Marc S Greenblatt

List of Publications by Year
in descending order

29 papers	3,397 citations	516710 16 h-index	552781 26 g-index
35 all docs	35 docs citations	35 times ranked	7420 citing authors

#	Article	IF	Citations
1	Risk-reducing hysterectomy and bilateral salpingo-oophorectomy in female heterozygotes of pathogenic mismatch repair variants: a Prospective Lynch Syndrome Database report. Genetics in Medicine, 2021, 23, 705-712.	2.4	28
2	Uptake of hysterectomy and bilateral salpingo-oophorectomy in carriers of pathogenic mismatch repair variants: a Prospective Lynch Syndrome Database report. European Journal of Cancer, 2021, 148, 124-133.	2.8	11
3	No Difference in Penetrance between Truncating and Missense/Aberrant Splicing Pathogenic Variants in MLH1 and MSH2: A Prospective Lynch Syndrome Database Study. Journal of Clinical Medicine, 2021, 10, 2856.	2.4	11
4	Cancer risks by gene, age, and gender in 6350 carriers of pathogenic mismatch repair variants: findings from the Prospective Lynch Syndrome Database. Genetics in Medicine, 2020, 22, 15-25.	2.4	365
5	Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Medicine, 2020, 12, 3.	8.2	312
6	Curated multiple sequence alignment for the Adenomatous Polyposis Coli (APC) gene and accuracy of in silico pathogenicity predictions. PLoS ONE, 2020, 15, e0233673.	2.5	1
7	Two integrated and highly predictive functional analysis-based procedures for the classification of MSH6 variants in Lynch syndrome. Genetics in Medicine, 2020, 22, 847-856.	2.4	16
8	Title is missing!. , 2020, 15, e0233673.		0
9	Title is missing!. , 2020, 15, e0233673.		0
10	Title is missing!. , 2020, 15, e0233673.		0
11	Title is missing!. , 2020, 15, e0233673.		0
12	Determining the clinical validity of hereditary colorectal cancer and polyposis susceptibility genes using the Clinical Genome Resource Clinical Validity Framework. Genetics in Medicine, 2019, 21, 1507-1516.	2.4	19
13	A functional assayâ€"based procedure to classify mismatch repair gene variants in Lynch syndrome. Genetics in Medicine, 2019, 21, 1486-1496.	2.4	36
14	Modeling the ACMG/AMP variant classification guidelines as a Bayesian classification framework. Genetics in Medicine, 2018, 20, 1054-1060.	2.4	366
15	Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. Human Mutation, 2017, 38, 460-463.	2.5	1
16	Placing negative multi-gene panel results into clinical context. Familial Cancer, 2017, 16, 595-595.	1.9	0
17	Multi-gene panel testing for hereditary cancer susceptibility in a rural Familial Cancer Program. Familial Cancer, 2017, 16, 159-166.	1.9	16
18	Universal Versus Targeted Screening for Lynch Syndrome: Comparing Ascertainment and Costs Based on Clinical Experience. Digestive Diseases and Sciences, 2016, 61, 2887-2895.	2.3	20

#	Article	IF	Citations
19	HGVS Recommendations for the Description of Sequence Variants: 2016 Update. Human Mutation, 2016, 37, 564-569.	2.5	1,194
20	Sequence Variants of Uncertain Significance. Surgical Oncology Clinics of North America, 2015, 24, 833-846.	1.5	11
21	The MLH1 c.-27C>A and c.85G>T variants are linked to dominantly inherited MLH1 epimutation and are borne on a European ancestral haplotype. European Journal of Human Genetics, 2014, 22, 617-624.	2.8	36
22	Application of a 5-tiered scheme for standardized classification of 2,360 unique mismatch repair gene variants in the InSiGHT locus-specific database. Nature Genetics, 2014, 46, 107-115.	21.4	410
23	Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265.	2.5	80
24	Classifying the Effects of BRCA1 and BRCA2 Variants on Splicing - A Systematic Study. Human Mutation, 2013, 34, v-v.	2.5	0
25	Classifying variants of CDKN2A using computational and laboratory studies. Human Mutation, 2011, 32, 900-911.	2.5	31
26	Locus-specific databases and recommendations to strengthen their contribution to the classification of variants in cancer susceptibility genes. Human Mutation, 2008, 29, 1273-1281.	2.5	41
27	In silico analysis of missense substitutions using sequence-alignment based methods. Human Mutation, 2008, 29, 1327-1336.	2.5	181
28	Genetic evidence and integration of various data sources for classifying uncertain variants into a single model. Human Mutation, 2008, 29, 1265-1272.	2.5	169
29	The Familial Cancer Program of the Vermont Cancer Center: Development of a Cancer Genetics Program in a Rural Area. Journal of Genetic Counseling, 1997, 6, 131-145.	1.6	7