

# Christian Schönbach

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

7,378  
citations

279798

23  
h-index

91884

69  
g-index

77  
all docs

77  
docs citations

77  
times ranked

9992  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548
3	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	27.8	653
4	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
5	Impact of Alternative Initiation, Splicing, and Termination on the Diversity of the mRNA Transcripts Encoded by the Mouse Transcriptome. <i>Genome Research</i> , 2003, 13, 1290-1300.	5.5	168
6	Methods for Prediction of Peptide Binding to MHC Molecules: A Comparative Study. <i>Molecular Medicine</i> , 2002, 8, 137-148.	4.4	133
7	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	3.5	95
8	Novel peroxisomal protease Tysnd1 processes PTS1- and PTS2-containing enzymes involved in $\beta$ -oxidation of fatty acids. <i>EMBO Journal</i> , 2007, 26, 835-845.	7.8	94
9	Mouse Proteome Analysis. <i>Genome Research</i> , 2003, 13, 1335-1344.	5.5	91
10	Id4, a New Candidate Gene for Senile Osteoporosis, Acts as a Molecular Switch Promoting Osteoblast Differentiation. <i>PLoS Genetics</i> , 2010, 6, e1001019.	3.5	67
11	HLA-B*3501 peptide interactions: role of anchor residues of peptides in their binding to HLA-B* 3501 molecules. <i>International Immunology</i> , 1994, 6, 255-261.	4.0	55
12	Identification of novel PPAR $\beta$ target genes by integrated analysis of ChIP-on-chip and microarray expression data during adipocyte differentiation. <i>Biochemical and Biophysical Research Communications</i> , 2008, 372, 362-366.	2.1	52
13	FIMM, a database of functional molecular immunology. <i>Nucleic Acids Research</i> , 2000, 28, 222-224.	14.5	48
14	FIMM, a database of functional molecular immunology: update 2002. <i>Nucleic Acids Research</i> , 2002, 30, 226-229.	14.5	38
15	Data warehousing in molecular biology. <i>Briefings in Bioinformatics</i> , 2000, 1, 190-198.	6.5	36
16	Mhc-DRB genes of the pigtail macaque ( <i>Macaca nemestrina</i> ): implications for the evolution of human DRB genes. <i>Molecular Biology and Evolution</i> , 1991, 8, 563-78.	8.9	35
17	Efficient discovery of immune response targets by cyclical refinement of QSAR models of peptide binding. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 405-411.	2.4	35
18	Methods for prediction of peptide binding to MHC molecules: a comparative study. <i>Molecular Medicine</i> , 2002, 8, 137-48.	4.4	35

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19	Tysnd1 Deficiency in Mice Interferes with the Peroxisomal Localization of PTS2 Enzymes, Causing Lipid Metabolic Abnormalities and Male Infertility. <i>PLoS Genetics</i> , 2013, 9, e1003286.	3.5	32
20	Conservative evolution of the Mhc-DP region in anthropoid primates. <i>Human Immunology</i> , 1993, 37, 75-84.	2.4	31
21	Multiplication of Mhc-DRB5 loci in the orangutan: implications for the evolution of DRB haplotypes. <i>Mammalian Genome</i> , 1993, 4, 159-170.	2.2	30
22	Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. <i>BMC Bioinformatics</i> , 2006, 7, S8.	2.6	26
23	Gorilla major histocompatibility complex-DRB pseudogene orthologous to HLA-DRBVIII. <i>Human Immunology</i> , 1991, 32, 211-220.	2.4	25
24	The Mammalian Protein-Protein Interaction Database and Its Viewing System That Is Linked to the Main FANTOM2 Viewer. <i>Genome Research</i> , 2003, 13, 1534-1541.	5.5	23
25	BlockLogo: Visualization of peptide and sequence motif conservation. <i>Journal of Immunological Methods</i> , 2013, 400-401, 37-44.	1.4	22
26	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. <i>Genome Research</i> , 2002, 12, 367-378.	5.5	21
27	Identification of HTLV-1-Specific CTL Directed against Synthetic and Naturally Processed Peptides in HLA-B*3501 Transgenic Mice. <i>Virology</i> , 1996, 226, 102-112.	2.4	20
28	Residue 116 determines the C-terminal anchor residue of HLA-B * 3501 and -B * 5101 binding peptides but does not explain the general affinity difference. <i>Immunogenetics</i> , 1998, 47, 256-263.	2.4	20
29	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. <i>BMC Bioinformatics</i> , 2011, 12, S1.	2.6	20
30	Large-scale computational identification of HIV T-cell epitopes. <i>Immunology and Cell Biology</i> , 2002, 80, 300-306.	2.3	19
31	Effects of a Single Escape Mutation on T Cell and HIV-1 Co-adaptation. <i>Cell Reports</i> , 2016, 15, 2279-2291.	6.4	19
32	Refined peptide HLA-B * 3501 binding motif reveals differences in 9-mer to 11-mer peptide binding. <i>Immunogenetics</i> , 1996, 45, 121-129.	2.4	18
33	Predominant role of N-terminal residue of nonamer peptides in their binding to HLA-B * 5101 molecules. <i>Immunogenetics</i> , 1997, 46, 245-248.	2.4	17
34	An Update on the Functional Molecular Immunology (FIMM) Database. <i>Applied Bioinformatics</i> , 2005, 4, 25-31.	1.6	15
35	Predicted mouse peroxisome-targeted proteins and their actual subcellular locations. <i>BMC Bioinformatics</i> , 2008, 9, S16.	2.6	15
36	Inferring Higher Functional Information for RIKEN Mouse Full-Length cDNA Clones With FACTS. <i>Genome Research</i> , 2003, 13, 1520-1533.	5.5	14

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37	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). BMC Genomics, 2010, 11, S1.	2.8	14
38	Phylogeny of primate major histocompatibility complex DRB alleles. Human Immunology, 1991, 31, 28-33.	2.4	12
39	Sequence-Based Discovery of the Human and Rodent Peroxisomal Proteome. Applied Bioinformatics, 2005, 4, 93-104.	1.6	12
40	Computational vaccinology and the ICoVax 2012 workshop. BMC Bioinformatics, 2013, 14, 11.	2.6	10
41	Textmining in support of knowledge discovery for vaccine development. Methods, 2004, 34, 488-495.	3.8	8
42	From Immunogenetics to Immunomics: Functional Prospecting of Genes and Transcripts. Novartis Foundation Symposium, 2008, , 177-192.	1.1	7
43	Molecular docking analysis of 2009-H1N1 and 2004-H5N1 influenza virus HLA-B*4405-restricted HA epitope candidates: implications for TCR cross-recognition and vaccine development. BMC Bioinformatics, 2013, 14, S21.	2.6	7
44	APBioNetâ€”Transforming Bioinformatics in the Asia-Pacific Region. PLoS Computational Biology, 2013, 9, e1003317.	3.2	7
45	Computational and Bioinformatics Techniques for Immunology. BioMed Research International, 2014, 2014, 1-2.	1.9	7
46	Top soil physical and chemical properties in Kazakhstan across a north-south gradient. Scientific Data, 2018, 5, 180242.	5.3	7
47	FREP: a database of functional repeats in mouse cDNAs. Nucleic Acids Research, 2004, 32, 471D-475.	14.5	6
48	Identification of "pathologs" (disease-related genes) from the RIKEN mouse cDNA dataset using human curation plus FACTS, a new biological information extraction system. BMC Genomics, 2004, 5, 28.	2.8	6
49	InCoB2013 introduces Systems Biology as a major conference theme. BMC Systems Biology, 2013, 7, S1.	3.0	6
50	Distribution of potentially toxic soil elements along a transect across Kazakhstan. Geoderma Regional, 2020, 21, e00281.	2.1	6
51	From masking repeats to identifying functional repeats in the mouse transcriptome. Briefings in Bioinformatics, 2004, 5, 107-117.	6.5	5
52	Crucial role of N-terminal residue of binding peptides in recognition of the monoclonal antibody specific for the peptide-HLA-B5, -B35 complex. Immunogenetics, 1997, 47, 149-158.	2.4	4
53	InCoB2014: Systems Biology update from the Asia-Pacific. BMC Systems Biology, 2014, 8, 11.	3.0	4
54	Epitope Predictions. , 2019, , 952-971.		4

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55	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. BMC Bioinformatics, 2010, 11, S1.	2.6	3
56	InCoB2014: mining biological data from genomics for transforming industry and health. BMC Genomics, 2014, 15, 11.	2.8	3
57	Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). BMC Bioinformatics, 2016, 17, 524.	2.6	3
58	Cytokine-Related Genes Identified From the RIKEN Full-Length Mouse cDNA Data Set. Genome Research, 2003, 13, 1307-1317.	5.5	2
59	Identification of Potential Peroxisomal Proteins in Mouse. Genome Research, 2003, 13, 1560-1560.	5.5	2
60	Camostat Does Not Inhibit the Proteolytic Activity of Neutrophil Serine Proteases. Pharmaceuticals, 2022, 15, 500.	3.8	2
61	Identification of Novel "Pathologs" (Human Disease-Related Gene Candidates) From the RIKEN Full-Length Mouse cDNA Data Set. Genome Research, 2003, 13, 1559-1559.	5.5	1
62	A possible mutation that enables H1N1 influenza a virus to escape antibody recognition. , 2010, , .		1
63	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. BMC Bioinformatics, 2015, 16, 11.	2.6	1
64	A bioinformatics potpourri. BMC Genomics, 2018, 19, 920.	2.8	1
65	APBioNet's annual International Conference on Bioinformatics (InCoB) returns to India in 2018. BMC Genomics, 2019, 19, 266.	2.8	1
66	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. Genome Research, 2002, 12, 367-378.	5.5	1
67	The Contribution of Alternative Transcription and Alternative Splicing to the Complexity of Mammalian Transcriptomes. , 2006, , 351-380.		0
68	The RIKEN Mouse Transcriptome: Lessons Learned and Implications for the Regulation of Immune Reactions. Novartis Foundation Symposium, 2007, 281, 25-37.	1.1	0
69	InCoB2014: bioinformatics to tackle the data to knowledge challenge. BMC Bioinformatics, 2014, 15, 11.	2.6	0
70	Further characterization of anchor and non-anchor residues on deca- and undeca-peptides in addition to nona-peptides, which bind to the HLA Class I molecules (HLA-B*3501). , 2002, , 797-798.		0