# Christiane Schaffitzel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10770653/publications.pdf

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| 57 | 4,175 | 147566 | 155451 |
|---|---|---|---|
| papers | citations | 31 h-index | 55 g-index |

| 69 | 69 | 69 | 5150 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Picomolar affinity antibodies from a fully synthetic naive library selected and evolved by ribosome display. Nature Biotechnology, 2000, 18, 1287-1292. | 9.4 | 362 |
| 2 | Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein. Science, 2020, 370, 725-730. | 6.0 | 348 |
| 3 | Protein complex expression by using multigene baculoviral vectors. Nature Methods, 2006, 3, 1021-1032. | 9.0 | 330 |
| 4 | Structure of the E. coli protein-conducting channel bound to a translating ribosome. Nature, 2005, 438, 318-324. | 13.7 | 243 |
| 5 | Ribosome display: an in vitro method for selection and evolution of antibodies from libraries. Journal of Immunological Methods, 1999, 231, 119-135. | 0.6 | 202 |
| 6 | Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. EMBO Journal, 2008, 27, 1622-1632. | 3.5 | 142 |
| 7 | The architecture of human general transcription factor TFIID core complex. Nature, 2013, 493, 699-702. | 13.7 | 142 |
| 8 | Structure of the E. coli signal recognition particle bound to a translating ribosome. Nature, 2006, 444, 503-506. | 13.7 | 126 |
| 9 | Membrane protein insertion and proton-motive-force-dependent secretion through the bacterial holo-translocon SecYEGâ€“SecDFâ€“YajCâ€“YidC. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4844-4849. | 3.3 | 124 |
| 10 | Molecular Basis of the Rapamycin Insensitivity of Target Of Rapamycin Complex 2. Molecular Cell, 2015, 58, 977-988. | 4.5 | 120 |
| 11 | YidC and Oxa1 Form Dimeric Insertion Pores on the Translating Ribosome. Molecular Cell, 2009, 34, 344-353. | 4.5 | 117 |
| 12 | Membrane association of myotubularin-related protein 2 is mediated by a pleckstrin homology-GRAM domain and a coiled-coil dimerization module. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12177-12182. | 3.3 | 113 |
| 13 | Automated unrestricted multigene recombineering for multiprotein complex production. Nature Methods, 2009, 6, 447-450. | 9.0 | 98 |
| 14 | Multiple conformational switches in a GTPase complex control co-translational protein targeting. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1754-1759. | 3.3 | 95 |
| 15 | Multi-level regulation of myotubularin-related protein-2 phosphatase activity by myotubularin-related protein-13/set-binding factor-2. Human Molecular Genetics, 2006, 15, 569-579. | 1.4 | 92 |
| 16 | Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. Journal of Structural Biology, 2011, 175, 198-208. | 1.3 | 92 |
| 17 | Dual function of UPF3B in early and late translation termination. EMBO Journal, 2017, 36, 2968-2986. | 3.5 | 89 |
| 18 | Dynamics of Trigger Factor Interaction with Translating Ribosomes. Journal of Biological Chemistry, 2008, 283, 4124-4132. | 1.6 | 82 |

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|---|---|---|---|
| 19 | The SARS-CoV-2 spike protein: balancing stability and infectivity. Cell Research, 2020, 30, 1059-1060. | 5.7 | 82 |
| 20 | Elongation Arrest by SecM via a Cascade of Ribosomal RNA Rearrangements. Molecular Cell, 2006, 22, 533-543. | 4.5 | 78 |
| 21 | Cytoplasmic TAF2â€“TAF8â€“TAF10 complex provides evidence for nuclear holoâ€“TFIID assembly from preformed submodules. Nature Communications, 2015, 6, 6011. | 5.8 | 77 |
| 22 | Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein**. Angewandte Chemie - International Edition, 2021, 60, 7098-7110. | 7.2 | 77 |
| 23 | Structure of a human cap-dependent 48S translation pre-initiation complex. Nucleic Acids Research, 2018, 46, 2678-2689. | 6.5 | 76 |
| 24 | Generation of ribosome nascent chain complexes for structural and functional studies. Journal of Structural Biology, 2007, 158, 463-471. | 1.3 | 72 |
| 25 | Cryo-EM structure of the E. coli translating ribosome in complex with SRP and its receptor. Nature Structural and Molecular Biology, 2011, 18, 88-90. | 3.6 | 69 |
| 26 | Membrane protein insertion and assembly by the bacterial holo-translocon SecYEGâ€“SecDFâ€“YajCâ€“YidC. Biochemical Journal, 2016, 473, 3341-3354. | 1.7 | 61 |
| 27 | Comparison ofEscherichia coliand rabbit reticulocyte ribosome display systems. FEBS Letters, 1999, 450, 105-110. | 1.3 | 55 |
| 28 | A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. Scientific Reports, 2016, 6, 38399. | 1.6 | 54 |
| 29 | Multiprotein Expression Strategy for Structural Biology of Eukaryotic Complexes. Structure, 2007, 15, 275-279. | 1.6 | 50 |
| 30 | In vitro selection and evolution of proteins. Advances in Protein Chemistry, 2001, 55, 367-403. | 4.4 | 46 |
| 31 | Cryo-EM structure of Saccharomyces cerevisiae target of rapamycin complex 2. Nature Communications, 2017, 8, 1729. | 5.8 | 46 |
| 32 | Advances and challenges of membraneâ€“protein complex production. Current Opinion in Structural Biology, 2015, 32, 123-130. | 2.6 | 32 |
| 33 | Ribosomeâ€“SRPâ€–FtsY cotranslational targeting complex in the closed state. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3943-3948. | 3.3 | 26 |
| 34 | Probing Telomeric G-Quadruplex DNA Structures in Cells with In Vitro Generated Single-Chain Antibody Fragments. Methods in Molecular Biology, 2010, 608, 159-181. | 0.4 | 26 |
| 35 | MultiBac: Baculovirus-Mediated Multigene DNA Cargo Delivery in Insect and Mammalian Cells. Viruses, 2019, 11, 198. | 1.5 | 25 |
| 36 | Pathogen-sugar interactions revealed by universal saturation transfer analysis. Science, 2022, 377, . | 6.0 | 24 |

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|---|---|---|---|
| 37 | Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2. Nature Communications, 2022, 13, 222. | 5.8 | 23 |
| 38 | Structure and Dynamics of the Central Lipid Pool and Proteins of the Bacterial Holo-Translocon. Biophysical Journal, 2019, 116, 1931-1940. | 0.2 | 22 |
| 39 | Structural biology in the fight against COVID-19. Nature Structural and Molecular Biology, 2021, 28, 2-7. | 3.6 | 20 |
| 40 | Synthetic virions reveal fatty acid-coupled adaptive immunogenicity of SARS-CoV-2 spike glycoprotein. Nature Communications, 2022, 13, 868. | 5.8 | 20 |
| 41 | The fatty acid site is coupled to functional motifs in the SARS-CoV-2 spike protein and modulates spike allosteric behaviour. Computational and Structural Biotechnology Journal, 2022, 20, 139-147. | 1.9 | 19 |
| 42 | ACEMBL Tool-Kits for High-Throughput Multigene Delivery and Expression in Prokaryotic and Eukaryotic Hosts. Advances in Experimental Medicine and Biology, 2016, 896, 27-42. | 0.8 | 17 |
| 43 | Structural basis of signal sequence surveillance and selection by the SRPâ€“FtsY complex. Nature Structural and Molecular Biology, 2013, 20, 604-610. | 3.6 | 16 |
| 44 | Highly efficient CRISPR-mediated large DNA docking and multiplexed prime editing using a single baculovirus. Nucleic Acids Research, 2022, 50, 7783-7799. | 6.5 | 15 |
| 45 | Protein-fold evolution in the test tube. Trends in Biochemical Sciences, 2001, 26, 577-579. | 3.7 | 14 |
| 46 | Cryoâ€electron microscopy of ribosomal complexes in cotranslational folding, targeting, and translocation. Wiley Interdisciplinary Reviews RNA, 2012, 3, 429-441. | 3.2 | 13 |
| 47 | Blasticidin S inhibits mammalian translation and enhances production of protein encoded by nonsense mRNA. Nucleic Acids Research, 2021, 49, 7665-7679. | 6.5 | 13 |
| 48 | Reprint of â€œGeneration of ribosome nascent chain complexes for structural and functional studiesâ€• [J. Struct. Biol. 158 (2007) 463â€“471]â˜†. Journal of Structural Biology, 2007, 159, 302-310. | 1.3 | 10 |
| 49 | ACEMBLing a Multiprotein Transmembrane Complex. Methods in Enzymology, 2015, 556, 23-49. | 0.4 | 9 |
| 50 | VLPâ€factoryâ„¢ and ADDomer<sup>Â©</sup>: Selfâ€assembling Virusâ€Like Particle (VLP) Technologies for Multiple Protein and Peptide Epitope Display. Current Protocols, 2021, 1, e55. | 1.3 | 9 |
| 51 | 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. Nucleic Acids Research, 2022, 50, 5934-5947. | 6.5 | 8 |
| 52 | High-Throughput Production of Influenza Virus-Like Particle (VLP) Array by Using VLP-factoryâ„¢, a MultiBac Baculoviral Genome Customized for Enveloped VLP Expression. Methods in Molecular Biology, 2019, 2025, 213-226. | 0.4 | 7 |
| 53 | Molecular Simulations suggest Vitamins, Retinoids and Steroids as Ligands of the Free Fatty Acid Pocket of the SARSâ€CoVâ€2 Spike Protein**. Angewandte Chemie, 2021, 133, 7174-7186. | 1.6 | 6 |
| 54 | Efficient production of a mature and functional gamma secretase protease. Scientific Reports, 2018, 8, 12834. | 1.6 | 5 |

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|---|---|---|---|
| 55 | Multiprotein Complex Production in E. coli: The SecYEG-SecDFYajC-YidC Holotranslocon. Methods in Molecular Biology, 2017, 1586, 279-290. | 0.4 | 2 |
| 56 | Production of Multi-subunit Membrane Protein Complexes. Methods in Molecular Biology, 2021, 2247, 3-16. | 0.4 | 1 |
| 57 | Cell-Free Synthesis of Macromolecular Complexes. Advances in Experimental Medicine and Biology, 2016, 896, 79-95. | 0.8 | 0 |