Andreas Beyer

List of Publications by Year
in descending order

92 papers	7,190 citations	117453 34 h-index	66788 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. Cell, 2016, 165, 535-550.	13.5	2,216
2	Assessing Long-Range Transport Potential of Persistent Organic Pollutants. Environmental Science & Technology, 2000, 34, 699-703.	4.6	322
3	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. Nature, 2013, 494, 266-270.	13.7	307
4	Post-transcriptional Expression Regulation in the Yeast Saccharomyces cerevisiae on a Genomic Scale. Molecular and Cellular Proteomics, 2004, 3, 1083-1092.	2.5	217
5	STITCH 2: an interaction network database for small molecules and proteins. Nucleic Acids Research, 2010, 38, D552-D556.	6.5	215
6	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. Cell, 2015, 163, 1539-1554.	13.5	200
7	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. Plant Cell, 2019, 31, 2430-2455.	3.1	198
8	Integrating physical and genetic maps: from genomes to interaction networks. Nature Reviews Genetics, 2007, 8, 699-710.	7.7	192
9	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. Genome Biology, 2017, 18, 56.	3.8	164
10	Posttranscriptional Expression Regulation: What Determines Translation Rates?. PLoS Computational Biology, 2007, 3, e57.	1.5	157
11	Selecting internally consistent physicochemical properties of organic compounds. Environmental Toxicology and Chemistry, 2002, 21, 941-953.	2.2	149
12	Comparing Estimates of Persistence and Long-Range Transport Potential among Multimedia Models. Environmental Science & Technology, 2005, 39, 1932-1942.	4.6	138
13	eQED: an efficient method for interpreting eQTL associations using protein networks. Molecular Systems Biology, 2008, 4, 162.	3.2	117
14	Detection and interpretation of expression quantitative trait loci (eQTL). Methods, 2009, 48, 265-276.	1.9	115
15	Constitutive upregulation of the transforming growth factor-Î² pathway in rheumatoid arthritis synovial fibroblasts. Arthritis Research and Therapy, 2007, 9, R59.	1.6	114
16	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. Nature Communications, 2017, 8, 1212.	5.8	112
17	Temperature Dependence of the Characteristic Travel Distance. Environmental Science & Technology, 2003, 37, 766-771.	4.6	91
18	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	9.4	88

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19	Landscape of nuclear transport receptor cargoÂspecificity. Molecular Systems Biology, 2017, 13, 962.	3.2	88
20	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2006, 2, e70.	1.5	82
21	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. Cell, 2021, 184, 545-559.e22.	13.5	82
22	A nutritional memory effect counteracts the benefits of dietary restriction in old mice. Nature Metabolism, 2019, 1, 1059-1073.	5.1	80
23	A random forest approach to capture genetic effects in the presence of population structure. Nature Communications, 2015, 6, 7432.	5.8	79
24	Protein networks markedly improve prediction of subcellular localization in multiple eukaryotic species. Nucleic Acids Research, 2008, 36, e136-e136.	6.5	69
25	Natural genetic variation impacts expression levels of coding, nonâ€coding, and antisense transcripts in fission yeast. Molecular Systems Biology, 2014, 10, 764.	3.2	65
26	Data-driven assessment of eQTL mapping methods. BMC Genomics, 2010, 11, 502.	1.2	55
27	Assessing Computational Methods for Transcription Factor Target Gene Identification Based on ChIP-seq Data. PLoS Computational Biology, 2013, 9, e1003342.	1.5	55
28	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. Kidney International, 2019, 95, 333-349.	2.6	55
29	Global analysis reveals SRp20- and SRp75-specific mRNPs in cycling and neural cells. Nature Structural and Molecular Biology, 2010, 17, 962-970.	3.6	53
30	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. Life Science Alliance, 2018, 1, e201800042.	1.3	51
31	The Footprint of Polygenic Adaptation on Stress-Responsive *Cis*-Regulatory Divergence in the *Arabidopsis Genus*. Molecular Biology and Evolution, 2016, 33, 2088-2101.	3.5	50
32	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. Kidney International, 2018, 93, 1308-1319.	2.6	49
33	Large-scale De Novo Prediction of Physical Protein-Protein Association. Molecular and Cellular Proteomics, 2011, 10, M111.010629.	2.5	44
34	A proteomic atlas of insulin signalling reveals tissueâ€specific mechanisms of longevity assurance. Molecular Systems Biology, 2017, 13, 939.	3.2	42
35	Long-Range transport potential of semivolatile organic chemicals in coupled air-water systems. Environmental Science and Pollution Research, 2001, 8, 173-179.	2.7	40
36	Predicting functionality of proteinâ€"DNA interactions by integrating diverse evidence. Bioinformatics, 2009, 25, i137-i144.	1.8	38

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37	Meiotic Cohesin SMC1Î² Provides Prophase I Centromeric Cohesion and Is Required for Multiple Synapsis-Associated Functions. PLoS Genetics, 2013, 9, e1003985.	1.5	36
38	Impact of Natural Genetic Variation on Gene Expression Dynamics. PLoS Genetics, 2013, 9, e1003514.	1.5	35
39	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	5.8	35
40	Pathway and Time-Resolved Benzo[*a*]pyrene Toxicity on Hepa1c1c7 Cells at Toxic and Subtoxic Exposure. Journal of Proteome Research, 2015, 14, 164-182.	1.8	34
41	Testing and Validation of Computational Methods for Mass Spectrometry. Journal of Proteome Research, 2016, 15, 809-814.	1.8	34
42	Assessing Persistence and Long-Range Transport Potential of Current-Use Pesticides. Environmental Science & Technology, 2009, 43, 9223-9229.	4.6	33
43	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. PLoS Computational Biology, 2014, 10, e1003657.	1.5	32
44	Cooperative genetic networks drive embryonic stem cell transition from naÃ¯ve to formative pluripotency. EMBO Journal, 2021, 40, e105776.	3.5	31
45	The proteomic landscape of small urinary extracellular vesicles during kidney transplantation. Journal of Extracellular Vesicles, 2020, 10, e12026.	5.5	30
46	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. Nature Communications, 2021, 12, 3804.	5.8	30
47	Predicting the Fission Yeast Protein Interaction Network. G3: Genes, Genomes, Genetics, 2012, 2, 453-467.	0.8	29
48	Associations between DNA methylation and schizophrenia-related intermediate phenotypes â€" A gene set enrichment analysis. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2015, 59, 31-39.	2.5	29
49	PROBABILISTIC UNCERTAINTY ANALYSIS OF THE EUROPEAN UNION SYSTEM FOR THE EVALUATION OF SUBSTANCES MULTIMEDIA REGIONAL DISTRIBUTION MODEL. Environmental Toxicology and Chemistry, 2004, 23, 2494.	2.2	28
50	Transcriptional signatures of regulatory and toxic responses to benzo-[a]-pyrene exposure. BMC Genomics, 2011, 12, 502.	1.2	28
51	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. Molecular and Cellular Proteomics, 2013, 12, 1741-1751.	2.5	28
52	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. Molecular Systems Biology, 2020, 16, e9270.	3.2	27
53	The Integrated RNA Landscape of Renal Preconditioning against Ischemia-Reperfusion Injury. Journal of the American Society of Nephrology: JASN, 2020, 31, 716-730.	3.0	26
54	Biological mechanisms of aging predict ageâ€related disease coâ€occurrence in patients. Aging Cell, 2022, 21, e13524.	3.0	26

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55	Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. Nature Communications, 2021, 12, 3376.	5.8	25
56	Identification and characterization of protein subcomplexes in yeast. Proteomics, 2005, 5, 2082-2089.	1.3	22
57	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. Cell Systems, 2021, 12, 401-418.e12.	2.9	22
58	DASS: efficient discovery and p-value calculation of substructures in unordered data. Bioinformatics, 2007, 23, 77-83.	1.8	21
59	Stress induces remodelling of yeast interaction and co-expression networks. Molecular BioSystems, 2013, 9, 1697.	2.9	21
60	Importance of rare gene copy number alterations for personalized tumor characterization and survival analysis. Genome Biology, 2016, 17, 204.	3.8	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. Journal of Proteome Research, 2011, 10, 379-393.	1.8	17
62	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	3.8	17
63	NMD is required for timely cell fate transitions by fine-tuning gene expression and regulating translation. Genes and Development, 2022, 36, 348-367.	2.7	17
64	THE NEW CLASSIFICATION SCHEME OF THE GENETIC CODE, ITS EARLY EVOLUTION, AND tRNA USAGE. Journal of Bioinformatics and Computational Biology, 2006, 04, 609-620.	0.3	16
65	Comparing representations of the environmental spatial scale of organic chemicals. Environmental Toxicology and Chemistry, 2001, 20, 922-927.	2.2	15
66	Systematic Detection of Epistatic Interactions Based on Allele Pair Frequencies. PLoS Genetics, 2012, 8, e1002463.	1.5	15
67	regNet: an R package for network-based propagation of gene expression alterations. Bioinformatics, 2018, 34, 308-311.	1.8	13
68	Dynamic simulation of protein complex formation on a genomic scale. Bioinformatics, 2005, 21, 1610-1616.	1.8	12
69	Reconstruction and Validation of RefRec: A Global Model for the Yeast Molecular Interaction Network. PLoS ONE, 2010, 5, e10662.	1.1	12
70	Proteomics-Based Monitoring of Pathway Activity Reveals that Blocking Diacylglycerol Biosynthesis Rescues from Alpha-Synuclein Toxicity. Cell Systems, 2019, 9, 309-320.e8.	2.9	12
71	Tissue-specific modulation of gene expression in response to lowered insulin signalling in Drosophila. ELife, 2021, 10, .	2.8	12
72	Integrative Analysis of Low- and High-Resolution eQTL. PLoS ONE, 2010, 5, e13920.	1.1	12

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73	Common patterns in type II restriction enzyme binding sites. Nucleic Acids Research, 2005, 33, 2726-2733.	6.5	11
74	Teamwork: Improved eQTL Mapping Using Combinations of Machine Learning Methods. PLoS ONE, 2012, 7, e40916.	1.1	10
75	The impact of genomic variation on protein phosphorylation states and regulatory networks. Molecular Systems Biology, 2022, 18, e10712.	3.2	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. PLoS ONE, 2014, 9, e111748.	1.1	8
77	Hepatic gene body hypermethylation is a shared epigenetic signature of murine longevity. PLoS Genetics, 2018, 14, e1007766.	1.5	8
78	Influence of Distributional Shape of Substance Parameters on Exposure Model Output. Risk Analysis, 2005, 25, 1137-1145.	1.5	7
79	Selecting internally consistent physicochemical properties of organic compounds. , 2002, 21, 941.		7
80	Optimizing network propagation for multi-omics data integration. PLoS Computational Biology, 2021, 17, e1009161.	1.5	7
81	Detection of *COPB2* as a *KRAS* synthetic lethal partner through integration of functional genomics screens. Oncotarget, 2017, 8, 34283-34297.	0.8	6
82	Topology of functional networks predicts physical binding of proteins. Bioinformatics, 2012, 28, 2137-2145.	1.8	5
83	Accounting for Redundancy when Integrating Gene Interaction Databases. PLoS ONE, 2009, 4, e7492.	1.1	5
84	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. PLoS Computational Biology, 2022, 18, e1009849.	1.5	5
85	Role of vegetation on the overall persistence and long-range transport potential. Stochastic Environmental Research and Risk Assessment, 2003, 17, 252-255.	1.9	3
86	Protein Subcomplexes-Molecular Machines With Highly Specialized Functions. IEEE Transactions on Nanobioscience, 2007, 6, 86-93.	2.2	3
87	Revealing Molecular Mechanisms by Integrating High-Dimensional Functional Screens with Protein Interaction Data. PLoS Computational Biology, 2014, 10, e1003801.	1.5	3
88	Comparing representations of the environmental spatial scale of organic chemicals. Environmental Toxicology and Chemistry, 2001, 20, 922-7.	2.2	2
89	Network-Based Models in Molecular Biology. , 2009, , 35-56.		1
90	Computational approaches for the systematic analysis of aging-associated molecular alterations. Drug Discovery Today: Disease Models, 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