termination. <i>EMBO Journal</i> , 2017 , 36, 2968-2986	13	60

41	Cryo-EM structure of <i>Saccharomyces cerevisiae</i> target of rapamycin complex 2. <i>Nature Communications</i> , 2017 , 8, 1729	17.4	38
40	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016 , 6, 38399	4.9	38
39	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
38	Cell-Free Synthesis of Macromolecular Complexes. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 896, 79-95	3.6	
37	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
36	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
35	Advances and challenges of membrane-protein complex production. <i>Current Opinion in Structural Biology</i> , 2015 , 32, 123-30	8.1	24
34	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
33	Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. <i>Molecular Cell</i> , 2015 , 58, 977-88	17.6	101
32	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
31	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
30	Structural basis of signal sequence surveillance and selection by the SRP-FtsY complex. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 604-10	17.6	15
29	The architecture of human general transcription factor TFIID core complex. <i>Nature</i> , 2013 , 493, 699-702	50.4	116
28	Cryo-electron microscopy of ribosomal complexes in cotranslational folding, targeting, and translocation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012 , 3, 429-41	9.3	11
27	Robots, pipelines, polyproteins: enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011 , 175, 198-208	3.4	80
26	Cryo-EM structure of the <i>E. coli</i> translating ribosome in complex with SRP and its receptor. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 88-90	17.6	61
25	Probing telomeric G-quadruplex DNA structures in cells with in vitro generated single-chain antibody fragments. <i>Methods in Molecular Biology</i> , 2010 , 608, 159-81	1.4	24
24	Multiple conformational switches in a GTPase complex control co-translational protein targeting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 1754-9	11.5	90

23	Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009 , 6, 447-50	21.6	84
22	YidC and Oxa1 form dimeric insertion pores on the translating ribosome. <i>Molecular Cell</i> , 2009 , 34, 344-53	17.6	103
21	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. <i>EMBO Journal</i> , 2008 , 27, 1622-32	13	124
20	Dynamics of trigger factor interaction with translating ribosomes. <i>Journal of Biological Chemistry</i> , 2008 , 283, 4124-32	5.4	72
19	Multiprotein expression strategy for structural biology of eukaryotic complexes. <i>Structure</i> , 2007 , 15, 275-9	5.2	45
18	Generation of ribosome nascent chain complexes for structural and functional studies. <i>Journal of Structural Biology</i> , 2007 , 158, 463-71	3.4	63
17	Reprint of "Generation of ribosome nascent chain complexes for structural and functional studies" [J. Struct. Biol. 158 (2007) 463-471]. <i>Journal of Structural Biology</i> , 2007 , 159, 302-10	3.4	10
16	Multi-level regulation of myotubularin-related protein-2 phosphatase activity by myotubularin-related protein-13/set-binding factor-2. <i>Human Molecular Genetics</i> , 2006 , 15, 569-79	5.6	87
15	Elongation arrest by SecM via a cascade of ribosomal RNA rearrangements. <i>Molecular Cell</i> , 2006 , 22, 533-43	17.6	70
14	Protein complex expression by using multigene baculoviral vectors. <i>Nature Methods</i> , 2006 , 3, 1021-32	21.6	262
13	Structure of the E. coli signal recognition particle bound to a translating ribosome. <i>Nature</i> , 2006 , 444, 503-6	50.4	109
12	Structure of the E. coli protein-conducting channel bound to a translating ribosome. <i>Nature</i> , 2005 , 438, 318-24	50.4	226
11	Membrane association of myotubularin-related protein 2 is mediated by a pleckstrin homology-GRAM domain and a coiled-coil dimerization module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12177-82	11.5	97
10	In vitro selection and evolution of proteins. <i>Advances in Protein Chemistry</i> , 2000 , 55, 367-403		36
9	Picomolar affinity antibodies from a fully synthetic naive library selected and evolved by ribosome display. <i>Nature Biotechnology</i> , 2000 , 18, 1287-92	44.5	308
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	Comparison of Escherichia coli and rabbit reticulocyte ribosome display systems. <i>FEBS Letters</i> , 1999 , 450, 105-10	3.8	51
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