

Andreas Beyer

List of Publications by Year in descending order

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Version: 2024-02-01

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	Regulatory network-based imputation of dropouts in single-cell RNA sequencing data. <i>PLoS Computational Biology</i> , 2022, 18, e1009849.	1.5	5
2	Biological mechanisms of aging predict age-related disease co-occurrence in patients. <i>Aging Cell</i> , 2022, 21, e13524.	3.0	26
3	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.	2.7	17
4	The impact of genomic variation on protein phosphorylation states and regulatory networks. <i>Molecular Systems Biology</i> , 2022, 18, e10712.	3.2	9
5	Dynamic 3D proteomes reveal protein functional alterations at high resolution in situ. <i>Cell</i> , 2021, 184, 545-559.e22.	13.5	82
6	Cooperative genetic networks drive embryonic stem cell transition from naïve to formative pluripotency. <i>EMBO Journal</i> , 2021, 40, e105776.	3.5	31
7	Tissue-specific modulation of gene expression in response to lowered insulin signalling in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, .	2.8	12
8	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. <i>Cell Systems</i> , 2021, 12, 401-418.e12.	2.9	22
9	Genomic imprinting in mouse blastocysts is predominantly associated with H3K27me3. <i>Nature Communications</i> , 2021, 12, 3804.	5.8	30
10	Cis-regulatory evolution spotlights species differences in the adaptive potential of gene expression plasticity. <i>Nature Communications</i> , 2021, 12, 3376.	5.8	25
11	Optimizing network propagation for multi-omics data integration. <i>PLoS Computational Biology</i> , 2021, 17, e1009161.	1.5	7
12	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	3.8	17
13	The proteomic landscape of small urinary extracellular vesicles during kidney transplantation. <i>Journal of Extracellular Vesicles</i> , 2020, 10, e12026.	5.5	30
14	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.	3.0	26
15	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. <i>Molecular Systems Biology</i> , 2020, 16, e9270.	3.2	27
16	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.	2.9	12
17	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	5.8	35
18	A Coevolved EDS1-SAG101-NRG1 Module Mediates Cell Death Signaling by TIR-Domain Immune Receptors. <i>Plant Cell</i> , 2019, 31, 2430-2455.	3.1	198

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19	A nutritional memory effect counteracts the benefits of dietary restriction in old mice. <i>Nature Metabolism</i> , 2019, 1, 1059-1073.	5.1	80
20	The proteome microenvironment determines the protective effect of preconditioning in cisplatin-induced acute kidney injury. <i>Kidney International</i> , 2019, 95, 333-349.	2.6	55
21	Single-nephron proteomes connect morphology and function in proteinuric kidney disease. <i>Kidney International</i> , 2018, 93, 1308-1319.	2.6	49
22	regNet: an R package for network-based propagation of gene expression alterations. <i>Bioinformatics</i> , 2018, 34, 308-311.	1.8	13
23	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
24	Hepatic gene body hypermethylation is a shared epigenetic signature of murine longevity. <i>PLoS Genetics</i> , 2018, 14, e1007766.	1.5	8
25	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018, 1, e201800042.	1.3	51
26	Dietary restriction protects from age-associated DNA methylation and induces epigenetic reprogramming of lipid metabolism. <i>Genome Biology</i> , 2017, 18, 56.	3.8	164
27	Systematic proteome and proteostasis profiling in human Trisomy 21 fibroblast cells. <i>Nature Communications</i> , 2017, 8, 1212.	5.8	112
28	A proteomic atlas of insulin signalling reveals tissue-specific mechanisms of longevity assurance. <i>Molecular Systems Biology</i> , 2017, 13, 939.	3.2	42
29	Landscape of nuclear transport receptor cargo-specificity. <i>Molecular Systems Biology</i> , 2017, 13, 962.	3.2	88
30	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.	0.8	6
31	Abstract 5565: Multi-omic profiling of prostate cancer evolution in 39 patients. , 2017, , .		1
32	On the Dependency of Cellular Protein Levels on mRNA Abundance. <i>Cell</i> , 2016, 165, 535-550.	13.5	2,216
33	Importance of rare gene copy number alterations for personalized tumor characterization and survival analysis. <i>Genome Biology</i> , 2016, 17, 204.	3.8	19
34	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.	3.5	50
35	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	1.8	34
36	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. <i>Cell</i> , 2015, 163, 1539-1554.	13.5	200

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37	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
38	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.	1.8	34
39	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.	2.5	29
40	A random forest approach to capture genetic effects in the presence of population structure. <i>Nature Communications</i> , 2015, 6, 7432.	5.8	79
41	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.	1.1	8
42	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. <i>PLoS Computational Biology</i> , 2014, 10, e1003657.	1.5	32
43	Revealing Molecular Mechanisms by Integrating High-Dimensional Functional Screens with Protein Interaction Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003801.	1.5	3
44	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	3.2	65
45	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , 2013, 9, 1697.	2.9	21
46	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	13.7	307
47	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1741-1751.	2.5	28
48	Assessing Computational Methods for Transcription Factor Target Gene Identification Based on CHIP-seq Data. <i>PLoS Computational Biology</i> , 2013, 9, e1003342.	1.5	55
49	Impact of Natural Genetic Variation on Gene Expression Dynamics. <i>PLoS Genetics</i> , 2013, 9, e1003514.	1.5	35
50	Meiotic Cohesin SMC1 ² Provides Prophase I Centromeric Cohesion and Is Required for Multiple Synapsis-Associated Functions. <i>PLoS Genetics</i> , 2013, 9, e1003985.	1.5	36
51	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	0.8	29
52	Systematic Detection of Epistatic Interactions Based on Allele Pair Frequencies. <i>PLoS Genetics</i> , 2012, 8, e1002463.	1.5	15
53	Teamwork: Improved eQTL Mapping Using Combinations of Machine Learning Methods. <i>PLoS ONE</i> , 2012, 7, e40916.	1.1	10
54	Topology of functional networks predicts physical binding of proteins. <i>Bioinformatics</i> , 2012, 28, 2137-2145.	1.8	5

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55	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.	1.8	17
56	Transcriptional signatures of regulatory and toxic responses to benzo-[a]-pyrene exposure. <i>BMC Genomics</i> , 2011, 12, 502.	1.2	28
57	Large-scale De Novo Prediction of Physical Protein-Protein Association. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010629.	2.5	44
58	Data-driven assessment of eQTL mapping methods. <i>BMC Genomics</i> , 2010, 11, 502.	1.2	55
59	Global analysis reveals SRp20- and SRp75-specific mRNPs in cycling and neural cells. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 962-970.	3.6	53
60	Reconstruction and Validation of RefRec: A Global Model for the Yeast Molecular Interaction Network. <i>PLoS ONE</i> , 2010, 5, e10662.	1.1	12
61	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556.	6.5	215
62	Integrative Analysis of Low- and High-Resolution eQTL. <i>PLoS ONE</i> , 2010, 5, e13920.	1.1	12
63	Predicting functionality of protein-DNA interactions by integrating diverse evidence. <i>Bioinformatics</i> , 2009, 25, i137-i144.	1.8	38
64	Detection and interpretation of expression quantitative trait loci (eQTL). <i>Methods</i> , 2009, 48, 265-276.	1.9	115
65	Network-Based Models in Molecular Biology. , 2009, , 35-56.		1
66	Assessing Persistence and Long-Range Transport Potential of Current-Use Pesticides. <i>Environmental Science & Technology</i> , 2009, 43, 9223-9229.	4.6	33
67	Accounting for Redundancy when Integrating Gene Interaction Databases. <i>PLoS ONE</i> , 2009, 4, e7492.	1.1	5
68	eQED: an efficient method for interpreting eQTL associations using protein networks. <i>Molecular Systems Biology</i> , 2008, 4, 162.	3.2	117
69	Protein networks markedly improve prediction of subcellular localization in multiple eukaryotic species. <i>Nucleic Acids Research</i> , 2008, 36, e136-e136.	6.5	69
70	Posttranscriptional Expression Regulation: What Determines Translation Rates?. <i>PLoS Computational Biology</i> , 2007, 3, e57.	1.5	157
71	DASS: efficient discovery and p-value calculation of substructures in unordered data. <i>Bioinformatics</i> , 2007, 23, 77-83.	1.8	21
72	Constitutive upregulation of the transforming growth factor- β pathway in rheumatoid arthritis synovial fibroblasts. <i>Arthritis Research and Therapy</i> , 2007, 9, R59.	1.6	114

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73	Uncovering Regulatory Pathways with Expression Quantitative Trait Loci. , 2007, , .		0
74	Protein Subcomplexes-Molecular Machines With Highly Specialized Functions. IEEE Transactions on Nanobioscience, 2007, 6, 86-93.	2.2	3
75	Integrating physical and genetic maps: from genomes to interaction networks. Nature Reviews Genetics, 2007, 8, 699-710.	7.7	192
76	Integrated Assessment and Prediction of Transcription Factor Binding. PLoS Computational Biology, 2006, 2, e70.	1.5	82
77	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
78	Influence of Distributional Shape of Substance Parameters on Exposure Model Output. Risk Analysis, 2005, 25, 1137-1145.	1.5	7
79	Identification and characterization of protein subcomplexes in yeast. Proteomics, 2005, 5, 2082-2089.	1.3	22
80	Dynamic simulation of protein complex formation on a genomic scale. Bioinformatics, 2005, 21, 1610-1616.	1.8	12
81	Common patterns in type II restriction enzyme binding sites. Nucleic Acids Research, 2005, 33, 2726-2733.	6.5	11
82	Comparing Estimates of Persistence and Long-Range Transport Potential among Multimedia Models. Environmental Science & Technology, 2005, 39, 1932-1942.	4.6	138
83	Post-transcriptional Expression Regulation in the Yeast <i>Saccharomyces cerevisiae</i> on a Genomic Scale. Molecular and Cellular Proteomics, 2004, 3, 1083-1092.	2.5	217
84	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
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	Temperature Dependence of the Characteristic Travel Distance. Environmental Science & Technology, 2003, 37, 766-771.	4.6	91
87	Selecting internally consistent physicochemical properties of organic compounds. Environmental Toxicology and Chemistry, 2002, 21, 941-953.	2.2	149
88	Selecting internally consistent physicochemical properties of organic compounds. , 2002, 21, 941.		7
89	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
90	Comparing representations of the environmental spatial scale of organic chemicals. Environmental Toxicology and Chemistry, 2001, 20, 922-927.	2.2	15

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91	Comparing representations of the environmental spatial scale of organic chemicals. <i>Environmental Toxicology and Chemistry</i> , 2001, 20, 922-7.	2.2	2
92	Assessing Long-Range Transport Potential of Persistent Organic Pollutants. <i>Environmental Science & Technology</i> , 2000, 34, 699-703.	4.6	322