

Bo Torben Porse

List of Publications by Year in descending order

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93
papers

9,309
citations

50170

46
h-index

43802

91
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98
all docs

98
docs citations

98
times ranked

17424
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiomic Profiling of Central Nervous System Leukemia Identifies mRNA Translation as a Therapeutic Target. <i>Blood Cancer Discovery</i> , 2022, 3, 16-31.	2.6	4
2	Dynamic intron retention modulates gene expression in the monocytic differentiation pathway. <i>Immunology</i> , 2022, 165, 274-286.	2.0	7
3	Real-Time Search-Assisted Acquisition on a Tribrid Mass Spectrometer Improves Coverage in Multiplexed Single-Cell Proteomics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100219.	2.5	44
4	H3K9 dimethylation safeguards cancer cells against activation of the interferon pathway. <i>Science Advances</i> , 2022, 8, eabf8627.	4.7	10
5	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. <i>Cell Reports</i> , 2022, 39, 110793.	2.9	3
6	Transcription factor-driven coordination of cell cycle exit and lineage-specification in vivo during granulocytic differentiation. <i>Nature Communications</i> , 2022, 13, .	5.8	16
7	Targeted inhibition of cooperative mutation- and therapy-induced AKT activation in AML effectively enhances response to chemotherapy. <i>Leukemia</i> , 2021, 35, 2030-2042.	3.3	14
8	The ASXL1-G643W variant accelerates the development of CEBPA mutant acute myeloid leukemia. <i>Haematologica</i> , 2021, 106, 1000-1007.	1.7	9
9	Basement membrane stiffness determines metastases formation. <i>Nature Materials</i> , 2021, 20, 892-903.	13.3	94
10	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. <i>Nature Communications</i> , 2021, 12, 3341.	5.8	197
11	The EHA Research Roadmap: Normal Hematopoiesis. <i>HemaSphere</i> , 2021, 5, e669.	1.2	1
12	Myelodysplastic syndrome patient-derived xenografts: from no options to many. <i>Haematologica</i> , 2020, 105, 864-869.	1.7	17
13	CCAAT enhancer binding protein alpha (CEBPA) biallelic acute myeloid leukaemia: cooperating lesions, molecular mechanisms and clinical relevance. <i>British Journal of Haematology</i> , 2020, 190, 495-507.	1.2	31
14	Heterozygous loss of Srp72 in mice is not associated with major hematological phenotypes. <i>European Journal of Haematology</i> , 2019, 103, 319-328.	1.1	5
15	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. <i>Science Advances</i> , 2019, 5, eaaw4304.	4.7	28
16	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 172.	5.8	42
17	Inhibition of Upf2-Dependent Nonsense-Mediated Decay Leads to Behavioral and Neurophysiological Abnormalities by Activating the Immune Response. <i>Neuron</i> , 2019, 104, 665-679.e8.	3.8	43
18	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. <i>Cell Reports</i> , 2019, 29, 2756-2769.e6.	2.9	7

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19	A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. <i>Cell Research</i> , 2019, 29, 221-232.	5.7	48
20	SinaPlot: An Enhanced Chart for Simple and Truthful Representation of Single Observations Over Multiple Classes. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 673-676.	0.9	37
21	Human adult HSCs can be discriminated from lineage-committed HPCs by the expression of endomucin. <i>Blood Advances</i> , 2018, 2, 1628-1632.	2.5	10
22	Testosterone is an endogenous regulator of BAFF and splenic B cell number. <i>Nature Communications</i> , 2018, 9, 2067.	5.8	66
23	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in <i>Cebpa</i> null Progenitors. <i>Cell Reports</i> , 2018, 23, 2744-2757.	2.9	45
24	A new genetic tool to improve immune-compromised mouse models: Derivation and CRISPR/Cas9-mediated targeting of NRG embryonic stem cell lines. <i>Genesis</i> , 2018, 56, e23238.	0.8	1
25	Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. <i>Cell Reports</i> , 2018, 24, 766-780.	2.9	40
26	Leukemogenic nucleophosmin mutation disrupts the transcription factor hub that regulates granulomonocytic fates. <i>Journal of Clinical Investigation</i> , 2018, 128, 4260-4279.	3.9	97
27	EZH2 is a potential therapeutic target for H3K27M-mutant pediatric gliomas. <i>Nature Medicine</i> , 2017, 23, 483-492.	15.2	392
28	Peak-valley-peak pattern of histone modifications delineates active regulatory elements and their directionality. <i>Nucleic Acids Research</i> , 2016, 44, 4037-4051.	6.5	26
29	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
30	C/EBP β creates elite cells for iPSC reprogramming by upregulating Klf4 and increasing the levels of Lsd1 and Brd4. <i>Nature Cell Biology</i> , 2016, 18, 371-381.	4.6	94
31	BloodSpot: a database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2016, 44, D917-D924.	6.5	242
32	UPF2-Dependent Nonsense-Mediated mRNA Decay Pathway Is Essential for Spermatogenesis by Selectively Eliminating Longer 3'UTR Transcripts. <i>PLoS Genetics</i> , 2016, 12, e1005863.	1.5	94
33	Disease evolution and outcomes in familial AML with germline CEBPA mutations. <i>Blood</i> , 2015, 126, 1214-1223.	0.6	157
34	UPF2, a nonsense-mediated mRNA decay factor, is required for prepubertal Sertoli cell development and male fertility by ensuring fidelity of the transcriptome. <i>Development (Cambridge)</i> , 2015, 142, 352-62.	1.2	30
35	Amplification of pico-scale DNA mediated by bacterial carrier DNA for small-cell-number transcription factor ChIP-seq. <i>BMC Genomics</i> , 2015, 16, 46.	1.2	27
36	Loss of TET2 in hematopoietic cells leads to DNA hypermethylation of active enhancers and induction of leukemogenesis. <i>Genes and Development</i> , 2015, 29, 910-922.	2.7	213

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37	ERG promotes the maintenance of hematopoietic stem cells by restricting their differentiation. <i>Genes and Development</i> , 2015, 29, 1915-1929.	2.7	71
38	Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. <i>Cell</i> , 2015, 163, 1663-1677.	13.5	875
39	Liver is the major source of elevated serum lipocalin α 2 levels after bacterial infection or partial hepatectomy: A critical role for IL α 6/STAT3. <i>Hepatology</i> , 2015, 61, 692-702.	3.6	143
40	C/EBP β Is Dispensable for the Ontogeny of PD-1+ CD4+ Memory T Cells but Restricts Their Expansion in an Age-Dependent Manner. <i>PLoS ONE</i> , 2014, 9, e84728.	1.1	15
41	C/EBP β Is Required for Long-Term Self-Renewal and Lineage Priming of Hematopoietic Stem Cells and for the Maintenance of Epigenetic Configurations in Multipotent Progenitors. <i>PLoS Genetics</i> , 2014, 10, e1004079.	1.5	85
42	Initiation of MLL-rearranged AML is dependent on C/EBP β . <i>Journal of Experimental Medicine</i> , 2014, 211, 5-13.	4.2	62
43	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. <i>Bioinformatics</i> , 2014, 30, 1154-1162.	1.8	31
44	Comparing cancer vs normal gene expression profiles identifies new disease entities and common transcriptional programs in AML patients. <i>Blood</i> , 2014, 123, 894-904.	0.6	133
45	The functional consequences of intron retention: Alternative splicing coupled to \langle scn \rangle NMD \langle /scn \rangle as a regulator of gene expression. <i>BioEssays</i> , 2014, 36, 236-243.	1.2	190
46	spliceR: an R package for classification of alternative splicing and prediction of coding potential from RNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 81.	1.2	100
47	Regulation of Trib2 by an E2F1-C/EBP β feedback loop in AML cell proliferation. <i>Blood</i> , 2014, 123, 2389-2400.	0.6	44
48	shRNA screening identifies JMJD1C as being required for leukemia maintenance. <i>Blood</i> , 2014, 123, 1870-1882.	0.6	73
49	Lack of the p42 form of C/EBP β leads to spontaneous immortalization and lineage infidelity of committed myeloid progenitors. <i>Experimental Hematology</i> , 2013, 41, 882-893.e16.	0.2	8
50	PRDM11 is dispensable for the maintenance and function of hematopoietic stem and progenitor cells. <i>Stem Cell Research</i> , 2013, 11, 1129-1136.	0.3	5
51	Temporal mapping of CEBPA and CEBPB binding during liver regeneration reveals dynamic occupancy and specific regulatory codes for homeostatic and cell cycle gene batteries. <i>Genome Research</i> , 2013, 23, 592-603.	2.4	73
52	Regulation of Axon Guidance by Compartmentalized Nonsense-Mediated mRNA Decay. <i>Cell</i> , 2013, 153, 1252-1265.	13.5	174
53	HemaExplorer: a database of mRNA expression profiles in normal and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2013, 41, D1034-D1039.	6.5	65
54	HemaExplorer: a Web server for easy and fast visualization of gene expression in normal and malignant hematopoiesis. <i>Blood</i> , 2012, 119, 6394-6395.	0.6	32

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55	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. <i>Genome Biology</i> , 2012, 13, R35.	13.9	113
56	PSD-95 is post-transcriptionally repressed during early neural development by PTBP1 and PTBP2. <i>Nature Neuroscience</i> , 2012, 15, 381-388.	7.1	212
57	Allelic methylation levels of the noncoding VTRNA2-1 located on chromosome 5q31.1 predict outcome in AML. <i>Blood</i> , 2012, 119, 206-216.	0.6	97
58	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
59	Phosphorylation of Serine 248 of C/EBP β Is Dispensable for Myelopoiesis but Its Disruption Leads to a Low Penetrant Myeloid Disorder with Long Latency. <i>PLoS ONE</i> , 2012, 7, e38841.	1.1	3
60	Technical Advance: Immunophenotypical characterization of human neutrophil differentiation. <i>Journal of Leukocyte Biology</i> , 2011, 90, 629-634.	1.5	37
61	Leukemia "ABC" methods and protocols. <i>European Journal of Haematology</i> , 2010, 84, 94-94.	1.1	0
62	UFP2 Is a Critical Regulator of Liver Development, Function and Regeneration. <i>PLoS ONE</i> , 2010, 5, e11650.	1.1	80
63	Characterization of an antagonistic switch between histone H3 lysine 27 methylation and acetylation in the transcriptional regulation of Polycomb group target genes. <i>Nucleic Acids Research</i> , 2010, 38, 4958-4969.	6.5	317
64	C/EBP β in leukemogenesis: Identity and origin of the leukemia-initiating cell. <i>BioFactors</i> , 2009, 35, 227-231.	2.6	9
65	Modeling of C/EBP β Mutant Acute Myeloid Leukemia Reveals a Common Expression Signature of Committed Myeloid Leukemia-Initiating Cells. <i>Cancer Cell</i> , 2008, 13, 299-310.	7.7	225
66	Effect of Apolipoprotein M on High Density Lipoprotein Metabolism and Atherosclerosis in Low Density Lipoprotein Receptor Knock-out Mice. <i>Journal of Biological Chemistry</i> , 2008, 283, 1839-1847.	1.6	165
67	NMD is essential for hematopoietic stem and progenitor cells and for eliminating by-products of programmed DNA rearrangements. <i>Genes and Development</i> , 2008, 22, 1381-1396.	2.7	231
68	Mutation of C/EBP β predisposes to the development of myeloid leukemia in a retroviral insertional mutagenesis screen. <i>Blood</i> , 2008, 111, 4309-4321.	0.6	11
69	The Polycomb group proteins bind throughout the INK4A-ARF locus and are disassociated in senescent cells. <i>Genes and Development</i> , 2007, 21, 525-530.	2.7	775
70	Distinct C/EBP β motifs regulate lipogenic and gluconeogenic gene expression in vivo. <i>EMBO Journal</i> , 2007, 26, 1081-1093.	3.5	85
71	Activation of the canonical Wnt pathway leads to loss of hematopoietic stem cell repopulation and multilineage differentiation block. <i>Nature Immunology</i> , 2006, 7, 1048-1056.	7.0	407
72	Systems biology of neutrophil differentiation and immune response. <i>Current Opinion in Immunology</i> , 2006, 18, 54-60.	2.4	73

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73	C/EBP β : A tumour suppressor in multiple tissues?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2006, 1766, 88-103.	3.3	64
74	The Proline-Histidine-Rich CDK2/CDK4 Interaction Region of C/EBP β Is Dispensable for C/EBP β -Mediated Growth Regulation In Vivo. <i>Molecular and Cellular Biology</i> , 2006, 26, 1028-1037.	1.1	21
75	Messenger RNA Surveillance: Neutralizing Natural Nonsense. <i>Current Biology</i> , 2005, 15, R559-R562.	1.8	79
76	Highly glycosylated β 1-acid glycoprotein is synthesized in myelocytes, stored in secondary granules, and released by activated neutrophils. <i>Journal of Leukocyte Biology</i> , 2005, 78, 462-470.	1.5	45
77	Loss of C/EBP β cell cycle control increases myeloid progenitor proliferation and transforms the neutrophil granulocyte lineage. <i>Journal of Experimental Medicine</i> , 2005, 202, 85-96.	4.2	101
78	A novel partial modification at C2501 in Escherichia coli 23S ribosomal RNA. <i>Rna</i> , 2004, 10, 907-913.	1.6	83
79	A conserved chloramphenicol binding site at the entrance to the ribosomal peptide exit tunnel. <i>Nucleic Acids Research</i> , 2003, 31, 7208-7215.	6.5	38
80	E2F Repression by C/EBP β Is Required for Adipogenesis and Granulopoiesis In Vivo. <i>Cell</i> , 2001, 107, 247-258.	13.5	292
81	Puromycinâ€rRNA interaction sites at the peptidyl transferase center. <i>Rna</i> , 2000, 6, 744-754.	1.6	26
82	Peptidyl transferase antibiotics perturb the relative positioning of the 3â€2-terminal adenosine of P/Pâ€2-site-bound tRNA and 23S rRNA in the ribosome. <i>Rna</i> , 1999, 5, 1003-1013.	1.6	31
83	UV-induced modifications in the peptidyl transferase loop of 23S rRNA dependent on binding of the streptogramin B antibiotic, pristinamycin IA. <i>Rna</i> , 1999, 5, 585-595.	1.6	18
84	Ribosomal Mechanics, Antibiotics, and GTP Hydrolysis. <i>Cell</i> , 1999, 97, 423-426.	13.5	45
85	Sites of interaction of streptogramin A and B antibiotics in the peptidyl transferase loop of 23 S rRNA and the synergism of their inhibitory mechanisms 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1999, 286, 375-387.	2.0	74
86	The antibiotic micrococin acts on protein L11 at the ribosomal GTPase centre 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1999, 287, 33-45.	2.0	56
87	The antibiotic thiostrepton inhibits a functional transition within protein L11 at the ribosomal GTPase centre 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1998, 276, 391-404.	2.0	114
88	Assembly of proteins and 5 S rRNA to transcripts of the major structural domains of 23 S rRNA 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1998, 284, 227-240.	2.0	36
89	Movement of the 3â€2-end of tRNA through the peptidyl transferase centre and its inhibition by antibiotics. <i>FEBS Letters</i> , 1997, 406, 223-233.	1.3	54
90	A Sparsomycin-resistant Mutant of Halobacterium salinarium Lacks a Modification at Nucleotide U2603 in the Peptidyl Transferase Centre of 23 S rRNA. <i>Journal of Molecular Biology</i> , 1996, 261, 231-238.	2.0	42

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91	The Donor Substrate Site within the Peptidyl Transferase Loop of 23 S rRNA and its Putative Interactions with the CCA-end of N-blocked Aminoacyl-tRNAPhe. <i>Journal of Molecular Biology</i> , 1996, 264, 472-483.	2.0	37
92	Mapping Important Nucleotides in the Peptidyl Transferase Centre of 23 S rRNA using a Random Mutagenesis Approach. <i>Journal of Molecular Biology</i> , 1995, 249, 1-10.	2.0	76
93	Antibiotic inhibition of the movement of tRNA substrates through a peptidyl transferase cavity. <i>Biochemistry and Cell Biology</i> , 1995, 73, 877-885.	0.9	21