Robert Huether

List of Publications by Year
in descending order

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53	9,794	236925	254184
papers	citations	25 h-index	43 g-index

54	54	54	16691
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
2	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. Nature Genetics, 2012, 44, 251-253.	21.4	1,402
3	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
4	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742
5	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
6	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
7	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
8	C11orf95â€“RELA fusions drive oncogenic NF-Î²B signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
9	Associations Between Cancer Predisposition Testing Panel Genes and Breast Cancer. JAMA Oncology, 2017, 3, 1190.	7.1	472
10	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
11	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
12	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1386-1391.	21.4	238
13	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
14	Association of Breast and Ovarian Cancers With Predisposition Genes Identified by Large-Scale Sequencing. JAMA Oncology, 2019, 5, 51.	7.1	145
15	Geneâ€specific criteria for PTEN variant curation: Recommendations from the ClinGen PTEN Expert Panel. Human Mutation, 2018, 39, 1581-1592.	2.5	123
16	Clinical validation of the tempus xT next-generation targeted oncology sequencing assay. Oncotarget, 2019, 10, 2384-2396.	1.8	119
17	RB1 gene inactivation by chromothripsis in human retinoblastoma. Oncotarget, 2014, 5, 438-450.	1.8	104
18	Integrated genomic profiling expands clinical options for patients with cancer. Nature Biotechnology, 2019, 37, 1351-1360.	17.5	103

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19	Specifications of the ACMG/AMP variant interpretation guidelines for germline TP53 variants. Human Mutation, 2021, 42, 223-236.	2.5	81
20	Mutations in RASA1 and GDF2 identified in patients with clinical features of hereditary hemorrhagic telangiectasia. Human Genome Variation, 2015, 2, 15040.	0.7	53
21	A recurrent mutation in KCNA2 as a novel cause of hereditary spastic paraplegia and ataxia. Annals of Neurology, 2016, 80, .	5.3	49
22	Candidate-gene criteria for clinical reporting: diagnostic exome sequencing identifies altered candidate genes among 8% of patients with undiagnosed diseases. Genetics in Medicine, 2017, 19, 224-235.	2.4	47
23	Clinical validation of the Tempus xO assay. Oncotarget, 2018, 9, 25826-25832.	1.8	43
24	Tumor Mutational Burden From Tumor-Only Sequencing Compared With Germline Subtraction From Paired Tumor and Normal Specimens. JAMA Network Open, 2020, 3, e200202.	5.9	40
25	Loss of function of the retinoid-related nuclear receptor (RORB) gene and epilepsy. European Journal of Human Genetics, 2016, 24, 1761-1770.	2.8	36
26	Further evidence that de novo missense and truncating variants in <scp>ZBTB18</scp> cause intellectual disability with variable features. Clinical Genetics, 2017, 91, 697-707.	2.0	29
27	Damaging de novo missense variants inEEF1A2lead to a developmental and degenerative epilepticâ€dyskinetic encephalopathy. Human Mutation, 2020, 41, 1263-1279.	2.5	24
28	Germline activating MTOR mutation arising through gonadal mosaicism in two brothers with megalencephaly and neurodevelopmental abnormalities. BMC Medical Genetics, 2015, 16, 102.	2.1	23
29	Expansion and further delineation of the SETD5 phenotype leading to global developmental delay, variable dysmorphic features, and reduced penetrance. Clinical Genetics, 2018, 93, 752-761.	2.0	23
30	Mutations in MAP3K1 that cause 46,XY disorders of sex development disrupt distinct structural domains in the protein. Human Molecular Genetics, 2019, 28, 1620-1628.	2.9	21
31	Determining Structure and Function of Steroid Dehydrogenase Enzymes by Sequence Analysis, Homology Modeling, and Rational Mutational Analysis. Annals of the New York Academy of Sciences, 2005, 1061, 135-148.	3.8	19
32	Structure/function of human type 1 3Î²-hydroxysteroid dehydrogenase: An intrasubunit disulfide bond in the Rossmann-fold domain and a Cys residue in the active site are critical for substrate and coenzyme utilization. Journal of Steroid Biochemistry and Molecular Biology, 2007, 107, 80-87.	2.5	14
33	Rational genomics I: Antisense open reading frames and codon bias in short-chain oxido reductase enzymes and the evolution of the genetic code. Proteins: Structure, Function and Bioinformatics, 2005, 61, 900-906.	2.6	13
34	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. Scientific Reports, 2014, 4, 7455.	3.3	13
35	Real-world Evidence of Diagnostic Testing and Treatment Patterns in US Patients With Breast Cancer With Implications for Treatment Biomarkers From RNA Sequencing Data. Clinical Breast Cancer, 2021, 21, e340-e361.	2.4	10
36	Divergent evolution of a Rossmann fold and identification of its oldest surviving ancestor. International Journal of Bioinformatics Research and Applications, 2009, 5, 280.	0.2	9

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37	De novo variants in KLF7 are a potential novel cause of developmental delay/intellectual disability, neuromuscular and psychiatric symptoms. Clinical Genetics, 2018, 93, 1030-1038.	2.0	9
38	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	1.4	9
39	Rational proteomics of PKD1. I. Modeling the three dimensional structure and ligand specificity of the C_lectin binding domain of Polycystin-1.. Journal of Molecular Modeling, 2007, 13, 891-896.	1.8	7
40	Divergent evolution of a Rossmann fold and identification of its oldest surviving ancestor. International Journal of Bioinformatics Research and Applications, 2009, 5, 280-94.	0.2	5
41	Abstract PR03: The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. , 2014, , .		2
42	The shortâ€chain oxidoreductase Q9HYA2 from Pseudomonas aeruginosa PAO1 contains an atypical catalytic center. Protein Science, 2010, 19, 1097-1103.	7.6	1
43	Sequence fingerprint and structural analysis of the SCOR enzyme A3DFK9 from Clostridium thermocellum. Proteins: Structure, Function and Bioinformatics, 2010, 78, 603-613.	2.6	1
44	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	1.2	1
45	Abstract 2597: Breast and ovarian cancer risks associated with cancer predisposition gene mutations identified by multigene panel testing. , 2016, , .		1
46	Evolution of bacterial ribosomal protein L1. International Journal of Bioinformatics Research and Applications, 2012, 8, 99.	0.2	0
47	Multiple open reading frames, codon bias and the evolution of the genetic code. FASEB Journal, 2006, 20, A927.	0.5	0
48	Multiple open reading frames GARP content and a 32-letter genetic code. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s163-s163.	0.3	0
49	Correlation in species, cofactor, oligomerization and substrate specificity in shortâ€chain oxidoreductase enzymes. FASEB Journal, 2010, 24, lb163.	0.5	0
50	Ribosomal protein structures and sequences define the prokaryotic tree of life. Acta Crystallographica Section A: Foundations and Advances, 2010, 66, s21-s21.	0.3	0
51	Discovery of Novel Recurrent Mutations in Childhood Early T-Cell Precursor Acute Lymphoblastic Leukemia by Whole Genome Sequencing - a Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 68-68.	1.4	0
52	Use of whole genome sequencing to identify novel mutations in distinct subgroups of medulloblastoma.. Journal of Clinical Oncology, 2012, 30, 9518-9518.	1.6	0
53	Abstract 2930: Global chromatin profiling reveals NSD2 mutation in pediatric ALL. , 2014, , .		0