

Bart Deplancke

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

12,824
citations

36203

51
h-index

30848

102
g-index

154
all docs

154
docs citations

154
times ranked

22140
citing authors

#	ARTICLE	IF	CITATIONS
1	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
2	Microbial modulation of innate defense: goblet cells and the intestinal mucus layer. <i>American Journal of Clinical Nutrition</i> , 2001, 73, 1131S-1141S.	2.2	786
3	Exhaustion of tumor-specific CD8+ T cells in metastases from melanoma patients. <i>Journal of Clinical Investigation</i> , 2011, 121, 2350-2360.	3.9	707
4	Natural variation in genome architecture among 205 <i>Drosophila melanogaster</i> Genetic Reference Panel lines. <i>Genome Research</i> , 2014, 24, 1193-1208.	2.4	565
5	Morphological and Molecular Characterization of Adult Midgut Compartmentalization in <i>Drosophila</i> . <i>Cell Reports</i> , 2013, 3, 1725-1738.	2.9	421
6	Tetracyclines Disturb Mitochondrial Function across Eukaryotic Models: A Call for Caution in Biomedical Research. <i>Cell Reports</i> , 2015, 10, 1681-1691.	2.9	385
7	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. <i>Science</i> , 2013, 342, 744-747.	6.0	364
8	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches. <i>Cell</i> , 2022, 185, 379-396.e38.	13.5	343
9	The Genetics of Transcription Factor DNA Binding Variation. <i>Cell</i> , 2016, 166, 538-554.	13.5	331
10	A stromal cell population that inhibits adipogenesis in mammalian fat depots. <i>Nature</i> , 2018, 559, 103-108.	13.7	327
11	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , 2015, 4, .	2.8	316
12	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. <i>Science</i> , 2022, 375, eabk2432.	6.0	295
13	Chromatin immunoprecipitation (ChIP) coupled to detection by quantitative real-time PCR to study transcription factor binding to DNA in <i>Caenorhabditis elegans</i> . <i>Nature Protocols</i> , 2008, 3, 698-709.	5.5	237
14	A Gene-Centered <i>C. elegans</i> Protein-DNA Interaction Network. <i>Cell</i> , 2006, 125, 1193-1205.	13.5	224
15	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. <i>Cell</i> , 2015, 162, 1039-1050.	13.5	210
16	A Gateway-Compatible Yeast One-Hybrid System. <i>Genome Research</i> , 2004, 14, 2093-2101.	2.4	189
17	Hydrogen sulfide induces serum-independent cell cycle entry in nontransformed rat intestinal epithelial cells. <i>FASEB Journal</i> , 2003, 17, 1310-1312.	0.2	184
18	Genome-Wide RNA Polymerase II Profiles and RNA Accumulation Reveal Kinetics of Transcription and Associated Epigenetic Changes During Diurnal Cycles. <i>PLoS Biology</i> , 2012, 10, e1001442.	2.6	178

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19	Fermentation by Gut Microbiota Cultured in a Simulator of the Human Intestinal Microbial Ecosystem Is Improved by Supplementing a Soygerm Powder. <i>Journal of Nutrition</i> , 2000, 130, 2599-2606.	1.3	177
20	A compendium of <i>Caenorhabditis elegans</i> regulatory transcription factors: a resource for mapping transcription regulatory networks. <i>Genome Biology</i> , 2005, 6, R110.	13.9	175
21	A First Version of the <i>Caenorhabditis elegans</i> Promoterome. <i>Genome Research</i> , 2004, 14, 2169-2175.	2.4	155
22	Systematic dissection of genomic features determining transcription factor binding and enhancer function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1291-E1300.	3.3	150
23	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. <i>Genome Research</i> , 2014, 24, 1157-1168.	2.4	143
24	The NAD-Booster Nicotinamide Riboside Potently Stimulates Hematopoiesis through Increased Mitochondrial Clearance. <i>Cell Stem Cell</i> , 2019, 24, 405-418.e7.	5.2	143
25	Molecular Ecological Analysis of the Succession and Diversity of Sulfate-Reducing Bacteria in the Mouse Gastrointestinal Tract. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2166-2174.	1.4	140
26	Selective growth of mucolytic bacteria including <i>Clostridium perfringens</i> in a neonatal piglet model of total parenteral nutrition,,. <i>American Journal of Clinical Nutrition</i> , 2002, 76, 1117-1125.	2.2	133
27	BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. <i>Genome Biology</i> , 2019, 20, 71.	3.8	125
28	<i>C. elegans</i> 14-3-3 proteins regulate life span and interact with SIR-2.1 and DAF-16/FOXO. <i>Mechanisms of Ageing and Development</i> , 2006, 127, 741-747.	2.2	117
29	Reversible De-differentiation of Mature White Adipocytes into Preadipocyte-like Precursors during Lactation. <i>Cell Metabolism</i> , 2018, 28, 282-288.e3.	7.2	116
30	GLUT3 is induced during epithelial-mesenchymal transition and promotes tumor cell proliferation in non-small cell lung cancer. <i>Cancer & Metabolism</i> , 2014, 2, 11.	2.4	115
31	Roles of <i>Vibrio fischeri</i> and Nonsymbiotic Bacteria in the Dynamics of Mucus Secretion during Symbiont Colonization of the <i>Euprymna scolopes</i> Light Organ. <i>Applied and Environmental Microbiology</i> , 2002, 68, 5113-5122.	1.4	112
32	ASAP: a web-based platform for the analysis and interactive visualization of single-cell RNA-seq data. <i>Bioinformatics</i> , 2017, 33, 3123-3125.	1.8	112
33	<i>C. elegans</i> tubby regulates life span and fat storage by two independent mechanisms. <i>Cell Metabolism</i> , 2005, 2, 35-42.	7.2	110
34	Topology and Dynamics of the Zebrafish Segmentation Clock Core Circuit. <i>PLoS Biology</i> , 2012, 10, e1001364.	2.6	108
35	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108
36	Genomic Analysis of European <i>Drosophila melanogaster</i> Populations Reveals Longitudinal Structure, Continent-Wide Selection, and Previously Unknown DNA Viruses. <i>Molecular Biology and Evolution</i> , 2020, 37, 2661-2678.	3.5	104

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37	Genomic Variation and Its Impact on Gene Expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2012, 8, e1003055.	1.5	102
38	Identification of the transcription factor ZEB1 as a central component of the adipogenic gene regulatory network. <i>ELife</i> , 2014, 3, e03346.	2.8	101
39	Effects of Tylosin on Bacterial Mucolysis, <i>Clostridium perfringens</i> Colonization, and Intestinal Barrier Function in a Chick Model of Necrotic Enteritis. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 3311-3317.	1.4	97
40	Integrative Genomics Identifies the Corepressor SMRT as a Gatekeeper of Adipogenesis through the Transcription Factors C/EBP β and KAISO. <i>Molecular Cell</i> , 2012, 46, 335-350.	4.5	96
41	SMiLE-seq identifies binding motifs of single and dimeric transcription factors. <i>Nature Methods</i> , 2017, 14, 316-322.	9.0	90
42	Complex expression dynamics and robustness in <i>C. elegans</i> insulin networks. <i>Genome Research</i> , 2013, 23, 954-965.	2.4	87
43	Absolute quantification of transcription factors during cellular differentiation using multiplexed targeted proteomics. <i>Nature Methods</i> , 2013, 10, 570-576.	9.0	82
44	Disparate temperature-dependent virus-host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. <i>PLoS Biology</i> , 2021, 19, e3001158.	2.6	79
45	Automated protein-DNA interaction screening of <i>Drosophila</i> regulatory elements. <i>Nature Methods</i> , 2011, 8, 1065-1070.	9.0	76
46	Gastrointestinal and Microbial Responses to Sulfate-Supplemented Drinking Water in Mice. <i>Experimental Biology and Medicine</i> , 2003, 228, 424-433.	1.1	75
47	Toward a Consensus View of Mammalian Adipocyte Stem and Progenitor Cell Heterogeneity. <i>Trends in Cell Biology</i> , 2020, 30, 937-950.	3.6	69
48	Transcriptional regulatory logic of the diurnal cycle in the mouse liver. <i>PLoS Biology</i> , 2017, 15, e2001069.	2.6	68
49	Gateway-Compatible Yeast One-Hybrid Screens. <i>Cold Spring Harbor Protocols</i> , 2006, 2006, pdb.prot4590-pdb.prot4590.	0.2	67
50	A Comprehensive <i>Drosophila melanogaster</i> Transcription Factor Interactome. <i>Cell Reports</i> , 2019, 27, 955-970.e7.	2.9	66
51	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. <i>Nature Communications</i> , 2017, 8, 15842.	5.8	64
52	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. <i>Nature Methods</i> , 2007, 4, 659-664.	9.0	62
53	Hippo, TGF- β , and Src-MAPK pathways regulate transcription of the <i>upd3</i> cytokine in <i>Drosophila</i> enterocytes upon bacterial infection. <i>PLoS Genetics</i> , 2017, 13, e1007091.	1.5	61
54	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. <i>ELife</i> , 2019, 8, .	2.8	61

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55	A multiplicity of factors contributes to selective RNA polymerase III occupancy of a subset of RNA polymerase III genes in mouse liver. <i>Genome Research</i> , 2012, 22, 666-680.	2.4	56
56	Genetic, molecular and physiological basis of variation in <i>Drosophila</i> gut immunocompetence. <i>Nature Communications</i> , 2015, 6, 7829.	5.8	54
57	Transcription factor proteomics—Tools, applications, and challenges. <i>Proteomics</i> , 2017, 17, 1600317.	1.3	52
58	Chromosome-Biased Binding and Gene Regulation by the <i>Caenorhabditis elegans</i> DRM Complex. <i>PLoS Genetics</i> , 2011, 7, e1002074.	1.5	50
59	An Evolutionarily Conserved Role for the Aryl Hydrocarbon Receptor in the Regulation of Movement. <i>PLoS Genetics</i> , 2014, 10, e1004673.	1.5	50
60	Primate-restricted KRAB zinc finger proteins and target retrotransposons control gene expression in human neurons. <i>Science Advances</i> , 2020, 6, eaba3200.	4.7	50
61	PDF Signaling Is an Integral Part of the <i>Drosophila</i> Circadian Molecular Oscillator. <i>Cell Reports</i> , 2016, 17, 708-719.	2.9	49
62	Primer-initiated sequence synthesis to detect and assemble structural variants. <i>Nature Methods</i> , 2010, 7, 485-486.	9.0	48
63	A large-scale, in vivo transcription factor screen defines bivalent chromatin as a key property of regulatory factors mediating <i>Drosophila</i> wing development. <i>Genome Research</i> , 2015, 25, 514-523.	2.4	45
64	GETPrime: a gene- or transcript-specific primer database for quantitative real-time PCR. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar040.	1.4	43
65	Global and Stage Specific Patterns of Krüppel-Associated-Box Zinc Finger Protein Gene Expression in Murine Early Embryonic Cells. <i>PLoS ONE</i> , 2013, 8, e56721.	1.1	43
66	Cross-talk between emulsion drops: how are hydrophilic reagents transported across oil phases?. <i>Lab on A Chip</i> , 2018, 18, 3903-3912.	3.1	43
67	Mitochondrial gene signature in the prefrontal cortex for differential susceptibility to chronic stress. <i>Scientific Reports</i> , 2020, 10, 18308.	1.6	43
68	Engineered Multivalent Sensors to Detect Coexisting Histone Modifications in Living Stem Cells. <i>Cell Chemical Biology</i> , 2018, 25, 51-56.e6.	2.5	39
69	The <i>C. elegans</i> Snail homolog CES-1 can activate gene expression in vivo and share targets with bHLH transcription factors. <i>Nucleic Acids Research</i> , 2009, 37, 3689-3698.	6.5	36
70	A yeast one-hybrid and microfluidics-based pipeline to map mammalian gene regulatory networks. <i>Molecular Systems Biology</i> , 2013, 9, 682.	3.2	35
71	Deterministic scRNA-seq captures variation in intestinal crypt and organoid composition. <i>Nature Methods</i> , 2022, 19, 323-330.	9.0	33
72	ZFP30 promotes adipogenesis through the KAP1-mediated activation of a retrotransposon-derived <i>Pparg2</i> enhancer. <i>Nature Communications</i> , 2019, 10, 1809.	5.8	30

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73	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. <i>ELife</i> , 2021, 10, .	2.8	29
74	GETPrime 2.0: gene- and transcript-specific qPCR primers for 13 species including polymorphisms. <i>Nucleic Acids Research</i> , 2017, 45, D56-D60.	6.5	25
75	Inter-embryo gene expression variability recapitulates the hourglass pattern of evo-devo. <i>BMC Biology</i> , 2020, 18, 129.	1.7	23
76	Simplified Drop-seq workflow with minimized bead loss using a bead capture and processing microfluidic chip. <i>Lab on A Chip</i> , 2019, 19, 1610-1620.	3.1	22
77	DNA-centered approaches to characterize regulatory proteinâ€“DNA interaction complexes. <i>Molecular BioSystems</i> , 2010, 6, 462-468.	2.9	21
78	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. <i>Bioinformatics</i> , 2014, 30, 165-171.	1.8	21
79	Extensive tissue-specific expression variation and novel regulators underlying circadian behavior. <i>Science Advances</i> , 2021, 7, .	4.7	21
80	Dissecting the brown adipogenic regulatory network using integrative genomics. <i>Scientific Reports</i> , 2017, 7, 42130.	1.6	20
81	LncRNA <i><i>Ctcflos</i></i> orchestrates transcription and alternative splicing in thermogenic adipogenesis. <i>EMBO Reports</i> , 2021, 22, e51289.	2.0	19
82	Recent advances in trajectory inference from single-cell omics data. <i>Current Opinion in Systems Biology</i> , 2021, 27, 100344.	1.3	19
83	Quantification of Cooperativity in Heterodimer-DNA Binding Improves the Accuracy of Binding Specificity Models. <i>Journal of Biological Chemistry</i> , 2016, 291, 10293-10306.	1.6	18
84	iSLIM: a comprehensive approach to mapping and characterizing gene regulatory networks. <i>Nucleic Acids Research</i> , 2013, 41, e52-e52.	6.5	17
85	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. <i>Nucleic Acids Research</i> , 2020, 48, W403-W414.	6.5	17
86	Potential Direct Regulators of the <i><i>Drosophila yellow</i></i> Gene Identified by Yeast One-Hybrid and RNAi Screens. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3419-3430.	0.8	16
87	Profiling of Singleâ€“Cell Transcriptomes. <i>Current Protocols in Mouse Biology</i> , 2017, 7, 145-175.	1.2	16
88	The Movement Tracker: A Flexible System for Automated Movement Analysis in Invertebrate Model Organisms. <i>Current Protocols in Neuroscience</i> , 2016, 77, 8.37.1-8.37.21.	2.6	15
89	The <i>Zic</i> family homologue <i>Odd-paired</i> regulates <i>Alk</i> expression in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2017, 13, e1006617.	1.5	15
90	cis-regulatory variation modulates susceptibility to enteric infection in the <i>Drosophila</i> genetic reference panel. <i>Genome Biology</i> , 2020, 21, 6.	3.8	14

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91	Context-dependent transcriptional interpretation of mitogen activated protein kinase signaling in the <i>Drosophila</i> embryo. <i>Chaos</i> , 2013, 23, 025105.	1.0	13
92	Commensal Gut Bacteria Buffer the Impact of Host Genetic Variants on <i>Drosophila</i> Developmental Traits under Nutritional Stress. <i>IScience</i> , 2019, 19, 436-447.	1.9	12
93	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , 2019, 47, 1786-1796.	6.5	12
94	Single-cell transcriptional profiling of splenic fibroblasts reveals subset-specific innate immune signatures in homeostasis and during viral infection. <i>Communications Biology</i> , 2021, 4, 1355.	2.0	12
95	Experimental advances in the characterization of metazoan gene regulatory networks. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 8, 12-27.	3.8	11
96	Mitochondrial haplotypes affect metabolic phenotypes in the <i>Drosophila</i> Genetic Reference Panel. <i>Nature Metabolism</i> , 2019, 1, 1226-1242.	5.1	11
97	Selective Retrieval of Individual Cells from Microfluidic Arrays Combining Dielectrophoretic Force and Directed Hydrodynamic Flow. <i>Micromachines</i> , 2020, 11, 322.	1.4	11
98	Systems-Genetics-Based Inference of a Core Regulatory Network Underlying White Fat Browning. <i>Cell Reports</i> , 2019, 29, 4099-4113.e5.	2.9	10
99	Tissue-specific enhancer repression through molecular integration of cell signaling inputs. <i>PLoS Genetics</i> , 2017, 13, e1006718.	1.5	9
100	A parallelized, automated platform enabling individual or sequential CHIP of histone marks and transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13828-13838.	3.3	8
101	A High-throughput Gateway-Compatible Yeast One-Hybrid Screen to Detect Protein-DNA Interactions. <i>Methods in Molecular Biology</i> , 2012, 786, 335-355.	0.4	8
102	Cross-Tissue Identification of Somatic Stem and Progenitor Cells Using a Single-Cell RNA-Sequencing Derived Gene Signature. <i>Stem Cells</i> , 2017, 35, 2390-2402.	1.4	6
103	Genome-Wide Profiling of DNA-Binding Proteins Using Barcode-Based Multiplex Solexa Sequencing. <i>Methods in Molecular Biology</i> , 2012, 786, 247-262.	0.4	6
104	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation. <i>Nature Communications</i> , 2022, 13, 2042.	5.8	6
105	A Tead1-Apelin axis directs paracrine communication from myogenic to endothelial cells in skeletal muscle. <i>IScience</i> , 2022, 25, 104589.	1.9	6
106	WebPrInSeS: automated full-length clone sequence identification and verification using high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2010, 38, W378-W384.	6.5	5
107	Morphological and Molecular Characterization of Adult Midgut Compartmentalization in <i>Drosophila</i> . <i>Cell Reports</i> , 2013, 3, 1755.	2.9	5
108	Multilevel regulation of the glass locus during <i>Drosophila</i> eye development. <i>PLoS Genetics</i> , 2019, 15, e1008269.	1.5	5

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109	A mammalian transcription factor-specific peptide repository for targeted proteomics. <i>Proteomics</i> , 2015, 15, 752-756.	1.3	4
110	Sex-dependent and sex-independent regulatory systems of size variation in natural populations. <i>Molecular Systems Biology</i> , 2019, 15, e9012.	3.2	4
111	Enteric infection induces Lark-mediated intron retention at the 5' end of <i>Drosophila</i> genes. <i>Genome Biology</i> , 2020, 21, 4.	3.8	4
112	Variable Outcome of Mutations. <i>Science</i> , 2012, 335, 44-45.	6.0	3
113	Gene regulatory mechanisms underlying the intestinal innate immune response. <i>Current Opinion in Genetics and Development</i> , 2017, 43, 46-52.	1.5	3
114	Shared acute phase traits in effector and memory human CD8 T cells. <i>Current Research in Immunology</i> , 2022, 3, 1-12.	1.2	2
115	Rounding Up Natural Gene Expression Variation during Development. <i>Developmental Cell</i> , 2013, 27, 601-603.	3.1	1
116	SMiLE-seq: Selective Microfluidics-based Ligand Enrichment followed by sequencing. <i>Protocol Exchange</i> , 0, , .	0.3	1
117	Editorial overview: Genome architecture and expression. <i>Current Opinion in Genetics and Development</i> , 2017, 43, iv-v.	1.5	0