Valtteri Wirta

List of Publications by Year
in descending order

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15	504	933447 10	996975 15
papers	citations	h-index	g-index

16	16	16	1126
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Trailblazing precision medicine in Europe: A joint view by Genomic Medicine Sweden and the Centers for Personalized Medicine, ZPM, in Germany. Seminars in Cancer Biology, 2022, 84, 242-254.	9.6	22
2	PatientMatcher: A customizable Pythonâ€based openâ€source tool for matching undiagnosed rare disease patients via the Matchmaker Exchange network. Human Mutation, 2022, , .	2.5	5
3	A Study Protocol for Validation and Implementation of Whole-Genome and -Transcriptome Sequencing as a Comprehensive Precision Diagnostic Test in Acute Leukemias. Frontiers in Medicine, 2022, 9, 842507.	2.6	15
4	Integration of whole genome sequencing into a healthcare setting: high diagnostic rates across multiple clinical entities in 3219 rare disease patients. Genome Medicine, 2021, 13, 40.	8.2	116
5	High diagnostic yield in skeletal ciliopathies using massively parallel genome sequencing, structural variant screening and RNA analyses. Journal of Human Genetics, 2021, 66, 995-1008.	2.3	19
6	Loqusdb: added value of an observations database of local genomic variation. BMC Bioinformatics, 2020, 21, 273.	2.6	5
7	Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. Nature Medicine, 2020, 26, 992-994.	30.7	56
8	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 2020, 9, 63.	1.6	21
9	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. Genome Medicine, 2019, 11, 68.	8.2	88
10	Replicative and non-replicative mechanisms in the formation of clustered CNVs are indicated by whole genome characterization. PLoS Genetics, 2018, 14, e1007780.	3.5	28
11	Eleven percent intact PGM3 in a severely immunodeficient patient with a novel splice-site mutation, a case report. BMC Pediatrics, 2018, 18, 285.	1.7	10
12	Bioinformatoryâ€assisted analysis of nextâ€generation sequencing data for precision medicine in pancreatic cancer. Molecular Oncology, 2017, 11, 1413-1429.	4.6	20
13	Whole-Genome Sequencing of Cytogenetically Balanced Chromosome Translocations Identifies Potentially Pathological Gene Disruptions and Highlights the Importance of Microhomology in the Mechanism of Formation. Human Mutation, 2017, 38, 180-192.	2.5	58
14	CTNND2â€”a candidate gene for reading problems and mild intellectual disability. Journal of Medical Genetics, 2015, 52, 111-122.	3.2	35
15	Assembly of a gene sequence tag microarray by reversible biotin-streptavidin capture for transcript analysis of Arabidopsis thaliana. BMC Biotechnology, 2005, 5, 5.	3.3	6