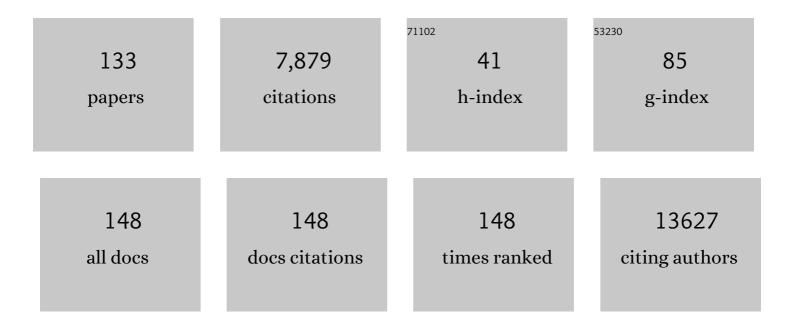
Jaroslaw Meller

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The active kinome: The modern view of how active protein kinase networks fit in biological research. Current Opinion in Pharmacology, 2022, 62, 117-129.	3.5	10
2	Complimentary transcriptomic-metallomic analysis identifies risk of relapse for clear-cell renal cell carcinoma (ccRCC) patients Journal of Clinical Oncology, 2022, 40, 378-378.	1.6	0
3	Assessing the effects of antipsychotic medications on schizophrenia functional analysis: a postmortem proteome study. Neuropsychopharmacology, 2022, 47, 2033-2041.	5.4	5
4	Differential genetic associations and expression of PAPST1/SLC35B2 in bipolar disorder and schizophrenia. Journal of Neural Transmission, 2022, 129, 913-924.	2.8	0
5	Signature-based approaches for informed drug repurposing: targeting CNS disorders. Neuropsychopharmacology, 2021, 46, 116-130.	5.4	38
6	The mycobiomes and bacteriomes of sputum, saliva, and home dust. Indoor Air, 2021, 31, 357-368.	4.3	3
7	Identification of candidate repurposable drugs to combat COVID-19 using a signature-based approach. Scientific Reports, 2021, 11, 4495.	3.3	22
8	Molecular and Metabolic Subtypes in Sporadic and Inherited Clear Cell Renal Cell Carcinoma. Genes, 2021, 12, 388.	2.4	10
9	Selective MAP1LC3C (LC3C) autophagy requires noncanonical regulators and the C-terminal peptide. Journal of Cell Biology, 2021, 220, .	5.2	10
10	Transcriptional profile of pyramidal neurons in chronic schizophrenia reveals lamina-specific dysfunction of neuronal immunity. Molecular Psychiatry, 2021, 26, 7699-7708.	7.9	11
11	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. Journal of Clinical Investigation, 2021, 131, .	8.2	14
12	KRSA: An R package and R Shiny web application for an end-to-end upstream kinase analysis of kinome array data. PLoS ONE, 2021, 16, e0260440.	2.5	8
13	Transcriptional Profile of Pyramidal Neurons in Chronic Schizophrenia Reveals Lamina-Specific Dysfunction of Neuronal Immunity. Biological Psychiatry, 2020, 87, S347-S348.	1.3	2
14	Transcriptional Regulation of Cancer Immune Checkpoints: Emerging Strategies for Immunotherapy. Vaccines, 2020, 8, 735.	4.4	18
15	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic Acids Research, 2020, 48, W85-W93.	14.5	18
16	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. PLoS ONE, 2020, 15, e0229801.	2.5	4
17	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
18	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0

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#	Article	IF	CITATIONS
19	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
20	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
21	S181. Kaleidoscope: A New Bioinformatics Pipeline Application for in Silico Hypothesis Testing of Gene Expression Changes in Severe Mental Illness. Biological Psychiatry, 2019, 85, S367.	1.3	0
22	Kinase network dysregulation in a human induced pluripotent stem cell model of DISC1 schizophrenia. Molecular Omics, 2019, 15, 173-188.	2.8	33
23	Enrichment of Genomic Pathways Based on Differential DNA Methylation Associated With Chronic Postsurgical Pain and Anxiety in Children: A Prospective, Pilot Study. Journal of Pain, 2019, 20, 771-785.	1.4	28
24	Structural Adaptations of Norovirus GII.17/13/21 Lineage through Two Distinct Evolutionary Paths. Journal of Virology, 2019, 93, .	3.4	16
25	Connectivity Analyses of Bioenergetic Changes in Schizophrenia: Identification of Novel Treatments. Molecular Neurobiology, 2019, 56, 4492-4517.	4.0	34
26	Rational identification of a Cdc42 inhibitor presents a new regimen for long-term hematopoietic stem cell mobilization. Leukemia, 2019, 33, 749-761.	7.2	48
27	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
28	Significant variation between SNP-based HLA imputations in diverse populations: the last mile is the hardest. Pharmacogenomics Journal, 2018, 18, 367-376.	2.0	32
29	Variability of indoor fungal microbiome of green and non-green low-income homes in Cincinnati, Ohio. Science of the Total Environment, 2018, 610-611, 212-218.	8.0	21
30	F201. KINASE NETWORK DYSREGULATION IN SCHIZOPHRENIA: IMPLICATIONS FOR NEW TREATMENT STRATEGIES. Schizophrenia Bulletin, 2018, 44, S299-S299.	4.3	1
31	Data Portal for the Library of Integrated Network-based Cellular Signatures (LINCS) program: integrated access to diverse large-scale cellular perturbation response data. Nucleic Acids Research, 2018, 46, D558-D566.	14.5	143
32	ABCC3 genetic variants are associated with postoperative morphine-induced respiratory depression and morphine pharmacokinetics in children. Pharmacogenomics Journal, 2017, 17, 162-169.	2.0	27
33	Traumatic Brain Injury Induces Alterations in Cortical Glutamate Uptake without a Reduction in Glutamate Transporter-1 Protein Expression. Journal of Neurotrauma, 2017, 34, 220-234.	3.4	49
34	A Point Mutation in the Rhesus Rotavirus VP4 Protein Generated through a Rotavirus Reverse Genetics System Attenuates Biliary Atresia in the Murine Model. Journal of Virology, 2017, 91, .	3.4	11
35	Abnormalities of signal transduction networks in chronic schizophrenia. NPJ Schizophrenia, 2017, 3, 30.	3.6	62
36	The SRL peptide of rhesus rotavirus VP4 protein governs cholangiocyte infection and the murine model of biliary atresia. Hepatology, 2017, 65, 1278-1292.	7.3	13

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37	Leveraging Food and Drug Administration Adverse Event Reports for the Automated Monitoring of Electronic Health Records in a Pediatric Hospital. Biomedical Informatics Insights, 2017, 9, 117822261771301.	4.6	13
38	UQlust: combining profile hashing with linear-time ranking for efficient clustering and analysis of big macromolecular data. BMC Bioinformatics, 2016, 17, 546.	2.6	1
39	Comprehensive analysis of sequences of a protein switch. Protein Science, 2016, 25, 135-146.	7.6	20
40	Dynamics of C-terminus Motion of Norwalk Virus Capsid by Molecular Dynamics (All-Atom &) Tj ETQq0 0 0 rg	BT /Overlo 0.5	ock 10 Tf 50
41	Toward Pediatric Precision Medicine: Examples of Genomics-Based Stratification Strategies. Translational Bioinformatics, 2016, , 339-361.	0.0	0
42	Targeting substrate-site in Jak2 kinase prevents emergence of genetic resistance. Scientific Reports, 2015, 5, 14538.	3.3	45
43	Analysis of Domain Movement and Dynamics of Norwalk Virus Capsid by Molecular Dynamics (All-Atom) Tj ETQq1	1,0,78431 0.5	l4 rgBT /Ove
44	Combined Rational Design and a High Throughput Screening Platform for Identifying Chemical Inhibitors of a Ras-activating Enzyme. Journal of Biological Chemistry, 2015, 290, 12879-12898.	3.4	27
45	Novel associations between FAAH genetic variants and postoperative central opioid-related adverse effects. Pharmacogenomics Journal, 2015, 15, 436-442.	2.0	31
46	Rhesus rotavirus VP4 sequence-specific activation of mononuclear cells is associated with cholangiopathy in murine biliary atresia. American Journal of Physiology - Renal Physiology, 2015, 309, G466-G474.	3.4	14
47	Increased susceptibility of estrogen-induced bladder outlet obstruction in a novel mouse model. Laboratory Investigation, 2015, 95, 546-560.	3.7	8
48	Opioid-induced respiratory depression: ABCB1 transporter pharmacogenetics. Pharmacogenomics Journal, 2015, 15, 119-126.	2.0	77
49	Interaction between Na-K-ATPase and Bcl-2 proteins BclXL and Bak. American Journal of Physiology - Cell Physiology, 2015, 308, C51-C60.	4.6	22
50	Rational Design of Small Molecule Inhibitors Targeting the Ras GEF, SOS1. Chemistry and Biology, 2014, 21, 1618-1628.	6.0	53
51	Association of Streptomyces community composition determined by PCR-denaturing gradient gel electrophoresis with indoor mold status. Environmental Monitoring and Assessment, 2014, 186, 8773-8783.	2.7	3
52	Genetic risk signatures of opioid-induced respiratory depression following pediatric tonsillectomy. Pharmacogenomics, 2014, 15, 1749-1762.	1.3	26
53	TRPM3 and miR-204 Establish a Regulatory Circuit that Controls Oncogenic Autophagy in Clear Cell Renal Cell Carcinoma. Cancer Cell, 2014, 26, 738-753.	16.8	156

⁵⁴Secretory phospholipase A2-IIa upregulates HER/HER2-elicited signaling in lung cancer cells.3.33054International Journal of Oncology, 2014, 45, 978-984.3.330

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55	Abstract LB-10: Rational design of small molecules targeting the Ras GEF, SOS1. , 2014, , .		0
56	Canonical Bcl-2 Motifs of the Na ⁺ /K ⁺ Pump Revealed by the BH3 Mimetic Chelerythrine: Early Signal Transducers of Apoptosis?. Cellular Physiology and Biochemistry, 2013, 31, 257-276.	1.6	11
57	Substrate specificity of Tulane virus protease. Virology, 2013, 436, 24-32.	2.4	3
58	Inhibition of Histo-blood Group Antigen Binding as a Novel Strategy to Block Norovirus Infections. PLoS ONE, 2013, 8, e69379.	2.5	39
59	Folliculin Contributes to VHL Tumor Suppressing Activity in Renal Cancer through Regulation of Autophagy. PLoS ONE, 2013, 8, e70030.	2.5	23
60	Novel Mechanism of Na/K Pump Inhibition by Chelerythrine (CET), a PKC Inhibitor, Uncovers Potential Early Signal Transducers of Apoptosis FASEB Journal, 2013, 27, 726.13.	0.5	0
61	Rotavirus VP8*: Phylogeny, Host Range, and Interaction with Histo-Blood Group Antigens. Journal of Virology, 2012, 86, 9899-9910.	3.4	152
62	Not all autophagy is equal. Autophagy, 2012, 8, 1155-1156.	9.1	18
63	On Setting Up and Assessing Docking Simulations for Virtual Screening. Methods in Molecular Biology, 2012, 928, 1-16.	0.9	3
64	VHL-Regulated MiR-204 Suppresses Tumor Growth through Inhibition of LC3B-Mediated Autophagy in Renal Clear Cell Carcinoma. Cancer Cell, 2012, 21, 532-546.	16.8	290
65	Rational Design of Small Molecule Inhibitors Targeting the Rac GTPase-p67 Signaling Axis in Inflammation. Chemistry and Biology, 2012, 19, 228-242.	6.0	53
66	Identifying a small set of marker genes using minimum expected cost of misclassification. Artificial Intelligence in Medicine, 2012, 55, 51-59.	6.5	3
67	Analysis of Current Antifungal Agents and Their Targets within the Pneumocystis carinii Genome. Current Drug Targets, 2012, 13, 1575-1585.	2.1	21
68	COMPUTATIONAL APPROACH TO UNDERSTANDING AUTISM SPECTRUM DISORDERS. Computer Science, 2012, 13, 47.	0.6	17
69	From SNP Genotyping to Improved Pediatric Healthcare. Translational Bioinformatics, 2012, , 359-378.	0.0	0
70	Solvent and Lipid Accessibility Prediction as a Basis for Model Quality Assessment in Soluble and Membrane Proteins. Current Protein and Peptide Science, 2011, 12, 563-573.	1.4	9
71	Hypomorphic mutations in PRF1, MUNC13-4, and STXBP2 are associated with adult-onset familial HLH. Blood, 2011, 118, 5794-5798.	1.4	349
72	Survey of public domain software for docking simulations and virtual screening. Human Genomics, 2011, 5, 497.	2.9	48

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73	Fast Geometric Consensus Approach for Protein Model Quality Assessment. Journal of Computational Biology, 2011, 18, 1807-1818.	1.6	10
74	Identification of a Conserved Anti-Apoptotic Protein That Modulates the Mitochondrial Apoptosis Pathway. PLoS ONE, 2011, 6, e25284.	2.5	20
75	Genomics Portals: integrative web-platform for mining genomics data. BMC Genomics, 2010, 11, 27.	2.8	13
76	Genetic and Phenotypic Characterization of GII-4 Noroviruses That Circulated during 1987 to 2008. Journal of Virology, 2010, 84, 9595-9607.	3.4	61
77	POLYVIEW-MM: web-based platform for animation and analysis of molecular simulations. Nucleic Acids Research, 2010, 38, W662-W666.	14.5	25
78	von Hippel-Lindau–Dependent Patterns of RNA Polymerase II Hydroxylation in Human Renal Clear Cell Carcinomas. Clinical Cancer Research, 2010, 16, 5142-5152.	7.0	26
79	Dual-Channel Single-Molecule Imaging of pRNA on phi29 DNA-Packaging Motor. Biophysical Journal, 2010, 98, 579a.	0.5	1
80	Dual-Channel Single-Molecule Fluorescence Resonance Energy Transfer to Establish Distance Parameters for RNA Nanoparticles. ACS Nano, 2010, 4, 6843-6853.	14.6	25
81	45-OR: Fine-Mapping of MHC Region Variants in Juvenile Idiopathic Arthritis (JIA) Reveals Evidence of Additional Predisposing Sites Telomeric to Class I. Human Immunology, 2010, 71, S141.	2.4	0
82	Enhanced Prediction of Conformational Flexibility and Phosphorylation in Proteins. Advances in Experimental Medicine and Biology, 2010, 680, 307-319.	1.6	11
83	Comprehensive Identification and Modified-Site Mapping of S-Nitrosylated Targets in Prostate Epithelial Cells. PLoS ONE, 2010, 5, e9075.	2.5	75
84	Mapping critical structural elements in divalent metalâ€ion transporterâ€1 (DMT1). FASEB Journal, 2010, 24, 609.7.	0.5	0
85	Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. Molecular Vision, 2010, 16, 72-8.	1.1	29
86	Building and assessing atomic models of proteins from structural templates: Learning and benchmarks. Proteins: Structure, Function and Bioinformatics, 2009, 76, 930-945.	2.6	25
87	iTRAQ proteomic identification of pVHL-dependent and -independent targets of Egln1 prolyl hydroxylase knockdown in renal carcinoma cells. Advances in Enzyme Regulation, 2009, 49, 121-132.	2.6	9
88	Conservation of Carbohydrate Binding Interfaces — Evidence of Human HBGA Selection in Norovirus Evolution. PLoS ONE, 2009, 4, e5058.	2.5	103
89	Cyclin D3 action in androgen receptor regulation and prostate cancer. Oncogene, 2008, 27, 3111-3121.	5.9	34
90	Elucidation of strain-specific interaction of a GII-4 norovirus with HBGA receptors by site-directed mutagenesis study. Virology, 2008, 379, 324-334.	2.4	71

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91	The von Hippel-Lindau Tumor Suppressor Protein and Egl-9-Type Proline Hydroxylases Regulate the Large Subunit of RNA Polymerase II in Response to Oxidative Stress. Molecular and Cellular Biology, 2008, 28, 2701-2717.	2.3	115
92	Differential transmission of MEKK1 morphogenetic signals by JNK1 and JNK2. Development (Cambridge), 2008, 135, 23-32.	2.5	45
93	Artificial Intelligence Approaches for Rational Drug Design and Discovery. Current Pharmaceutical Design, 2007, 13, 1497-1508.	1.9	152
94	Phosphorylation-dependent Conformational Transition of the Cardiac Specific N-Extension of Troponin I in Cardiac Troponin. Journal of Molecular Biology, 2007, 373, 706-722.	4.2	80
95	Versatile annotation and publication quality visualization of protein complexes using POLYVIEW-3D. BMC Bioinformatics, 2007, 8, 316.	2.6	91
96	Cinteny: flexible analysis and visualization of synteny and genome rearrangements in multiple organisms. BMC Bioinformatics, 2007, 8, 82.	2.6	112
97	Transcriptome of Pneumocystis carinii during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.	2.5	58
98	SENSITIVITY ANALYSIS FOR REVERSAL DISTANCE AND BREAKPOINT REUSE IN GENOME REARRANGEMENTS. , 2007, , .		2
99	Prediction-based fingerprints of protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2006, 66, 630-645.	2.6	342
100	Draft Assembly and Annotation of the Pneumocystis carinii Genome. Journal of Eukaryotic Microbiology, 2006, 53, S89-S91.	1.7	31
101	Large-Scale Characterization of Introns in the Pneumocystis carinii Genome. Journal of Eukaryotic Microbiology, 2006, 53, S151-S153.	1.7	8
102	Enhanced recognition of protein transmembrane domains with prediction-based structural profiles. Bioinformatics, 2006, 22, 303-309.	4.1	88
103	C-Terminal Arginine Cluster Is Essential for Receptor Binding of Norovirus Capsid Protein. Journal of Virology, 2006, 80, 7322-7331.	3.4	56
104	A central domain of cyclin D1 mediates nuclear receptor corepressor activity. Oncogene, 2005, 24, 431-444.	5.9	63
105	Combining prediction of secondary structure and solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2005, 59, 467-475.	2.6	265
106	Linear Regression Models for Solvent Accessibility Prediction in Proteins. Journal of Computational Biology, 2005, 12, 355-369.	1.6	100
107	Characterization of Disulfide Bonds in Human Nucleoside Triphosphate Diphosphohydrolase 3 (NTPDase3):  Implications for NTPDase Structural Modeling. Biochemistry, 2005, 44, 8998-9012.	2.5	39
108	POLYVIEW: a flexible visualization tool for structural and functional annotations of proteins. Bioinformatics, 2004, 20, 2460-2462.	4.1	133

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109	Localization of Rac2 via the C terminus and aspartic acid 150 specifies superoxide generation, actin polarity and chemotaxis in neutrophils. Nature Immunology, 2004, 5, 744-751.	14.5	119
110	Large-scale linear programming techniques for the design of protein folding potentials. Mathematical Programming, 2004, 101, 301.	2.4	21
111	Accurate prediction of solvent accessibility using neural networks-based regression. Proteins: Structure, Function and Bioinformatics, 2004, 56, 753-767.	2.6	249
112	On the transferability of folding and threading potentials and sequence-independent filters for protein folding simulations. Molecular Physics, 2004, 102, 1291-1305.	1.7	7
113	von Hippel–Lindau tumor suppressor: not only HIF's executioner. Trends in Molecular Medicine, 2004, 10, 146-149.	6.7	68
114	Deuterium Isotope Effects on Hydrophobic Interactions:Â The Importance of Dispersion Interactions in the Hydrophobic Phase. Journal of the American Chemical Society, 2003, 125, 13836-13849.	13.7	196
115	Mutations within the P2 Domain of Norovirus Capsid Affect Binding to Human Histo-Blood Group Antigens: Evidence for a Binding Pocket. Journal of Virology, 2003, 77, 12562-12571.	3.4	171
116	von Hippel-Lindau protein binds hyperphosphorylated large subunit of RNA polymerase II through a proline hydroxylation motif and targets it for ubiquitination. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2706-2711.	7.1	206
117	Size-consistent multireference configuration interaction method through the dressing of the norm of determinants. Molecular Physics, 2003, 101, 2029-2041.	1.7	17
118	Protein Recognition by Sequence-to-Structure Fitness: Bridging Efficiency and Capacity of Threading Models. Advances in Chemical Physics, 2002, , 77-130.	0.3	10
119	Maximum feasibility guideline in the design and analysis of protein folding potentials. Journal of Computational Chemistry, 2002, 23, 111-118.	3.3	24
120	Linear programming optimization and a double statistical filter for protein threading protocols. Proteins: Structure, Function and Bioinformatics, 2001, 45, 241-261.	2.6	117
121	fw2.2: A Quantitative Trait Locus Key to the Evolution of Tomato Fruit Size. Science, 2000, 289, 85-88.	12.6	1,290
122	Electronic excitation spectra of furan and pyrrole: Revisited by the symmetry adapted cluster–configuration interaction method. Journal of Chemical Physics, 2000, 113, 7853-7866.	3.0	88
123	SGA derivation of matrix elements between spin-adapted perturbative wave functions. International Journal of Quantum Chemistry, 1999, 74, 123-133.	2.0	0
124	Stochastic Path Approach to Compute Atomically Detailed Trajectories:  Application to the Folding of C Peptide. Journal of Physical Chemistry B, 1999, 103, 899-911.	2.6	104
125	Computer Simulations of Carbon Monoxide Photodissociation in Myoglobin: Structural Interpretation of the B States. Biophysical Journal, 1998, 74, 789-802.	0.5	58
126	A general bridge between configuration interaction and coupled-cluster methods: a multistate solution. Chemical Physics Letters, 1996, 259, 619-626.	2.6	7

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127	Stateâ€specific coupled clusterâ€type dressing of multireference singles and doubles configuration interaction matrix. Journal of Chemical Physics, 1996, 104, 4068-4076.	3.0	75
128	Multireference self-consistent size-consistent configuration interaction method. A few applications to ground and excited states. Chemical Physics Letters, 1995, 244, 440-447.	2.6	40
129	On multireference superdirect configuration interaction in third order. International Journal of Quantum Chemistry, 1994, 50, 243-271.	2.0	8
130	Size-consistent self-consistent combination of selected CI and perturbation theory. Chemical Physics Letters, 1994, 218, 276-282.	2.6	11
131	Temperatures in linguistics as a model of thermodynamics. Open Systems and Information Dynamics, 1994, 2, 211-230.	1.2	4
132	Enumeration of the order-14 invariants formed from the Riemann tensor. Journal of Physics A, 1992, 25, 5999-6003.	1.6	2
133	Computational Methods for Prediction of Protein-Protein Interaction Sites. , 0, , .		10