Oliver Stegle

List of Publications by Year
in descending order

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139 papers	49,265 citations	11639 70 h-index	11601 135 g-index
209 all docs	209 docs citations	209 times ranked	71942 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
3	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
4	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
5	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547
6	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nature Biotechnology, 2015, 33, 155-160.	9.4	1,068
7	Deep learning for computational biology. Molecular Systems Biology, 2016, 12, 878.	3.2	1,059
8	Computational and analytical challenges in single-cell transcriptomics. Nature Reviews Genetics, 2015, 16, 133-145.	7.7	1,043
9	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. Nature Methods, 2014, 11, 817-820.	9.0	954
10	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	9.4	910
11	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
12	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
13	Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. Nature Protocols, 2012, 7, 500-507.	5.5	799
14	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
15	Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. Nature, 2011, 480, 245-249.	13.7	681
16	Multiâ€Omics Factor Analysisâ€”a framework for unsupervised integration of multiâ€omics data sets. Molecular Systems Biology, 2018, 14, e8124.	3.2	659
17	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
18	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	9.0	602

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19	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. Nature, 2011, 477, 419-423.	13.7	593
20	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
21	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
22	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Nature Communications, 2018, 9, 781.	5.8	513
23	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	13.7	491
24	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ELife, 2015, 4, e05255.	2.8	457
25	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	1.5	439
26	A Bayesian Framework to Account for Complex Non-Genetic Factors in Gene Expression Levels Greatly Increases Power in eQTL Studies. PLoS Computational Biology, 2010, 6, e1000770.	1.5	408
27	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
28	SpatialDE: identification of spatially variable genes. Nature Methods, 2018, 15, 343-346.	9.0	382
29	Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods, 2015, 85, 54-61.	1.9	381
30	Expression Atlas: gene and protein expression across multiple studies and organisms. Nucleic Acids Research, 2018, 46, D246-D251.	6.5	365
31	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. Genome Biology, 2017, 18, 67.	3.8	361
32	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
33	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
34	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. Genome Biology, 2020, 21, 111.	3.8	344
35	Single-cell epigenomics: Recording the past and predicting the future. Science, 2017, 358, 69-75.	6.0	343
36	Multi-tissue DNA methylation age predictor in mouse. Genome Biology, 2017, 18, 68.	3.8	341

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37	Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. Cell, 2017, 169, 807-823.e19.	13.5	339
38	Arabidopsis Defense against Botrytis cinerea: Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis Â Â. Plant Cell, 2012, 24, 3530-3557.	3.1	337
39	Cell2location maps fine-grained cell types in spatial transcriptomics. Nature Biotechnology, 2022, 40, 661-671.	9.4	335
40	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	9.4	313
41	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	13.7	307
42	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
43	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves T _H 1/T _{FH} fate bifurcation in malaria. Science Immunology, 2017, 2, .	5.6	258
44	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
45	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	5.8	235
46	DNA Methylation and Transcription Patterns in Intestinal Epithelial Cells From Pediatric Patients With Inflammatory BowelÂDiseases Differentiate Disease Subtypes and Associate With Outcome. Gastroenterology, 2018, 154, 585-598.	0.6	226
47	Computational principles and challenges in single-cell data integration. Nature Biotechnology, 2021, 39, 1202-1215.	9.4	223
48	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. Genome Biology, 2020, 21, 36.	3.8	216
49	Gaussian Process Robust Regression for Noisy Heart Rate Data. IEEE Transactions on Biomedical Engineering, 2008, 55, 2143-2151.	2.5	177
50	Vireo: Bayesian demultiplexing of pooled single-cell RNA-seq data without genotype reference. Genome Biology, 2019, 20, 273.	3.8	152
51	Century-scale Methylome Stability in a Recently Diverged Arabidopsis thaliana Lineage. PLoS Genetics, 2015, 11, e1004920.	1.5	148
52	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. Nature Genetics, 2021, 53, 304-312.	9.4	146
53	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	13.5	144
54	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	4.1	134

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55	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. Cell Reports, 2019, 29, 202-211.e6.	2.9	133
56	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
57	f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. Genome Biology, 2017, 18, 212.	3.8	119
58	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. Nature Biotechnology, 2019, 37, 592-600.	9.4	118
59	Estimation of Free-Living Energy Expenditure by Heart Rate and Movement Sensing: A Doubly-Labelled Water Study. PLoS ONE, 2015, 10, e0137206.	1.1	116
60	DNA methylation defines regional identity of human intestinal epithelial organoids and undergoes dynamic changes during development. Gut, 2019, 68, 49-61.	6.1	116
61	A linear mixed-model approach to study multivariate geneâ€“environment interactions. Nature Genetics, 2019, 51, 180-186.	9.4	112
62	Genetic Variation in the Social Environment Contributes to Health and Disease. PLoS Genetics, 2017, 13, e1006498.	1.5	110
63	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
64	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	1.8	99
65	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. Plant Cell, 2017, 29, 5-19.	3.1	98
66	Efficient set tests for the genetic analysis of correlated traits. Nature Methods, 2015, 12, 755-758.	9.0	97
67	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	3.8	97
68	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	9.4	96
69	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	2.9	95
70	Joint Modelling of Confounding Factors and Prominent Genetic Regulators Provides Increased Accuracy in Genetical Genomics Studies. PLoS Computational Biology, 2012, 8, e1002330.	1.5	94
71	Limited Contribution of DNA Methylation Variation to Expression Regulation in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006141.	1.5	94
72	Effects of the COVID-19 pandemic on life scientists. Genome Biology, 2020, 21, 113.	3.8	90

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73	Predicting and understanding the stability of G-quadruplexes. Bioinformatics, 2009, 25, i374-i1382.	1.8	89
74	A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series. Journal of Computational Biology, 2010, 17, 355-367.	0.8	84
75	A random forest approach to capture genetic effects in the presence of population structure. Nature Communications, 2015, 6, 7432.	5.8	79
76	Extensivecis-Regulatory Variation Robust to Environmental Perturbation inArabidopsis. Plant Cell, 2014, 26, 4298-4310.	3.1	77
77	Joint Genetic Analysis of Gene Expression Data with Inferred Cellular Phenotypes. PLoS Genetics, 2011, 7, e1001276.	1.5	76
78	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	9.4	74
79	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	1.5	72
80	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	2.9	70
81	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	0.7	67
82	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. Nature Communications, 2020, 11, 2927.	5.8	67
83	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. Genome Biology, 2019, 20, 146.	3.8	66
84	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO. Nature Methods, 2022, 19, 179-186.	9.0	63
85	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. Genome Biology, 2019, 20, 30.	3.8	61
86	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511.	5.8	60
87	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. Cell Systems, 2020, 11, 25-41.e9.	2.9	59
88	Genetic variants regulating expression levels and isoform diversity during embryogenesis. Nature, 2017, 541, 402-406.	13.7	56
89	Subclone-specific microenvironmental impact and drug response in refractory multiple myeloma revealed by singleâ€cell transcriptomics. Nature Communications, 2021, 12, 6960.	5.8	53
90	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	5.8	52

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91	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
92	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. Nature Methods, 2020, 17, 414-421.	9.0	48
93	A Toolbox for Predicting G-Quadruplex Formation and Stability. Journal of Nucleic Acids, 2010, 2010, 1-6.	0.8	47
94	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	5.8	47
95	MUON: multimodal omics analysis framework. Genome Biology, 2022, 23, 42.	3.8	47
96	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. Nature Genetics, 2021, 53, 313-321.	9.4	42
97	A Palaeolithicâ€type diet causes strong tissueâ€specific effects on ectopic fat deposition in obese postmenopausal women. Journal of Internal Medicine, 2013, 274, 67-76.	2.7	41
98	A high-content platform to characterise human induced pluripotent stem cell lines. Methods, 2016, 96, 85-96.	1.9	41
99	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	15.2	40
100	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	2.8	40
101	Accurate detection of differential RNA processing. Nucleic Acids Research, 2013, 41, 5189-5198.	6.5	39
102	The germline genetic component of drug sensitivity in cancer cell lines. Nature Communications, 2018, 9, 3385.	5.8	38
103	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. Cell Stem Cell, 2020, 27, 470-481.e6.	5.2	38
104	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. Cell Reports, 2019, 26, 2078-2087.e3.	2.9	36
105	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. Genome Biology, 2019, 20, 27.	3.8	35
106	Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. ELife, 2019, 8, .	2.8	34
107	IceR improves proteome coverage and data completeness in global and single-cell proteomics. Nature Communications, 2021, 12, 4787.	5.8	29
108	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. Nature Communications, 2022, 13, 1779.	5.8	25

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109	Modelling local gene networks increases power to detect trans-acting genetic effects on gene expression. Genome Biology, 2016, 17, 33.	3.8	24
110	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. Cell Reports, 2021, 35, 109032.	2.9	23
111	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	9.4	23
112	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. Nature Communications, 2020, 11, 2928.	5.8	22
113	Genomic Rearrangements inArabidopsisConsidered as Quantitative Traits. Genetics, 2017, 205, 1425-1441.	1.2	21
114	GeneCodeq: quality score compression and improved genotyping using a Bayesian framework. Bioinformatics, 2016, 32, 3124-3132.	1.8	20
115	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18
116	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. Molecular and Cellular Proteomics, 2019, 18, S114-S125.	2.5	16
117	Joint genetic analysis using variant sets reveals polygenic gene-context interactions. PLoS Genetics, 2017, 13, e1006693.	1.5	15
118	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. Nature Precedings, 2010, , .	0.1	13
119	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
120	Detecting regulatory geneâ€“environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	1.8	12
121	Personalized medicine: from genotypes, molecular phenotypes and the quantified self, towards improved medicine. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 342-6.	0.7	12
122	scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation. Genome Biology, 2022, 23, 8.	3.8	11
123	Generalized correlation measure using count statistics for gene expression data with ordered samples. Bioinformatics, 2018, 34, 617-624.	1.8	9
124	Inference algorithms and learning theory for Bayesian sparse factor analysis. Journal of Physics: Conference Series, 2009, 197, 012002.	0.3	5
125	Dissecting indirect genetic effects from peers in laboratory mice. Genome Biology, 2021, 22, 216.	3.8	5
126	Integrative genome-wide analysis of the determinants of RNA splicing in kidney renal clear cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 44-55.	0.7	5

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127	ShapePheno: unsupervised extraction of shape phenotypes from biological image collections. Bioinformatics, 2012, 28, 1001-1008.	1.8	4
128	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3
129	Simultaneous cellular and molecular phenotyping of embryonic mutants using single-cell regulatory trajectories. Developmental Cell, 2022, 57, 496-511.e8.	3.1	3
130	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
131	Efficient branch-and-bound techniques for two-locus association mapping. BMC Bioinformatics, 2011, 12, .	1.2	1
132	Warped Matrix Factorisation for Multi-view Data Integration. Lecture Notes in Computer Science, 2016, , 789-804.	1.0	1
133	A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series. Lecture Notes in Computer Science, 2009, , 201-216.	1.0	1
134	Accurate modeling of confounding variation in eQTL studies leads to a great increase in power to detect trans-regulatory effects. Nature Precedings, 2011, , .	0.1	0
135	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. , 2011, , .		0
136	THE FUTURE OF GENOME-BASED MEDICINE. , 2012, , .		0
137	Reply. Gastroenterology, 2018, 155, 230-231.	0.6	0
138	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, 18, 171-174.	0.7	0
139	OAB-007: Single-cell multiomic analysis identifies regulatory programs in relapsed/refractory multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S5.	0.2	0