

# Bart Deplancke

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

123  
papers

8,459  
citations

46  
h-index

91  
g-index

154  
ext. papers

11,005  
ext. citations

12.8  
avg, IF

5.79  
L-index

#	Paper	IF	Citations
123	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches.. <i>Cell</i> , <b>2022</b> , 185, 379-396.e38	56.2	20
122	Shared acute phase traits in effector and memory human CD8 T cells.. <i>Current Research in Immunology</i> , <b>2022</b> , 3, 1-12	1	
121	Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly.. <i>Science</i> , <b>2022</b> , 375, eabk2432	33.3	23
120	A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation.. <i>Nature Communications</i> , <b>2022</b> , 13, 2042	17.4	1
119	Disparate temperature-dependent virus-host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001158	9.7	36
118	LncRNA Ctcfls orchestrates transcription and alternative splicing in thermogenic adipogenesis. <i>EMBO Reports</i> , <b>2021</b> , 22, e51289	6.5	5
117	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. <i>ELife</i> , <b>2021</b> , 10,	8.9	8
116	Recent advances in trajectory inference from single-cell omics data. <i>Current Opinion in Systems Biology</i> , <b>2021</b> , 27, 100344	3.2	0
115	Extensive tissue-specific expression variation and novel regulators underlying circadian behavior. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	7
114	Single-cell transcriptional profiling of splenic fibroblasts reveals subset-specific innate immune signatures in homeostasis and during viral infection. <i>Communications Biology</i> , <b>2021</b> , 4, 1355	6.7	1
113	Toward a Consensus View of Mammalian Adipocyte Stem and Progenitor Cell Heterogeneity. <i>Trends in Cell Biology</i> , <b>2020</b> , 30, 937-950	18.3	19
112	ASAP 2020 update: an open, scalable and interactive web-based portal for (single-cell) omics analyses. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W403-W414	20.1	9
111	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> , <b>2020</b> , 117, 13828-13838	11.5	4
110	Selective Retrieval of Individual Cells from Microfluidic Arrays Combining Dielectrophoretic Force and Directed Hydrodynamic Flow. <i>Micromachines</i> , <b>2020</b> , 11,	3.3	5
109	cis-regulatory variation modulates susceptibility to enteric infection in the Drosophila genetic reference panel. <i>Genome Biology</i> , <b>2020</b> , 21, 6	18.3	7
108	Enteric infection induces Lark-mediated intron retention at the 5Send of Drosophila genes. <i>Genome Biology</i> , <b>2020</b> , 21, 4	18.3	2
107	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , <b>2020</b> , 587, 377-386	50.4	56

106	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> , <b>2020</b> , 37, 2661-2678	8.3	41
105	Mitochondrial gene signature in the prefrontal cortex for differential susceptibility to chronic stress. <i>Scientific Reports</i> , <b>2020</b> , 10, 18308	4.9	12
104	Inter-embryo gene expression variability recapitulates the hourglass pattern of evo-devo. <i>BMC Biology</i> , <b>2020</b> , 18, 129	7.3	7
103	Primate-restricted KRAB zinc finger proteins and target retrotransposons control gene expression in human neurons. <i>Science Advances</i> , <b>2020</b> , 6, eaba3200	14.3	16
102	Commensal Gut Bacteria Buffer the Impact of Host Genetic Variants on <i>Drosophila</i> Developmental Traits under Nutritional Stress. <i>iScience</i> , <b>2019</b> , 19, 436-447	6.1	5
101	BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. <i>Genome Biology</i> , <b>2019</b> , 20, 71	18.3	47
100	ZFP30 promotes adipogenesis through the KAP1-mediated activation of a retrotransposon-derived Pparg2 enhancer. <i>Nature Communications</i> , <b>2019</b> , 10, 1809	17.4	14
99	A Comprehensive <i>Drosophila melanogaster</i> Transcription Factor Interactome. <i>Cell Reports</i> , <b>2019</b> , 27, 955-970.e7	10.6	22
98	Simplified Drop-seq workflow with minimized bead loss using a bead capture and processing microfluidic chip. <i>Lab on A Chip</i> , <b>2019</b> , 19, 1610-1620	7.2	13
97	The NAD-Booster Nicotinamide Riboside Potently Stimulates Hematopoiesis through Increased Mitochondrial Clearance. <i>Cell Stem Cell</i> , <b>2019</b> , 24, 405-418.e7	18	81
96	Multilevel regulation of the glass locus during <i>Drosophila</i> eye development. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008269	6	2
95	Dynamic regulation of chromatin accessibility by pluripotency transcription factors across the cell cycle. <i>ELife</i> , <b>2019</b> , 8,	8.9	27
94	Sex-dependent and sex-independent regulatory systems of size variation in natural populations. <i>Molecular Systems Biology</i> , <b>2019</b> , 15, e9012	12.2	3
93	Mitochondrial haplotypes affect metabolic phenotypes in the <i>Drosophila</i> Genetic Reference Panel. <i>Nature Metabolism</i> , <b>2019</b> , 1, 1226-1242	14.6	5
92	Systems-Genetics-Based Inference of a Core Regulatory Network Underlying White Fat Browning. <i>Cell Reports</i> , <b>2019</b> , 29, 4099-4113.e5	10.6	5
91	Differential regulation of RNA polymerase III genes during liver regeneration. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 1786-1796	20.1	7
90	Reversible De-differentiation of Mature White Adipocytes into Preadipocyte-like Precursors during Lactation. <i>Cell Metabolism</i> , <b>2018</b> , 28, 282-288.e3	24.6	69
89	A stromal cell population that inhibits adipogenesis in mammalian fat depots. <i>Nature</i> , <b>2018</b> , 559, 103-108	30.4	183

88	Engineered Multivalent Sensors to Detect Coexisting Histone Modifications in Living Stem Cells. <i>Cell Chemical Biology</i> , <b>2018</b> , 25, 51-56.e6	8.2	20
87	Cross-talk between emulsion drops: how are hydrophilic reagents transported across oil phases?. <i>Lab on A Chip</i> , <b>2018</b> , 18, 3903-3912	7.2	27
86	GETPrime 2.0: gene- and transcript-specific qPCR primers for 13 species including polymorphisms. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D56-D60	20.1	17
85	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> , <b>2017</b> , 114, E1291-E1300	11.5	30
84	SMiLE-seq identifies binding motifs of single and dimeric transcription factors. <i>Nature Methods</i> , <b>2017</b> , 14, 316-322	21.6	58
83	Dissecting the brown adipogenic regulatory network using integrative genomics. <i>Scientific Reports</i> , <b>2017</b> , 7, 42130	4.9	14
82	ASAP: a web-based platform for the analysis and interactive visualization of single-cell RNA-seq data. <i>Bioinformatics</i> , <b>2017</b> , 33, 3123-3125	7.2	71
81	Gene regulatory mechanisms underlying the intestinal innate immune response. <i>Current Opinion in Genetics and Development</i> , <b>2017</b> , 43, 46-52	4.9	3
80	Cross-Tissue Identification of Somatic Stem and Progenitor Cells Using a Single-Cell RNA-Sequencing Derived Gene Signature. <i>Stem Cells</i> , <b>2017</b> , 35, 2390-2402	5.8	5
79	Transcriptional regulatory logic of the diurnal cycle in the mouse liver. <i>PLoS Biology</i> , <b>2017</b> , 15, e2001069	9.7	51
78	Profiling of Single-Cell Transcriptomes. <i>Current Protocols in Mouse Biology</i> , <b>2017</b> , 7, 145-175	1.1	10
77	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. <i>Nature Communications</i> , <b>2017</b> , 8, 15842	17.4	39
76	Transcription factor proteomics-Tools, applications, and challenges. <i>Proteomics</i> , <b>2017</b> , 17, 1600317	4.8	17
75	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
74	The Zic family homologue Odd-paired regulates Alk expression in Drosophila. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006617	6	7
73	Tissue-specific enhancer repression through molecular integration of cell signaling inputs. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006718	6	7
72	Hippo, TGF- $\beta$ and Src-MAPK pathways regulate transcription of the upd3 cytokine in Drosophila enterocytes upon bacterial infection. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007091	6	37
71	Author response: The Human Cell Atlas <b>2017</b> ,		10

70	Quantification of Cooperativity in Heterodimer-DNA Binding Improves the Accuracy of Binding Specificity Models. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 10293-306	5.4	18
69	Potential Direct Regulators of the Drosophila yellow Gene Identified by Yeast One-Hybrid and RNAi Screens. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 3419-3430	3.2	11
68	PDF Signaling Is an Integral Part of the Drosophila Circadian Molecular Oscillator. <i>Cell Reports</i> , <b>2016</b> , 17, 708-719	10.6	31
67	The Movement Tracker: A Flexible System for Automated Movement Analysis in Invertebrate Model Organisms. <i>Current Protocols in Neuroscience</i> , <b>2016</b> , 77, 8.37.1-8.37.21	2.7	10
66	The Genetics of Transcription Factor DNA Binding Variation. <i>Cell</i> , <b>2016</b> , 166, 538-554	56.2	201
65	Genetic, molecular and physiological basis of variation in Drosophila gut immunocompetence. <i>Nature Communications</i> , <b>2015</b> , 6, 7829	17.4	42
64	Tetracyclines Disturb Mitochondrial Function across Eukaryotic Models: A Call for Caution in Biomedical Research. <i>Cell Reports</i> , <b>2015</b> , 10, 1681-1691	10.6	280
63	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. <i>Cell</i> , <b>2015</b> , 162, 1039-50	56.2	156
62	A mammalian transcription factor-specific peptide repository for targeted proteomics. <i>Proteomics</i> , <b>2015</b> , 15, 752-6	4.8	4
61	A large-scale, in vivo transcription factor screen defines bivalent chromatin as a key property of regulatory factors mediating Drosophila wing development. <i>Genome Research</i> , <b>2015</b> , 25, 514-23	9.7	28
60	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , <b>2015</b> , 4,	8.9	140
59	Author response: Conservation of transcription factor binding specificities across 600 million years of bilateria evolution <b>2015</b> ,		2
58	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. <i>Bioinformatics</i> , <b>2014</b> , 30, 165-71	7.2	17
57	GLUT3 is induced during epithelial-mesenchymal transition and promotes tumor cell proliferation in non-small cell lung cancer. <i>Cancer &amp; Metabolism</i> , <b>2014</b> , 2, 11	5.4	81
56	Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. <i>Genome Research</i> , <b>2014</b> , 24, 1157-68	9.7	106
55	Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. <i>Genome Research</i> , <b>2014</b> , 24, 1193-208	9.7	372
54	An evolutionarily conserved role for the aryl hydrocarbon receptor in the regulation of movement. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004673	6	36
53	Identification of the transcription factor ZEB1 as a central component of the adipogenic gene regulatory network. <i>ELife</i> , <b>2014</b> , 3, e03346	8.9	60

52	Morphological and molecular characterization of adult midgut compartmentalization in <i>Drosophila</i> . <i>Cell Reports</i> , <b>2013</b> , 3, 1725-38	10.6	308
51	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. <i>Science</i> , <b>2013</b> , 342, 744-7	33.3	278
50	Morphological and Molecular Characterization of Adult Midgut Compartmentalization in <i>Drosophila</i> . <i>Cell Reports</i> , <b>2013</b> , 3, 1755	10.6	3
49	Rounding up natural gene expression variation during development. <i>Developmental Cell</i> , <b>2013</b> , 27, 601-310.2	10.2	0
48	Absolute quantification of transcription factors during cellular differentiation using multiplexed targeted proteomics. <i>Nature Methods</i> , <b>2013</b> , 10, 570-6	21.6	72
47	Complex expression dynamics and robustness in <i>C. elegans</i> insulin networks. <i>Genome Research</i> , <b>2013</b> , 23, 954-65	9.7	64
46	Context-dependent transcriptional interpretation of mitogen activated protein kinase signaling in the <i>Drosophila</i> embryo. <i>Chaos</i> , <b>2013</b> , 23, 025105	3.3	11
45	A yeast one-hybrid and microfluidics-based pipeline to map mammalian gene regulatory networks. <i>Molecular Systems Biology</i> , <b>2013</b> , 9, 682	12.2	31
44	iSLIM: a comprehensive approach to mapping and characterizing gene regulatory networks. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e52	20.1	14
43	Global and stage specific patterns of Krüppel-associated-box zinc finger protein gene expression in murine early embryonic cells. <i>PLoS ONE</i> , <b>2013</b> , 8, e56721	3.7	40
42	Genetics. Variable outcome of mutations. <i>Science</i> , <b>2012</b> , 335, 44-5	33.3	3
41	Integrative genomics identifies the corepressor SMRT as a gatekeeper of adipogenesis through the transcription factors C/EBP $\beta$ and KAISO. <i>Molecular Cell</i> , <b>2012</b> , 46, 335-50	17.6	62
40	Genome-wide RNA polymerase II profiles and RNA accumulation reveal kinetics of transcription and associated epigenetic changes during diurnal cycles. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001442	9.7	142
39	Topology and dynamics of the zebrafish segmentation clock core circuit. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001364	9.7	84
38	Genomic variation and its impact on gene expression in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003055	6	85
37	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> , <b>2012</b> , 22, 666-80	9.7	49
36	Genome-wide profiling of DNA-binding proteins using barcode-based multiplex Solexa sequencing. <i>Methods in Molecular Biology</i> , <b>2012</b> , 786, 247-62	1.4	6
35	A high-throughput gateway-compatible yeast one-hybrid screen to detect protein-DNA interactions. <i>Methods in Molecular Biology</i> , <b>2012</b> , 786, 335-55	1.4	7

34	Automated protein-DNA interaction screening of Drosophila regulatory elements. <i>Nature Methods</i> , <b>2011</b> , 8, 1065-70	21.6	65
33	GETPrime: a gene- or transcript-specific primer database for quantitative real-time PCR. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2011</b> , 2011, bar040	5	35
32	Chromosome-biased binding and gene regulation by the Caenorhabditis elegans DRM complex. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002074	6	39
31	Exhaustion of tumor-specific CD8+ T cells in metastases from melanoma patients. <i>Journal of Clinical Investigation</i> , <b>2011</b> , 121, 2350-60	15.9	549
30	Primer-initiated sequence synthesis to detect and assemble structural variants. <i>Nature Methods</i> , <b>2010</b> , 7, 485-6	21.6	25
29	WebPrInSeS: automated full-length clone sequence identification and verification using high-throughput sequencing data. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W378-84	20.1	5
28	DNA-centered approaches to characterize regulatory protein-DNA interaction complexes. <i>Molecular BioSystems</i> , <b>2010</b> , 6, 462-8		19
27	The C. elegans Snail homolog CES-1 can activate gene expression in vivo and share targets with bHLH transcription factors. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 3689-98	20.1	30
26	Experimental advances in the characterization of metazoan gene regulatory networks. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2009</b> , 8, 12-27		11
25	Chromatin immunoprecipitation (ChIP) coupled to detection by quantitative real-time PCR to study transcription factor binding to DNA in Caenorhabditis elegans. <i>Nature Protocols</i> , <b>2008</b> , 3, 698-709	18.8	205
24	Matrix and Steiner-triple-system smart pooling assays for high-performance transcription regulatory network mapping. <i>Nature Methods</i> , <b>2007</b> , 4, 659-64	21.6	59
23	C. elegans 14-3-3 proteins regulate life span and interact with SIR-2.1 and DAF-16/FOXO. <i>Mechanisms of Ageing and Development</i> , <b>2006</b> , 127, 741-7	5.6	107
22	A gene-centered C. elegans protein-DNA interaction network. <i>Cell</i> , <b>2006</b> , 125, 1193-205	56.2	194
21	Gateway-compatible yeast one-hybrid screens. <i>Cold Spring Harbor Protocols</i> , <b>2006</b> , 2006,	1.2	51
20	C. elegans tubby regulates life span and fat storage by two independent mechanisms. <i>Cell Metabolism</i> , <b>2005</b> , 2, 35-42	24.6	91
19	A compendium of Caenorhabditis elegans regulatory transcription factors: a resource for mapping transcription regulatory networks. <i>Genome Biology</i> , <b>2005</b> , 6, R110	18.3	142
18	A first version of the Caenorhabditis elegans Promoterome. <i>Genome Research</i> , <b>2004</b> , 14, 2169-75	9.7	133
17	A gateway-compatible yeast one-hybrid system. <i>Genome Research</i> , <b>2004</b> , 14, 2093-101	9.7	162



16	Hydrogen sulfide induces serum-independent cell cycle entry in nontransformed rat intestinal epithelial cells. <i>FASEB Journal</i> , <b>2003</b> , 17, 1310-2	0.9	161
15	Gastrointestinal and microbial responses to sulfate-supplemented drinking water in mice. <i>Experimental Biology and Medicine</i> , <b>2003</b> , 228, 424-33	3.7	63
14	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> , <b>2003</b> , 47, 3311-7	5.9	82
13	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> , <b>2002</b> , 68, 5113-22	4.8	99
12	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> , <b>2002</b> , 76, 1117-25	7	118
11	Microbial modulation of innate defense: goblet cells and the intestinal mucus layer. <i>American Journal of Clinical Nutrition</i> , <b>2001</b> , 73, 1131S-1141S	7	639
10	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> , <b>2000</b> , 130, 2599-606	4.1	141
9	Molecular ecological analysis of the succession and diversity of sulfate-reducing bacteria in the mouse gastrointestinal tract. <i>Applied and Environmental Microbiology</i> , <b>2000</b> , 66, 2166-74	4.8	128
8	Selection against expression noise explains the origin of the hourglass pattern of Evo-Devo		1
7	Disparate temperature-dependent virus-host dynamics for SARS-CoV-2 and SARS-CoV in the human respiratory epithelium		23
6	Time- and cost-efficient high-throughput transcriptomics enabled by Bulk RNA Barcoding and sequencing		2
5	Genomic analysis of European <i>Drosophila melanogaster</i> populations reveals longitudinal structure, continent-wide selection, and previously unknown DNA viruses		13
4	Extensive mitochondrial population structure and haplotype-specific phenotypic variation in the <i>Drosophila</i> Genetic Reference Panel		2
3	A highly parallel, automated platform enabling individual or sequential ChIP of histone marks and transcription factors		1
2	Genome-wide molecular recording using Live-seq		3
1	Fly Cell Atlas: a single-cell transcriptomic atlas of the adult fruit fly		16