

# Bruno P Klaholz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1760768/publications.pdf>

Version: 2024-02-01

48  
papers

3,083  
citations

236925

25  
h-index

189892

50  
g-index

52  
all docs

52  
docs citations

52  
times ranked

5387  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Structural basis for safe and efficient energy conversion in a respiratory supercomplex. <i>Nature Communications</i> , 2022, 13, 545.  | 12.8 | 10        |
| 2  | Setup and Troubleshooting of Volta Phase Plate Cryo-EM Data Collection. <i>Methods in Molecular Biology</i> , 2021, 2305, 291-299.  | 0.9  | 3         |
| 3  | Identification of Mg <sup>2+</sup> ions next to nucleotides in cryo-EM maps using electrostatic potential maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 534-539.                      | 2.3  | 9         |
| 4  | Myod1 and GR coordinate myofiber-specific transcriptional enhancers. <i>Nucleic Acids Research</i> , 2021, 49, 4472-4492.   | 14.5 | 18        |
| 5  | MeCP2 is a microsatellite binding protein that protects CA repeats from nucleosome invasion. <i>Science</i> , 2021, 372, .  | 12.6 | 36        |
| 6  | Studying the Structural Organization of Polyribosomes with Alexander S. Spirin. <i>Biochemistry (Moscow)</i> , 2021, 86, 1053-1059.   | 1.5  | 1         |
| 7  | Practical Aspects of Super-Resolution Imaging and Segmentation of Macromolecular Complexes by dSTORM. <i>Methods in Molecular Biology</i> , 2021, 2247, 271-286.  | 0.9  | 5         |
| 8  | Structural basis of nanobody recognition of grapevine fanleaf virus and of virus resistance loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10848-10855.    | 7.1  | 10        |
| 9  | Targeting the Human 80S Ribosome in Cancer: From Structure to Function and Drug Design for Innovative Adjuvant Therapeutic Strategies. <i>Cells</i> , 2020, 9, 629.   | 4.1  | 45        |
| 10 | Dynamics of uS19 C-Terminal Tail during the Translation Elongation Cycle in Human Ribosomes. <i>Cell Reports</i> , 2020, 31, 107473.  | 6.4  | 32        |
| 11 | Ribosomal RNA 2'-O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , 2020, 2, zcaa036.   | 3.1  | 40        |
| 12 | CENP-A nucleosome clusters form rosette-like structures around HJURP during G1. <i>Nature Communications</i> , 2019, 10, 4436.  | 12.8 | 25        |
| 13 | N6-Methyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. <i>Nature Chemical Biology</i> , 2019, 15, 88-94.   | 8.0  | 258       |
| 14 | Deriving and refining atomic models in crystallography and cryo-EM: the latest <i>Phenix</i> tools to facilitate structure analysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 878-881. | 2.3  | 28        |
| 15 | Structure-function analyses unravel distinct effects of allosteric inhibitors of HIV-1 integrase on viral maturation and integration. <i>Journal of Biological Chemistry</i> , 2018, 293, 6172-6186.                  | 3.4  | 31        |
| 16 | 3DClusterViSu: 3D clustering analysis of super-resolution microscopy data by 3D Voronoi tessellations. <i>Bioinformatics</i> , 2018, 34, 3004-3012.   | 4.1  | 37        |
| 17 | Volta phase plate data collection facilitates image processing and cryo-EM structure determination. <i>Journal of Structural Biology</i> , 2018, 202, 191-199.  | 2.8  | 24        |
| 18 | Structural features of the salivary gland hypertrophy virus of the tsetse fly revealed by cryo-electron microscopy and tomography. <i>Virology</i> , 2018, 514, 165-169.  | 2.4  | 5         |

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|----|---|------|-----------|
| 19 | Tetracyclines Modify Translation by Targeting Key Human rRNA Substructures. <i>Cell Chemical Biology</i> , 2018, 25, 1506-1518.e13.   | 5.2  | 35        |
| 20 | Visualizing the Role of 2â€™-OH rRNA Methylations in the Human Ribosome Structure. <i>Biomolecules</i> , 2018, 8, 125.  | 4.0  | 32        |
| 21 | New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.   | 2.3  | 575       |
| 22 | Focused classification and refinement in high-resolution cryo-EM structural analysis of ribosome complexes. <i>Current Opinion in Structural Biology</i> , 2017, 46, 140-148.   | 5.7  | 53        |
| 23 | The Ribosome Holds the RNA Polymerase on Track in Bacteria. <i>Trends in Biochemical Sciences</i> , 2017, 42, 686-689.  | 7.5  | 5         |
| 24 | Visualization of chemical modifications in the human 80S ribosome structure. <i>Nature</i> , 2017, 551, 472-477.  | 27.8 | 277       |
| 25 | The integrative role of cryo electron microscopy in molecular and cellular structural biology. <i>Biology of the Cell</i> , 2017, 109, 81-93.   | 2.0  | 58        |
| 26 | Importance of the Sequence-Directed DNA Shape for Specific Binding Site Recognition by the Estrogen-Related Receptor. <i>Frontiers in Endocrinology</i> , 2017, 8, 140.   | 3.5  | 12        |
| 27 | The HIV-1 integrase-LEDGF allosteric inhibitor MUT-A: resistance profile, impairment of virus maturation and infectivity but without influence on RNA packaging or virus immunoreactivity. <i>Retrovirology</i> , 2017, 14, 50. | 2.0  | 18        |
| 28 | ClusterViSu, a method for clustering of protein complexes by Voronoi tessellation in super-resolution microscopy. <i>Scientific Reports</i> , 2016, 6, 24084.   | 3.3  | 125       |
| 29 | Structureâ€™function insights reveal the human ribosome as a cancer target for antibiotics. <i>Nature Communications</i> , 2016, 7, 12856.  | 12.8 | 75        |
| 30 | Cryo-EM study of start codon selection during archaeal translation initiation. <i>Nature Communications</i> , 2016, 7, 13366.   | 12.8 | 25        |
| 31 | SharpViSu: integrated analysis and segmentation of super-resolution microscopy data. <i>Bioinformatics</i> , 2016, 32, 2239-2241.   | 4.1  | 40        |
| 32 | X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. <i>Journal of Biological Chemistry</i> , 2015, 290, 13191-13201.  | 3.4  | 33        |
| 33 | Structural insight into the mechanism of stabilization of the 7SK small nuclear RNA by LARP7. <i>Nucleic Acids Research</i> , 2015, 43, 3373-3388.  | 14.5 | 54        |
| 34 | Live cell immunogold labelling of RNA polymerase II. <i>Scientific Reports</i> , 2015, 5, 8324.   | 3.3  | 17        |
| 35 | Conformation transitions of eukaryotic polyribosomes during multi-round translation. <i>Nucleic Acids Research</i> , 2015, 43, 618-628.   | 14.5 | 43        |
| 36 | IBISS, a versatile and interactive tool for integrated sequence and 3D structure analysis of large macromolecular complexes. <i>Bioinformatics</i> , 2015, 31, 3339-3344.   | 4.1  | 3         |

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|----|--|------|-----------|
| 37 | Structureâ€“function relationships in nuclear receptors: the facts. Trends in Biochemical Sciences, 2015, 40, 287-290.   | 7.5  | 12        |
| 38 | Structure of the human 80S ribosome. Nature, 2015, 520, 640-645.   | 27.8 | 406       |
| 39 | Structure Sorting of Multiple Macromolecular States in Heterogeneous Cryo-EM Samples by 3D Multivariate Statistical Analysis. Open Journal of Statistics, 2015, 05, 820-836.             | 0.7  | 27        |
| 40 | The palindromic DNA-bound USP/EcR nuclear receptor adopts an asymmetric organization with allosteric domain positioning. Nature Communications, 2014, 5, 4139.                           | 12.8 | 33        |
| 41 | Nuclear position dictates DNA repair pathway choice. Genes and Development, 2014, 28, 2450-2463.   | 5.9  | 167       |
| 42 | The molecular structure of the left-handed supra-molecular helix of eukaryotic polyribosomes. Nature Communications, 2014, 5, 5294.  | 12.8 | 43        |
| 43 | Structure of the protein core of translation initiation factor 2 in apo, GTP-bound and GDP-bound forms. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 925-933. | 2.5  | 26        |
| 44 | On effective and optical resolutions of diffraction data sets. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1921-1934.  | 2.5  | 19        |
| 45 | Molecular recognition and catalysis in translation termination complexes. Trends in Biochemical Sciences, 2011, 36, 282-292.   | 7.5  | 29        |
| 46 | Let's see how tmRNA rescues a stuck ribosome. EMBO Journal, 2010, 29, 3747-3749.   | 7.8  | 1         |
| 47 | Visualization of release factor 3 on the ribosome during termination of protein synthesis. Nature, 2004, 427, 862-865.   | 27.8 | 131       |
| 48 | Câ€“Hâ€“â€“O Hydrogen Bonds in the Nuclear Receptor RARÎ³â€“a Potential Tool for Drug Selectivity. Structure, 2002, 10, 1197-1204.   | 3.3  | 84        |