

Dominika M Borek

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

4,209
citations

147726

31
h-index

118793

62
g-index

71
all docs

71
docs citations

71
times ranked

6853
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiparametric scaling of diffraction intensities. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2003, 59, 228-234.	0.3	623
2	Structure and control of the actin regulatory WAVE complex. <i>Nature</i> , 2010, 468, 533-538.	13.7	424
3	Structural Basis for CoREST-Dependent Demethylation of Nucleosomes by the Human LSD1 Histone Demethylase. <i>Molecular Cell</i> , 2006, 23, 377-387.	4.5	306
4	Crystal structure of the human sterol transporter ABCG5/ABCG8. <i>Nature</i> , 2016, 533, 561-564.	13.7	233
5	Ebola Virus VP24 Targets a Unique NLS Binding Site on Karyopherin Alpha 5 to Selectively Compete with Nuclear Import of Phosphorylated STAT1. <i>Cell Host and Microbe</i> , 2014, 16, 187-200.	5.1	198
6	Structural basis for dsRNA recognition and interferon antagonism by Ebola VP35. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 165-172.	3.6	177
7	Structure and gating mechanism of the $\alpha 7$ nicotinic acetylcholine receptor. <i>Cell</i> , 2021, 184, 2121-2134.e13.	13.5	137
8	An Intrinsically Disordered Peptide from Ebola Virus VP35 Controls Viral RNA Synthesis by Modulating Nucleoprotein-RNA Interactions. <i>Cell Reports</i> , 2015, 11, 376-389.	2.9	136
9	Structure of Tracheal Cytotoxin in Complex with a Heterodimeric Pattern-Recognition Receptor. <i>Science</i> , 2006, 311, 1761-1764.	6.0	127
10	Data publication with the structural biology data grid supports live analysis. <i>Nature Communications</i> , 2016, 7, 10882.	5.8	113
11	Crystal structure of the cohesin loader Scc2 and insight into cohesinopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12444-12449.	3.3	104
12	Structural basis for Marburg virus VP35-mediated immune evasion mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20661-20666.	3.3	90
13	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Reports</i> , 2015, 10, 910-919.	2.9	77
14	In Silico Derived Small Molecules Bind the Filovirus VP35 Protein and Inhibit Its Polymerase Cofactor Activity. <i>Journal of Molecular Biology</i> , 2014, 426, 2045-2058.	2.0	75
15	Development of RNA Aptamers Targeting Ebola Virus VP35. <i>Biochemistry</i> , 2013, 52, 8406-8419.	1.2	73
16	Structure of the human cohesin inhibitor Wapl. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11355-11360.	3.3	62
17	Structural and Functional Characterization of Reston Ebola Virus VP35 Interferon Inhibitory Domain. <i>Journal of Molecular Biology</i> , 2010, 399, 347-357.	2.0	61
18	Measurement errors and their consequences in protein crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2031-2038.	2.5	59

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19	Expression, purification and catalytic activity of <i>Lupinus luteus</i> asparagine β -amidohydrolase and its <i>Escherichia coli</i> homolog. <i>FEBS Journal</i> , 2004, 271, 3215-3226.	0.2	59
20	Extracellular Architecture of the SYG-1/SYG-2 Adhesion Complex Instructs Synaptogenesis. <i>Cell</i> , 2014, 156, 482-494.	13.5	59
21	Disruption of Wnt/ β -Catenin Signaling and Telomeric Shortening Are Inextricable Consequences of Tankyrase Inhibition in Human Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 2425-2435.	1.1	58
22	Diffraction data analysis in the presence of radiation damage. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 426-436.	2.5	57
23	The many faces of radiation-induced changes. <i>Journal of Synchrotron Radiation</i> , 2007, 14, 24-33.	1.0	48
24	Complete genome of <i>Pieris rapae</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016, 5, 2631.	0.8	47
25	Divergent kinase regulates membrane ultrastructure of the <i>Toxoplasma</i> parasitophorous vacuole. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6361-6370.	3.3	46
26	Structure and Mechanism of a Eukaryotic FMN Adenylyltransferase. <i>Journal of Molecular Biology</i> , 2009, 389, 388-400.	2.0	45
27	Comparative genome sequencing reveals chemotype-specific gene clusters in the toxigenic black mold <i>Stachybotrys</i> . <i>BMC Genomics</i> , 2014, 15, 590.	1.2	45
28	Complete genomes of Hairstreak butterflies, their speciation and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> , 2016, 6, 24863.	1.6	44
29	A trimethoprim derivative impedes antibiotic resistance evolution. <i>Nature Communications</i> , 2021, 12, 2949.	5.8	41
30	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biology and Evolution</i> , 2016, 8, 915-931.	1.1	40
31	When COI barcodes deceive: complete genomes reveal introgression in hairstreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20161735.	1.2	39
32	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , 2015, 16, 639.	1.2	38
33	Structure of the Type III Secretion Effector Protein ExoU in Complex with Its Chaperone SpcU. <i>PLoS ONE</i> , 2012, 7, e49388.	1.1	36
34	Crystal structure of the human NK-1 tachykinin receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13264-13269.	3.3	30
35	Structural basis for human respiratory syncytial virus NS1-mediated modulation of host responses. <i>Nature Microbiology</i> , 2017, 2, 17101.	5.9	29
36	Identification of patterns in diffraction intensities affected by radiation exposure. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 37-48.	1.0	27

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37	Crystal structure of active site mutant of antileukemic <i>Asparaginase</i> reveals conserved zinc-binding site. <i>FEBS Journal</i> , 2014, 281, 4097-4111.	2.2	27
38	Crystal structure and putative function of small Toprim domain-containing protein from <i>Bacillus stearothermophilus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 311-319.	1.5	23
39	To automate or not to automate: this is the question. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 211-221.	1.2	23
40	Complete Genome of <i>Achalarus lyciades</i> , The First Representative of the Eudaminae Subfamily of Skippers. <i>Current Genomics</i> , 2017, 18, 366-374.	0.7	22
41	Crystallization and preliminary crystallographic studies of five crystal forms of <i>Escherichia coli</i> L-asparaginase II (Asp90Glu mutant). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 130-132.	2.5	21
42	Crystallization and preliminary crystallographic studies of a new L-asparaginase encoded by the <i>Escherichia coli</i> genome. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1505-1507.	2.5	20
43	The first complete genomes of <i>Metalmarks</i> and the classification of butterfly families. <i>Genomics</i> , 2017, 109, 485-493.	1.3	20
44	Functional diversification of the NleG effector family in enterohemorrhagic <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10004-10009.	3.3	19
45	Structures of teixobactin-producing nonribosomal peptide synthetase condensation and adenylation domains. <i>Current Research in Structural Biology</i> , 2020, 2, 14-24.	1.1	18
46	Crystal packing of plant-type L-asparaginase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 309-320.	2.5	17
47	Inhibition of Marburg Virus RNA Synthesis by a Synthetic Anti-VP35 Antibody. <i>ACS Infectious Diseases</i> , 2019, 5, 1385-1396.	1.8	14
48	The crystal structure of the effector-binding domain of the trehalose repressor TreR from <i>Bacillus subtilis</i> 168 reveals a unique quaternary assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 679-682.	1.5	12
49	Structural basis for IFN antagonism by human respiratory syncytial virus nonstructural protein 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2020587118.	3.3	12
50	Crystallization and preliminary X-ray analysis of Ebola VP35 interferon inhibitory domain mutant proteins. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 689-692.	0.7	11
51	High-resolution cryo-EM reconstructions in the presence of substantial aberrations. <i>IUCr</i> , 2020, 7, 445-452.	1.0	11
52	X-Ray Diffraction Experiment. <i>Advances in Protein Chemistry and Structural Biology</i> , 2009, 77, 23-40.	1.0	10
53	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. <i>Molecular Genetics and Genomics</i> , 2019, 294, 211-226.	1.0	10
54	NMR and crystallographic structural studies of the extremely stable monomeric variant of human cystatin C with single amino acid substitution. <i>FEBS Journal</i> , 2020, 287, 361-376.	2.2	10

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55	Structural characterization of V57D and V57P mutants of human cystatin C, an amyloidogenic protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 577-586.	2.5	8
56	Real-space analysis of radiation-induced specific changes with independent component analysis. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 451-467.	1.0	8
57	Expression, purification and preliminary crystallographic studies of human ketohexokinase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 586-588.	2.5	6
58	Optimal structure determination from sub-optimal diffraction data. <i>Protein Science</i> , 2022, 31, 259-268.	3.1	6
59	Crystallization and preliminary X-ray diffraction analysis of Val57 mutants of the amyloidogenic protein human cystatin C. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1608-1611.	0.7	5
60	Crystal Structure of Cardiac Troponin C Regulatory Domain in Complex with Cadmium and Deoxycholic Acid Reveals Novel Conformation. <i>Journal of Molecular Biology</i> , 2011, 413, 699-711.	2.0	4
61	Taking a look at the calibration of a CCD detector with a fiber-optic taper. <i>Journal of Applied Crystallography</i> , 2016, 49, 415-425.	1.9	3
62	Kinetic control of eukaryotic chromatin structure by recursive topological restraints. <i>Nature Precedings</i> , 2008, , .	0.1	1
63	Everything Happens at Once – Deconvolving Systematic Effects in X-ray Data Processing. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2013, , 105-112.	0.5	1
64	Molecular analysis and essentiality of Aro1 shikimate biosynthesis multi-enzyme in <i>Candida albicans</i> . <i>Life Science Alliance</i> , 2022, 5, e202101358.	1.3	1