

# 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	Camostat Does Not Inhibit the Proteolytic Activity of Neutrophil Serine Proteases. <i>Pharmaceuticals</i> , 2022, 15, 500.	3.8	2
2	Distribution of potentially toxic soil elements along a transect across Kazakhstan. <i>Geoderma Regional</i> , 2020, 21, e00281.	2.1	6
3	Epitope Predictions. , 2019, , 952-971.		4
4	APBioNet's annual International Conference on Bioinformatics (InCoB) returns to India in 2018. <i>BMC Genomics</i> , 2019, 19, 266.	2.8	1
5	Top soil physical and chemical properties in Kazakhstan across a north-south gradient. <i>Scientific Data</i> , 2018, 5, 180242.	5.3	7
6	A bioinformatics potpourri. <i>BMC Genomics</i> , 2018, 19, 920.	2.8	1
7	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
8	Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). <i>BMC Bioinformatics</i> , 2016, 17, 524.	2.6	3
9	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. <i>BMC Bioinformatics</i> , 2015, 16, 11.	2.6	1
10	Computational and Bioinformatics Techniques for Immunology. <i>BioMed Research International</i> , 2014, 2014, 1-2.	1.9	7
11	InCoB2014: mining biological data from genomics for transforming industry and health. <i>BMC Genomics</i> , 2014, 15, 11.	2.8	3
12	InCoB2014: bioinformatics to tackle the data to knowledge challenge. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	0
13	InCoB2014: Systems Biology update from the Asia-Pacific. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	4
14	Computational vaccinology and the ICoVax 2012 workshop. <i>BMC Bioinformatics</i> , 2013, 14, 11.	2.6	10
15	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. <i>BMC Bioinformatics</i> , 2013, 14, S21.	2.6	7
16	InCoB2013 introduces Systems Biology as a major conference theme. <i>BMC Systems Biology</i> , 2013, 7, S1.	3.0	6
17	BlockLogo: Visualization of peptide and sequence motif conservation. <i>Journal of Immunological Methods</i> , 2013, 400-401, 37-44.	1.4	22
18	APBioNetâ€™s Transforming Bioinformatics in the Asia-Pacific Region. <i>PLoS Computational Biology</i> , 2013, 9, e1003317.	3.2	7

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19	Tysnd1 Deficiency in Mice Interferes with the Peroxisomal Localization of PTS2 Enzymes, Causing Lipid Metabolic Abnormalities and Male Infertility. PLoS Genetics, 2013, 9, e1003286.	3.5	32
20	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. BMC Bioinformatics, 2011, 12, S1.	2.6	20
21	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. BMC Bioinformatics, 2010, 11, S1.	2.6	3
22	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
23	Id4, a New Candidate Gene for Senile Osteoporosis, Acts as a Molecular Switch Promoting Osteoblast Differentiation. PLoS Genetics, 2010, 6, e1001019.	3.5	67
24	A possible mutation that enables H1N1 influenza a virus to escape antibody recognition. , 2010, , .		1
25	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
26	Predicted mouse peroxisome-targeted proteins and their actual subcellular locations. BMC Bioinformatics, 2008, 9, S16.	2.6	15
27	Identification of novel PPAR $\alpha$ target genes by integrated analysis of ChIP-on-chip and microarray expression data during adipocyte differentiation. Biochemical and Biophysical Research Communications, 2008, 372, 362-366.	2.1	52
28	From Immunogenetics to Immunomics: Functional Prospecting of Genes and Transcripts. Novartis Foundation Symposium, 2008, , 177-192.	1.1	7
29	The RIKEN Mouse Transcriptome: Lessons Learned and Implications for the Regulation of Immune Reactions. Novartis Foundation Symposium, 2007, 281, 25-37.	1.1	0
30	Novel peroxisomal protease Tysnd1 processes PTS1- and PTS2-containing enzymes involved in $\beta$ -oxidation of fatty acids. EMBO Journal, 2007, 26, 835-845.	7.8	94
31	The Contribution of Alternative Transcription and Alternative Splicing to the Complexity of Mammalian Transcriptomes. , 2006, , 351-380.		0
32	Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. BMC Bioinformatics, 2006, 7, S8.	2.6	26
33	Mice and Men: Their Promoter Properties. PLoS Genetics, 2006, 2, e54.	3.5	95
34	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	12.6	3,227
35	Sequence-Based Discovery of the Human and Rodent Peroxisomal Proteome. Applied Bioinformatics, 2005, 4, 93-104.	1.6	12
36	An Update on the Functional Molecular Immunology (FIMM) Database. Applied Bioinformatics, 2005, 4, 25-31.	1.6	15

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37	From masking repeats to identifying functional repeats in the mouse transcriptome. Briefings in Bioinformatics, 2004, 5, 107-117.	6.5	5
38	FREP: a database of functional repeats in mouse cDNAs. Nucleic Acids Research, 2004, 32, 471D-475.	14.5	6
39	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
40	Textmining in support of knowledge discovery for vaccine development. Methods, 2004, 34, 488-495.	3.8	8
41	Impact of Alternative Initiation, Splicing, and Termination on the Diversity of the mRNA Transcripts Encoded by the Mouse Transcriptome. Genome Research, 2003, 13, 1290-1300.	5.5	168
42	Cytokine-Related Genes Identified From the RIKEN Full-Length Mouse cDNA Data Set. Genome Research, 2003, 13, 1307-1317.	5.5	2
43	Mouse Proteome Analysis. Genome Research, 2003, 13, 1335-1344.	5.5	91
44	Inferring Higher Functional Information for RIKEN Mouse Full-Length cDNA Clones With FACTS. Genome Research, 2003, 13, 1520-1533.	5.5	14
45	The Mammalian Protein-Protein Interaction Database and Its Viewing System That Is Linked to the Main FANTOM2 Viewer. Genome Research, 2003, 13, 1534-1541.	5.5	23
46	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
47	Identification of Potential Peroxisomal Proteins in Mouse. Genome Research, 2003, 13, 1560-1560.	5.5	2
48	FIMM, a database of functional molecular immunology: update 2002. Nucleic Acids Research, 2002, 30, 226-229.	14.5	38
49	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. Genome Research, 2002, 12, 367-378.	5.5	21
50	Methods for Prediction of Peptide Binding to MHC Molecules: A Comparative Study. Molecular Medicine, 2002, 8, 137-148.	4.4	133
51	Large-scale computational identification of HIV T-cell epitopes. Immunology and Cell Biology, 2002, 80, 300-306.	2.3	19
52	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	27.8	1,548
53	Exploration of Novel Motifs Derived from Mouse cDNA Sequences. Genome Research, 2002, 12, 367-378.	5.5	1
54	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

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55	Methods for prediction of peptide binding to MHC molecules: a comparative study. <i>Molecular Medicine</i> , 2002, 8, 137-48.	4.4	35
56	Functional annotation of a full-length mouse cDNA collection. <i>Nature</i> , 2001, 409, 685-690.	27.8	653
57	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
58	FIMM, a database of functional molecular immunology. <i>Nucleic Acids Research</i> , 2000, 28, 222-224.	14.5	48
59	Data warehousing in molecular biology. <i>Briefings in Bioinformatics</i> , 2000, 1, 190-198.	6.5	36
60	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
61	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
62	Crucial role of N-terminal residue of binding peptides in recognition of the monoclonal antibody specific for the peptide-HLA-B5, -B35 complex. <i>Immunogenetics</i> , 1997, 47, 149-158.	2.4	4
63	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
64	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
65	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
66	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
67	Conservative evolution of the Mhc-DP region in anthropoid primates. <i>Human Immunology</i> , 1993, 37, 75-84.	2.4	31
68	Phylogeny of primate major histocompatibility complex DRB alleles. <i>Human Immunology</i> , 1991, 31, 28-33.	2.4	12
69	Gorilla major histocompatibility complex-DRB pseudogene orthologous to HLA-DRBVIII. <i>Human Immunology</i> , 1991, 32, 211-220.	2.4	25
70	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