

Imre Berger

List of Publications by Year in descending order

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Version: 2024-02-01

112
papers

6,181
citations

81743

39
h-index

82410

72
g-index

134
all docs

134
docs citations

134
times ranked

7875
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. | 1.9 | 19 |
| 2 | Structural insights in cell-type specific evolution of intra-host diversity by SARS-CoV-2. <i>Nature Communications</i> , 2022, 13, 222. | 5.8 | 23 |
| 3 | HR-Bac, a toolbox based on homologous recombination for expression, screening and production of multiprotein complexes using the baculovirus expression system. <i>Scientific Reports</i> , 2022, 12, 2030. | 1.6 | 5 |
| 4 | Synthetic virions reveal fatty acid-coupled adaptive immunogenicity of SARS-CoV-2 spike glycoprotein. <i>Nature Communications</i> , 2022, 13, 868. | 5.8 | 20 |
| 5 | 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. | 6.5 | 8 |
| 6 | Pathogen-sugar interactions revealed by universal saturation transfer analysis. <i>Science</i> , 2022, 377, . | 6.0 | 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. | 6.5 | 15 |
| 8 | Microfluidic production and characterization of biofunctionalized giant unilamellar vesicles for targeted intracellular cargo delivery. <i>Biomaterials</i> , 2021, 264, 120203. | 5.7 | 45 |
| 9 | SynBac: Enhanced Baculovirus Genomes by Iterative Recombineering. <i>Methods in Molecular Biology</i> , 2021, 2305, 141-152. | 0.4 | 0 |
| 10 | 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. | 7.2 | 77 |
| 11 | 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. | 1.6 | 6 |
| 12 | 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, . | 1.6 | 7 |
| 13 | 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, . | 7.2 | 0 |
| 14 | VLP ^{factory} and ADDomer ^Å : Self-assembling Virus-Like Particle (VLP) Technologies for Multiple Protein and Peptide Epitope Display. <i>Current Protocols</i> , 2021, 1, e55. | 1.3 | 9 |
| 15 | Young infants exhibit robust functional antibody responses and restrained IFN- β production to SARS-CoV-2. <i>Cell Reports Medicine</i> , 2021, 2, 100327. | 3.3 | 29 |
| 16 | TAF8 regions important for TFIID lobe B assembly or for TAF2 interactions are required for embryonic stem cell survival. <i>Journal of Biological Chemistry</i> , 2021, 297, 101288. | 1.6 | 4 |
| 17 | The MultiBac BEVS: Basics, applications, performance and recent developments. <i>Methods in Enzymology</i> , 2021, 660, 129-154. | 0.4 | 5 |
| 18 | The SARS-CoV-2 Spike protein disrupts human cardiac pericytes function through CD147 receptor-mediated signalling: a potential non-infective mechanism of COVID-19 microvascular disease. <i>Clinical Science</i> , 2021, 135, 2667-2689. | 1.8 | 97 |

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|----|---|------|-----------|
| 19 | Structure of the Human Cation-Independent Mannose 6-Phosphate/IGF2 Receptor Domains 7Å Uncovers the Mannose 6-Phosphate Binding Site of Domain 9. <i>Structure</i> , 2020, 28, 1300-1312.e5. | 1.6 | 8 |
| 20 | Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein. <i>Science</i> , 2020, 370, 725-730. | 6.0 | 348 |
| 21 | Synthetic Virus-Derived Nanosystems (SVNs) for Delivery and Precision Docking of Large Multifunctional DNA Circuitry in Mammalian Cells. <i>Pharmaceutics</i> , 2020, 12, 759. | 2.0 | 13 |
| 22 | TBPL2/TFIIA complex establishes the maternal transcriptome through oocyte-specific promoter usage. <i>Nature Communications</i> , 2020, 11, 6439. | 5.8 | 23 |
| 23 | The SARS-CoV-2 spike protein: balancing stability and infectivity. <i>Cell Research</i> , 2020, 30, 1059-1060. | 5.7 | 82 |
| 24 | DNA origami-based single-molecule force spectroscopy elucidates RNA Polymerase III pre-initiation complex stability. <i>Nature Communications</i> , 2020, 11, 2828. | 5.8 | 36 |
| 25 | X-ray Structure of the Human Karyopherin RanBP5, an Essential Factor for Influenza Polymerase Nuclear Trafficking. <i>Journal of Molecular Biology</i> , 2020, 432, 3353-3359. | 2.0 | 6 |
| 26 | TFIID Enables RNA Polymerase II Promoter-Proximal Pausing. <i>Molecular Cell</i> , 2020, 78, 785-793.e8. | 4.5 | 55 |
| 27 | The structure of human thyroglobulin. <i>Nature</i> , 2020, 578, 627-630. | 13.7 | 81 |
| 28 | AMPfret: synthetic nanosensor for cellular energy states. <i>Biochemical Society Transactions</i> , 2020, 48, 103-111. | 1.6 | 4 |
| 29 | 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. | 0.4 | 7 |
| 30 | Synthetic self-assembling ADDomer platform for highly efficient vaccination by genetically encoded multiepitope display. <i>Science Advances</i> , 2019, 5, eaaw2853. | 4.7 | 29 |
| 31 | Synthetic energy sensor AMPfret deciphers adenylate-dependent AMPK activation mechanism. <i>Nature Communications</i> , 2019, 10, 1038. | 5.8 | 47 |
| 32 | MultiBac: Baculovirus-Mediated Multigene DNA Cargo Delivery in Insect and Mammalian Cells. <i>Viruses</i> , 2019, 11, 198. | 1.5 | 25 |
| 33 | Sequential Digestion with Trypsin and Elastase in Cross-Linking Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 4472-4478. | 3.2 | 26 |
| 34 | The MultiBac system: a perspective. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 477-482. | 1.1 | 3 |
| 35 | Homozygous TAF8 mutation in a patient with intellectual disability results in undetectable TAF8 protein, but preserved RNA polymerase II transcription. <i>Human Molecular Genetics</i> , 2018, 27, 2171-2186. | 1.4 | 22 |
| 36 | Chaperonin CCT checkpoint function in basal transcription factor TFIID assembly. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1119-1127. | 3.6 | 43 |

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|----|---|-----|-----------|
| 37 | XLF and APLF bind Ku80 at two remote sites to ensure DNA repair by non-homologous end joining. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 971-980. | 3.6 | 78 |
| 38 | Efficient production of a mature and functional gamma secretase protease. <i>Scientific Reports</i> , 2018, 8, 12834. | 1.6 | 5 |
| 39 | MultiBacMam Bimolecular Fluorescence Complementation (BiFC) tool-kit identifies new small-molecule inhibitors of the CDK5-p25 protein-protein interaction (PPI). <i>Scientific Reports</i> , 2018, 8, 5083. | 1.6 | 11 |
| 40 | Multiprotein Complex Production in <i>E. coli</i> : The SecYEG-SecDFYajC-YidC Holotranslocon. <i>Methods in Molecular Biology</i> , 2017, 1586, 279-290. | 0.4 | 2 |
| 41 | Retriever is a multiprotein complex for retromer-independent endosomal cargo recycling. <i>Nature Cell Biology</i> , 2017, 19, 1214-1225. | 4.6 | 243 |
| 42 | MultiBac: from protein complex structures to synthetic viral nanosystems. <i>BMC Biology</i> , 2017, 15, 99. | 1.7 | 29 |
| 43 | New insights into HCV replication in original cells from <i>Aedes</i> mosquitoes. <i>Virology Journal</i> , 2017, 14, 161. | 1.4 | 4 |
| 44 | Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, . | 2.8 | 29 |
| 45 | Targeted supplementation design for improved production and quality of enveloped viral particles in insect cell-baculovirus expression system. <i>Journal of Biotechnology</i> , 2016, 233, 34-41. | 1.9 | 20 |
| 46 | Glutathione-conjugating and membrane-remodeling activity of GDAP1 relies on amphipathic C-terminal domain. <i>Scientific Reports</i> , 2016, 6, 36930. | 1.6 | 27 |
| 47 | A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016, 6, 38399. | 1.6 | 54 |
| 48 | Membrane protein insertion and assembly by the bacterial holo-translocon SecYEG- SecDF- YajC- YidC. <i>Biochemical Journal</i> , 2016, 473, 3341-3354. | 1.7 | 61 |
| 49 | Zooming in on Transcription Preinitiation. <i>Journal of Molecular Biology</i> , 2016, 428, 2581-2591. | 2.0 | 36 |
| 50 | 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. | 0.8 | 17 |
| 51 | The MultiBac Baculovirus/Insect Cell Expression Vector System for Producing Complex Protein Biologics. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 199-215. | 0.8 | 59 |
| 52 | Genetic code expansion for multiprotein complex engineering. <i>Nature Methods</i> , 2016, 13, 997-1000. | 9.0 | 63 |
| 53 | Genetically Encoded Fluorescent Biosensors to Explore AMPK Signaling and Energy Metabolism. <i>Exs</i> , 2016, 107, 491-523. | 1.4 | 9 |
| 54 | Structural characterization of recombinant IAV polymerase reveals a stable complex between viral PA-PB1 heterodimer and host RanBP5. <i>Scientific Reports</i> , 2016, 6, 24727. | 1.6 | 19 |

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|----|---|------|-----------|
| 55 | Highly efficient baculovirus-mediated multigene delivery in primary cells. <i>Nature Communications</i> , 2016, 7, 11529. | 5.8 | 83 |
| 56 | Tuneable endogenous mammalian target complementation via multiplexed plasmid-based recombineering. <i>Scientific Reports</i> , 2015, 5, 17432. | 1.6 | 4 |
| 57 | Polyproteins in structural biology. <i>Current Opinion in Structural Biology</i> , 2015, 32, 139-146. | 2.6 | 21 |
| 58 | Editorial overview: New protein production tools for structural biology. <i>Current Opinion in Structural Biology</i> , 2015, 32, v-vii. | 2.6 | 0 |
| 59 | Subunits of ADA-two-A-containing (ATAC) or Spt-Ada-Gcn5-acetyltransferase (SAGA) Coactivator Complexes Enhance the Acetyltransferase Activity of GCN5. <i>Journal of Biological Chemistry</i> , 2015, 290, 28997-29009. | 1.6 | 41 |
| 60 | Cytoplasmic TAF2â€“TAF8â€“TAF10 complex provides evidence for nuclear holoâ€“TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015, 6, 6011. | 5.8 | 77 |
| 61 | ACEMBLing a Multiprotein Transmembrane Complex. <i>Methods in Enzymology</i> , 2015, 556, 23-49. | 0.4 | 9 |
| 62 | Chemical crossâ€“linking and mass spectrometry to determine the subunit interaction network in a recombinant human SAGA HAT subcomplex. <i>Protein Science</i> , 2015, 24, 1232-1246. | 3.1 | 17 |
| 63 | 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. | 3.3 | 26 |
| 64 | Baculovirus expression: old dog, new tricks. <i>Bioengineered</i> , 2015, 6, 316-322. | 1.4 | 14 |
| 65 | Characterization and Production of Protein Complexes by Co-expression in <i>Escherichia coli</i> . <i>Methods in Molecular Biology</i> , 2015, 1261, 63-89. | 0.4 | 14 |
| 66 | The Production of Multiprotein Complexes in Insect Cells Using the Baculovirus Expression System. <i>Methods in Molecular Biology</i> , 2015, 1261, 91-114. | 0.4 | 14 |
| 67 | Multiprotein Complex Production in Insect Cells by Using Polyproteins. <i>Methods in Molecular Biology</i> , 2014, 1091, 131-141. | 0.4 | 34 |
| 68 | More pieces to the puzzle: recent structural insights into class II transcription initiation. <i>Current Opinion in Structural Biology</i> , 2014, 24, 91-97. | 2.6 | 22 |
| 69 | Structural insight into cap-snatching and RNA synthesis by influenza polymerase. <i>Nature</i> , 2014, 516, 361-366. | 13.7 | 376 |
| 70 | 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. | 3.3 | 124 |
| 71 | OmniBac: Universal Multigene Transfer Plasmids for Baculovirus Expression Vector Systems. <i>Methods in Molecular Biology</i> , 2014, 1091, 123-130. | 0.4 | 9 |
| 72 | Structural basis of signal sequence surveillance and selection by the SRPâ€“FtsY complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 604-610. | 3.6 | 16 |

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|----|--|------|-----------|
| 73 | The architecture of human general transcription factor TFIID core complex. <i>Nature</i> , 2013, 493, 699-702. | 13.7 | 142 |
| 74 | Protein production for structural biology: new solutions to new challenges. <i>Current Opinion in Structural Biology</i> , 2013, 23, 317-318. | 2.6 | 4 |
| 75 | Baculovirus expression: tackling the complexity challenge. <i>Current Opinion in Structural Biology</i> , 2013, 23, 357-364. | 2.6 | 28 |
| 76 | MultiBac turns sweet. <i>Bioengineered</i> , 2013, 4, 78-83. | 1.4 | 29 |
| 77 | Gene gymnastics. <i>Bioengineered</i> , 2013, 4, 279-287. | 1.4 | 37 |
| 78 | The MultiBac Protein Complex Production Platform at the EMBL. <i>Journal of Visualized Experiments</i> , 2013, , e50159. | 0.2 | 22 |
| 79 | Tandem Recombineering by SLIC Cloning and Cre-LoxP Fusion to Generate Multigene Expression Constructs for Protein Complex Research. <i>Methods in Molecular Biology</i> , 2013, 1073, 131-140. | 0.4 | 23 |
| 80 | MultiBac complexomics. <i>Expert Review of Proteomics</i> , 2012, 9, 363-373. | 1.3 | 16 |
| 81 | Architecture of the Mediator Head Module. <i>Biophysical Journal</i> , 2012, 102, 287a. | 0.2 | 0 |
| 82 | SweetBac: A New Approach for the Production of Mammalianised Glycoproteins in Insect Cells. <i>PLoS ONE</i> , 2012, 7, e34226. | 1.1 | 73 |
| 83 | MultiBac: expanding the research toolbox for multiprotein complexes. <i>Trends in Biochemical Sciences</i> , 2012, 37, 49-57. | 3.7 | 201 |
| 84 | Architecture of the Mediator head module. <i>Nature</i> , 2011, 475, 240-243. | 13.7 | 104 |
| 85 | Robots, pipelines, polyproteins: Enabling multiprotein expression in prokaryotic and eukaryotic cells. <i>Journal of Structural Biology</i> , 2011, 175, 198-208. | 1.3 | 92 |
| 86 | Recombinant Heptameric Coatomer Complexes: Novel Tools to Study Isoform-specific Functions. <i>Traffic</i> , 2011, 12, 682-692. | 1.3 | 26 |
| 87 | Light it up: Highly efficient multigene delivery in mammalian cells. <i>BioEssays</i> , 2011, 33, 946-955. | 1.2 | 12 |
| 88 | A plasmid-based multigene expression system for mammalian cells. <i>Nature Communications</i> , 2010, 1, 120. | 5.8 | 55 |
| 89 | New baculovirus expression tools for recombinant protein complex production. <i>Journal of Structural Biology</i> , 2010, 172, 45-54. | 1.3 | 182 |
| 90 | Towards eukaryotic structural complexomics. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 37-46. | 1.2 | 11 |

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|-----|---|------|-----------|
| 91 | Automated unrestricted multigene recombineering for multiprotein complex production. <i>Nature Methods</i> , 2009, 6, 447-450. | 9.0 | 98 |
| 92 | Getting a Grip on Complexes. <i>Current Genomics</i> , 2009, 10, 558-572. | 0.7 | 27 |
| 93 | MultiBac: Multigene Baculovirus-Based Eukaryotic Protein Complex Production. <i>Current Protocols in Protein Science</i> , 2008, 51, Unit 5.20. | 2.8 | 130 |
| 94 | Nucleic Acid Science – The Excitement of Discovery: Annual Symposium of the Chemical Society Zürich CGZ, Zürich, October 26, 2007. <i>Chimia</i> , 2007, 61, 837. | 0.3 | 0 |
| 95 | Multiprotein Expression Strategy for Structural Biology of Eukaryotic Complexes. <i>Structure</i> , 2007, 15, 275-279. | 1.6 | 50 |
| 96 | Protein complex expression by using multigene baculoviral vectors. <i>Nature Methods</i> , 2006, 3, 1021-1032. | 9.0 | 330 |
| 97 | Structure of the E. coli signal recognition particle bound to a translating ribosome. <i>Nature</i> , 2006, 444, 503-506. | 13.7 | 126 |
| 98 | 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, 569-579. | 1.4 | 92 |
| 99 | Syntheses of 4'-thioribonucleosides and thermodynamic stability and crystal structure of RNA oligomers with incorporated 4'-thiocytosine. <i>Nucleic Acids Research</i> , 2005, 33, 3965-3975. | 6.5 | 33 |
| 100 | Baculovirus expression system for heterologous multiprotein complexes. <i>Nature Biotechnology</i> , 2004, 22, 1583-1587. | 9.4 | 427 |
| 101 | Reaction cycle of the yeast Isw2 chromatin remodeling complex. <i>EMBO Journal</i> , 2004, 23, 3836-3843. | 3.5 | 54 |
| 102 | Formation Pathways of a Guanine-Quadruplex DNA Revealed by Molecular Dynamics and Thermodynamic Analysis of the Substates. <i>Biophysical Journal</i> , 2003, 85, 1787-1804. | 0.2 | 128 |
| 103 | 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, 12177-12182. | 3.3 | 113 |
| 104 | Direct Interaction of Ca ²⁺ /Calmodulin Inhibits Histone Deacetylase 5 Repressor Core Binding to Myocyte Enhancer Factor 2. <i>Journal of Biological Chemistry</i> , 2003, 278, 17625-17635. | 1.6 | 39 |
| 105 | Structural Dynamics and Cation Interactions of DNA Quadruplex Molecules Containing Mixed Guanine/Cytosine Quartets Revealed by Large-Scale MD Simulations. <i>Journal of the American Chemical Society</i> , 2001, 123, 3295-3307. | 6.6 | 93 |
| 106 | Molecular Dynamics of DNA Quadruplex Molecules Containing Inosine, 6-Thioguanine and 6-Thiopurine. <i>Biophysical Journal</i> , 2001, 80, 455-468. | 0.2 | 54 |
| 107 | Nanosecond Molecular Dynamics of Zipper-like DNA Duplex Structures Containing Sheared G•A Mismatch Pairs. <i>Journal of the American Chemical Society</i> , 2000, 122, 7564-7572. | 6.6 | 47 |
| 108 | Four-Stranded Intercalated Cytosine-Rich Molecules: Novel Insights into DNA Structure and Stability. <i>Nucleosides & Nucleotides</i> , 1999, 18, 1583-1585. | 0.5 | 1 |

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|-----|---|-----|-----------|
| 109 | Nanosecond Molecular Dynamics Simulations of Parallel and Antiparallel Guanine Quadruplex DNA Molecules. <i>Journal of the American Chemical Society</i> , 1999, 121, 5519-5534. | 6.6 | 162 |
| 110 | Molecular Dynamics of Hemiprotonated Intercalated Four-Stranded i-DNA:Â Stable Trajectories on a Nanosecond Scale. <i>Journal of the American Chemical Society</i> , 1998, 120, 6147-6151. | 6.6 | 77 |
| 111 | The Role of Backbone Oxygen Atoms in the Organization of Nucleic Acid Tertiary Structure: Zippers, Networks, Clamps, and Câ€Hâ€ ï,Ö Hydrogen Bonds. <i>Chemistry - A European Journal</i> , 1997, 3, 1400-1404. | 1.7 | 35 |
| 112 | Molecular structure of the halogenated anti-cancer drug iododoxorubicin complexed with d(TGTACA) and d(CGATCG). <i>Nucleic Acids Research</i> , 1995, 23, 4488-4494. | 6.5 | 20 |