

Andreas Beyer

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

7,190
citations

117625

34
h-index

66911

78
g-index

118
all docs

118
docs citations

118
times ranked

13665
citing authors

#	ARTICLE	IF	CITATIONS
1	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016, 165, 535-550.	28.9	2,216
2	Assessing Long-Range Transport Potential of Persistent Organic Pollutants. <i>Environmental Science & Technology</i> , 2000, 34, 699-703.	10.0	322
3	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	27.8	307
4	Post-transcriptional Expression Regulation in the Yeast <i>Saccharomyces cerevisiae</i> on a Genomic Scale. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1083-1092.	3.8	217
5	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556.	14.5	215
6	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. <i>Cell</i> , 2015, 163, 1539-1554.	28.9	200
7	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. <i>Plant Cell</i> , 2019, 31, 2430-2455.	6.6	198
8	Integrating physical and genetic maps: from genomes to interaction networks. <i>Nature Reviews Genetics</i> , 2007, 8, 699-710.	16.3	192
9	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. <i>Genome Biology</i> , 2017, 18, 56.	8.8	164
10	Posttranscriptional Expression Regulation: What Determines Translation Rates?. <i>PLoS Computational Biology</i> , 2007, 3, e57.	3.2	157
11	Selecting internally consistent physicochemical properties of organic compounds. <i>Environmental Toxicology and Chemistry</i> , 2002, 21, 941-953.	4.3	149
12	Comparing Estimates of Persistence and Long-Range Transport Potential among Multimedia Models. <i>Environmental Science & Technology</i> , 2005, 39, 1932-1942.	10.0	138
13	eQED: an efficient method for interpreting eQTL associations using protein networks. <i>Molecular Systems Biology</i> , 2008, 4, 162.	7.2	117
14	Detection and interpretation of expression quantitative trait loci (eQTL). <i>Methods</i> , 2009, 48, 265-276.	3.8	115
15	Constitutive upregulation of the transforming growth factor- β^2 pathway in rheumatoid arthritis synovial fibroblasts. <i>Arthritis Research and Therapy</i> , 2007, 9, R59.	3.5	114
16	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017, 8, 1212.	12.8	112
17	Temperature Dependence of the Characteristic Travel Distance. <i>Environmental Science & Technology</i> , 2003, 37, 766-771.	10.0	91
18	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88

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19	Landscape of nuclear transport receptor cargo specificity. <i>Molecular Systems Biology</i> , 2017, 13, 962.	7.2	88
20	Integrated Assessment and Prediction of Transcription Factor Binding. <i>PLoS Computational Biology</i> , 2006, 2, e70.	3.2	82
21	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <i>Cell</i> , 2021, 184, 545-559.e22.	28.9	82
22	A nutritional memory effect counteracts the benefits of dietary restriction in old mice. <i>Nature Metabolism</i> , 2019, 1, 1059-1073.	11.9	80
23	A random forest approach to capture genetic effects in the presence of population structure. <i>Nature Communications</i> , 2015, 6, 7432.	12.8	79
24	Protein networks markedly improve prediction of subcellular localization in multiple eukaryotic species. <i>Nucleic Acids Research</i> , 2008, 36, e136-e136.	14.5	69
25	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	7.2	65
26	Data-driven assessment of eQTL mapping methods. <i>BMC Genomics</i> , 2010, 11, 502.	2.8	55
27	Assessing Computational Methods for Transcription Factor Target Gene Identification Based on CHIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003342.	3.2	55
28	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	5.2	55
29	Global analysis reveals SRp20- and SRp75-specific mRNPs in cycling and neural cells. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 962-970.	8.2	53
30	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018, 1, e201800042.	2.8	51
31	The Footprint of Polygenic Adaptation on Stress-Responsive <i>Cis</i> -Regulatory Divergence in the <i>Arabidopsis</i> Genus. <i>Molecular Biology and Evolution</i> , 2016, 33, 2088-2101.	8.9	50
32	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. <i>Kidney International</i> , 2018, 93, 1308-1319.	5.2	49
33	Large-scale De Novo Prediction of Physical Protein-Protein Association. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010629.	3.8	44
34	A proteomic atlas of insulin signalling reveals tissue-specific mechanisms of longevity assurance. <i>Molecular Systems Biology</i> , 2017, 13, 939.	7.2	42
35	Long-Range transport potential of semivolatile organic chemicals in coupled air-water systems. <i>Environmental Science and Pollution Research</i> , 2001, 8, 173-179.	5.3	40
36	Predicting functionality of protein-DNA interactions by integrating diverse evidence. <i>Bioinformatics</i> , 2009, 25, i137-i144.	4.1	38

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37	Meiotic Cohesin SMC1 ² Provides Prophase I Centromeric Cohesion and Is Required for Multiple Synapsis-Associated Functions. <i>PLoS Genetics</i> , 2013, 9, e1003985.	3.5	36
38	Impact of Natural Genetic Variation on Gene Expression Dynamics. <i>PLoS Genetics</i> , 2013, 9, e1003514.	3.5	35
39	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	12.8	35
40	Pathway and Time-Resolved Benzo[<i>a</i>]pyrene Toxicity on Hepa1c1c7 Cells at Toxic and Subtoxic Exposure. <i>Journal of Proteome Research</i> , 2015, 14, 164-182.	3.7	34
41	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	3.7	34
42	Assessing Persistence and Long-Range Transport Potential of Current-Use Pesticides. <i>Environmental Science & Technology</i> , 2009, 43, 9223-9229.	10.0	33
43	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. <i>PLoS Computational Biology</i> , 2014, 10, e1003657.	3.2	32
44	Cooperative genetic networks drive embryonic stem cell transition from naïve to formative pluripotency. <i>EMBO Journal</i> , 2021, 40, e105776.	7.8	31
45	The proteomic landscape of small urinary extracellular vesicles during kidney transplantation. <i>Journal of Extracellular Vesicles</i> , 2020, 10, e12026.	12.2	30
46	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. <i>Nature Communications</i> , 2021, 12, 3804.	12.8	30
47	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	1.8	29
48	Associations between DNA methylation and schizophrenia-related intermediate phenotypes – A gene set enrichment analysis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2015, 59, 31-39.	4.8	29
49	PROBABILISTIC UNCERTAINTY ANALYSIS OF THE EUROPEAN UNION SYSTEM FOR THE EVALUATION OF SUBSTANCES MULTIMEDIA REGIONAL DISTRIBUTION MODEL. <i>Environmental Toxicology and Chemistry</i> , 2004, 23, 2494.	4.3	28
50	Transcriptional signatures of regulatory and toxic responses to benzo-[a]-pyrene exposure. <i>BMC Genomics</i> , 2011, 12, 502.	2.8	28
51	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1741-1751.	3.8	28
52	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. <i>Molecular Systems Biology</i> , 2020, 16, e9270.	7.2	27
53	The Integrated RNA Landscape of Renal Preconditioning against Ischemia-Reperfusion Injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2020, 31, 716-730.	6.1	26
54	Biological mechanisms of aging predict age-related disease occurrence in patients. <i>Aging Cell</i> , 2022, 21, e13524.	6.7	26

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55	Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. <i>Nature Communications</i> , 2021, 12, 3376.	12.8	25
56	Identification and characterization of protein subcomplexes in yeast. <i>Proteomics</i> , 2005, 5, 2082-2089.	2.2	22
57	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	6.2	22
58	DASS: efficient discovery and p-value calculation of substructures in unordered data. <i>Bioinformatics</i> , 2007, 23, 77-83.	4.1	21
59	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , 2013, 9, 1697.	2.9	21
60	Importance of rare gene copy number alterations for personalized tumor characterization and survival analysis. <i>Genome Biology</i> , 2016, 17, 204.	8.8	19
61	DIGE-Based Protein Expression Analysis of B[a]P-Exposed Hepatoma Cells Reveals a Complex Stress Response Including Alterations in Oxidative Stress, Cell Cycle Control, and Cytoskeleton Motility at Toxic and Subacute Concentrations. <i>Journal of Proteome Research</i> , 2011, 10, 379-393.	3.7	17
62	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	8.8	17
63	NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation. <i>Genes and Development</i> , 2022, 36, 348-367.	5.9	17
64	THE NEW CLASSIFICATION SCHEME OF THE GENETIC CODE, ITS EARLY EVOLUTION, AND tRNA USAGE. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 609-620.	0.8	16
65	Comparing representations of the environmental spatial scale of organic chemicals. <i>Environmental Toxicology and Chemistry</i> , 2001, 20, 922-927.	4.3	15
66	Systematic Detection of Epistatic Interactions Based on Allele Pair Frequencies. <i>PLoS Genetics</i> , 2012, 8, e1002463.	3.5	15
67	regNet: an R package for network-based propagation of gene expression alterations. <i>Bioinformatics</i> , 2018, 34, 308-311.	4.1	13
68	Dynamic simulation of protein complex formation on a genomic scale. <i>Bioinformatics</i> , 2005, 21, 1610-1616.	4.1	12
69	Reconstruction and Validation of RefRec: A Global Model for the Yeast Molecular Interaction Network. <i>PLoS ONE</i> , 2010, 5, e10662.	2.5	12
70	Proteomics-Based Monitoring of Pathway Activity Reveals that Blocking Diacylglycerol Biosynthesis Rescues from Alpha-Synuclein Toxicity. <i>Cell Systems</i> , 2019, 9, 309-320.e8.	6.2	12
71	Tissue-specific modulation of gene expression in response to lowered insulin signalling in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, .	6.0	12
72	Integrative Analysis of Low- and High-Resolution eQTL. <i>PLoS ONE</i> , 2010, 5, e13920.	2.5	12

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73	Common patterns in type II restriction enzyme binding sites. <i>Nucleic Acids Research</i> , 2005, 33, 2726-2733.	14.5	11
74	Teamwork: Improved eQTL Mapping Using Combinations of Machine Learning Methods. <i>PLoS ONE</i> , 2012, 7, e40916.	2.5	10
75	The impact of genomic variation on protein phosphorylation states and regulatory networks. <i>Molecular Systems Biology</i> , 2022, 18, e10712.	7.2	9
76	Stage-Specific Binding Profiles of Cohesin in Resting and Activated B Lymphocytes Suggest a Role for Cohesin in Immunoglobulin Class Switching and Maturation. <i>PLoS ONE</i> , 2014, 9, e111748.	2.5	8
77	Hepatic gene body hypermethylation is a shared epigenetic signature of murine longevity. <i>PLoS Genetics</i> , 2018, 14, e1007766.	3.5	8
78	Influence of Distributional Shape of Substance Parameters on Exposure Model Output. <i>Risk Analysis</i> , 2005, 25, 1137-1145.	2.7	7
79	SELECTING INTERNALLY CONSISTENT PHYSICOCHEMICAL PROPERTIES OF ORGANIC COMPOUNDS. <i>Environmental Toxicology and Chemistry</i> , 2002, 21, 941.	4.3	7
80	Optimizing network propagation for multi-omics data integration. <i>PLoS Computational Biology</i> , 2021, 17, e1009161.	3.2	7
81	Detection of <i>COPB2</i> as a <i>KRAS</i> synthetic lethal partner through integration of functional genomics screens. <i>Oncotarget</i> , 2017, 8, 34283-34297.	1.8	6
82	Topology of functional networks predicts physical binding of proteins. <i>Bioinformatics</i> , 2012, 28, 2137-2145.	4.1	5
83	Accounting for Redundancy when Integrating Gene Interaction Databases. <i>PLoS ONE</i> , 2009, 4, e7492.	2.5	5
84	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849.	3.2	5
85	Role of vegetation on the overall persistence and long-range transport potential. <i>Stochastic Environmental Research and Risk Assessment</i> , 2003, 17, 252-255.	4.0	3
86	Protein Subcomplexes-Molecular Machines With Highly Specialized Functions. <i>IEEE Transactions on Nanobioscience</i> , 2007, 6, 86-93.	3.3	3
87	Revealing Molecular Mechanisms by Integrating High-Dimensional Functional Screens with Protein Interaction Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003801.	3.2	3
88	Comparing representations of the environmental spatial scale of organic chemicals. <i>Environmental Toxicology and Chemistry</i> , 2001, 20, 922-7.	4.3	2
89	Network-Based Models in Molecular Biology. , 2009, , 35-56.		1
90	Computational approaches for the systematic analysis of aging-associated molecular alterations. <i>Drug Discovery Today: Disease Models</i> , 2018, 27, 51-59.	1.2	1

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91	Abstract 5565: Multi-omic profiling of prostate cancer evolution in 39 patients. , 2017, , .		1
92	Uncovering Regulatory Pathways with Expression Quantitative Trait Loci. , 2007, , .		0