Jaroslaw Meller

List of Publications by Year in Descending Order

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129	6,383	38	78
papers	citations	h-index	g-index
148	7,277	5.8	5.45
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
129	Complimentary transcriptomic-metallomic analysis identifies risk of relapse for clear-cell renal cell carcinoma (ccRCC) patients.. *Journal of Clinical Oncology*, **2022**, 40, 378-378	2.2	
128	The active kinome: The modern view of how active protein kinase networks fit in biological research.. *Current Opinion in Pharmacology*, **2021**, 62, 117-129	5.1	2
127	Molecular and Metabolic Subtypes in Sporadic and Inherited Clear Cell Renal Cell Carcinoma. *Genes*, **2021**, 12,	4.2	3
126	Selective MAP1LC3C (LC3C) autophagy requires noncanonical regulators and the C-terminal peptide. *Journal of Cell Biology*, **2021**, 220,	7.3	1
125	Signature-based approaches for informed drug repurposing: targeting CNS disorders. *Neuropsychopharmacology*, **2021**, 46, 116-130	8.7	13
124	The mycobiomes and bacteriomes of sputum, saliva, and home dust. *Indoor Air*, **2021**, 31, 357-368	5.4	1
123	Identification of candidate repurposable drugs to combat COVID-19 using a signature-based approach. *Scientific Reports*, **2021**, 11, 4495	4.9	14
122	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. *Journal of Clinical Investigation*, **2021**, 131,	15.9	5
121	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	3.7	0
120	Transcriptional Regulation of Cancer Immune Checkpoints: Emerging Strategies for Immunotherapy. *Vaccines*, **2020**, 8,	5.3	10
119	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. *Nucleic Acids Research*, **2020**, 48, W85-W93	20.1	9
118	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. *PLoS ONE*, **2020**, 15, e0229801	3.7	2
117	Identification of new drug treatments to combat COVID19: A signature-based approach using iLINCS **2020**,		4
116	Transcriptional Profile of Pyramidal Neurons in Chronic Schizophrenia Reveals Lamina-Specific Dysfunction of Neuronal Immunity. *Biological Psychiatry*, **2020**, 87, S347-S348	7.9	2
115	Kinase network dysregulation in a human induced pluripotent stem cell model of DISC1 schizophrenia. *Molecular Omics*, **2019**, 15, 173-188	4.4	20
114	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	5.2	20
113	Structural Adaptations of Norovirus GII.17/13/21 Lineage through Two Distinct Evolutionary Paths. *Journal of Virology*, **2019**, 93,	6.6	12

112	Connectivity Analyses of Bioenergetic Changes in Schizophrenia: Identification of Novel Treatments. *Molecular Neurobiology*, **2019**, 56, 4492-4517	6.2	22
111	Rational identification of a Cdc42 inhibitor presents a new regimen for long-term hematopoietic stem cell mobilization. *Leukemia*, **2019**, 33, 749-761	10.7	29
110	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	10.6	199
109	Significant variation between SNP-based HLA imputations in diverse populations: the last mile is the hardest. *Pharmacogenomics Journal*, **2018**, 18, 367-376	3.5	21
108	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	10.2	11
107	F201. KINASE NETWORK DYSREGULATION IN SCHIZOPHRENIA: IMPLICATIONS FOR NEW TREATMENT STRATEGIES. *Schizophrenia Bulletin*, **2018**, 44, S299-S299	1.3	1
106	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	20.1	84
105	ABCC3 genetic variants are associated with postoperative morphine-induced respiratory depression and morphine pharmacokinetics in children. *Pharmacogenomics Journal*, **2017**, 17, 162-169	3.5	21
104	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	5.4	29
103	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,	6.6	6
102	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, 1178222617713018	4.9	8
101	Abnormalities of signal transduction networks in chronic schizophrenia. *NPJ Schizophrenia*, **2017**, 3, 30	5.5	36
100	The SRL peptide of rhesus rotavirus VP4 protein governs cholangiocyte infection and the murine model of biliary atresia. *Hepatology*, **2017**, 65, 1278-1292	11.2	9
99	UQlust: combining profile hashing with linear-time ranking for efficient clustering and analysis of big macromolecular data. *BMC Bioinformatics*, **2016**, 17, 546	3.6	0
98	Comprehensive analysis of sequences of a protein switch. *Protein Science*, **2016**, 25, 135-46	6.3	11
97	Toward Pediatric Precision Medicine: Examples of Genomics-Based Stratification Strategies. *Translational Bioinformatics*, **2016**, 339-361		
96	Combined rational design and a high throughput screening platform for identifying chemical inhibitors of a Ras-activating enzyme. *Journal of Biological Chemistry*, **2015**, 290, 12879-98	5.4	19
95	Novel associations between FAAH genetic variants and postoperative central opioid-related adverse effects. *Pharmacogenomics Journal*, **2015**, 15, 436-42	3.5	22

94	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, G466-74	5.1	11
93	Increased susceptibility of estrogen-induced bladder outlet obstruction in a novel mouse model. *Laboratory Investigation*, **2015**, 95, 546-60	5.9	5
92	Opioid-induced respiratory depression: ABCB1 transporter pharmacogenetics. *Pharmacogenomics Journal*, **2015**, 15, 119-26	3.5	67
91	Interaction between Na-K-ATPase and Bcl-2 proteins BclXL and Bak. *American Journal of Physiology - Cell Physiology*, **2015**, 308, C51-60	5.4	19
90	Targeting substrate-site in Jak2 kinase prevents emergence of genetic resistance. *Scientific Reports* , **2015**, 5, 14538	4.9	24
89	TRPM3 and miR-204 establish a regulatory circuit that controls oncogenic autophagy in clear cell renal cell carcinoma. *Cancer Cell*, **2014**, 26, 738-53	24.3	125
88	Secretory phospholipase A2-IIa upregulates HER/HER2-elicited signaling in lung cancer cells. *International Journal of Oncology*, **2014**, 45, 978-84	4.4	17
87	Rational design of small molecule inhibitors targeting the Ras GEF, SOS1. *Chemistry and Biology*, **2014**, 21, 1618-28		37
86	Association of Streptomyces community composition determined by PCR-denaturing gradient gel electrophoresis with indoor mold status. *Environmental Monitoring and Assessment*, **2014**, 186, 8773-83	3.1	2
85	Genetic risk signatures of opioid-induced respiratory depression following pediatric tonsillectomy. *Pharmacogenomics*, **2014**, 15, 1749-1762	2.6	20
84	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, 257-76	3.9	9
83	Substrate specificity of Tulane virus protease. *Virology*, **2013**, 436, 24-32	3.6	2
82	Inhibition of histo-blood group antigen binding as a novel strategy to block norovirus infections. *PLoS ONE*, **2013**, 8, e69379	3.7	35
81	Folliculin contributes to VHL tumor suppressing activity in renal cancer through regulation of autophagy. *PLoS ONE*, **2013**, 8, e70030	3.7	19
80	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	0.9	
79	On setting up and assessing docking simulations for virtual screening. *Methods in Molecular Biology*, **2012**, 928, 1-16	1.4	2
78	VHL-regulated MiR-204 suppresses tumor growth through inhibition of LC3B-mediated autophagy in renal clear cell carcinoma. *Cancer Cell*, **2012**, 21, 532-46	24.3	253
77	Rational design of small molecule inhibitors targeting the Rac GTPase-p67(phox) signaling axis in inflammation. *Chemistry and Biology*, **2012**, 19, 228-42		46

76	Identifying a small set of marker genes using minimum expected cost of misclassification. *Artificial Intelligence in Medicine*, **2012**, 55, 51-9	7.4	3
75	Rotavirus VP8*: phylogeny, host range, and interaction with histo-blood group antigens. *Journal of Virology*, **2012**, 86, 9899-910	6.6	128
74	Not all autophagy is equal. *Autophagy*, **2012**, 8, 1155-6	10.2	15
73	Analysis of current antifungal agents and their targets within the Pneumocystis carinii genome. *Current Drug Targets*, **2012**, 13, 1575-85	3	16
72	COMPUTATIONAL APPROACH TO UNDERSTANDING AUTISM SPECTRUM DISORDERS. *Computer Science*, **2012**, 13, 47	1.2	12
71	From SNP Genotyping to Improved Pediatric Healthcare. *Translational Bioinformatics*, **2012**, 359-378		
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, 563-73	2.8	8
69	Hypomorphic mutations in PRF1, MUNC13-4, and STXBP2 are associated with adult-onset familial HLH. *Blood*, **2011**, 118, 5794-8	2.2	283
68	Survey of public domain software for docking simulations and virtual screening. *Human Genomics*, **2011**, 5, 497-505	6.8	30
67	Fast geometric consensus approach for protein model quality assessment. *Journal of Computational Biology*, **2011**, 18, 1807-18	1.7	9
66	Identification of a conserved anti-apoptotic protein that modulates the mitochondrial apoptosis pathway. *PLoS ONE*, **2011**, 6, e25284	3.7	15
65	Genetic and phenotypic characterization of GII-4 noroviruses that circulated during 1987 to 2008. *Journal of Virology*, **2010**, 84, 9595-607	6.6	57
64	POLYVIEW-MM: web-based platform for animation and analysis of molecular simulations. *Nucleic Acids Research*, **2010**, 38, W662-6	20.1	23
63	von Hippel-Lindau-dependent patterns of RNA polymerase II hydroxylation in human renal clear cell carcinomas. *Clinical Cancer Research*, **2010**, 16, 5142-52	12.9	21
62	Molecular Dynamics **2010**,		5
61	Dual-channel single-molecule fluorescence resonance energy transfer to establish distance parameters for RNA nanoparticles. *ACS Nano*, **2010**, 4, 6843-53	16.7	20
60	Genomics Portals: integrative web-platform for mining genomics data. *BMC Genomics*, **2010**, 11, 27	4.5	9
59	Comprehensive identification and modified-site mapping of S-nitrosylated targets in prostate epithelial cells. *PLoS ONE*, **2010**, 5, e9075	3.7	72

58	Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. *Molecular Vision*, **2010**, 16, 72-8	2.3	29
57	Mapping critical structural elements in divalent metal-ion transporter-1 (DMT1). *FASEB Journal*, **2010**, 24, 609.7	0.9	
56	Enhanced prediction of conformational flexibility and phosphorylation in proteins. *Advances in Experimental Medicine and Biology*, **2010**, 680, 307-19	3.6	8
55	Building and assessing atomic models of proteins from structural templates: learning and benchmarks. *Proteins: Structure, Function and Bioinformatics*, **2009**, 76, 930-45	4.2	23
54	iTRAQ proteomic identification of pVHL-dependent and -independent targets of Egln1 prolyl hydroxylase knockdown in renal carcinoma cells. *Advances in Enzyme Regulation*, **2009**, 49, 121-32		7
53	Conservation of carbohydrate binding interfaces: evidence of human HBGA selection in norovirus evolution. *PLoS ONE*, **2009**, 4, e5058	3.7	89
52	Cyclin D3 action in androgen receptor regulation and prostate cancer. *Oncogene*, **2008**, 27, 3111-21	9.2	28
51	Elucidation of strain-specific interaction of a GII-4 norovirus with HBGA receptors by site-directed mutagenesis study. *Virology*, **2008**, 379, 324-34	3.6	67
50	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, 2701-17	4.8	99
49	Differential transmission of MEKK1 morphogenetic signals by JNK1 and JNK2. *Development (Cambridge)*, **2008**, 135, 23-32	6.6	37
48	Versatile annotation and publication quality visualization of protein complexes using POLYVIEW-3D. *BMC Bioinformatics*, **2007**, 8, 316	3.6	87
47	Cinteny: flexible analysis and visualization of synteny and genome rearrangements in multiple organisms. *BMC Bioinformatics*, **2007**, 8, 82	3.6	93
46	Artificial intelligence approaches for rational drug design and discovery. *Current Pharmaceutical Design*, **2007**, 13, 1497-508	3.3	102
45	Phosphorylation-dependent conformational transition of the cardiac specific N-extension of troponin I in cardiac troponin. *Journal of Molecular Biology*, **2007**, 373, 706-22	6.5	73
44	Prediction-based fingerprints of protein-protein interactions. *Proteins: Structure, Function and Bioinformatics*, **2007**, 66, 630-45	4.2	247
43	Transcriptome of Pneumocystis carinii during fulminate infection: carbohydrate metabolism and the concept of a compatible parasite. *PLoS ONE*, **2007**, 2, e423	3.7	50
42	Enhanced recognition of protein transmembrane domains with prediction-based structural profiles. *Bioinformatics*, **2006**, 22, 303-9	7.2	78
41	C-terminal arginine cluster is essential for receptor binding of norovirus capsid protein. *Journal of Virology*, **2006**, 80, 7322-31	6.6	51

40	Draft assembly and annotation of the Pneumocystis carinii genome. *Journal of Eukaryotic Microbiology*, **2006**, 53 Suppl 1, S89-91	3.6	20
39	Large-scale characterization of introns in the Pneumocystis carinii genome. *Journal of Eukaryotic Microbiology*, **2006**, 53 Suppl 1, S151-3	3.6	5
38	Characterization of disulfide bonds in human nucleoside triphosphate diphosphohydrolase 3 (NTPDase3): implications for NTPDase structural modeling. *Biochemistry*, **2005**, 44, 8998-9012	3.2	30
37	A central domain of cyclin D1 mediates nuclear receptor corepressor activity. *Oncogene*, **2005**, 24, 431-44	9.2	57
36	Combining prediction of secondary structure and solvent accessibility in proteins. *Proteins: Structure, Function and Bioinformatics*, **2005**, 59, 467-75	4.2	222
35	Linear regression models for solvent accessibility prediction in proteins. *Journal of Computational Biology*, **2005**, 12, 355-69	1.7	84
34	POLYVIEW: a flexible visualization tool for structural and functional annotations of proteins. *Bioinformatics*, **2004**, 20, 2460-2	7.2	112
33	Mutations within the P2 Domain of Norovirus Capsid Affect Binding to Human Histo-Blood Group Antigens: Evidence for a Binding Pocket. *Journal of Virology*, **2004**, 78, 3201-3201	6.6	78
32	Localization of Rac2 via the C terminus and aspartic acid 150 specifies superoxide generation, actin polarity and chemotaxis in neutrophils. *Nature Immunology*, **2004**, 5, 744-51	19.1	112
31	Large-scale linear programming techniques for the design of protein folding potentials. *Mathematical Programming*, **2004**, 101, 301	2.1	17
30	Accurate prediction of solvent accessibility using neural networks-based regression. *Proteins: Structure, Function and Bioinformatics*, **2004**, 56, 753-67	4.2	205
29	On the transferability of folding and threading potentials and sequence-independent filters for protein folding simulations. *Molecular Physics*, **2004**, 102, 1291-1305	1.7	6
28	von Hippel-Lindau tumor suppressor: not only HIFα executioner. *Trends in Molecular Medicine*, **2004** , 10, 146-9	11.5	60
27	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, 2706-11	11.5	179
26	Size-consistent multireference configuration interaction method through the dressing of the norm of determinants. *Molecular Physics*, **2003**, 101, 2029-2041	1.7	13
25	Deuterium isotope effects on hydrophobic interactions: the importance of dispersion interactions in the hydrophobic phase. *Journal of the American Chemical Society*, **2003**, 125, 13836-49	16.4	165
24	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, 12562-71	6.6	148
23	Maximum feasibility guideline in the design and analysis of protein folding potentials. *Journal of Computational Chemistry*, **2002**, 23, 111-8	3.5	21

22	Protein Recognition by Sequence-to-Structure Fitness: Bridging Efficiency and Capacity of Threading Models. *Advances in Chemical Physics*, **2002**, 77-130		4
21	Linear programming optimization and a double statistical filter for protein threading protocols. *Proteins: Structure, Function and Bioinformatics*, **2001**, 45, 241-61	4.2	113
20	fw2.2: a quantitative trait locus key to the evolution of tomato fruit size. *Science*, **2000**, 289, 85-8	33.3	1084
19	Electronic excitation spectra of furan and pyrrole: Revisited by the symmetry adapted cluster‐configuration interaction method. *Journal of Chemical Physics*, **2000**, 113, 7853-7866	3.9	82
18	SGA derivation of matrix elements between spin-adapted perturbative wave functions. *International Journal of Quantum Chemistry*, **1999**, 74, 123-133	2.1	
17	Stochastic Path Approach to Compute Atomically Detailed Trajectories: Application to the Folding of C Peptide. *Journal of Physical Chemistry B*, **1999**, 103, 899-911	3.4	96
16	Computer simulations of carbon monoxide photodissociation in myoglobin: structural interpretation of the B states. *Biophysical Journal*, **1998**, 74, 789-802	2.9	53
15	A general bridge between configuration interaction and coupled-cluster methods: a multistate solution. *Chemical Physics Letters*, **1996**, 259, 619-626	2.5	7
14	State-specific coupled cluster-type dressing of multireference singles and doubles configuration interaction matrix. *Journal of Chemical Physics*, **1996**, 104, 4068-4076	3.9	72
13	Multireference self-consistent size-consistent configuration interaction method. A few applications to ground and excited states. *Chemical Physics Letters*, **1995**, 244, 440-447	2.5	38
12	On multireference superdirect configuration interaction in third order. *International Journal of Quantum Chemistry*, **1994**, 50, 243-271	2.1	6
11	Size-consistent self-consistent combination of selected CI and perturbation theory. *Chemical Physics Letters*, **1994**, 218, 276-282	2.5	10
10	Temperatures in linguistics as a model of thermodynamics. *Open Systems and Information Dynamics*, **1994**, 2, 211-230	0.4	3
9	Enumeration of the order-14 invariants formed from the Riemann tensor. *Journal of Physics A*, **1992**, 25, 5999-6003		2
8	Computational Methods for Prediction of Protein-Protein Interaction Sites		5
7	Integrative Omics for Informed Drug Repurposing: Targeting CNS Disorders		1
6	Kaleidoscope: A New Bioinformatics Pipeline Web Application for In Silico Hypothesis Exploration of Omics Signatures		8
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