

Valtteri Wirta

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

504
citations

933447

10
h-index

996975

15
g-index

16
all docs

16
docs citations

16
times ranked

1126
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of whole genome sequencing into a healthcare setting: high diagnostic rates across multiple clinical entities in 3219 rare disease patients. <i>Genome Medicine</i> , 2021, 13, 40.	8.2	116
2	From cytogenetics to cytogenomics: whole-genome sequencing as a first-line test comprehensively captures the diverse spectrum of disease-causing genetic variation underlying intellectual disability. <i>Genome Medicine</i> , 2019, 11, 68.	8.2	88
3	Whole-Genome Sequencing of Cytogenetically Balanced Chromosome Translocations Identifies Potentially Pathological Gene Disruptions and Highlights the Importance of Microhomology in the Mechanism of Formation. <i>Human Mutation</i> , 2017, 38, 180-192.	2.5	58
4	Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. <i>Nature Medicine</i> , 2020, 26, 992-994.	30.7	56
5	<i>CTNND2</i> a candidate gene for reading problems and mild intellectual disability. <i>Journal of Medical Genetics</i> , 2015, 52, 111-122.	3.2	35
6	Replicative and non-replicative mechanisms in the formation of clustered CNVs are indicated by whole genome characterization. <i>PLoS Genetics</i> , 2018, 14, e1007780.	3.5	28
7	Trailblazing precision medicine in Europe: A joint view by Genomic Medicine Sweden and the Centers for Personalized Medicine, ZPM, in Germany. <i>Seminars in Cancer Biology</i> , 2022, 84, 242-254.	9.6	22
8	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. <i>F1000Research</i> , 2020, 9, 63.	1.6	21
9	Bioinformatory-assisted analysis of next-generation sequencing data for precision medicine in pancreatic cancer. <i>Molecular Oncology</i> , 2017, 11, 1413-1429.	4.6	20
10	High diagnostic yield in skeletal ciliopathies using massively parallel genome sequencing, structural variant screening and RNA analyses. <i>Journal of Human Genetics</i> , 2021, 66, 995-1008.	2.3	19
11	A Study Protocol for Validation and Implementation of Whole-Genome and -Transcriptome Sequencing as a Comprehensive Precision Diagnostic Test in Acute Leukemias. <i>Frontiers in Medicine</i> , 2022, 9, 842507.	2.6	15
12	Eleven percent intact PGM3 in a severely immunodeficient patient with a novel splice-site mutation, a case report. <i>BMC Pediatrics</i> , 2018, 18, 285.	1.7	10
13	Assembly of a gene sequence tag microarray by reversible biotin-streptavidin capture for transcript analysis of <i>Arabidopsis thaliana</i> . <i>BMC Biotechnology</i> , 2005, 5, 5.	3.3	6
14	Loqusdb: added value of an observations database of local genomic variation. <i>BMC Bioinformatics</i> , 2020, 21, 273.	2.6	5
15	PatientMatcher: A customizable Python-based open-source tool for matching undiagnosed rare disease patients via the Matchmaker Exchange network. <i>Human Mutation</i> , 2022, , .	2.5	5