

# Corey T Watson

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

4,569  
citations

147566

31  
h-index

123241

61  
g-index

93  
all docs

93  
docs citations

93  
times ranked

7665  
citing authors

#	ARTICLE	IF	CITATIONS
1	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. <i>Genome Research</i> , 2010, 20, 1352-1360.	2.4	737
2	Slow Delivery Immunization Enhances HIV Neutralizing Antibody and Germinal Center Responses via Modulation of Immunodominance. <i>Cell</i> , 2019, 177, 1153-1171.e28.	13.5	293
3	Complete Haplotype Sequence of the Human Immunoglobulin Heavy-Chain Variable, Diversity, and Joining Genes and Characterization of Allelic and Copy-Number Variation. <i>American Journal of Human Genetics</i> , 2013, 92, 530-546.	2.6	223
4	Tumor-derived exosomes drive immunosuppressive macrophages in a pre-metastatic niche through glycolytic dominant metabolic reprogramming. <i>Cell Metabolism</i> , 2021, 33, 2040-2058.e10.	7.2	200
5	A Potently Neutralizing Antibody Protects Mice against SARS-CoV-2 Infection. <i>Journal of Immunology</i> , 2020, 205, 915-922.	0.4	186
6	The immunoglobulin heavy chain locus: genetic variation, missing data, and implications for human disease. <i>Genes and Immunity</i> , 2012, 13, 363-373.	2.2	179
7	IGHV1-69 polymorphism modulates anti-influenza antibody repertoires, correlates with IGHV utilization shifts and varies by ethnicity. <i>Scientific Reports</i> , 2016, 6, 20842.	1.6	167
8	Genome-wide DNA methylation profiling in the superior temporal gyrus reveals epigenetic signatures associated with Alzheimer's disease. <i>Genome Medicine</i> , 2016, 8, 5.	3.6	163
9	Adaptive Immune Receptor Repertoire Community recommendations for sharing immune-repertoire sequencing data. <i>Nature Immunology</i> , 2017, 18, 1274-1278.	7.0	163
10	The Genetics of Microdeletion and Microduplication Syndromes: An Update. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 215-244.	2.5	145
11	Genome-Wide DNA Methylation Profiling Reveals Epigenetic Changes in the Rat Nucleus Accumbens Associated With Cross-Generational Effects of Adolescent THC Exposure. <i>Neuropsychopharmacology</i> , 2015, 40, 2993-3005.	2.8	143
12	The Individual and Population Genetics of Antibody Immunity. <i>Trends in Immunology</i> , 2017, 38, 459-470.	2.9	134
13	Reproducibility and Reuse of Adaptive Immune Receptor Repertoire Data. <i>Frontiers in Immunology</i> , 2017, 8, 1418.	2.2	102
14	Identification of rare de novo epigenetic variations in congenital disorders. <i>Nature Communications</i> , 2018, 9, 2064.	5.8	82
15	A specific low-density neutrophil population correlates with hypercoagulation and disease severity in hospitalized COVID-19 patients. <i>JCI Insight</i> , 2021, 6, .	2.3	79
16	Identification of Subject-Specific Immunoglobulin Alleles From Expressed Repertoire Sequencing Data. <i>Frontiers in Immunology</i> , 2019, 10, 129.	2.2	67
17	DNA Methylation Profiling of Uniparental Disomy Subjects Provides a Map of Parental Epigenetic Bias in the Human Genome. <i>American Journal of Human Genetics</i> , 2016, 99, 555-566.	2.6	66
18	A survey of inter-individual variation in DNA methylation identifies environmentally responsive co-regulated networks of epigenetic variation in the human genome. <i>PLoS Genetics</i> , 2018, 14, e1007707.	1.5	65

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19	Integrative transcriptomic analysis reveals key drivers of acute peanut allergic reactions. <i>Nature Communications</i> , 2017, 8, 1943.	5.8	64
20	Immunoglobulin Light Chain Gene Rearrangements, Receptor Editing and the Development of a Self-Tolerant Antibody Repertoire. <i>Frontiers in Immunology</i> , 2018, 9, 2249.	2.2	64
21	Inferred Allelic Variants of Immunoglobulin Receptor Genes: A System for Their Evaluation, Documentation, and Naming. <i>Frontiers in Immunology</i> , 2019, 10, 435.	2.2	63
22	A Novel Framework for Characterizing Genomic Haplotype Diversity in the Human Immunoglobulin Heavy Chain Locus. <i>Frontiers in Immunology</i> , 2020, 11, 2136.	2.2	54
23	Mechanisms Underlying Metabolic and Neural Defects in Zebrafish and Human Multiple Acyl-CoA Dehydrogenase Deficiency (MADD). <i>PLoS ONE</i> , 2009, 4, e8329.	1.1	52
24	Vitamin D receptor binding, chromatin states and association with multiple sclerosis. <i>Human Molecular Genetics</i> , 2012, 21, 3575-3586.	1.4	50
25	Gene Duplication and Divergence of Long Wavelength-Sensitive Opsin Genes in the Guppy, <i>Poecilia reticulata</i> . <i>Journal of Molecular Evolution</i> , 2011, 72, 240-252.	0.8	47
26	Comment on "A Database of Human Immune Receptor Alleles Recovered from Population Sequencing Data". <i>Journal of Immunology</i> , 2017, 198, 3371-3373.	0.4	46
27	Dual transcriptomic and epigenomic study of reaction severity in peanut-allergic children. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1219-1230.	1.5	44
28	DNA methylation profiling in X;autosome translocations supports a role for L1 repeats in the spread of X chromosome inactivation. <i>Human Molecular Genetics</i> , 2014, 23, 1224-1236.	1.4	43
29	Sequencing of the human IG light chain loci from a hydatidiform mole BAC library reveals locus-specific signatures of genetic diversity. <i>Genes and Immunity</i> , 2015, 16, 24-34.	2.2	43
30	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021, 18, 588-591.	9.0	40
31	Vaccine genetics of IGHV1-2 VRC01-class broadly neutralizing antibody precursor naïve human B cells. <i>Npj Vaccines</i> , 2021, 6, 113.	2.9	40
32	VDJbase: an adaptive immune receptor genotype and haplotype database. <i>Nucleic Acids Research</i> , 2020, 48, D1051-D1056.	6.5	39
33	Body Mass Index in Multiple Sclerosis modulates ceramide-induced DNA methylation and disease course. <i>EBioMedicine</i> , 2019, 43, 392-410.	2.7	36
34	Genomic organization of duplicated short wave-sensitive and long wave-sensitive opsin genes in the green swordtail, <i>Xiphophorus helleri</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 87.	3.2	32
35	The Effect of Single Nucleotide Polymorphisms from Genome Wide Association Studies in Multiple Sclerosis on Gene Expression. <i>PLoS ONE</i> , 2010, 5, e10142.	1.1	32
36	Germline immunoglobulin genes: Disease susceptibility genes hidden in plain sight?. <i>Current Opinion in Systems Biology</i> , 2020, 24, 100-108.	1.3	31

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37	OGRDB: a reference database of inferred immune receptor genes. <i>Nucleic Acids Research</i> , 2020, 48, D964-D970.	6.5	30
38	The induction of peripheral trained immunity in the pancreas incites anti-tumor activity to control pancreatic cancer progression. <i>Nature Communications</i> , 2022, 13, 759.	5.8	30
39	A comparison of immunoglobulin <scp>IGHV</scp>, <scp>IGHD</scp> and <scp>IGHJ</scp> genes in wildâ€derived and classical inbred mouse strains. <i>Immunology and Cell Biology</i> , 2019, 97, 888-901.	1.0	25
40	The ADC API: A Web API for the Programmatic Query of the AIRR Data Commons. <i>Frontiers in Big Data</i> , 2020, 3, 22.	1.8	24
41	T cell receptor beta germline variability is revealed by inference from repertoire data. <i>Genome Medicine</i> , 2022, 14, 2.	3.6	24
42	Fumarates target the metabolic-epigenetic interplay of brain-homing T cells in multiple sclerosis. <i>Brain</i> , 2019, 142, 647-661.	3.7	22
43	DNase hypersensitive sites and association with multiple sclerosis. <i>Human Molecular Genetics</i> , 2014, 23, 942-948.	1.4	21
44	Month of Birth and Thymic Output. <i>JAMA Neurology</i> , 2013, 70, 527.	4.5	19
45	Proteomic Analysis Reveals Novel Mechanisms by Which Polychlorinated Biphenyls Compromise the Liver Promoting Diet-Induced Steatohepatitis. <i>Journal of Proteome Research</i> , 2019, 18, 1582-1594.	1.8	19
46	Age-Associated Hyper-Methylated Regions in the Human Brain Overlap with Bivalent Chromatin Domains. <i>PLoS ONE</i> , 2012, 7, e43840.	1.1	18
47	Commentary on Population matched (pm) germline allelic variants of immunoglobulin (IG) loci: relevance in infectious diseases and vaccination studies in human populations. <i>Genes and Immunity</i> , 2021, 22, 335-338.	2.2	18
48	Phosphatidylinositol synthase is required for lens structural integrity and photoreceptor cell survival in the zebrafish eye. <i>Experimental Eye Research</i> , 2011, 93, 460-474.	1.2	16
49	Estimating the proportion of variation in susceptibility to multiple sclerosis captured by common SNPs. <i>Scientific Reports</i> , 2012, 2, 770.	1.6	16
50	HYBRIDIZATION LEADS TO SENSORY REPERTOIRE EXPANSION IN A GYNOGENETIC FISH, THE AMAZON MOLLY (<i>POECILIA FORMOSA</i>): A TEST OF THE HYBRID-SENSORY EXPANSION HYPOTHESIS. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 120-130.	1.1	16
51	Genomic Environment Impacts Color Vision Evolution in a Family with Visually Based Sexual Selection. <i>Genome Biology and Evolution</i> , 2017, 9, 3100-3107.	1.1	16
52	Gut Microbiota Composition Modulates the Magnitude and Quality of Germinal Centers during Plasmodium Infections. <i>Cell Reports</i> , 2020, 33, 108503.	2.9	16
53	Hepatic signalling disruption by pollutant Polychlorinated biphenyls in steatohepatitis. <i>Cellular Signalling</i> , 2019, 53, 132-139.	1.7	15
54	Genotyping and Copy Number Analysis of Immunoglobulin Heavy Chain Variable Genes Using Long Reads. <i>IScience</i> , 2020, 23, 100883.	1.9	15

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55	Igh Locus Polymorphism May Dictate Topological Chromatin Conformation and V Gene Usage in the Ig Repertoire. <i>Frontiers in Immunology</i> , 2021, 12, 682589.	2.2	13
56	Revisiting the T-cell receptor alpha/delta locus and possible associations with multiple sclerosis. <i>Genes and Immunity</i> , 2011, 12, 59-66.	2.2	9
57	Regulatory function of conserved sequences upstream of the long-wave sensitive opsin genes in teleost fishes. <i>Vision Research</i> , 2011, 51, 2295-2303.	0.7	9
58	Variations in antibody repertoires correlate with vaccine responses. <i>Genome Research</i> , 2022, 32, 791-804.	2.4	7
59	A BALB/c IGHV Reference Set, Defined by Haplotype Analysis of Long-Read VDJ-C Sequences From F1 (BALB/c x C57BL/6) Mice. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	7
60	IGHV4-39 deletion polymorphism does not associate with risk or outcome of multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2010, 225, 164-166.	1.1	5
61	A Proposed New Nomenclature for the Immunoglobulin Genes of <i>Mus musculus</i> . <i>Frontiers in Immunology</i> , 2019, 10, 2961.	2.2	5
62	Using High-Throughput Sequencing to Characterize the Development of the Antibody Repertoire During Infections: A Case Study of HIV-1. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1053, 245-263.	0.8	4
63	Limitations of lymphoblastoid cell lines for establishing genetic reference datasets in the immunoglobulin loci. <i>PLoS ONE</i> , 2021, 16, e0261374.	1.1	4
64	Comment on "Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome". <i>PLoS Genetics</i> , 2013, 9, e1003332.	1.5	3
65	Immunoglobulin genes, reproductive isolation and vertebrate speciation. <i>Immunology and Cell Biology</i> , 0, , .	1.0	3
66	Establishing Best Practices for Effective Online Learning Modules: a Single Institution Study. <i>Medical Science Educator</i> , 2018, 28, 683-691.	0.7	2
67	Integrin CD11b Negatively Regulates B Cell Receptor Signaling to Shape Humoral Response during Immunization and Autoimmunity. <i>Journal of Immunology</i> , 2021, 207, 1785-1797.	0.4	2
68	Tumor-Derived Exosomes Drive Immunosuppressive Macrophages in a Pre-Metastatic Niche Through NF-Kb Dependent Glycolytic Metabolic Reprogramming. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
69	Analysis of Serial Peripheral Blood Transcriptomes from Peanut Allergic Children Undergoing Double-blind, Placebo-controlled Oral Food Challenges Reveals Key Drivers of the Acute Allergic Response to Peanut. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, AB189.	1.5	0
70	Common genetic variants in the immunoglobulin heavy chain locus and their differential impact on group A streptococcal disease susceptibility: a comparative meta-analysis of genetic susceptibility studies. <i>Lancet, The</i> , 2017, 389, S76.	6.3	0
71	Tree-Guided Construction of Antibody Repertoires and Its Applications to CDR Annotation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
72	"Epic-Genetics": An exploration of preservice helping professionals' (mis)understanding of epigenetic influences on human development. <i>Teaching and Learning Inquiry</i> , 2020, 8, 122-137.	0.5	0