

# Jörg Labahn

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2705424/publications.pdf>

Version: 2024-02-01

36  
papers

3,042  
citations

516710

16  
h-index

361022

35  
g-index

38  
all docs

38  
docs citations

38  
times ranked

3842  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fibril structure of amyloid-Î²(1-42) by cryo-electron microscopy. <i>Science</i> , 2017, 358, 116-119.	12.6	801
2	Molecular basis of transmembrane signalling by sensory rhodopsin II-transducer complex. <i>Nature</i> , 2002, 419, 484-487.	27.8	380
3	Chapter 27 Immobilized-Metal Affinity Chromatography (IMAC). <i>Methods in Enzymology</i> , 2009, 463, 439-473.	1.0	309
4	Structural Basis for the Excision Repair of Alkylation-Damaged DNA. <i>Cell</i> , 1996, 86, 321-329.	28.9	258
5	X-ray crystal structure of arrestin from bovine rod outer segments. <i>Nature</i> , 1998, 391, 918-921.	27.8	227
6	Three-dimensional structure of the E. coli DMA-binding protein FIS. <i>Nature</i> , 1991, 349, 178-180.	27.8	178
7	Three-dimensional structure of the adenine-specific DNA methyltransferase M.Taq I in complex with the cofactor S-adenosylmethionine.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10957-10961.	7.1	173
8	Development of the signal in sensory rhodopsin and its transfer to the cognate transducer. <i>Nature</i> , 2006, 440, 115-119.	27.8	169
9	The archaeal sensory rhodopsin II/transducer complex: a model for transmembrane signal transfer. <i>FEBS Letters</i> , 2004, 564, 219-224.	2.8	103
10	An Alternative Mechanism for Amidase Signature Enzymes. <i>Journal of Molecular Biology</i> , 2002, 322, 1053-1064.	4.2	80
11	Crystal structure of the factor for inversion stimulation FIS at 2.0 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 226, 209-226.	4.2	78
12	QTY code enables design of detergent-free chemokine receptors that retain ligand-binding activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8652-E8659.	7.1	39
13	A model for DNA binding and enzyme action derived from crystallographic studies of the TaqI N6-adenine-methyltransferase. <i>Gene</i> , 1995, 157, 131-134.	2.2	37
14	Production and comprehensive quality control of recombinant human Interleukin-1Î²: A case study for a process development strategy. <i>Protein Expression and Purification</i> , 2008, 57, 244-254.	1.3	26
15	Interaction of 2-oxoglutarate dehydrogenase OdhA with its inhibitor OdhI in <i>Corynebacterium glutamicum</i> : Mutants and a model. <i>Journal of Biotechnology</i> , 2014, 191, 99-105.	3.8	26
16	Sites for Interaction between Gal80p and Gal1p in <i>Kluyveromyces lactis</i> : Structural Model of Galactokinase based on Homology to the GHMP Protein Family. <i>Journal of Molecular Biology</i> , 2003, 333, 479-492.	4.2	21
17	Expression and Purification of Membrane Proteins. <i>Methods in Enzymology</i> , 2014, 541, 117-140.	1.0	17
18	Adrenergic Agonists Bind to Adrenergic-Receptor-Like Regions of the Mu Opioid Receptor, Enhancing Morphine and Methionine-Enkephalin Binding: A New Approach to "Biased Opioids". <i>International Journal of Molecular Sciences</i> , 2018, 19, 272.	4.1	15

#	ARTICLE	IF	CITATIONS
19	Single Stabilizing Point Mutation Enables High-Resolution Co-Crystal Structures of the Adenosine A <sub>2A</sub> Receptor with Preladenant Conjugates. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	14
20	Controlled In Meso Phase Crystallization – A Method for the Structural Investigation of Membrane Proteins. <i>PLoS ONE</i> , 2012, 7, e35458.	2.5	13
21	Structural basis for the regulatory interactions of proapoptotic Par-4. <i>Cell Death and Differentiation</i> , 2017, 24, 1540-1547.	11.2	12
22	Crystallization and preliminary X-ray data of the recombinant peptide amidase from <i>Stenotrophomonas maltophilia</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 333-335.	2.5	10
23	Mutual Enhancement of Opioid and Adrenergic Receptors by Combinations of Opioids and Adrenergic Ligands Is Reflected in Molecular Complementarity of Ligands: Drug Development Possibilities. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4137.	4.1	9
24	Crystallization of the DNA-binding <i>Escherichia coli</i> protein FIS. <i>Journal of Molecular Biology</i> , 1989, 208, 209-210.	4.2	8
25	Expression and Purification of Functional Human Mu Opioid Receptor from <i>E. coli</i> . <i>PLoS ONE</i> , 2013, 8, e56500.	2.5	7
26	Cloning, expression, purification, crystallization and preliminary crystallographic analysis of the C-terminal domain of Par-4 (PAWR). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1224-1227.	0.8	6
27	High-efficient production and biophysical characterisation of nicastrin and its interaction with APPC100. <i>Scientific Reports</i> , 2017, 7, 44297.	3.3	6
28	Crystallization and preliminary X-ray diffraction studies of $\beta$ -cyclodextrin glucanotransferase isolated from <i>Bacillus macerans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 348-349.	2.5	3
29	Signal relay from sensory rhodopsin I to the cognate transducer HtrI: Assessing the critical change in hydrogen-bonding between Tyr-210 and Asn-53. <i>Biophysical Chemistry</i> , 2010, 150, 23-28.	2.8	3
30	Influence of solubilization and AD-mutations on stability and structure of human presenilins. <i>Scientific Reports</i> , 2017, 7, 17970.	3.3	3
31	Data on solubilization, identification, and thermal stability of human Presenilin-2. <i>Data in Brief</i> , 2018, 17, 626-630.	1.0	2
32	Expression, purification, and preliminary characterization of human presenilin-2. <i>Process Biochemistry</i> , 2018, 64, 63-73.	3.7	2
33	Preliminary X-ray characterization of the ribonuclease P (C5 protein) from <i>Escherichia coli</i> : expression, crystallization and cryoconditions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 350-352.	2.5	1
34	Stray Light Correction in the Optical Spectroscopy of Crystals. <i>Applied Spectroscopy</i> , 2015, 69, 1106-1111.	2.2	1
35	Eine einzige stabilisierende Punktmutation ermöglicht hochaufgelöste Co-Kristallstrukturen des Adenosin A <sub>2A</sub> -Rezeptors mit Preladenant-Konjugaten. <i>Angewandte Chemie</i> , 0, , .	2.0	0
36	Innentitelbild: Eine einzige stabilisierende Punktmutation ermöglicht hochaufgelöste Co-Kristallstrukturen des Adenosin A <sub>2A</sub> -Rezeptors mit Preladenant-Konjugaten (Angew.) Tj ET 2020 0 0 0 0 BT /Overlo		