# JÃ¶rg Labahn

List of Publications by Year
in descending order

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| 36 | 3,042 | 516710 | 361022 |
|---|---|---|---|
| papers | citations | 16 h-index | 35 g-index |

| 38 | 38 | 38 | 3842 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Single Stabilizing Point Mutation Enables Highâ€Resolution Coâ€Crystal Structures of the Adenosine A<sub>2A</sub> Receptor with Preladenant Conjugates. Angewandte Chemie - International Edition, 2022, 61, . | 13.8 | 14 |
| 2 | Innentitelbild: Eine einzige stabilisierende Punktmutation ermÃ¶glicht hochaufgelÃ¶ste Coâ€Kristallstrukturen des Adenosinâ€A<sub>2A</sub>â€Rezeptors mit Preladenantâ€Konjugaten (Angew.) Tj ET Q q 0 0 0 rg BT /Overlo | 2.0 | 0 |
| 3 | Mutual Enhancement of Opioid and Adrenergic Receptors by Combinations of Opioids and Adrenergic Ligands Is Reflected in Molecular Complementarity of Ligands: Drug Development Possibilities. International Journal of Molecular Sciences, 2019, 20, 4137. | 4.1 | 9 |
| 4 | Data on solubilization, identification, and thermal stability of human Presenilin-2. Data in Brief, 2018, 17, 626-630. | 1.0 | 2 |
| 5 | Expression, purification, and preliminary characterization of human presenilin-2. Process Biochemistry, 2018, 64, 63-73. | 3.7 | 2 |
| 6 | Adrenergic Agonists Bind to Adrenergic-Receptor-Like Regions of the Mu Opioid Receptor, Enhancing Morphine and Methionine-Enkephalin Binding: A New Approach to â€œBiased Opioidsâ€?. International Journal of Molecular Sciences, 2018, 19, 272. | 4.1 | 15 |
| 7 | QTY code enables design of detergent-free chemokine receptors that retain ligand-binding activities. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8652-E8659. | 7.1 | 39 |
| 8 | High-efficient production and biophysical characterisation of nicastrin and its interaction with APPC100. Scientific Reports, 2017, 7, 44297. | 3.3 | 6 |
| 9 | Fibril structure of amyloid-Î²(1â€“42) by cryoâ€“electron microscopy. Science, 2017, 358, 116-119. | 12.6 | 801 |
| 10 | Structural basis for the regulatory interactions of proapoptotic Par-4. Cell Death and Differentiation, 2017, 24, 1540-1547. | 11.2 | 12 |
| 11 | Influence of solubilization and AD-mutations on stability and structure of human presenilins. Scientific Reports, 2017, 7, 17970. | 3.3 | 3 |
| 12 | Stray Light Correction in the Optical Spectroscopy of Crystals. Applied Spectroscopy, 2015, 69, 1106-1111. | 2.2 | 1 |
| 13 | Cloning, expression, purification, crystallization and preliminary crystallographic analysis of the C-terminal domain of Par-4 (PAWR). Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1224-1227. | 0.8 | 6 |
| 14 | Expression and Purification of Membrane Proteins. Methods in Enzymology, 2014, 541, 117-140. | 1.0 | 17 |
| 15 | Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in Corynebacterium glutamicum: Mutants and a model. Journal of Biotechnology, 2014, 191, 99-105. | 3.8 | 26 |
| 16 | Expression and Purification of Functional Human Mu Opioid Receptor from E.coli. PLoS ONE, 2013, 8, e56500. | 2.5 | 7 |
| 17 | Controlled In Meso Phase Crystallization â€“ A Method for the Structural Investigation of Membrane Proteins. PLoS ONE, 2012, 7, e35458. | 2.5 | 13 |
| 18 | Signal relay from sensory rhodopsin I to the cognate transducer HtrI: Assessing the critical change in hydrogen-bonding between Tyr-210 and Asn-53. Biophysical Chemistry, 2010, 150, 23-28. | 2.8 | 3 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Chapter 27 Immobilized-Metal Affinity Chromatography (IMAC). Methods in Enzymology, 2009, 463, 439-473. | 1.0 | 309 |
| 20 | Production and comprehensive quality control of recombinant human Interleukin-1Î²: A case study for a process development strategy. Protein Expression and Purification, 2008, 57, 244-254. | 1.3 | 26 |
| 21 | Development of the signal in sensory rhodopsin and its transfer to the cognate transducer. Nature, 2006, 440, 115-119. | 27.8 | 169 |
| 22 | The archaeal sensory rhodopsin II/transducer complex: a model for transmembrane signal transfer. FEBS Letters, 2004, 564, 219-224. | 2.8 | 103 |
| 23 | Preliminary X-ray characterization of the ribonuclease P (C5 protein) fromEscherichia coli: expression, crystallization and cryoconditions. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 350-352. | 2.5 | 1 |
| 24 | Crystallization and preliminary X-ray diffraction studies of Î±-cyclodextrin glucanotransferase isolated fromBacillus macerans. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 348-349. | 2.5 | 3 |
| 25 | Sites for Interaction between Gal80p and Gal1p in Kluyveromyces lactis: Structural Model of Galactokinase based on Homology to the GHMP Protein Family. Journal of Molecular Biology, 2003, 333, 479-492. | 4.2 | 21 |
| 26 | An Alternative Mechanism for Amidase Signature Enzymes. Journal of Molecular Biology, 2002, 322, 1053-1064. | 4.2 | 80 |
| 27 | Crystallization and preliminary X-ray data of the recombinant peptide amidase fromStenotrophomonas maltophilia. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 333-335. | 2.5 | 10 |
| 28 | Molecular basis of transmembrane signalling by sensory rhodopsin IIâ€“transducer complex. Nature, 2002, 419, 484-487. | 27.8 | 380 |
| 29 | X-ray crystal structure of arrestin from bovine rod outer segments. Nature, 1998, 391, 918-921. | 27.8 | 227 |
| 30 | Structural Basis for the Excision Repair of Alkylation-Damaged DNA. Cell, 1996, 86, 321-329. | 28.9 | 258 |
| 31 | A model for DNA binding and enzyme action derived from crystallographic studies of the TaqI N6-adenine-methyltransferase. Gene, 1995, 157, 131-134. | 2.2 | 37 |
| 32 | Three-dimensional structure of the adenine-specific DNA methyltransferase M.Taq I in complex with the cofactor S-adenosylmethionine.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 10957-10961. | 7.1 | 173 |
| 33 | Crystal structure of the factor for inversion stimulation FIS at 2.0 Ã... resolution. Journal of Molecular Biology, 1992, 226, 209-226. | 4.2 | 78 |
| 34 | Three-dimensional structure of the E. coli DMA-binding protein FIS. Nature, 1991, 349, 178-180. | 27.8 | 178 |
| 35 | Crystallization of the DNA-binding Escherichia coli protein FIS. Journal of Molecular Biology, 1989, 208, 209-210. | 4.2 | 8 |
| 36 | Eine einzige stabilisierende Punktmutation ermÃ¶glicht hochaufgelÃ¶ste Coâ€Kristallstrukturen des Adenosinâ€A <sub>2A</sub> â€Rezeptors mit Preladenantâ€Konjugaten. Angewandte Chemie, 0, , . | 2.0 | 0 |