

John C Castle

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

5,577
citations

331670

21
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

9570
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutation-Derived Neoantigens for Cancer Immunotherapy. <i>Frontiers in Immunology</i> , 2019, 10, 1856.	4.8	78
2	Bioinformatic methods for cancer neoantigen prediction. <i>Progress in Molecular Biology and Translational Science</i> , 2019, 164, 25-60.	1.7	27
3	Human Leukocyte Antigen Typing Using High-Throughput DNA and RNA Sequencing and Application for Cell Line Identification. <i>Advances in Molecular Pathology</i> , 2019, 2, 187-199.	0.4	1
4	Actively personalized vaccination trial for newly diagnosed glioblastoma. <i>Nature</i> , 2019, 565, 240-245.	27.8	637
5	HLA and proteasome expression body map. <i>BMC Medical Genomics</i> , 2018, 11, 36.	1.5	95
6	In Silico Typing of Classical and Non-classical HLA Alleles from Standard RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2018, 1802, 177-191.	0.9	6
7	TCLP: an online cancer cell line catalogue integrating HLA type, predicted neo-epitopes, virus and gene expression. <i>Genome Medicine</i> , 2015, 7, 118.	8.2	78
8	Mutant MHC class II epitopes drive therapeutic immune responses to cancer. <i>Nature</i> , 2015, 520, 692-696.	27.8	1,030
9	Immunic, genomic and transcriptomic characterization of CT26 colorectal carcinoma. <i>BMC Genomics</i> , 2014, 15, 190.	2.8	334
10	A catalog of HLA type, HLA expression, and neo-epitope candidates in human cancer cell lines. <i>Oncolmmunology</i> , 2014, 3, e954893.	4.6	92
11	Mutated tumor alleles are expressed according to their DNA frequency. <i>Scientific Reports</i> , 2014, 4, 4743.	3.3	40
12	Genomics Meets Cancer Immunotherapy. , 2014, , 229-236.		0
13	Confidence-based Somatic Mutation Evaluation and Prioritization. <i>PLoS Computational Biology</i> , 2012, 8, e1002714.	3.2	30
14	Exploiting the Mutanome for Tumor Vaccination. <i>Cancer Research</i> , 2012, 72, 1081-1091.	0.9	706
15	Targeting the tumor mutanome for personalized vaccination therapy. <i>Oncolmmunology</i> , 2012, 1, 768-769.	4.6	55
16	HLA typing from RNA-Seq sequence reads. <i>Genome Medicine</i> , 2012, 4, 102.	8.2	204
17	Activity of the <i>Rhodopseudomonas palustris</i> p-Coumaroyl-Homoserine Lactone-Responsive Transcription Factor RpaR. <i>Journal of Bacteriology</i> , 2011, 193, 2598-2607.	2.2	45
18	NSR-seq transcriptional profiling enables identification of a gene signature of <i>Plasmodium falciparum</i> parasites infecting children. <i>Journal of Clinical Investigation</i> , 2011, 121, 1119-1129.	8.2	72

#	ARTICLE	IF	CITATIONS
19	Global regulation of alternative splicing during myogenic differentiation. <i>Nucleic Acids Research</i> , 2010, 38, 7651-7664.	14.5	135
20	Unique Signatures of Long Noncoding RNA Expression in Response to Virus Infection and Altered Innate Immune Signaling. <i>MBio</i> , 2010, 1, .	4.1	237
21	Digital Genome-Wide ncRNA Expression, Including SnoRNAs, across 11 Human Tissues Using PolyA-Neutral Amplification. <i>PLoS ONE</i> , 2010, 5, e11779.	2.5	108
22	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009, 6, 647-649.	19.0	160
23	Expression of 24,426 human alternative splicing events and predicted cis regulation in 48 tissues and cell lines. <i>Nature Genetics</i> , 2008, 40, 1416-1425.	21.4	272
24	Genome-Scale RNAi Screen for Host Factors Required for HIV Replication. <i>Cell Host and Microbe</i> , 2008, 4, 495-504.	11.0	689
25	A postnatal switch of CELF and MBNL proteins reprograms alternative splicing in the developing heart. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20333-20338.	7.1	433