## Jesús Jvd Del Valle

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Solving the enigma of POLD1 p.V295M as a potential cause of increased cancer risk. European Journal of Human Genetics, 2022, 30, 485-489.	2.8	2
2	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
3	Variants of uncertain significance (VUS) in cancer predisposing genes: What are we learning from multigene panels?. European Journal of Medical Genetics, 2022, 65, 104400.	1.3	4
4	Mosaicism in PTEN—new case and comment on the literature. European Journal of Human Genetics, 2022, 30, 641-644.	2.8	6
5	Characteristics of Adrenocortical Carcinoma Associated With Lynch Syndrome. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 318-325.	3.6	20
6	BARD1 Pathogenic Variants Are Associated with Triple-Negative Breast Cancer in a Spanish Hereditary Breast and Ovarian Cancer Cohort. Genes, 2021, 12, 150.	2.4	11
7	The Challenge of Diagnosing Constitutional Mismatch Repair Deficiency Syndrome in Brain Malignancies from Young Individuals. International Journal of Molecular Sciences, 2021, 22, 4629.	4.1	9
8	CNVfilteR: an R/Bioconductor package to identify false positives produced by germline NGS CNV detection tools. Bioinformatics, 2021, 37, 4227-4229.	4.1	1
9	Response to letter entitled: Re: ERCC3 a new ovarian cancer susceptibility gene?. European Journal of Cancer, 2021, 150, 281-282.	2.8	0
10	Genetic Screening for TLR7 Variants in Young and Previously Healthy Men With Severe COVID-19. Frontiers in Immunology, 2021, 12, 719115.	4.8	76
11	Paired Somatic-Germline Testing of 15 Polyposis and Colorectal Cancer–Predisposing Genes Highlights the Role of APC Mosaicism in de Novo Familial Adenomatous Polyposis. Journal of Molecular Diagnostics, 2021, 23, 1452-1459.	2.8	10
12	RNA assay identifies a previous misclassification of BARD1 c.1977A>G variant. Scientific Reports, 2021, 11, 22948.	3.3	0
13	Comprehensive Constitutional Genetic and Epigenetic Characterization of Lynch-Like Individuals. Cancers, 2020, 12, 1799.	3.7	15
14	Screening of CNVs using NGS data improves mutation detection yield and decreases costs in genetic testing for hereditary cancer. Journal of Medical Genetics, 2020, , jmedgenet-2020-107366.	3.2	3
15	Role of POLE and POLD1 in familial cancer. Genetics in Medicine, 2020, 22, 2089-2100.	2.4	76
16	ERCC3, a new ovarian cancer susceptibility gene?. European Journal of Cancer, 2020, 141, 1-8.	2.8	8
17	Comprehensive analysis and ACMGâ€based classification of <i>CHEK2</i> variants in hereditary cancer patients. Human Mutation, 2020, 41, 2128-2142.	2.5	10
18	Evaluation of CNV detection tools for NGS panel data in genetic diagnostics. European Journal of Human Genetics, 2020, 28, 1645-1655.	2.8	67

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19	The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292.	3.7	11
20	Exploring the Role of Mutations in Fanconi Anemia Genes in Hereditary Cancer Patients. Cancers, 2020, 12, 829.	3.7	41
21	Improving Genetic Testing in Hereditary Cancer by RNA Analysis. Journal of Molecular Diagnostics, 2020, 22, 1453-1468.	2.8	9
22	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	2.5	102
23	Opportunistic testing of <i>BRCA1</i> , <i>BRCA2</i> and mismatch repair genes improves the yield of phenotype driven hereditary cancer gene panels. International Journal of Cancer, 2019, 145, 2682-2691.	5.1	30
24	Highly sensitive MLH1 methylation analysis in blood identifies a cancer patient with low-level mosaic MLH1 epimutation. Clinical Epigenetics, 2019, 11, 171.	4.1	7
25	Does multilocus inherited neoplasia alleles syndrome have severe clinical expression?. Journal of Medical Genetics, 2019, 56, 521-525.	3.2	11
26	Primary constitutional MLH1 epimutations: a focal epigenetic event. British Journal of Cancer, 2018, 119, 978-987.	6.4	22
27	Genetic Testing in Hereditary Colorectal Cancer. , 2018, , 209-232.		Ο
28	Elucidating the clinical significance of two PMS2 missense variants coexisting in a family fulfilling hereditary cancer criteria. Familial Cancer, 2017, 16, 501-507.	1.9	3
29	Elucidating the molecular basis of MSH2â€deficient tumors by combined germline and somatic analysis. International Journal of Cancer, 2017, 141, 1365-1380.	5.1	26
30	Benchmarking of Whole Exome Sequencing and Ad Hoc Designed Panels for Genetic Testing of Hereditary Cancer. Scientific Reports, 2017, 7, 37984.	3.3	35
31	A comprehensive custom panel design for routine hereditary cancer testing: preserving control, improving diagnostics and revealing a complex variation landscape. Scientific Reports, 2017, 7, 39348.	3.3	45
32	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	1.6	152
33	Identification of a founder <i><scp>BRCA1</scp></i> mutation in the Moroccan population. Clinical Genetics, 2016, 90, 361-365.	2.0	13
34	Investigating the effect of 28 BRCA1 and BRCA2 mutations on their related transcribed mRNA. Breast Cancer Research and Treatment, 2016, 155, 253-260.	2.5	6
35	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	5.0	26
36	ICO Amplicon NGS Data Analysis: A Web Tool for Variant Detection in Common High-Risk Hereditary Cancer Genes Analyzed by Amplicon GS Junior Next-Generation Sequencing. Human Mutation, 2014, 35, 271-277.	2.5	2

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37	Identification of a founder EPCAM deletion in Spanish Lynch syndrome families. Clinical Genetics, 2014, 85, 260-266.	2.0	12
38	Refining the role of <i>pms2</i> in Lynch syndrome: germline mutational analysis improved by comprehensive assessment of variants. Journal of Medical Genetics, 2013, 50, 552-563.	3.2	47
39	Next-generation sequencing meets genetic diagnostics: development of a comprehensive workflow for the analysis of BRCA1 and BRCA2 genes. European Journal of Human Genetics, 2013, 21, 864-870.	2.8	94
40	Assessing the RNA effect of 26 DNA variants in the BRCA1 and BRCA2 genes. Breast Cancer Research and Treatment, 2012, 132, 979-992.	2.5	20
41	Analysis of SLX4/FANCP in non-BRCA1/2-mutated breast cancer families. BMC Cancer, 2012, 12, 84.	2.6	14
42	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	5.0	78
43	Abstract 4445: Defining a pipeline to use next generation sequencing for genetic testing in hereditary cancer. , 2012, , .		0
44	Identification of a new complex rearrangement affecting exon 20 of BRCA1. Breast Cancer Research and Treatment, 2011, 130, 341-344.	2.5	3
45	Identification and comprehensive characterization of large genomic rearrangements in the BRCA1 and BRCA2 genes. Breast Cancer Research and Treatment, 2010, 122, 733-743.	2.5	34
46	Comments on: Sluiter MD and van Rensburg EJ, Large genomic rearrangements of the BRCA1 and BRCA2 genes: review of the literature and report of a novel BRCA1 mutation. Breast Cancer Research and Treatment, 2010, 124, 295-296.	2.5	1
47	Small supernumerary marker chromosome causing partial trisomy 6p in a child with craniosynostosis. American Journal of Medical Cenetics, Part A, 2007, 1434, 1108-1113	1.2	15