Daniel Hoffmann

List of Publications by Year
in descending order

135 papers	5,251 citations	94415 37 h-index	102480 66 g-index
152 all docs	152 docs citations	152 times ranked	7535 citing authors

#	Article	IF	Citations
1	DNA-methylation patterns imply a common cellular origin of virus- and UV-associated Merkel cell carcinoma. Oncogene, 2022, 41, 37-45.	5.9	8
2	Clinical and molecular characteristics associated with response to therapeutic PD-1/PD-L1 inhibition in advanced Merkel cell carcinoma. , 2022, 10, e003198.		21
3	HAMdetector: a Bayesian regression model that integrates information to detect HLA-associated mutations. Bioinformatics, 2022, 38, 2428-2436.	4.1	1
4	BRAF and MEK inhibition in melanoma patients enables reprogramming of tumor infiltrating lymphocytes. Cancer Immunology, Immunotherapy, 2021, 70, 1635-1647.	4.2	13
5	Hepatitis B virus particles activate B cells through the TLR2â€"MyD88â€"mTOR axis. Cell Death and Disease, 2021, 12, 34.	6.3	13
6	UMI or not UMI, that is the question for scRNA-seq zero-inflation. Nature Biotechnology, 2021, 39, 158-159.	17.5	24
7	Specific inhibition of the Survivinâ€"CRM1 interaction by peptide-modified molecular tweezers. Nature Communications, 2021, 12, 1505.	12.8	18
8	Classifier uncertainty: evidence, potential impact, and probabilistic treatment. PeerJ Computer Science, 2021, 7, e398.	4.5	12
9	Epigenetic profiling of articular chondrocytes. Osteoarthritis and Cartilage, 2021, 29, S309.	1.3	0
10	Comprehensive Comparison of RNA-Seq Data of SARS-CoV-2, SARS-CoV and MERS-CoV Infections: Alternative Entry Routes and Innate Immune Responses. Frontiers in Immunology, 2021, 12, 656433.	4.8	11
11	Computational Tools for Discovery of CD8 T cell Epitopes and CTL Immune Escape in Viruses Causing Persistent Infections. , 2021, , 141-156.		0
12	Human Cord Blood B Cells Differ from the Adult Counterpart by Conserved Ig Repertoires and Accelerated Response Dynamics. Journal of Immunology, 2021, 206, 2839-2851.	0.8	18
13	Rhinovirus prevalence as indicator for efficacy of measures against SARS-CoV-2. BMC Public Health, 2021, 21, 1178.	2.9	13
14	Classical and Variant Merkel Cell Carcinoma Cell Lines Display Different Degrees of Neuroendocrine Differentiation and Epithelial-Mesenchymal Transition. Journal of Investigative Dermatology, 2021, 141, 1675-1686.e4.	0.7	13
15	Abstract 3065: Modeling common aspects of the metabolic response of cancer cells to ionizing radiation. , 2021, , .		0
16	Metabolism of cancer cells commonly responds to irradiation by a transient early mitochondrial shutdown. IScience, 2021, 24, 103366.	4.1	15
17	A Pro-Inflammatory Gut Microbiome Characterizes SARS-CoV-2 Infected Patients and a Reduction in the Connectivity of an Anti-Inflammatory Bacterial Network Associates With Severe COVID-19. Frontiers in Cellular and Infection Microbiology, 2021, 11, 747816.	3.9	51
18	Wnt5a is a transcriptional target of Gli3 and Trps1 at the onset of chondrocyte hypertrophy. Developmental Biology, 2020, 457, 104-118.	2.0	14

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19	Excessive Neutrophils and Neutrophil Extracellular Traps in COVID-19. Frontiers in Immunology, 2020, 11, 2063.	4.8	198
20	Accelerated trypsin autolysis by affinity polymer templates. RSC Advances, 2020, 10, 28711-28719.	3.6	2
21	Rapid Uptake of Pre-Exposure Prophylaxis After Significant Price Reduction in Germany Highlights Importance of Pre-Exposure Prophylaxis Accessibility. AIDS Research and Human Retroviruses, 2020, 36, 721-733.	1.1	4
22	IgGeneUsage: differential gene usage in immune repertoires. Bioinformatics, 2020, 36, 3590-3591.	4.1	2
23	Predominance of Central Memory T Cells with High T-Cell Receptor Repertoire Diversity is Associated with Response to PD-1/PD-L1 Inhibition in Merkel Cell Carcinoma. Clinical Cancer Research, 2020, 26, 2257-2267.	7.0	39
24	Chondrocytes respond to an altered heparan sulfate composition with distinct changes of heparan sulfate structure and increased levels of chondroitin sulfate. Matrix Biology, 2020, 93, 43-59.	3.6	13
25	An altered heparan sulfate structure in the articular cartilage protects against osteoarthritis. Osteoarthritis and Cartilage, 2020, 28, 977-987.	1.3	13
26	Epigenetic Mechanisms Mediating Cell State Transitions in Chondrocytes. Journal of Bone and Mineral Research, 2020, 36, 968-985.	2.8	4
27	Integrin Alpha E (CD103) Limits Virus-Induced IFN-I Production in Conventional Dendritic Cells. Frontiers in Immunology, 2020, 11, 607889.	4.8	1
28	intePareto: an R package for integrative analyses of RNA-Seq and ChIP-Seq data. BMC Genomics, 2020, 21, 802.	2.8	11
29	Bayesian Data Integration Questions Classic Study on Protease Self-Digest Kinetics. ACS Omega, 2020, 5, 15162-15168.	3.5	2
30	Atoh8 acts as a regulator of chondrocyte proliferation and differentiation in endochondral bones. PLoS ONE, 2019, 14, e0218230.	2.5	11
31	A network of trans-cortical capillaries as mainstay for blood circulation in long bones. Nature Metabolism, 2019, 1, 236-250.	11.9	221
32	A new class of supramolecular ligands stabilizes 14-3-3 protein–protein interactions by up to two orders of magnitude. Chemical Communications, 2019, 55, 111-114.	4.1	11
33	Treatment of Chronic Hepatitis B Virus Infection Using Small Molecule Modulators of Nucleocapsid Assembly: Recent Advances and Perspectives. ACS Infectious Diseases, 2019, 5, 713-724.	3.8	57
34	Mutations in Hepatitis D Virus Allow It to Escape Detection by CD8+ T Cells and Evolve at the Population Level. Gastroenterology, 2019, 156, 1820-1833.	1.3	44
35	Gut Microbiota in Human Immunodeficiency Virus–Infected Individuals Linked to Coronary Heart Disease. Journal of Infectious Diseases, 2019, 219, 497-508.	4.0	39
36	Differential escape of HCV from CD8+ T cell selection pressure between China and Germany depends on the presenting HLA class I molecule. Journal of Viral Hepatitis, 2019, 26, 73-82.	2.0	4

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37	Atoh8 acts as a regulator of chondrocyte proliferation and differentiation in endochondral bones. , 2019, 14, e0218230.		0
38	Atoh8 acts as a regulator of chondrocyte proliferation and differentiation in endochondral bones. , 2019, 14, e0218230.		0
39	Atoh8 acts as a regulator of chondrocyte proliferation and differentiation in endochondral bones. , 2019, 14, e0218230.		0
40	Atoh8 acts as a regulator of chondrocyte proliferation and differentiation in endochondral bones. , 2019, 14, e0218230.		0
41	Amino Acid Substitutions within HLA-B*27-Restricted T Cell Epitopes Prevent Recognition by Hepatitis Delta Virus-Specific CD8$^+$T Cells. Journal of Virology, 2018, 92, .	3.4	23
42	Rational Design, Binding Studies, and Crystal†Structure Evaluation of the First Ligand Targeting the Dimerization Interface of the 14â€3â€3Î¶ Adapter Protein. ChemBioChem, 2018, 19, 591-595.	2.6	15
43	Locating Large, Flexible Ligands on Proteins. Journal of Chemical Information and Modeling, 2018, 58, 315-327.	5.4	6
44	Illumina sequencing for the identification of filamentous bulking and foaming bacteria in industrial activated sludge plants. International Journal of Environmental Science and Technology, 2018, 15, 1139-1158.	3.5	24
45	Signaling systems affecting the severity of multiple osteochondromas. Bone, 2018, 111, 71-81.	2.9	11
46	Biased IGH VDJ gene repertoire and clonal expansions in B cells of chronically hepatitis C virusâ€"infected individuals. Blood, 2018, 131, 546-557.	1.4	28
47	Evaluation of susceptibility of HIV-1 CRF01_AE variants to neutralization by a panel of broadly neutralizing antibodies. Archives of Virology, 2018, 163, 3303-3315.	2.1	9
48	Proteolytic processing of palmitoylated Hedgehog peptides specifies the 3-4 intervein region of the Drosophila wing. ELife, 2018, 7, .	6.0	15
49	Trade-off shapes diversity in eco-evolutionary dynamics. ELife, 2018, 7, .	6.0	37
50	Quantitative Assessment of Molecular Dynamics Sampling for Flexible Systems. Journal of Chemical Theory and Computation, 2017, 13, 400-414.	5.3	17
51	The spectrum of aseptic central nervous system infections in southern Germany â€" demographic, clinical and laboratory findings. European Journal of Neurology, 2017, 24, 1062-1070.	3.3	17
52	Calcium coordination controls sonic hedgehog structure and Scube2-cubulin domain regulated release. Journal of Cell Science, 2017, 130, 3261-3271.	2.0	20
53	Quantitative Comparison of Abundance Structures of Generalized Communities: From B-Cell Receptor Repertoires to Microbiomes. PLoS Computational Biology, 2017, 13, e1005362.	3.2	17
54	Granulocytic myeloid-derived suppressor cells suppress virus-specific CD8+ T cell responses during acute Friend retrovirus infection. Retrovirology, 2017, 14, 42.	2.0	20

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55	SeqFeatR for the Discovery of Feature-Sequence Associations. PLoS ONE, 2016, 11, e0146409.	2.5	10
56	Role of Gag mutations in PI resistance in the Swiss HIV cohort study: bystanders or contributors?. Journal of Antimicrobial Chemotherapy, 2016, 72, dkw493.	3.0	12
57	Protistan community analysis: key findings of a large-scale molecular sampling. ISME Journal, 2016, 10, 2269-2279.	9.8	145
58	Parameters Influencing Baseline HIV-1 Genotypic Tropism Testing Related to Clinical Outcome in Patients on Maraviroc. PLoS ONE, 2015, 10, e0125502.	2.5	7
59	Virus-Induced Type I Interferon Deteriorates Control of Systemic Pseudomonas Aeruginosa Infection. Cellular Physiology and Biochemistry, 2015, 36, 2379-2392.	1.6	14
60	Adaptation of the hepatitis B virus core protein to CD8+ Tâ€cell selection pressure. Hepatology, 2015, 62, 47-56.	7.3	45
61	Complexity of the human memory B-cell compartment is determined by the versatility of clonal diversification in germinal centers. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5281-9.	7.1	58
62	Pareto Optimization Identifies Diverse Set of Phosphorylation Signatures Predicting Response to Treatment with Dasatinib. PLoS ONE, 2015, 10, e0128542.	2.5	4
63	AmpliconDuo: A Split-Sample Filtering Protocol for High-Throughput Amplicon Sequencing of Microbial Communities. PLoS ONE, 2015, 10, e0141590.	2.5	53
64	Signaling Domain of Sonic Hedgehog as Cannibalistic Calcium-Regulated Zinc-Peptidase. PLoS Computational Biology, 2014, 10, e1003707.	3.2	10
65	Differential selection in HIV-1 gp120 between subtype B and East Asian variant Bâ€™. Virologica Sinica, 2014, 29, 40-47.	3.0	3
66	A simple structure-based model for the prediction of HIV-1 co-receptor tropism. BioData Mining, 2014, 7, 14.	4.0	27
67	Identification of Significant Features by the Global Mean Rank Test. PLoS ONE, 2014, 9, e104504.	2.5	18
68	Inference of global HIV-1 sequence patterns and preliminary feature analysis. Virologica Sinica, 2013, 28, 228-238.	3.0	1
69	Transient Domain Interactions Enhance the Affinity of the Mitotic Regulator Pin1 toward Phosphorylated Peptide Ligands. Structure, 2013, 21, 1769-1777.	3.3	24
70	A new approach to inhibit human Î²-tryptase by protein surface binding of four-armed peptide ligands with two different sets of arms. Organic and Biomolecular Chemistry, 2013, 11, 1631.	2.8	21
71	The amino acid substitutions rtP177G and rtF249A in the reverse transcriptase domain of hepatitis B virus polymerase reduce the susceptibility to tenofovir. Antiviral Research, 2013, 97, 93-100.	4.1	44
72	An emerging role of Sonic Hedgehog shedding as a modulator of heparan sulfate interactions.. Journal of Biological Chemistry, 2013, 288, 5049.	3.4	0

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73	Design of a Modular Protein-Based MRI Contrast Agent for Targeted Application. PLoS ONE, 2013, 8, e65346.	2.5	13
74	A Small Set of Succinct Signature Patterns Distinguishes Chinese and Non-Chinese HIV-1 Genomes. PLoS ONE, 2013, 8, e58804.	2.5	7
75	Novel Algorithm for Non-Invasive Assessment of Fibrosis in NAFLD. PLoS ONE, 2013, 8, e62439.	2.5	55
76	An Emerging Role of Sonic Hedgehog Shedding as a Modulator of Heparan Sulfate Interactions. Journal of Biological Chemistry, 2012, 287, 43708-43719.	3.4	49
77	Escape from a Dominant HLA-B*15-Restricted CD8 $^+$ T Cell Response against Hepatitis C Virus Requires Compensatory Mutations outside the Epitope. Journal of Virology, 2012, 86, 991-1000.	3.4	21
78	The Normal-Mode Entropy in the MM/GBSA Method: Effect of System Truncation, Buffer Region, and Dielectric Constant. Journal of Chemical Information and Modeling, 2012, 52, 2079-2088.	5.4	166
79	The imprinted NPAP1/C15orf2 gene in the Prader–Willi syndrome region encodes a nuclear pore complex associated protein. Human Molecular Genetics, 2012, 21, 4038-4048.	2.9	25
80	CD8+ T-Cell Response Promotes Evolution of Hepatitis C Virus Nonstructural Proteins. Gastroenterology, 2011, 140, 2064-2073.	1.3	42
81	Machine learning on normalized protein sequences. BMC Research Notes, 2011, 4, 94.	1.4	15
82	Sonic Hedgehog Shedding Results in Functional Activation of the Solubilized Protein. Developmental Cell, 2011, 20, 764-774.	7.0	78
83	Parental origin and functional relevance of a de novo UBE3A variant. European Journal of Medical Genetics, 2011, 54, 19-24.	1.3	8
84	An additional glucose dehydrogenase from *Sulfolobus solfataricus*: fine-tuning of sugar degradation?. Biochemical Society Transactions, 2011, 39, 77-81.	3.4	19
85	Interpol: An R package for preprocessing of protein sequences. BioData Mining, 2011, 4, 16.	4.0	18
86	Improved Bevirimat resistance prediction by combination of structural and sequence-based classifiers. BioData Mining, 2011, 4, 26.	4.0	20
87	Backbone rigidity and static presentation of guanidinium groups increases cellular uptake of arginine-rich cell-penetrating peptides. Nature Communications, 2011, 2, 453.	12.8	253
88	Single-Domain Parvulins Constitute a Specific Marker for Recently Proposed Deep-Branching Archaeal Subgroups. Evolutionary Bioinformatics, 2011, 7, EBO.S7683.	1.2	4
89	Widespread regulation of gene expression in the Drosophila genome by the histone acetyltransferase dTip60. Chromosoma, 2010, 119, 99-113.	2.2	10
90	Predicting Bevirimat resistance of HIV-1 from genotype. BMC Bioinformatics, 2010, 11, 37.	2.6	29

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91	The antiretroviral potency of emtricitabine is approximately 3-fold higher compared to lamivudine in dual human immunodeficiency virus type 1 infection/competition experiments in vitro. Antiviral Research, 2010, 86, 312-315.	4.1	6
92	Structure of HIV-1 quasi-species as early indicator for switches of co-receptor tropism. AIDS Research and Therapy, 2010, 7, 41.	1.7	17
93	Estimating affinities of calcium ions to proteins. Advances and Applications in Bioinformatics and Chemistry, 2010, 3, 1.	2.6	4
94	Rpd3-dependent boundary formation at telomeres by removal of Sir2 substrate. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5522-5527.	7.1	52
95	Prediction of Co-Receptor Usage of HIV-1 from Genotype. PLoS Computational Biology, 2010, 6, e1000743.	3.2	46
96	A Novel Algorithm for Macromolecular Epitope Matching. Algorithms, 2009, 2, 498-517.	2.1	6
97	Prevalence of C-terminal gag cleavage site mutations in HIV from therapy-naÃ¯ve patients. Journal of Infection, 2009, 58, 61-67.	3.3	22
98	Prevalence of minor variants of HIV strains at reverse transcriptase position 103 in therapy-naÃ¯ve patients and their impact on the virological failure. Journal of Clinical Virology, 2009, 45, 34-38.	3.1	47
99	L76V â€" clinically relevant resensitization of the protease inhibitors (PIs) saquinavir (SQV) and atazanavir (ATV). Journal of the International AIDS Society, 2008, 11, P43.	3.0	0
100	Evolutionary Pareto-optimization of stably folding peptides. BMC Bioinformatics, 2008, 9, 109.	2.6	22
101	Biallelic loss of function of the promyelocytic leukaemia zinc finger (PLZF) gene causes severe skeletal defects and genital hypoplasia. Journal of Medical Genetics, 2008, 45, 731-737.	3.2	56
102	The B-cell epitope of the monoclonal anti-factor VIII antibody ESH8 characterized by peptide array analysis. Thrombosis and Haemostasis, 2008, 99, 634-637.	3.4	20
103	SearchXLinks. A Program for the Identification of Disulfide Bonds in Proteins from Mass Spectra. Analytical Chemistry, 2006, 78, 1235-1241.	6.5	38
104	The enzyme-binding region of human GM2-activator protein. FEBS Journal, 2006, 273, 982-991.	4.7	28
105	A Multiobjective Evolutionary Method for the Design of Peptidic Mimotopes. Journal of Computational Biology, 2006, 13, 113-125.	1.6	14
106	Arevir: A Secure Platform for Designing Personalized Antiretroviral Therapies Against HIV. Lecture Notes in Computer Science, 2006, , 185-194.	1.3	11
107	Compensatory Mutations at the HIV Cleavage Sites P7/P1 and P1/P6-Gag in Therapy-Naive and Therapy-Experienced Patients. Antiviral Therapy, 2006, 11, 879-888.	1.0	58
108	A multi-objective evolutionary approach to peptide structure redesign and stabilization. , 2005, , .		0

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109	Estimating HIV Evolutionary Pathways and the Genetic Barrier to Drug Resistance. Journal of Infectious Diseases, 2005, 191, 1953-1960.	4.0	76
110	Learning Multiple Evolutionary Pathways from Cross-Sectional Data. Journal of Computational Biology, 2005, 12, 584-598.	1.6	105
111	Mtreemix: a software package for learning and using mixture models of mutagenetic trees. Bioinformatics, 2005, 21, 2106-2107.	4.1	68
112	Computational methods for the design of effective therapies against drug resistant HIV strains. Bioinformatics, 2005, 21, 3943-3950.	4.1	103
113	Evolution of HIV resistance during treatment interruption in experienced patients and after restarting a new therapy. Journal of Clinical Virology, 2005, 34, 277-287.	3.1	20
114	Characterization of Novel HIV Drug Resistance Mutations Using Clustering, Multidimensional Scaling and SVM-Based Feature Ranking. Lecture Notes in Computer Science, 2005, , 285-296.	1.3	18
115	Learning multiple evolutionary pathways from cross-sectional data. , 2004, , .		3
116	Photoaffinity labelling of the Human GM2-activator protein. Mechanistic insight into ganglioside GM2 degradation. FEBS Journal, 2004, 271, 614-627.	0.2	49
117	A Functional Study on Saposin B and C Using Experimentally Validated Models. , 2003, , 19-27.		0
118	Geno2pheno: estimating phenotypic drug resistance from HIV-1 genotypes. Nucleic Acids Research, 2003, 31, 3850-3855.	14.5	213
119	Tenofovir Resistance and Resensitization. Antimicrobial Agents and Chemotherapy, 2003, 47, 3478-3484.	3.2	77
120	Methods for optimizing antiviral combination therapies. Bioinformatics, 2003, 19, i16-i25.	4.1	39
121	Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8271-8276.	7.1	310
122	Screening for Disulfide Bonds in Proteins by MALDI In-Source Decay and LIFT-TOF/TOF-MS. Analytical Chemistry, 2002, 74, 4980-4988.	6.5	109
123	Partial Reduction and Two-Step Modification of Proteins for Identification of Disulfide Bonds. Analytical Chemistry, 2002, 74, 2386-2393.	6.5	20
124	Structural modeling of ataxin-3 reveals distant homology to adaptins. Proteins: Structure, Function and Bioinformatics, 2002, 50, 355-370.	2.6	31
125	A New Method for the Fast Solution of Protein-3D-Structures, Combining Experiments and Bioinformatics. , 2002, , 59-78.		1
126	Geno2pheno: interpreting genotypic HIV drug resistance tests. IEEE Intelligent Systems, 2001, 16, 35-41.	4.0	42

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127	Simulation of oligopeptide folding or how do residues talk. , 1999, , .		0
128	Band-flip and kink as novel structural motifs in Î±-(1â†'4)-d-glucose oligosaccharides. Crystal structures of cyclodeca- and cyclotetradecaamylose. Carbohydrate Research, 1999, 322, 228-246.	2.3	47
129	Two-Stage Method for Proteinâˆ'Ligand Docking. Journal of Medicinal Chemistry, 1999, 42, 4422-4433.	6.4	86
130	A structural role for glycosylation: lessons from the hp model. Folding & Design, 1998, 3, 337-343.	4.5	26
131	Strain-Induced â€œBand Flipsâ€•in Cyclodecaamylose and Higher Homologues. Angewandte Chemie - International Edition, 1998, 37, 605-609.	13.8	62
132	Structures of the Common Cyclodextrins and Their Larger AnaloguesBeyond the Doughnut. Chemical Reviews, 1998, 98, 1787-1802.	47.7	685
133	Folding Pathways of a Helixâˆ'Turnâˆ'Helix Model Protein. Journal of Physical Chemistry B, 1997, 101, 6734-6740.	2.6	23
134	Polypeptide folding with off-lattice Monte Carlo dynamics: the method. European Biophysics Journal, 1996, 24, 387-403.	2.2	43
135	Protein dynamics with off-lattice Monte Carlo moves. Physical Review E, 1996, 53, 4221-4224.	2.1	24