# Marc S Greenblatt

List of Publications by Year
in descending order

516710

552781

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

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | HGVS Recommendations for the Description of Sequence Variants: 2016 Update. Human Mutation, 2016, 37, 564-569. | 2.5 | 1,194 |
| 2 | 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 |
| 3 | Modeling the ACMG/AMP variant classification guidelines as a Bayesian classification framework. Genetics in Medicine, 2018, 20, 1054-1060. | 2.4 | 366 |
| 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 | In silico analysis of missense substitutions using sequence-alignment based methods. Human Mutation, 2008, 29, 1327-1336. | 2.5 | 181 |
| 7 | 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 |
| 8 | Calibration of Multiple In Silico Tools for Predicting Pathogenicity of Mismatch Repair Gene Missense Substitutions. Human Mutation, 2013, 34, 255-265. | 2.5 | 80 |
| 9 | 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 |
| 10 | The MLH1 c.-27C&gt;A and c.85G&gt;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 |
| 11 | A functional assay–based procedure to classify mismatch repair gene variants in Lynch syndrome. Genetics in Medicine, 2019, 21, 1486-1496. | 2.4 | 36 |
| 12 | Classifying variants of CDKN2A using computational and laboratory studies. Human Mutation, 2011, 32, 900-911. | 2.5 | 31 |
| 13 | 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 |
| 14 | 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 |
| 15 | 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 |
| 16 | Multi-gene panel testing for hereditary cancer susceptibility in a rural Familial Cancer Program. Familial Cancer, 2017, 16, 159-166. | 1.9 | 16 |
| 17 | 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 |
| 18 | Sequence Variants of Uncertain Significance. Surgical Oncology Clinics of North America, 2015, 24, 833-846. | 1.5 | 11 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | Non-Coding Variation: The 2016 Annual Scientific Meeting of the Human Genome Variation Society. Human Mutation, 2017, 38, 460-463. | 2.5 | 1 |
| 23 | 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 |
| 24 | Classifying the Effects of BRCA1 and BRCA2 Variants on Splicing - A Systematic Study. Human Mutation, 2013, 34, v-v. | 2.5 | 0 |
| 25 | Placing negative multi-gene panel results into clinical context. Familial Cancer, 2017, 16, 595-595. | 1.9 | 0 |
| 26 | Title is missing!. , 2020, 15, e0233673. | | 0 |
| 27 | Title is missing!. , 2020, 15, e0233673. | | 0 |
| 28 | Title is missing!. , 2020, 15, e0233673. | | 0 |
| 29 | Title is missing!. , 2020, 15, e0233673. | | 0 |