Bernhard Loll

List of Publications by Year
in descending order

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Version: 2024-02-01

93 papers	6,296 citations	136885 32 h-index	69214 77 g-index

111 all docs	111 docs citations	111 times ranked	5790 citing authors

#	Article	IF	Citations
1	CryoEM analysis of small plant biocatalysts at sub-2â€…Ã… resolution. Acta Crystallographica Section D: Structural Biology, 2022, 78, 113-123.	1.1	1
2	An Unusual Aspartic Acid Cluster in the Reovirus Attachment Fiber Ïƒ1 Mediates Stability at Low pH and Preserves Trimeric Organization. Journal of Virology, 2022, , e0033122.	1.5	1
3	Towards an understanding of oleate hydratases and their application in industrial processes. Microbial Cell Factories, 2022, 21, 58.	1.9	13
4	Biotechnological potential and initial characterization of two novel sesquiterpene synthases from Basidiomycota Coniophora puteana for heterologous production of Î´-cadinol. Microbial Cell Factories, 2022, 21, 64.	1.9	9
5	Molecular basis of antibiotic self-resistance in a bee larvae pathogen. Nature Communications, 2022, 13, 2349.	5.8	4
6	Fluorine-induced polarity increases inhibitory activity of BPTI towards chymotrypsin. RSC Chemical Biology, 2022, 3, 773-782.	2.0	8
7	Steps toward translocation-independent RNA polymerase inactivation by terminator ATPase Ï. Science, 2021, 371, .	6.0	78
8	A skipping rope translocation mechanism in a widespread family of DNA repair helicases. Nucleic Acids Research, 2021, 49, 504-518.	6.5	7
9	A Structural View on the Stereospecificity of Plant Borneolâ€Type Dehydrogenases. ChemCatChem, 2021, 13, 2262-2277.	1.8	9
10	Large-scale ratcheting in a bacterial DEAH/RHA-type RNA helicase that modulates antibiotics susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	6
11	Exchange catalysis by tapasin exploits conserved and allele-specific features of MHC-I molecules. Nature Communications, 2021, 12, 4236.	5.8	20
12	Structure-Based Mechanisms of a Molecular RNA Polymerase/Chaperone Machine Required for Ribosome Biosynthesis. Molecular Cell, 2020, 79, 1024-1036.e5.	4.5	41
13	Towards a sustainable generation of pseudopterosin-type bioactives. Green Chemistry, 2020, 22, 6033-6046.	4.6	9
14	The Impression of a Nonexisting Catalytic Effect: The Role of CotB2 in Guiding the Complex Biosynthesis of Cyclooctat-9-en-7-ol. Journal of the American Chemical Society, 2020, 142, 21562-21574.	6.6	20
15	A Snu114â€“GTPâ€“Prp8 module forms a relay station for efficient splicing in yeast. Nucleic Acids Research, 2020, 48, 4572-4584.	6.5	2
16	Conformational Plasticity of HLA-B27 Molecules Correlates Inversely With Efficiency of Negative T Cell Selection. Frontiers in Immunology, 2020, 11, 179.	2.2	6
17	Exploring the catalytic cascade of cembranoid biosynthesis by combination of genetic engineering and molecular simulations. Computational and Structural Biotechnology Journal, 2020, 18, 1819-1829.	1.9	3
18	A Conserved Kinase-Based Body-Temperature Sensor Globally Controls Alternative Splicing and Gene Expression. Molecular Cell, 2020, 78, 57-69.e4.	4.5	76

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19	Understanding the role of active site residues in CotB2 catalysis using a cluster model. Beilstein Journal of Organic Chemistry, 2020, 16, 50-59.	1.3	11
20	The Î´ subunit and NTPase HelD institute a two-pronged mechanism for RNA polymerase recycling. Nature Communications, 2020, 11, 6418.	5.8	32
21	RIM-binding protein couples synaptic vesicle recruitment to release sites. Journal of Cell Biology, 2020, 219, .	2.3	26
22	Metal-triggered conformational reorientation of a self-peptide bound to a disease-associated HLA-B*27 subtype. Journal of Biological Chemistry, 2019, 294, 13269-13279.	1.6	8
23	Current understanding and biotechnological application of the bacterial diterpene synthase CotB2. Beilstein Journal of Organic Chemistry, 2019, 15, 2355-2368.	1.3	17
24	Exon Inclusion Modulates Conformational Plasticity and Autoinhibition of the Intersectin 1 SH3A Domain. Structure, 2019, 27, 977-987.e5.	1.6	4
25	Structural basis for the function of SuhB as a transcription factor in ribosomal RNA synthesis. Nucleic Acids Research, 2019, 47, 6488-6503.	6.5	15
26	Increased versatility despite reduced molecular complexity: evolution, structure and function of metazoan splicing factor PRPF39. Nucleic Acids Research, 2019, 47, 5867-5879.	6.5	7
27	Structural Basis for the Action of an All-Purpose Transcription Anti-termination Factor. Molecular Cell, 2019, 74, 143-157.e5.	4.5	86
28	Ketonization of Proline Residues in the Peptide Chains of Actinomycins by a 4â€Oxoproline Synthase. ChemBioChem, 2018, 19, 706-715.	1.3	10
29	Rhodococcus erythropolis Oleate Hydratase: a New Member in the Oleate Hydratase Family Treeâ€"Biochemical and Structural Studies. ChemCatChem, 2018, 10, 407-414.	1.8	29
30	Towards a comprehensive understanding of the structural dynamics of a bacterial diterpene synthase during catalysis. Nature Communications, 2018, 9, 3971.	5.8	57
31	Tetracyanocorannulene â€" an Easily Accessible and Strongly Electronâ€Deficient Compound. European Journal of Organic Chemistry, 2018, 2018, 6338-6342.	1.2	9
32	Molecular insights into antibiotic resistance - how a binding protein traps albicidin. Nature Communications, 2018, 9, 3095.	5.8	32
33	Bacterial Polysaccharide Specificity of the Pattern Recognition Receptor Langerin Is Highly Species-dependent. Journal of Biological Chemistry, 2017, 292, 862-871.	1.6	33
34	Internal Dynamics of the 3-Pyrroline-N-Oxide Ring in Spin-Labeled Proteins. Journal of Physical Chemistry Letters, 2017, 8, 1113-1117.	2.1	2
35	Structural basis for Î»N-dependent processive transcription antitermination. Nature Microbiology, 2017, 2, 17062.	5.9	58
36	Combining EPR spectroscopy and X-ray crystallography to elucidate the structure and dynamics of conformationally constrained spin labels in T4 lysozyme single crystals. Physical Chemistry Chemical Physics, 2017, 19, 20723-20734.	1.3	5

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37	Increased Conformational Flexibility of HLAâ€“B*27 Subtypes Associated With Ankylosing Spondylitis. Arthritis and Rheumatology, 2016, 68, 1172-1182.	2.9	36
38	Identification, characterization and molecular adaptation of class I redox systems for the production of hydroxylated diterpenoids. Microbial Cell Factories, 2016, 15, 86.	1.9	9
39	Tracking Transient Conformational States of T4 Lysozyme at Room Temperature Combining X-ray Crystallography and Site-Directed Spin Labeling. Journal of the American Chemical Society, 2016, 138, 12868-12875.	6.6	13
40	Active zone scaffolds differentially accumulate Unc13 isoforms to tune Ca2+ channelâ€“vesicle coupling. Nature Neuroscience, 2016, 19, 1311-1320.	7.1	166
41	Combining Single Crystal Electron Paramagnetic Resonance and X-Ray Crystallography to Study the Orientation and Dynamics of MTSSL Spin Labels in T4 Lysozyme. Biophysical Journal, 2015, 108, 616a.	0.2	0
42	Fluorine teams up with water to restore inhibitor activity to mutant BPTI. Chemical Science, 2015, 6, 5246-5254.	3.7	32
43	Structures ofDrosophila melanogasterRab2 and Rab3 bound to GMPPNP. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 34-40.	0.4	5
44	Presynaptic spinophilin tunes neurexin signalling to control active zone architecture and function. Nature Communications, 2015, 6, 8362.	5.8	51
45	Detailed Structureâ€“Function Correlations of Bacillus subtilis Acetolactate Synthase. ChemBioChem, 2015, 16, 110-118.	1.3	20
46	A high affinity RIM-binding protein/Aplip1 interaction prevents the formation of ectopic axonal active zones. ELife, 2015, 4, .	2.8	26
47	Entrapment of DNA in an intersubunit tunnel system of a single-stranded DNA-binding protein. Nucleic Acids Research, 2014, 42, 6698-6708.	6.5	15
48	RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. Molecular Cell, 2014, 54, 975-986.	4.5	23
49	Cyclolization of D-Lysergic Acid Alkaloid Peptides. Chemistry and Biology, 2014, 21, 146-155.	6.2	45
50	Production of Macrocyclic Sesquiâ€•and Diterpenes in Heterologous Microbial Hosts: A Systems Approach to Harness Natureâ€™s Molecular Diversity. ChemCatChem, 2014, 6, 1142-1165.	1.8	11
51	The first structure of a bacterial diterpene cyclase: CotB2. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1528-1537.	2.5	48
52	Drep-2 is a novel synaptic protein important for learning and memory. ELife, 2014, 3, .	2.8	39
53	Dynamics of free versus complexed Î²2-microglobulin and the evolution of interfaces in MHC class I molecules. Immunogenetics, 2013, 65, 157-172.	1.2	27
54	Comparative biophysical characterization of chicken Î²2-microglobulin. Biophysical Chemistry, 2012, 167, 26-35.	1.5	7

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55	HLA class I-associated diseases with a suspected autoimmune etiology: HLA-B27 subtypes as a model system. European Journal of Cell Biology, 2012, 91, 274-286.	1.6	24
56	Influence of inflammationâ€related changes on conformational characteristics of HLAâ€B27 subtypes as detected by IR spectroscopy. FEBS Journal, 2011, 278, 1713-1727.	2.2	18
57	Loss of recognition by crossâ€reactive T cells and its relation to a Câ€terminusâ€induced conformational reorientation of an HLAâ€B*2705â€bound peptide. Protein Science, 2011, 20, 278-290.	3.1	5
58	The P-Loop Domain of Yeast Clp1 Mediates Interactions Between CF IA and CPF Factors in Pre-mRNA 3â€² End Formation. PLoS ONE, 2011, 6, e29139.	1.1	33
59	HLAâ€“B27 heavy chains distinguished by a micropolymorphism exhibit differential flexibility. Arthritis and Rheumatism, 2010, 62, 978-987.	6.7	34
60	Coupled RNA polymerase II transcription and 3â€² end formation with yeast whole-cell extracts. Rna, 2010, 16, 2205-2217.	1.6	7
61	Structure of a Classical MHC Class I Molecule That Binds â€œNon-Classicalâ€•Ligands. PLoS Biology, 2010, 8, e1000557.	2.6	41
62	Crystal structure of the EndoG/EndoGI complex: mechanism of EndoG inhibition. Nucleic Acids Research, 2009, 37, 7312-7320.	6.5	29
63	Implications of Structural and Thermodynamic Studies of HLA-B27 Subtypes Exhibiting Differential Association with Ankylosing Spondylitis. Advances in Experimental Medicine and Biology, 2009, 649, 177-195.	0.8	32
64	HLA-B27 Subtypes Differentially Associated with Disease Exhibit Conformational Differences in Solution. Journal of Molecular Biology, 2008, 376, 798-810.	2.0	53
65	Modeling of variant copies of subunit D1 in the structure of photosystem II from Thermosynechococcus elongatus. Biological Chemistry, 2008, 389, 609-617.	1.2	35
66	Snapshots of the RNA Processing Factor SCAF8 Bound to Different Phosphorylated Forms of the Carboxyl-terminal Domain of RNA Polymerase II. Journal of Biological Chemistry, 2008, 283, 22659-22669.	1.6	55
67	Molecular and Structural Characterization of the PezAT Chromosomal Toxin-Antitoxin System of the Human Pathogen Streptococcus pneumoniae. Journal of Biological Chemistry, 2007, 282, 19606-19618.	1.6	103
68	Function of two Î²-carotenes near the D1 and D2 proteins in photosystem II dimers. Biochimica Et Biophysica Acta - Bioenergetics, 2007, 1767, 79-87.	0.5	30
69	Lipids in photosystem II: Interactions with protein and cofactors. Biochimica Et Biophysica Acta - Bioenergetics, 2007, 1767, 509-519.	0.5	120
70	Structure of full-length transcription regulator CcpA in the apo form. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2007, 1774, 732-736.	1.1	10
71	Structure of the transcription regulator CcpA fromLactococcus lactis. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 431-436.	2.5	7
72	Structure of the Mn4â€“Ca cluster as derived from X-ray diffraction. Photosynthesis Research, 2007, 92, 389-405.	1.6	35

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73	How photosynthetic reaction centers control oxidation power in chlorophyll pairs P680, P700, and P870. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9855-9860.	3.3	104
74	Where Water Is Oxidized to Dioxygen: Structure of the Photosynthetic Mn4Ca Cluster. Science, 2006, 314, 821-825.	6.0	782
75	Energetics of a Possible Proton Exit Pathway for Water Oxidation in Photosystem II. Biochemistry, 2006, 45, 2063-2071.	1.2	167
76	Cationic State of Accessory Chlorophyll and Electron Transfer through Pheophytin to Plastoquinone in Photosystem II. Angewandte Chemie - International Edition, 2006, 45, 1964-1965.	7.2	21
77	Conformational Dimorphism of Self-peptides and Molecular Mimicry in a Disease-associated HLA-B27 Subtype. Journal of Biological Chemistry, 2006, 281, 2306-2316.	1.6	49
78	Towards complete cofactor arrangement in the 3.0â€‰Ã… resolution structure of photosystem II. Nature, 2005, 438, 1040-1044.	13.7	1,801
79	A cartilage-derived self peptide presented by HLA-B27 molecules? Comment on the article by Atagunduz et al. Arthritis and Rheumatism, 2005, 52, 2581-2582.	6.7	3
80	Cyanobacterial Photosystem II at 3.2 Ã… resolution â€“ the plastoquinone binding pockets. Photosynthesis Research, 2005, 84, 153-159.	1.6	50
81	The Antenna System of Photosystem II From Thermosynechococcus elongatus at 3.2 Ã… Resolution. Photosynthesis Research, 2005, 86, 175-184.	1.6	36
82	Purification, crystallization and preliminary X-ray diffraction analysis of the human major histocompatibility antigen HLA-B*2703 complexed with a viral peptide and with a self-peptide. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 372-374.	0.7	4
83	Preliminary X-ray diffraction analysis of crystals from the recombinantly expressed human major histocompatibility antigen HLA-B*2704 in complex with a viral peptide and with a self-peptide. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 939-941.	0.7	7
84	X-ray diffraction analysis of crystals from the human major histocompatibility antigen HLA-B*2706 in complex with a viral peptide and with a self-peptide. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 1097-1099.	0.7	7
85	X-ray damage to the Mn4Ca complex in single crystals of photosystem II: A case study for metalloprotein crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12047-12052.	3.3	585
86	Redox Potentials of Chlorophylls in the Photosystem II Reaction Centerâ€. Biochemistry, 2005, 44, 4118-4124.	1.2	80
87	Thermostability and Ca2+Binding Properties of Wild Type and Heterologously Expressed PsbO Protein from Cyanobacterial Photosystem IIâ€. Biochemistry, 2005, 44, 4691-4698.	1.2	22
88	Tuning electron transfer by ester-group of chlorophylls in bacterial photosynthetic reaction center. FEBS Letters, 2005, 579, 712-716.	1.3	20
89	Purification, characterisation and crystallisation of photosystem II from Thermosynechococcus elongatus cultivated in a new type of photobioreactor. Biochimica Et Biophysica Acta - Bioenergetics, 2005, 1706, 147-157.	0.5	144
90	Crystal structure of Homo sapiens protein hp14.5. Proteins: Structure, Function and Bioinformatics, 2004, 54, 797-800.	1.5	42

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91	Crystal structure of cyanobacterial photosystem II at 3.2 Ã... resolution: a closer look at the Mn-cluster. Physical Chemistry Chemical Physics, 2004, 6, 4733-4736.	1.3	290
92	Functional Role of CÎ±â€“Hâ‹¯O Hydrogen Bonds Between Transmembrane Î±-Helices in Photosystem I. Journal of Molecular Biology, 2003, 328, 737-747.	2.0	31
93	Functional implications on the mechanism of the function of photosystem II including water oxidation based on the structure of photosystem II. Philosophical Transactions of the Royal Society B: Biological Sciences, 2002, 357, 1337-1345.	1.8	44