Jaroslaw Meller

List of Publications by Year
in descending order

133 papers	7,879 citations	71102 41 h-index	53230 85 g-index
148 all docs	148 docs citations	148 times ranked	13627 citing authors

#	Article	IF	Citations
1	fw2.2: A Quantitative Trait Locus Key to the Evolution of Tomato Fruit Size. Science, 2000, 289, 85-88.	12.6	1,290
2	Hypomorphic mutations in PRF1, MUNC13-4, and STXBP2 are associated with adult-onset familial HLH. Blood, 2011, 118, 5794-5798.	1.4	349
3	Prediction-based fingerprints of protein-protein interactions. Proteins: Structure, Function and Bioinformatics, 2006, 66, 630-645.	2.6	342
4	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
5	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
6	Combining prediction of secondary structure and solvent accessibility in proteins. Proteins: Structure, Function and Bioinformatics, 2005, 59, 467-475.	2.6	265
7	Accurate prediction of solvent accessibility using neural networks-based regression. Proteins: Structure, Function and Bioinformatics, 2004, 56, 753-767.	2.6	249
8	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
9	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
10	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
11	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
12	Artificial Intelligence Approaches for Rational Drug Design and Discovery. Current Pharmaceutical Design, 2007, 13, 1497-1508.	1.9	152
13	Rotavirus VP8*: Phylogeny, Host Range, and Interaction with Histo-Blood Group Antigens. Journal of Virology, 2012, 86, 9899-9910.	3.4	152
14	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
15	POLYVIEW: a flexible visualization tool for structural and functional annotations of proteins. Bioinformatics, 2004, 20, 2460-2462.	4.1	133
16	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
17	Linear programming optimization and a double statistical filter for protein threading protocols. Proteins: Structure, Function and Bioinformatics, 2001, 45, 241-261.	2.6	117
18	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

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19	Cinteny: flexible analysis and visualization of synteny and genome rearrangements in multiple organisms. BMC Bioinformatics, 2007, 8, 82.	2.6	112
20	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
21	Conservation of Carbohydrate Binding Interfaces â€" Evidence of Human HBGA Selection in Norovirus Evolution. PLoS ONE, 2009, 4, e5058.	2.5	103
22	Linear Regression Models for Solvent Accessibility Prediction in Proteins. Journal of Computational Biology, 2005, 12, 355-369.	1.6	100
23	Versatile annotation and publication quality visualization of protein complexes using POLYVIEW-3D. BMC Bioinformatics, 2007, 8, 316.	2.6	91
24	Electronic excitation spectra of furan and pyrrole: Revisited by the symmetry adapted clusterâ€"configuration interaction method. Journal of Chemical Physics, 2000, 113, 7853-7866.	3.0	88
25	Enhanced recognition of protein transmembrane domains with prediction-based structural profiles. Bioinformatics, 2006, 22, 303-309.	4.1	88
26	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
27	Opioid-induced respiratory depression: ABCB1 transporter pharmacogenetics. Pharmacogenomics Journal, 2015, 15, 119-126.	2.0	77
28	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
29	Comprehensive Identification and Modified-Site Mapping of S-Nitrosylated Targets in Prostate Epithelial Cells. PLoS ONE, 2010, 5, e9075.	2.5	75
30	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
31	von Hippelâ€"Lindau tumor suppressor: not only HIF's executioner. Trends in Molecular Medicine, 2004, 10, 146-149.	6.7	68
32	A central domain of cyclin D1 mediates nuclear receptor corepressor activity. Oncogene, 2005, 24, 431-444.	5.9	63
33	Abnormalities of signal transduction networks in chronic schizophrenia. NPJ Schizophrenia, 2017, 3, 30.	3.6	62
34	Genetic and Phenotypic Characterization of GII-4 Noroviruses That Circulated during 1987 to 2008. Journal of Virology, 2010, 84, 9595-9607.	3.4	61
35	Computer Simulations of Carbon Monoxide Photodissociation in Myoglobin: Structural Interpretation of the B States. Biophysical Journal, 1998, 74, 789-802.	0.5	58
36	Transcriptome of Pneumocystis carinii during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.	2.5	58

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37	C-Terminal Arginine Cluster Is Essential for Receptor Binding of Norovirus Capsid Protein. Journal of Virology, 2006, 80, 7322-7331.	3.4	56
38	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
39	Rational Design of Small Molecule Inhibitors Targeting the Ras GEF, SOS1. Chemistry and Biology, 2014, 21, 1618-1628.	6.0	53
40	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
41	Survey of public domain software for docking simulations and virtual screening. Human Genomics, 2011, 5, 497.	2.9	48
42	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
43	Differential transmission of MEKK1 morphogenetic signals by JNK1 and JNK2. Development (Cambridge), 2008, 135, 23-32.	2.5	45
44	Targeting substrate-site in Jak2 kinase prevents emergence of genetic resistance. Scientific Reports, 2015, 5, 14538.	3.3	45
45	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
46	Characterization of Disulfide Bonds in Human Nucleoside Triphosphate Diphosphohydrolase 3 (NTPDase3):â€‰ Implications for NTPDase Structural Modeling. Biochemistry, 2005, 44, 8998-9012.	2.5	39
47	Inhibition of Histo-blood Group Antigen Binding as a Novel Strategy to Block Norovirus Infections. PLoS ONE, 2013, 8, e69379.	2.5	39
48	Signature-based approaches for informed drug repurposing: targeting CNS disorders. Neuropsychopharmacology, 2021, 46, 116-130.	5.4	38
49	Cyclin D3 action in androgen receptor regulation and prostate cancer. Oncogene, 2008, 27, 3111-3121.	5.9	34
50	Connectivity Analyses of Bioenergetic Changes in Schizophrenia: Identification of Novel Treatments. Molecular Neurobiology, 2019, 56, 4492-4517.	4.0	34
51	Kinase network dysregulation in a human induced pluripotent stem cell model of DISC1 schizophrenia. Molecular Omics, 2019, 15, 173-188.	2.8	33
52	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
53	Draft Assembly and Annotation of the Pneumocystis carinii Genome. Journal of Eukaryotic Microbiology, 2006, 53, S89-S91.	1.7	31
54	Novel associations between FAAH genetic variants and postoperative central opioid-related adverse effects. Pharmacogenomics Journal, 2015, 15, 436-442.	2.0	31

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55	Secretory phospholipase A2-IIa upregulates HER/HER2-elicited signaling in lung cancer cells. International Journal of Oncology, 2014, 45, 978-984.	3.3	30
56	Expression profiles during dedifferentiation in newt lens regeneration revealed by expressed sequence tags. Molecular Vision, 2010, 16, 72-8.	1.1	29
57	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
58	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
59	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
60	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
61	Genetic risk signatures of opioid-induced respiratory depression following pediatric tonsillectomy. Pharmacogenomics, 2014, 15, 1749-1762.	1.3	26
62	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
63	POLYVIEW-MM: web-based platform for animation and analysis of molecular simulations. Nucleic Acids Research, 2010, 38, W662-W666.	14.5	25
64	Dual-Channel Single-Molecule Fluorescence Resonance Energy Transfer to Establish Distance Parameters for RNA Nanoparticles. ACS Nano, 2010, 4, 6843-6853.	14.6	25
65	Maximum feasibility guideline in the design and analysis of protein folding potentials. Journal of Computational Chemistry, 2002, 23, 111-118.	3.3	24
66	Folliculin Contributes to VHL Tumor Suppressing Activity in Renal Cancer through Regulation of Autophagy. PLoS ONE, 2013, 8, e70030.	2.5	23
67	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
68	Identification of candidate repurposable drugs to combat COVID-19 using a signature-based approach. Scientific Reports, 2021, 11, 4495.	3.3	22
69	Large-scale linear programming techniques for the design of protein folding potentials. Mathematical Programming, 2004, 101, 301.	2.4	21
70	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
71	Analysis of Current Antifungal Agents and Their Targets within the Pneumocystis carinii Genome. Current Drug Targets, 2012, 13, 1575-1585.	2.1	21
72	Comprehensive analysis of sequences of a protein switch. Protein Science, 2016, 25, 135-146.	7.6	20

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73	Identification of a Conserved Anti-Apoptotic Protein That Modulates the Mitochondrial Apoptosis Pathway. PLoS ONE, 2011, 6, e25284.	2.5	20
74	Not all autophagy is equal. Autophagy, 2012, 8, 1155-1156.	9.1	18
75	Transcriptional Regulation of Cancer Immune Checkpoints: Emerging Strategies for Immunotherapy. Vaccines, 2020, 8, 735.	4.4	18
76	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic Acids Research, 2020, 48, W85-W93.	14.5	18
77	Size-consistent multireference configuration interaction method through the dressing of the norm of determinants. Molecular Physics, 2003, 101, 2029-2041.	1.7	17
78	COMPUTATIONAL APPROACH TO UNDERSTANDING AUTISM SPECTRUM DISORDERS. Computer Science, 2012, 13, 47.	0.6	17
79	Structural Adaptations of Norovirus GII.17/13/21 Lineage through Two Distinct Evolutionary Paths. Journal of Virology, 2019, 93, .	3.4	16
80	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
81	Tobacco smoking induces metabolic reprogramming of renal cell carcinoma. Journal of Clinical Investigation, 2021, 131, .	8.2	14
82	Genomics Portals: integrative web-platform for mining genomics data. BMC Genomics, 2010, 11, 27.	2.8	13
83	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
84	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
85	Size-consistent self-consistent combination of selected CI and perturbation theory. Chemical Physics Letters, 1994, 218, 276-282.	2.6	11
86	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
87	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
88	Transcriptional profile of pyramidal neurons in chronic schizophrenia reveals lamina-specific dysfunction of neuronal immunity. Molecular Psychiatry, 2021, 26, 7699-7708.	7.9	11
89	Enhanced Prediction of Conformational Flexibility and Phosphorylation in Proteins. Advances in Experimental Medicine and Biology, 2010, 680, 307-319.	1.6	11
90	Protein Recognition by Sequence-to-Structure Fitness: Bridging Efficiency and Capacity of Threading Models. Advances in Chemical Physics, 2002, , 77-130.	0.3	10

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91	Fast Geometric Consensus Approach for Protein Model Quality Assessment. Journal of Computational Biology, 2011, 18, 1807-1818.	1.6	10
92	Molecular and Metabolic Subtypes in Sporadic and Inherited Clear Cell Renal Cell Carcinoma. Genes, 2021, 12, 388.	2.4	10
93	Selective MAP1LC3C (LC3C) autophagy requires noncanonical regulators and the C-terminal peptide. Journal of Cell Biology, 2021, 220, .	5.2	10
94	Computational Methods for Prediction of Protein-Protein Interaction Sites. , 0, , .		10
95	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
96	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
97	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
98	On multireference superdirect configuration interaction in third order. International Journal of Quantum Chemistry, 1994, 50, 243-271.	2.0	8
99	Large-Scale Characterization of Introns in the Pneumocystis carinii Genome. Journal of Eukaryotic Microbiology, 2006, 53, S151-S153.	1.7	8
100	Increased susceptibility of estrogen-induced bladder outlet obstruction in a novel mouse model. Laboratory Investigation, 2015, 95, 546-560.	3.7	8
101	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
102	A general bridge between configuration interaction and coupled-cluster methods: a multistate solution. Chemical Physics Letters, 1996, 259, 619-626.	2.6	7
103	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
104	Assessing the effects of antipsychotic medications on schizophrenia functional analysis: a postmortem proteome study. Neuropsychopharmacology, 2022, 47, 2033-2041.	5.4	5
105	Temperatures in linguistics as a model of thermodynamics. Open Systems and Information Dynamics, 1994, 2, 211-230.	1.2	4
106	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. PLoS ONE, 2020, 15, e0229801.	2.5	4
107	On Setting Up and Assessing Docking Simulations for Virtual Screening. Methods in Molecular Biology, 2012, 928, 1-16.	0.9	3
108	Identifying a small set of marker genes using minimum expected cost of misclassification. Artificial Intelligence in Medicine, 2012, 55, 51-59.	6.5	3

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109	Substrate specificity of Tulane virus protease. Virology, 2013, 436, 24-32.	2.4	3
110	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
111	The mycobiomes and bacteriomes of sputum, saliva, and home dust. Indoor Air, 2021, 31, 357-368.	4.3	3
112	Enumeration of the order-14 invariants formed from the Riemann tensor. Journal of Physics A, 1992, 25, 5999-6003.	1.6	2
113	Transcriptional Profile of Pyramidal Neurons in Chronic Schizophrenia Reveals Lamina-Specific Dysfunction of Neuronal Immunity. Biological Psychiatry, 2020, 87, S347-S348.	1.3	2
114	SENSITIVITY ANALYSIS FOR REVERSAL DISTANCE AND BREAKPOINT REUSE IN GENOME REARRANGEMENTS. , 2007, , .		2
115	Dual-Channel Single-Molecule Imaging of pRNA on phi29 DNA-Packaging Motor. Biophysical Journal, 2010, 98, 579a.	0.5	1
116	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
117	F201. KINASE NETWORK DYSREGULATION IN SCHIZOPHRENIA: IMPLICATIONS FOR NEW TREATMENT STRATEGIES. Schizophrenia Bulletin, 2018, 44, S299-S299.	4.3	1
118	SGA derivation of matrix elements between spin-adapted perturbative wave functions. International Journal of Quantum Chemistry, 1999, 74, 123-133.	2.0	0
119	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
120	Analysis of Domain Movement and Dynamics of Norwalk Virus Capsid by Molecular Dynamics (All-Atom) Tj ETQq0 0.0 rgBT /Overlock 10	0.5	0
121	Dynamics of C-terminus Motion of Norwalk Virus Capsid by Molecular Dynamics (All-Atom &) Tj ETQq1 1 0.784314 rgBT /Overlock	0.5	0
122	Toward Pediatric Precision Medicine: Examples of Genomics-Based Stratification Strategies. Translational Bioinformatics, 2016, , 339-361.	0.0	0
123	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
124	Mapping critical structural elements in divalent metal–ion transporter–1 (DMT1). FASEB Journal, 2010, 24, 609.7.	0.5	0
125	From SNP Genotyping to Improved Pediatric Healthcare. Translational Bioinformatics, 2012, , 359-378.	0.0	0
126	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

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127	Abstract LB-10: Rational design of small molecules targeting the Ras GEF, SOS1. , 2014, , .		0
128	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
129	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
130	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
131	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
132	IODVA1, a guanidinobenzimidazole derivative, targets Rac activity and Ras-driven cancer models. , 2020, 15, e0229801.		0
133	Differential genetic associations and expression of PAPST1/SLC35B2 in bipolar disorder and schizophrenia. Journal of Neural Transmission, 2022, 129, 913-924.	2.8	0