

Brian A Walker

List of Publications by Year in Descending Order

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Version: 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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|--------------------|-------------------------|----------------|-----------------|
| 218 papers | 7,860 citations | 44 h-index | 87 g-index |
| 242 ext. papers | 9,500 ext. citations | 5.6 avg, IF | 5.45 L-index |

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 218 | Diagnostic Evidence GAUge of Single cells (DEGAS): a flexible deep transfer learning framework for prioritizing cells in relation to disease.. <i>Genome Medicine</i> , 2022 , 14, 11 | 14.4 | 0 |
| 217 | What Is Genomic High-Risk Myeloma?. <i>Hemato</i> , 2022 , 3, 287-297 | 0.2 | |
| 216 | Paradoxical sex-specific patterns of autoantibody response to SARS-CoV-2 infection.. <i>Journal of Translational Medicine</i> , 2021 , 19, 524 | 8.5 | 1 |
| 215 | Insights into high-risk multiple myeloma from an analysis of the role of PHF19 in cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021 , 40, 380 | 12.8 | 1 |
| 214 | Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. <i>Nature Communications</i> , 2021 , 12, 1861 | 17.4 | 16 |
| 213 | Cryopreservation Preserves Cell-Type Composition and Gene Expression Profiles in Bone Marrow Aspirates From Multiple Myeloma Patients. <i>Frontiers in Genetics</i> , 2021 , 12, 663487 | 4.5 | 2 |
| 212 | Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , 2021 , | 7.5 | 1 |
| 211 | Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , 2021 , | 10.7 | 3 |
| 210 | High-risk transcriptional profiles in multiple myeloma are an acquired feature that can occur in any subtype and more frequently with each subsequent relapse. <i>British Journal of Haematology</i> , 2021 , 195, 283-286 | 4.5 | 2 |
| 209 | PHF19 inhibition as a therapeutic target in multiple myeloma. <i>Current Research in Translational Medicine</i> , 2021 , 69, 103290 | 3.7 | 3 |
| 208 | Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. <i>Haematologica</i> , 2021 , 106, 736-745 | 6.6 | 7 |
| 207 | Monitoring treatment response and disease progression in myeloma with circulating cell-free DNA. <i>European Journal of Haematology</i> , 2021 , 106, 230-240 | 3.8 | 5 |
| 206 | The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. <i>Nature Communications</i> , 2021 , 12, 293 | 17.4 | 20 |
| 205 | Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. <i>Leukemia</i> , 2021 , 35, 3017-3020 | 10.7 | 3 |
| 204 | Plasma cells expression from smouldering myeloma to myeloma reveals the importance of the PRC2 complex, cell cycle progression, and the divergent evolutionary pathways within the different molecular subgroups. <i>Leukemia</i> , 2021 , | 10.7 | 3 |
| 203 | Chromosomal 1q21 abnormalities in multiple myeloma: a review of translational, clinical research, and therapeutic strategies. <i>Expert Review of Hematology</i> , 2021 , 1-16 | 2.8 | 0 |
| 202 | Intron retention-induced neoantigen load correlates with unfavorable prognosis in multiple myeloma. <i>Oncogene</i> , 2021 , 40, 6130-6138 | 9.2 | 2 |

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| 201 | Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. <i>Blood Cancer Journal</i> , 2020 , 10, 70 | 7 | 16 |
| 200 | The Chromosome 13 Conundrum in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020 , 1, 16-17 | 7 | 2 |
| 199 | Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020 , 34, 1866-1874 | 10.7 | 27 |
| 198 | and Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , 2020 , 26, 2422-2432 | 12.9 | 17 |
| 197 | Complete Genome Sequences of Four Isolates of Vancomycin-Resistant <i>Enterococcus faecium</i> with the Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , 2020 , 9, | 1.3 | 2 |
| 196 | Mutations in CRBN and Other Cereblon Pathway Genes Are Only Associated with Acquired Resistance to Immunomodulatory Drugs in a Subset of Patients and Cell Line Models. <i>Blood</i> , 2020 , 136, 6-7 | 2.2 | |
| 195 | Impact of Etiological Cytogenetic Abnormalities on Immunoparesis and Progression-Free and Overall Survival in Newly Diagnosed Multiple Myeloma. <i>Blood</i> , 2020 , 136, 6-6 | 2.2 | |
| 194 | Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , 2020 , 136, 8-9 | 2.2 | 1 |
| 193 | Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive Versus Stable Myeloma Precursor Disease. <i>Blood</i> , 2020 , 136, 47-48 | 2.2 | 2 |
| 192 | Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. <i>PLoS Medicine</i> , 2020 , 17, e1003323 | 11.6 | 10 |
| 191 | Inactivating Mutations Are Enriched in Advanced Breast Cancer and Contribute to Endocrine Therapy Resistance. <i>Clinical Cancer Research</i> , 2020 , 26, 608-622 | 12.9 | 31 |
| 190 | The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. <i>Journal of Hematology and Oncology</i> , 2020 , 13, 108 | 22.4 | 8 |
| 189 | Two Cases of Vancomycin-Resistant Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. <i>Open Forum Infectious Diseases</i> , 2020 , 7, ofaa180 | 1 | 2 |
| 188 | Microhomology-mediated end joining drives complex rearrangements and overexpression of and in multiple myeloma. <i>Haematologica</i> , 2020 , 105, 1055-1066 | 6.6 | 22 |
| 187 | TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. <i>BMC Bioinformatics</i> , 2020 , 21, 144 | 3.6 | 1 |
| 186 | Long-term outcomes after autologous stem cell transplantation for multiple myeloma. <i>Blood Advances</i> , 2020 , 4, 422-431 | 7.8 | 30 |
| 185 | Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. <i>Human Genomics</i> , 2019 , 13, 37 | 6.8 | 5 |
| 184 | A tailored molecular profiling programme for children with cancer to identify clinically actionable genetic alterations. <i>European Journal of Cancer</i> , 2019 , 121, 224-235 | 7.5 | 21 |

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| 183 | Daratumumab and dexamethasone is safe and effective for triple refractory myeloma patients: final results of the IFM 2014-04 (Etoile du Nord) trial. <i>British Journal of Haematology</i> , 2019 , 187, 319-327 | 4.5 | 12 |
| 182 | Draft Genome Sequences of 48 Vancomycin-Resistant <i>Enterococcus faecium</i> Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , 2019 , 8, 1-8 | 1.3 | 1 |
| 181 | Clonal evolution in myeloma: the impact of maintenance lenalidomide and depth of response on the genetics and sub-clonal structure of relapsed disease in uniformly treated newly diagnosed patients. <i>Haematologica</i> , 2019 , 104, 1440-1450 | 6.6 | 39 |
| 180 | A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019 , 33, 159-170 | 10.7 | 176 |
| 179 | An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. <i>Blood Cancer Journal</i> , 2019 , 9, 62 | 7 | 17 |
| 178 | Analysis of the Sub-Clonal Structure of Smoldering Myeloma over Time Provides a New Means of Disease Monitoring and Highlights Evolutionary Trajectories Leading to Myeloma. <i>Blood</i> , 2019 , 134, 4333-4333 | 2.2 | 2 |
| 177 | The Spectrum of Exomic Mutation in Elderly Myeloma Differs Substantially from Patients at Younger Ages Consistent with a Different Evolutionary Trajectory to Full Blown Disease Based on Age of Onset. <i>Blood</i> , 2019 , 134, 4346-4346 | 2.2 | 2 |
| 176 | Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregulate Gene Function By a Range of Mechanisms. <i>Blood</i> , 2019 , 134, 3767-3767 | 2.2 | 3 |
| 175 | Mutant KRAS Enhances Stress Granules and Resistance to Proteasome Inhibition Via 15-d-PGJ2 in Multiple Myeloma. <i>Blood</i> , 2019 , 134, 4383-4383 | 2.2 | 2 |
| 174 | EARLY Results of TOTAL Therapy 7 (TT7): High Response Rates of NEWLY Diagnosed High Risk Myeloma to Daratumumab. <i>Blood</i> , 2019 , 134, 4569-4569 | 2.2 | 2 |
| 173 | Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of. <i>Oncotarget</i> , 2019 , 10, 732-737 | 3.3 | 5 |
| 172 | Aberrant Epigenomic Regulatory Networks in Multiple Myeloma and Strategies for Their Targeted Reversal. <i>RNA Technologies</i> , 2019 , 543-572 | 0.2 | |
| 171 | The mTOR Component, Rictor, Is Regulated By the Microenvironment to Control Dormancy and Proliferative States in Myeloma Cells. <i>Blood</i> , 2019 , 134, 4412-4412 | 2.2 | |
| 170 | Long-Term Outcome of Total Therapy Regimens: Impact of Molecular Subgroups. <i>Blood</i> , 2019 , 134, 3309-3309 | 2.3 | 1 |
| 169 | The Role of PHF19 As a Promoter of Tumorigenicity and Therapeutic Target in Multiple Myeloma. <i>Blood</i> , 2019 , 134, 508-508 | 2.2 | |
| 168 | Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. <i>Blood</i> , 2019 , 134, 4370-4370 | 2.2 | |
| 167 | Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. <i>Leukemia</i> , 2019 , 33, 1713-1722 | 10.7 | 66 |
| 166 | Kinase domain activation through gene rearrangement in multiple myeloma. <i>Leukemia</i> , 2018 , 32, 2435-2444 | 14.7 | 15 |

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| 165 | Loss of heterozygosity as a marker of homologous repair deficiency in multiple myeloma: a role for PARP inhibition?. <i>Leukemia</i> , 2018 , 32, 1561-1566 | 10.7 | 29 |
| 164 | Investigating the feasibility of tumour molecular profiling in gastrointestinal malignancies in routine clinical practice. <i>Annals of Oncology</i> , 2018 , 29, 230-236 | 10.3 | 16 |
| 163 | Treatment to suppression of focal lesions on positron emission tomography-computed tomography is a therapeutic goal in newly diagnosed multiple myeloma. <i>Haematologica</i> , 2018 , 103, 1047-1053 | 6.6 | 29 |
| 162 | Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. <i>Leukemia</i> , 2018 , 32, 102-110 | 10.7 | 108 |
| 161 | A Rapid and Robust Protocol for Reduced Representation Bisulfite Sequencing in Multiple Myeloma. <i>Methods in Molecular Biology</i> , 2018 , 1792, 179-191 | 1.4 | 1 |
| 160 | MAFb protein confers intrinsic resistance to proteasome inhibitors in multiple myeloma. <i>BMC Cancer</i> , 2018 , 18, 724 | 4.8 | 13 |
| 159 | Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , 2018 , 132, 587-597 | 2.2 | 196 |
| 158 | Deep Immunoprofiling of the Bone Marrow Microenvironmental Changes Underlying the Multistep Progression of Multiple Myeloma. <i>Blood</i> , 2018 , 132, 243-243 | 2.2 | 1 |
| 157 | Long-Term Follow-up Identifies Double Hit and Key Mutations As Impacting Progression Free and Overall Survival in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 110-110 | 2.2 | 1 |
| 156 | Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. <i>Blood</i> , 2018 , 132, 1882-1882 | 2.2 | 2 |
| 155 | The Mutational Landscape of Primary Plasma Cell Leukemia. <i>Blood</i> , 2018 , 132, 114-114 | 2.2 | 2 |
| 154 | A High-Risk Multiple Myeloma Group Identified By Integrative Multi-Omics Segmentation of Newly Diagnosed Patients. <i>Blood</i> , 2018 , 132, 3165-3165 | 2.2 | 2 |
| 153 | Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 408-408 | 2.2 | 2 |
| 152 | Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. <i>Blood</i> , 2018 , 132, 4457-4457 | 2.2 | |
| 151 | Poor Overall Survival in Hyperhaploid Multiple Myeloma Is Defined By Double-Hit Bi-Allelic Inactivation of TP53. <i>Blood</i> , 2018 , 132, 4441-4441 | 2.2 | |
| 150 | Sequential Improvements in the Outcome of Autologous Stem Cell Transplantation for Multiple Myeloma over Time. <i>Blood</i> , 2018 , 132, 3168-3168 | 2.2 | |
| 149 | Expression Signature of Myeloma Residual Cells Is Characterized By Genes Associated with Proliferation, Epigenetic Modification, and Stem Cell Maintenance. <i>Blood</i> , 2018 , 132, 4465-4465 | 2.2 | 1 |
| 148 | Myeloma Patient-Derived Bone Marrow Serum Negatively Regulates Natural Killer Cell Activity. <i>Blood</i> , 2018 , 132, 4468-4468 | 2.2 | |

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| 147 | Mutations and Copy Number Changes Predict Progression from Smoldering Myeloma to Symptomatic Myeloma in the Era of Novel IMWG Criteria. <i>Blood</i> , 2018 , 132, 4456-4456 | 2.2 | |
| 146 | Global 3D-Epigenetic Dysregulation of Cyclin D1 and D2 Actively Controls Their Expression Pattern in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 3904-3904 | 2.2 | |
| 145 | Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. <i>Blood</i> , 2018 , 132, 3185-3185 | 2.2 | |
| 144 | Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. <i>Blood</i> , 2018 , 132, 1906-1906 | 2.2 | |
| 143 | Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. <i>Blood</i> , 2018 , 132, 4454-4454 | 2.2 | |
| 142 | High Levels of APOBEC3B Gene Expression Contribute to Poor Prognosis in Multiple Myeloma Patients. <i>Blood</i> , 2018 , 132, 3897-3897 | 2.2 | |
| 141 | Mutant KRAS and Braf Upregulate Stress Granules and Mediate Drug Resistance, Which Can be Modulated By Cox2 Inhibition in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 3166-3166 | 2.2 | |
| 140 | An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. <i>Blood</i> , 2018 , 132, 4489-4489 | 2.2 | 0 |
| 139 | Characterization of the Immune Impact of Daratumumab By Mass Cytometry in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 4466-4466 | 2.2 | |
| 138 | Proliferation and Molecular Risk Score of Low Risk Myeloma Cells Are Increased in High Risk Microenvironment Via Augmented Bioavailability of Growth Factors. <i>Blood</i> , 2018 , 132, 1929-1929 | 2.2 | |
| 137 | Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , 2018 , 9, 1 | 7 | 18 |
| 136 | Knick-knack PADIMAC. <i>Blood</i> , 2018 , 132, 2110-2111 | 2.2 | 7 |
| 135 | EAPH-05. MOLECULAR PROFILING AND IDENTIFICATION OF TARGETED THERAPIES FOR CHILDREN AND YOUNG ADULTS WITH PRIMARY CENTRAL NERVOUS SYSTEM TUMOURS IN THE UNITED KINGDOM. <i>Neuro-Oncology</i> , 2018 , 20, i66-i66 | 1 | 78 |
| 134 | 487. Severity and Clinical Outcomes of Clostridium difficile Infection Based on Toxin B Assay Results. <i>Open Forum Infectious Diseases</i> , 2018 , 5, S180-S181 | 1 | 78 |
| 133 | The genomic landscape of plasma cells in systemic light chain amyloidosis. <i>Blood</i> , 2018 , 132, 2775-2777 | 2.2 | 10 |
| 132 | Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018 , 9, 3707 | 17.4 | 57 |
| 131 | A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. <i>Blood Advances</i> , 2018 , 2, 2400-2411 | 7.8 | 3 |
| 130 | The presence of large focal lesions is a strong independent prognostic factor in multiple myeloma. <i>Blood</i> , 2018 , 132, 59-66 | 2.2 | 43 |

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| 129 | Whole Exome Sequencing in Multiple Myeloma to Identify Somatic Single Nucleotide Variants and Key Translocations Involving Immunoglobulin Loci and MYC. <i>Methods in Molecular Biology</i> , 2018 , 1792, 71-95 | 1.4 | 4 |
| 128 | Bi-allelic inactivation is more prevalent at relapse in multiple myeloma, identifying RB1 as an independent prognostic marker. <i>Blood Cancer Journal</i> , 2017 , 7, e535 | 7 | 39 |
| 127 | Comprehensive translocation and clonality detection in lymphoproliferative disorders by next-generation sequencing. <i>Haematologica</i> , 2017 , 102, e57-e60 | 6.6 | 26 |
| 126 | Low expression of hexokinase-2 is associated with false-negative FDG-positron emission tomography in multiple myeloma. <i>Blood</i> , 2017 , 130, 30-34 | 2.2 | 120 |
| 125 | Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. <i>Blood Cancer Journal</i> , 2017 , 7, e573 | 7 | 8 |
| 124 | The prognostic value of the depth of response in multiple myeloma depends on the time of assessment, risk status and molecular subtype. <i>Haematologica</i> , 2017 , 102, e313-e316 | 6.6 | 21 |
| 123 | The level of deletion 17p and bi-allelic inactivation of has a significant impact on clinical outcome in multiple myeloma. <i>Haematologica</i> , 2017 , 102, e364-e367 | 6.6 | 44 |
| 122 | The spectrum of somatic mutations in monoclonal gammopathy of undetermined significance indicates a less complex genomic landscape than that in multiple myeloma. <i>Haematologica</i> , 2017 , 102, 1617-1625 | 6.6 | 42 |
| 121 | Overexpression of EZH2 in multiple myeloma is associated with poor prognosis and dysregulation of cell cycle control. <i>Blood Cancer Journal</i> , 2017 , 7, e549 | 7 | 60 |
| 120 | Neutral tumor evolution in myeloma is associated with poor prognosis. <i>Blood</i> , 2017 , 130, 1639-1643 | 2.2 | 14 |
| 119 | Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. <i>Nature Communications</i> , 2017 , 8, 268 | 17.4 | 170 |
| 118 | Loss of heterozygosity in multiple myeloma: A role for PARP inhibition?. <i>Journal of Clinical Oncology</i> , 2017 , 35, 8026-8026 | 2.2 | 1 |
| 117 | The varied distribution and impact of RAS codon and other key DNA alterations across the translocation cyclin D subgroups in multiple myeloma. <i>Oncotarget</i> , 2017 , 8, 27854-27867 | 3.3 | 19 |
| 116 | Search for rare protein altering variants influencing susceptibility to multiple myeloma. <i>Oncotarget</i> , 2017 , 8, 36203-36210 | 3.3 | 9 |
| 115 | Molecular profiling of colorectal pulmonary metastases and primary tumours: implications for targeted treatment. <i>Oncotarget</i> , 2017 , 8, 64999-65008 | 3.3 | 11 |
| 114 | Development of a targeted sequencing approach to identify prognostic, predictive and diagnostic markers in paediatric solid tumours. <i>Oncotarget</i> , 2017 , 8, 112036-112050 | 3.3 | 12 |
| 113 | MYC Rearrangements in Multiple Myeloma Are Complex, Can Involve More Than Five Different Chromosomes, and Correlate with Increased Expression of MYC and a Distinct Downstream Gene Expression Pattern. <i>Blood</i> , 2017 , 130, 65-65 | 2.2 | 2 |
| 112 | Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , 2016 , 7, 12050 | 17.4 | 101 |

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| 111 | The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. <i>Clinical Cancer Research</i> , 2016 , 22, 5783-5794 | 12.9 | 56 |
| 110 | Genomewide profiling of copy-number alteration in monoclonal gammopathy of undetermined significance. <i>European Journal of Haematology</i> , 2016 , 97, 568-575 | 3.8 | 20 |
| 109 | Impact of Genes Highly Correlated with MMSET Myeloma on the Survival of Non-MMSET Myeloma Patients. <i>Clinical Cancer Research</i> , 2016 , 22, 4039-44 | 12.9 | 11 |
| 108 | Concurrent Amplification of MYC and 1q21 in Multiple Myeloma: Focal and Segmental Jumping Translocations of MYC. <i>Blood</i> , 2016 , 128, 3266-3266 | 2.2 | 1 |
| 107 | Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. <i>Blood</i> , 2016 , 128, 3278-3278 | 2.2 | 2 |
| 106 | Inhibition of the Epigenetic Modifier EZH2 Upregulates Cell Cycle Control Genes to Inhibit Myeloma Cell Growth and Overcome High-Risk Disease Features. <i>Blood</i> , 2016 , 128, 3289-3289 | 2.2 | 2 |
| 105 | The Impact of Maintenance Lenalidomide on the Mutational Status of the Myeloma Clone at Relapse in the NCRI Myeloma XI Trial for Newly Diagnosed Multiple Myeloma Patients (NDMM). <i>Blood</i> , 2016 , 128, 4412-4412 | 2.2 | 2 |
| 104 | The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. <i>Blood</i> , 2016 , 128, 4431-4431 | 2.2 | 7 |
| 103 | The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. <i>Blood</i> , 2016 , 128, 196-196 | 2.2 | 1 |
| 102 | High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , 2016 , 128, 4416-4416 | 2.2 | 0 |
| 101 | The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. <i>Blood</i> , 2016 , 128, 4441-4441 | 2.2 | |
| 100 | The Metabolic Phenotype of Myeloma Plasma Cells Differs Between Active and Residual Disease States. <i>Blood</i> , 2016 , 128, 4438-4438 | 2.2 | |
| 99 | Translocations and Jumping Rearrangements at 8q24 Result in over-Expression of MYC and are Key Drivers of Disease Progression. <i>Blood</i> , 2016 , 128, 115-115 | 2.2 | 2 |
| 98 | Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. <i>Blood</i> , 2016 , 128, 3271-3271 | 2.2 | |
| 97 | Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. <i>Blood</i> , 2016 , 128, 1735-44 | 2.2 | 129 |
| 96 | Understanding next generation sequencing in oncology: A guide for oncologists. <i>Critical Reviews in Oncology/Hematology</i> , 2015 , 96, 463-74 | 7 | 28 |
| 95 | APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. <i>Nature Communications</i> , 2015 , 6, 6997 | 17.4 | 176 |
| 94 | A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. <i>Leukemia and Lymphoma</i> , 2015 , 56, 594-601 | 1.9 | 3 |

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| 93 | Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. <i>Journal of Clinical Oncology</i> , 2015 , 33, 3911-20 | 2.2 | 348 |
| 92 | A molecular diagnostic approach able to detect the recurrent genetic prognostic factors typical of presenting myeloma. <i>Genes Chromosomes and Cancer</i> , 2015 , 54, 91-8 | 5 | 26 |
| 91 | Coexistent hyperdiploidy does not abrogate poor prognosis in myeloma with adverse cytogenetics and may precede IGH translocations. <i>Blood</i> , 2015 , 125, 831-40 | 2.2 | 48 |
| 90 | The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. <i>Haematologica</i> , 2015 , 100, e110-3 | 6.6 | 22 |
| 89 | The combination of HDAC and aminopeptidase inhibitors is highly synergistic in myeloma and leads to disruption of the NF κ B signalling pathway. <i>Oncotarget</i> , 2015 , 6, 17314-27 | 3.3 | 7 |
| 88 | Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. <i>Oncotarget</i> , 2015 , 6, 19132-47 | 3.3 | 37 |
| 87 | Molecular Subgroups of Hyperdiploidy and Their Prognostic Relevance - an Analysis of 1,036 Myeloma Trial Patients. <i>Blood</i> , 2015 , 126, 2983-2983 | 2.2 | |
| 86 | Specific Identification of High Risk Disease Using Molecular Profiling By Mymap (Myeloma MLPA and translocation PCR) of 1,036 Cases. <i>Blood</i> , 2015 , 126, 2981-2981 | 2.2 | |
| 85 | Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. <i>Leukemia</i> , 2014 , 28, 1705-15 | 10.7 | 162 |
| 84 | Cancer-selective targeting of the NF- κ B survival pathway with GADD45 β /MKK7 inhibitors. <i>Cancer Cell</i> , 2014 , 26, 495-508 | 24.3 | 77 |
| 83 | Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. <i>Blood</i> , 2014 , 123, 2513-7; quiz 2593 | 2.2 | 31 |
| 82 | B-cell malignancies: capture-sequencing strategies for identification of gene rearrangements and translocations into immunoglobulin gene loci. <i>Blood and Lymphatic Cancer: Targets and Therapy</i> , 2014 , 107 | 2.6 | |
| 81 | Translocations at 8q24 juxtapose MYC with genes that harbor superenhancers resulting in overexpression and poor prognosis in myeloma patients. <i>Blood Cancer Journal</i> , 2014 , 4, e191 | 7 | 114 |
| 80 | Biology and treatment of myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2014 , 14 Suppl, S65-70 | 2 | 13 |
| 79 | Intracloal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. <i>Leukemia</i> , 2014 , 28, 384-390 | 10.7 | 202 |
| 78 | A novel functional role for MMSET in RNA processing based on the link between the REIIBP isoform and its interaction with the SMN complex. <i>PLoS ONE</i> , 2014 , 9, e99493 | 3.7 | 4 |
| 77 | Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. <i>Nature Genetics</i> , 2013 , 45, 1221-1225 | 36.3 | 119 |
| 76 | The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. <i>Nature Genetics</i> , 2013 , 45, 522-525 | 36.3 | 79 |

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|----|---|------|-----|
| 75 | Identification of a novel t(7;14) translocation in multiple myeloma resulting in overexpression of EGFR. <i>Genes Chromosomes and Cancer</i> , 2013 , 52, 817-22 | 5 | 6 |
| 74 | Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. <i>Blood</i> , 2013 , 122, 219-26 | 2.2 | 128 |
| 73 | Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , 2013 , 162, 348-59 | 4.5 | 44 |
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