Oliver Stegle

List of Publications by Year
in descending order

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139 papers	49,265 citations	11651 70 h-index	11607 135 g-index
209 all docs	209 docs citations	209 times ranked	71942 citing authors

#	Article	IF	Citations
1	scDALI: modeling allelic heterogeneity in single cells reveals context-specific genetic regulation. Genome Biology, 2022, 23, 8.	8.8	11
2	Cell2location maps fine-grained cell types in spatial transcriptomics. Nature Biotechnology, 2022, 40, 661-671.	17.5	335
3	Identifying temporal and spatial patterns of variation from multimodal data using MEFISTO. Nature Methods, 2022, 19, 179-186.	19.0	63
4	MUON: multimodal omics analysis framework. Genome Biology, 2022, 23, 42.	8.8	47
5	Simultaneous cellular and molecular phenotyping of embryonic mutants using single-cell regulatory trajectories. Developmental Cell, 2022, 57, 496-511.e8.	7.0	3
6	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	21.4	23
7	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses. Nature Communications, 2022, 13, 1779.	12.8	25
8	Identification of rare and common regulatory variants in pluripotent cells using population-scale transcriptomics. Nature Genetics, 2021, 53, 313-321.	21.4	42
9	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. Nature Genetics, 2021, 53, 304-312.	21.4	146
10	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
11	Erosion of human X chromosome inactivation causes major remodeling of the iPSC proteome. Cell Reports, 2021, 35, 109032.	6.4	23
12	Computational principles and challenges in single-cell data integration. Nature Biotechnology, 2021, 39, 1202-1215.	17.5	223
13	Cell segmentation-free inference of cell types from in situ transcriptomics data. Nature Communications, 2021, 12, 3545.	12.8	52
14	Dissecting indirect genetic effects from peers in laboratory mice. Genome Biology, 2021, 22, 216.	8.8	5
15	IceR improves proteome coverage and data completeness in global and single-cell proteomics. Nature Communications, 2021, 12, 4787.	12.8	29
16	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	30.7	40
17	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.	21.4	590
18	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96

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19	Subclone-specific microenvironmental impact and drug response in refractory multiple myeloma revealed by singleâ€cell transcriptomics. Nature Communications, 2021, 12, 6960.	12.8	53
20	OAB-007: Single-cell multiomic analysis identifies regulatory programs in relapsed/refractory multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S5.	0.4	0
21	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
22	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	27.8	108
23	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. Cell Stem Cell, 2020, 27, 470-481.e6.	11.1	38
24	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. Genome Biology, 2020, 21, 111.	8.8	344
25	Effects of the COVID-19 pandemic on life scientists. Genome Biology, 2020, 21, 113.	8.8	90
26	Discovery and quality analysis of a comprehensive set of structural variants and short tandem repeats. Nature Communications, 2020, 11, 2928.	12.8	22
27	Properties of structural variants and short tandem repeats associated with gene expression and complex traits. Nature Communications, 2020, 11, 2927.	12.8	67
28	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. Nature Methods, 2020, 17, 414-421.	19.0	48
29	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
30	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. Cell Systems, 2020, 11, 25-41.e9.	6.2	59
31	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
32	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	12.8	235
33	Robustness and applicability of transcription factor and pathway analysis tools on single-cell RNA-seq data. Genome Biology, 2020, 21, 36.	8.8	216
34	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
35	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280
36	Population-scale proteome variation in human induced pluripotent stem cells. ELife, 2020, 9, .	6.0	40

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37	Screening for genes that accelerate the epigenetic aging clock in humans reveals a role for the H3K36 methyltransferase NSD1. Genome Biology, 2019, 20, 146.	8.8	66
38	A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 2019, 178, 1465-1477.e17.	28.9	144
39	Modeling Cell-Cell Interactions from Spatial Molecular Data with Spatial Variance Component Analysis. Cell Reports, 2019, 29, 202-211.e6.	6.4	133
40	Multi-omics Characterization of Interaction-mediated Control of Human Protein Abundance levels. Molecular and Cellular Proteomics, 2019, 18, S114-S125.	3.8	16
41	The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. Nature Biotechnology, 2019, 37, 592-600.	17.5	118
42	Structural rearrangements generate cell-specific, gene-independent CRISPR-Cas9 loss of fitness effects. Genome Biology, 2019, 20, 27.	8.8	35
43	Combined single-cell profiling of expression and DNA methylation reveals splicing regulation and heterogeneity. Genome Biology, 2019, 20, 30.	8.8	61
44	Identifying Extrinsic versus Intrinsic Drivers of Variation in Cell Behavior in Human iPSC Lines from Healthy Donors. Cell Reports, 2019, 26, 2078-2087.e3.	6.4	36
45	Vireo: Bayesian demultiplexing of pooled single-cell RNA-seq data without genotype reference. Genome Biology, 2019, 20, 273.	8.8	152
46	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	27.8	307
47	A linear mixed-model approach to study multivariate geneâ€“environment interactions. Nature Genetics, 2019, 51, 180-186.	21.4	112
48	DNA methylation defines regional identity of human intestinal epithelial organoids and undergoes dynamic changes during development. Gut, 2019, 68, 49-61.	12.1	116
49	Systematic genetic analysis of the MHC region reveals mechanistic underpinnings of HLA type associations with disease. ELife, 2019, 8, .	6.0	34
50	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Nature Communications, 2018, 9, 781.	12.8	513
51	Generalized correlation measure using count statistics for gene expression data with ordered samples. Bioinformatics, 2018, 34, 617-624.	4.1	9
52	Expression Atlas: gene and protein expression across multiple studies and organisms. Nucleic Acids Research, 2018, 46, D246-D251.	14.5	365
53	SpatialDE: identification of spatially variable genes. Nature Methods, 2018, 15, 343-346.	19.0	382
54	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.	1.3	226

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55	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	2.5	18
56	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
57	Genome-Scale Oscillations in DNA Methylation during Exit from Pluripotency. Cell Systems, 2018, 7, 63-76.e12.	6.2	70
58	Reply. Gastroenterology, 2018, 155, 230-231.	1.3	0
59	The germline genetic component of drug sensitivity in cancer cell lines. Nature Communications, 2018, 9, 3385.	12.8	38
60	Multiâ€Omics Factor Analysisâ€”a framework for unsupervised integration of multiâ€omics data sets. Molecular Systems Biology, 2018, 14, e8124.	7.2	659
61	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
62	Genomic Rearrangements inArabidopsisConsidered as Quantitative Traits. Genetics, 2017, 205, 1425-1441.	2.9	21
63	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, .	11.9	258
64	Promoter shape varies across populations and affects promoter evolution and expression noise. Nature Genetics, 2017, 49, 550-558.	21.4	74
65	DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning. Genome Biology, 2017, 18, 67.	8.8	361
66	Multi-tissue DNA methylation age predictor in mouse. Genome Biology, 2017, 18, 68.	8.8	341
67	Common genetic variation drives molecular heterogeneity in human iPSCs. Nature, 2017, 546, 370-375.	27.8	491
68	Vitamin A-Retinoic Acid Signaling Regulates Hematopoietic Stem Cell Dormancy. Cell, 2017, 169, 807-823.e19.	28.9	339
69	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
70	Genetic variants regulating expression levels and isoform diversity during embryogenesis. Nature, 2017, 541, 402-406.	27.8	56
71	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	14.5	355
72	easyGWAS: A Cloud-Based Platform for Comparing the Results of Genome-Wide Association Studies. Plant Cell, 2017, 29, 5-19.	6.6	98

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73	Single-cell epigenomics: Recording the past and predicting the future. Science, 2017, 358, 69-75.	12.6	343
74	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	6.4	95
75	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511.	12.8	60
76	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	12.8	50
77	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
78	Genetic Variation in the Social Environment Contributes to Health and Disease. PLoS Genetics, 2017, 13, e1006498.	3.5	110
79	f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. Genome Biology, 2017, 18, 212.	8.8	119
80	Joint genetic analysis using variant sets reveals polygenic gene-context interactions. PLoS Genetics, 2017, 13, e1006693.	3.5	15
81	Warped Matrix Factorisation for Multi-view Data Integration. Lecture Notes in Computer Science, 2016, , 789-804.	1.3	1
82	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	28.9	863
83	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
84	Deep learning for computational biology. Molecular Systems Biology, 2016, 12, 878.	7.2	1,059
85	Modelling local gene networks increases power to detect trans-acting genetic effects on gene expression. Genome Biology, 2016, 17, 33.	8.8	24
86	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	19.0	602
87	A high-content platform to characterise human induced pluripotent stem cell lines. Methods, 2016, 96, 85-96.	3.8	41
88	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
89	GeneCodeq: quality score compression and improved genotyping using a Bayesian framework. Bioinformatics, 2016, 32, 3124-3132.	4.1	20
90	Limited Contribution of DNA Methylation Variation to Expression Regulation in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006141.	3.5	94

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91	Estimation of Free-Living Energy Expenditure by Heart Rate and Movement Sensing: A Doubly-Labelled Water Study. PLoS ONE, 2015, 10, e0137206.	2.5	116
92	Computational and analytical challenges in single-cell transcriptomics. Nature Reviews Genetics, 2015, 16, 133-145.	16.3	1,043
93	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nature Biotechnology, 2015, 33, 155-160.	17.5	1,068
94	Efficient set tests for the genetic analysis of correlated traits. Nature Methods, 2015, 12, 755-758.	19.0	97
95	Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods, 2015, 85, 54-61.	3.8	381
96	Century-scale Methylome Stability in a Recently Diverged Arabidopsis thaliana Lineage. PLoS Genetics, 2015, 11, e1004920.	3.5	148
97	A random forest approach to capture genetic effects in the presence of population structure. Nature Communications, 2015, 6, 7432.	12.8	79
98	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
99	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
100	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
101	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.	1.3	67
102	DNA methylation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ELife, 2015, 4, e05255.	6.0	457
103	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
104	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
105	INTEGRATIVE GENOME-WIDE ANALYSIS OF THE DETERMINANTS OF RNA SPLICING IN KIDNEY RENAL CLEAR CELL CARCINOMA. , 2014, , .		3
106	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	12.8	47
107	PERSONALIZED MEDICINE: FROM GENOTYPES, MOLECULAR PHENOTYPES AND THE QUANTIFIED SELF, TOWARDS IMPROVED MEDICINE. , 2014, , .		13
108	Extensivecis-Regulatory Variation Robust to Environmental Perturbation inArabidopsis. Plant Cell, 2014, 26, 4298-4310.	6.6	77

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109	Single-cell genome-wide bisulfite sequencing for assessing epigenetic heterogeneity. Nature Methods, 2014, 11, 817-820.	19.0	954
110	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
111	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
112	A Lasso multi-marker mixed model for association mapping with population structure correction. Bioinformatics, 2013, 29, 206-214.	4.1	99
113	Genotype-Environment Interactions Reveal Causal Pathways That Mediate Genetic Effects on Phenotype. PLoS Genetics, 2013, 9, e1003803.	3.5	72
114	Accurate detection of differential RNA processing. Nucleic Acids Research, 2013, 41, 5189-5198.	14.5	39
115	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.	6.0	41
116	Detecting regulatory geneâ€“environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	4.1	12
117	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS THERAPY- SESSION INTRODUCTION. , 2013, 19, 224-8.		2
118	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
119	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	3.5	439
120	ShapePheno: unsupervised extraction of shape phenotypes from biological image collections. Bioinformatics, 2012, 28, 1001-1008.	4.1	4
121	THE FUTURE OF GENOME-BASED MEDICINE. , 2012, , .		0
122	Using probabilistic estimation of expression residuals (PEER) to obtain increased power and interpretability of gene expression analyses. Nature Protocols, 2012, 7, 500-507.	12.0	799
123	Arabidopsis Defense against Botrytis cinerea: Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis Â Â. Plant Cell, 2012, 24, 3530-3557.	6.6	337
124	Joint Modelling of Confounding Factors and Prominent Genetic Regulators Provides Increased Accuracy in Genetical Genomics Studies. PLoS Computational Biology, 2012, 8, e1002330.	3.2	94
125	Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. Nature, 2011, 480, 245-249.	27.8	681
126	Whole-genome sequencing of multiple Arabidopsis thaliana populations. Nature Genetics, 2011, 43, 956-963.	21.4	910

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127	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
128	PERSONALIZED MEDICINE: FROM GENOTYPES AND MOLECULAR PHENOTYPES TOWARDS COMPUTED THERAPY. , 2011, , .		0
129	Efficient branch-and-bound techniques for two-locus association mapping. BMC Bioinformatics, 2011, 12, .	2.6	1
130	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. Nature, 2011, 477, 419-423.	27.8	593
131	Joint Genetic Analysis of Gene Expression Data with Inferred Cellular Phenotypes. PLoS Genetics, 2011, 7, e1001276.	3.5	76
132	Statistical Tests for Detecting Differential RNA-Transcript Expression from Read Counts. Nature Precedings, 2010, , .	0.1	13
133	A Toolbox for Predicting G-Quadruplex Formation and Stability. Journal of Nucleic Acids, 2010, 2010, 1-6.	1.2	47
134	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.	1.6	84
135	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.	3.2	408
136	Predicting and understanding the stability of G-quadruplexes. Bioinformatics, 2009, 25, i374-i1382.	4.1	89
137	Inference algorithms and learning theory for Bayesian sparse factor analysis. Journal of Physics: Conference Series, 2009, 197, 012002.	0.4	5
138	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.	1.3	1
139	Gaussian Process Robust Regression for Noisy Heart Rate Data. IEEE Transactions on Biomedical Engineering, 2008, 55, 2143-2151.	4.2	177