# Christopher P Wardell

List of Publications by Year
in descending order



| 109 | 5,788 | 126708 33 | 79541 73 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 112 | 112 | 112 | 8034 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509. | 9.4 | 596 |
| 2 | Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. Journal of Clinical Oncology, 2015, 33, 3911-3920. | 0.8 | 463 |
| 3 | Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. Blood, 2018, 132, 587-597. | 0.6 | 335 |
| 4 | A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. Leukemia, 2019, 33, 159-170. | 3.3 | 313 |
| 5 | A novel prognostic model in myeloma based on co-segregating adverse FISH lesions and the ISS: analysis of patients treated in the MRC Myeloma IX trial. Leukemia, 2012, 26, 349-355. | 3.3 | 298 |
| 6 | Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. Nature Communications, 2017, 8, 268. | 5.8 | 277 |
| 7 | APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Nature Communications, 2015, 6, 6997. | 5.8 | 261 |
| 8 | Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969. | 1.8 | 254 |
| 9 | Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. Leukemia, 2014, 28, 384-390. | 3.3 | 252 |
| 10 | Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. Blood, 2012, 120, 1077-1086. | 0.6 | 231 |
| 11 | Aberrant global methylation patterns affect the molecular pathogenesis and prognosis of multiple myeloma. Blood, 2011, 117, 553-562. | 0.6 | 217 |
| 12 | Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. Leukemia, 2014, 28, 1705-1715. | 3.3 | 207 |
| 13 | Mapping of Chromosome 1p Deletions in Myeloma Identifies FAM46C at 1p12 and CDKN2C at 1p32.3 as Being Genes in Regions Associated with Adverse Survival. Clinical Cancer Research, 2011, 17, 7776-7784. | 3.2 | 147 |
| 14 | Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. Blood, 2013, 122, 219-226. | 0.6 | 147 |
| 15 | Translocations at 8q24 juxtapose MYC with genes that harbor superenhancers resulting in overexpression and poor prognosis in myeloma patients. Blood Cancer Journal, 2014, 4, e191-e191. | 2.8 | 142 |
| 16 | Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. Blood, 2013, 121, 3413-3419. | 0.6 | 128 |
| 17 | Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. Leukemia, 2019, 33, 1713-1722. | 3.3 | 112 |
| 18 | Cancer whole-genome sequencing: present and future. Oncogene, 2015, 34, 5943-5950. | 2.6 | 87 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794. | 3.2 | 81 |
| 20 | Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373. | 1.8 | 81 |
| 21 | The spectrum of somatic mutations in monoclonal gammopathy of undetermined significance indicates a less complex genomic landscape than that in multiple myeloma. Haematologica, 2017, 102, 1617-1625. | 1.7 | 71 |
| 22 | 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. Haematologica, 2019, 104, 1440-1450. | 1.7 | 67 |
| 23 | The clinical impact and molecular biology of del(17p) in multiple myeloma treated with conventional or thalidomideâ€based therapy. Genes Chromosomes and Cancer, 2011, 50, 765-774. | 1.5 | 59 |
| 24 | Emerging BRAF Mutations in Cancer Progression and Their Possible Effects on Transcriptional Networks. Genes, 2020, 11, 1342. | 1.0 | 58 |
| 25 | Coexistent hyperdiploidy does not abrogate poor prognosis in myeloma with adverse cytogenetics and may precede IGH translocations. Blood, 2015, 125, 831-840. | 0.6 | 57 |
| 26 | The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. Nature Communications, 2021, 12, 293. | 5.8 | 54 |
| 27 | Improved risk stratification in myeloma using a micro<scp>RNA</scp>â€based classifier. British Journal of Haematology, 2013, 162, 348-359. | 1.2 | 53 |
| 28 | Cleavage of BLOC1S1 mRNA by IRE1 Is Sequence Specific, Temporally Separate from XBP1 Splicing, and Dispensable for Cell Viability under Acute Endoplasmic Reticulum Stress. Molecular and Cellular Biology, 2015, 35, 2186-2202. | 1.1 | 53 |
| 29 | HSF1 Is Essential for Myeloma Cell Survival and A Promising Therapeutic Target. Clinical Cancer Research, 2018, 24, 2395-2407. | 3.2 | 46 |
| 30 | TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207. | 5.8 | 42 |
| 31 | Microhomology-mediated end joining drives complex rearrangements and overexpression of MYC and PVT1 in multiple myeloma. Haematologica, 2020, 105, 1055-1066. | 1.7 | 42 |
| 32 | MMSET is the key molecular target in t(4;14) myeloma. Blood Cancer Journal, 2013, 3, e114-e114. | 2.8 | 40 |
| 33 | Gender Disparities in the Tumor Genetics and Clinical Outcome of Multiple Myeloma. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1703-1707. | 1.1 | 39 |
| 34 | BRAF and DIS3 Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. Clinical Cancer Research, 2020, 26, 2422-2432. | 3.2 | 37 |
| 35 | A TC classification-based predictor for multiple myeloma using multiplexed real-time quantitative PCR. Leukemia, 2013, 27, 1754-1757. | 3.3 | 36 |
| 36 | A molecular diagnostic approach able to detect the recurrent genetic prognostic factors typical of presenting myeloma. Genes Chromosomes and Cancer, 2015, 54, 91-98. | 1.5 | 31 |

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|---|---|---|---|
| 37 | Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. Blood Cancer Journal, 2020, 10, 70. | 2.8 | 27 |
| 38 | High expression levels of the mammalian target of rapamycin inhibitorDEPTORare predictive of response to thalidomide in myeloma. Leukemia and Lymphoma, 2010, 51, 2126-2129. | 0.6 | 26 |
| 39 | Genomewide profiling of copyâ€number alteration in monoclonal gammopathy of undetermined significance. European Journal of Haematology, 2016, 97, 568-575. | 1.1 | 24 |
| 40 | A Modified Method for Whole Exome Resequencing from Minimal Amounts of Starting DNA. PLoS ONE, 2012, 7, e32617. | 1.1 | 24 |
| 41 | An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. Blood Cancer Journal, 2019, 9, 62. | 2.8 | 23 |
| 42 | Neutral tumor evolution in myeloma is associated with poor prognosis. Blood, 2017, 130, 1639-1643. | 0.6 | 20 |
| 43 | Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. Haematologica, 2021, 106, 736-745. | 1.7 | 20 |
| 44 | Daratumumab and dexamethasone is safe and effective for triple refractory myeloma patients: final results of the IFM 2014â€04 (Etoile du Nord) trial. British Journal of Haematology, 2019, 187, 319-327. | 1.2 | 18 |
| 45 | Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564. | 2.9 | 17 |
| 46 | A Functional Precision Medicine Pipeline Combines Comparative Transcriptomics and Tumor Organoid Modeling to Identify Bespoke Treatment Strategies for Glioblastoma. Cells, 2021, 10, 3400. | 1.8 | 15 |
| 47 | Proof of the Concept to Use a Malignant B Cell Line Drug Screen Strategy for Identification and Weight of Melphalan Resistance Genes in Multiple Myeloma. PLoS ONE, 2013, 8, e83252. | 1.1 | 13 |
| 48 | Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of TP53. Oncotarget, 2019, 10, 732-737. | 0.8 | 13 |
| 49 | The genomic landscape of plasma cells in systemic light chain amyloidosis. Blood, 2018, 132, 2775-2777. | 0.6 | 12 |
| 50 | Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. Leukemia, 2021, 35, 3017-3020. | 3.3 | 11 |
| 51 | Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget, 2017, 8, 36203-36210. | 0.8 | 11 |
| 52 | Identification of a novel t(7;14) translocation in multiple myeloma resulting in overexpression of EGFR. Genes Chromosomes and Cancer, 2013, 52, 817-822. | 1.5 | 7 |
| 53 | FiNGS: high quality somatic mutations using filters for next generation sequencing. BMC Bioinformatics, 2021, 22, 77. | 1.2 | 7 |
| 54 | Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. Blood Cancer Journal, 2022, 12, . | 2.8 | 7 |

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|---|---|---|---|
| 55 | 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. Leukemia, 2022, 36, 591-595. | 3.3 | 6 |
| 56 | Proteogenomic analysis of melanoma brain metastases from distinct anatomical sites identifies pathways of metastatic progression. Acta Neuropathologica Communications, 2020, 8, 157. | 2.4 | 5 |
| 57 | Spatiotemporal Analysis of Intraclonal Heterogeneity in Multiple Myeloma: Unravelling the Impact of Treatment and the Propagating Capacity of Subclones Using Whole Exome Sequencing. Blood, 2015, 126, 371-371. | 0.6 | 5 |
| 58 | A Novel Functional Role for MMSET in RNA Processing Based on the Link Between the REIIBP Isoform and Its Interaction with the SMN Complex. PLoS ONE, 2014, 9, e99493. | 1.1 | 5 |
| 59 | Highâ€risk transcriptional profiles in multiple myeloma are an acquired feature that can occur in any subtype and more frequently with each subsequent relapse. British Journal of Haematology, 2021, 195, 283-286. | 1.2 | 4 |
| 60 | Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. Blood, 2018, 132, 408-408. | 0.6 | 3 |
| 61 | Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. Blood, 2010, 116, 782-782. | 0.6 | 3 |
| 62 | 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. Blood, 2017, 130, 65-65. | 0.6 | 3 |
| 63 | TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. BMC Bioinformatics, 2020, 21, 144. | 1.2 | 2 |
| 64 | The Mutational Landscape of Primary Plasma Cell Leukemia. Blood, 2018, 132, 114-114. | 0.6 | 2 |
| 65 | 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. Blood, 2019, 134, 4333-4333. | 0.6 | 2 |
| 66 | 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. Blood, 2019, 134, 4346-4346. | 0.6 | 2 |
| 67 | Exome Sequencing To Define A Genetic Signature Of Plasma Cells In Systemic AL Amyloidosis. Blood, 2013, 122, 3098-3098. | 0.6 | 2 |
| 68 | The Spectrum of Epigenetic Mutations in Myeloma and Their Clinical Impact. Blood, 2014, 124, 2194-2194. | 0.6 | 2 |
| 69 | Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278. | 0.6 | 2 |
| 70 | 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). Blood, 2016, 128, 4412-4412. | 0.6 | 2 |
| 71 | MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. Blood, 2013, 122, 274-274. | 0.6 | 2 |
| 72 | The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. Blood, 2016, 128, 196-196. | 0.6 | 2 |

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|---|---|---|---|
| 73 | Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. Blood, 2016, 128, 3271-3271. | 0.6 | 2 |
| 74 | A detailed exploration of using RNA-Seq data in established multiple myeloma gene expression profile microarray based risk scores. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e57-e58. | 0.2 | 1 |
| 75 | Hypermethylation Is A Key Feature of the Transition of Multiple Myeloma to Plasma Cell Leukemia. Blood, 2010, 116, 535-535. | 0.6 | 1 |
| 76 | Somatic Mutation Spectrum in Monoclonal Gammopathy of Undetermined Significance Compared to Multiple Myeloma. Blood, 2014, 124, 3346-3346. | 0.6 | 1 |
| 77 | Mutational Patterns and Copy Number Changes at Diagnosis Are a Powerful Tool to Predict Outcome: Result of the Sequencing Study of 463 Newly Diagnosed Myeloma Trial Patients. Blood, 2014, 124, 637-637. | 0.6 | 1 |
| 78 | Exome Sequencing to Define a Genetic Signature of Plasma Cells in Systemic AL Amyloidosis. Blood, 2014, 124, 726-726. | 0.6 | 1 |
| 79 | Defining High Risk Myeloma Using Co-Segregating FISH Variables; Results of MRC Myeloma IX. Blood, 2010, 116, 1907-1907. | 0.6 | 1 |
| 80 | Whole Genome Sequencing Illuminates the Genetic and Biological Features Underlying the Transition of SMM to MM. Blood, 2011, 118, 296-296. | 0.6 | 1 |
| 81 | Improved Risk Stratification in Myeloma Using Microrna-Based Classifier. Blood, 2012, 120, 932-932. | 0.6 | 1 |
| 82 | Expression Quantitative Trait Loci Reveal Regulatory Regions Important In The Pathogenesis of Multiple Myeloma. Blood, 2013, 122, 1847-1847. | 0.6 | 1 |
| 83 | Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. Blood, 2018, 132, 1906-1906. | 0.6 | 1 |
| 84 | An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. Blood, 2018, 132, 4489-4489. | 0.6 | 1 |
| 85 | Oncogenic Mutation BRAF V600E Changes Phenotypic Behavior of THLE-2 Liver Cells through Alteration of Gene Expression. International Journal of Molecular Sciences, 2022, 23, 1548. | 1.8 | 1 |
| 86 | B-cell malignancies: capture-sequencing strategies for identification of gene rearrangements and translocations into immunoglobulin gene loci. Blood and Lymphatic Cancer: Targets and Therapy, 2014, , 107. | 1.2 | 0 |
| 87 | Neutral Tumor Evolution in Myeloma is Associated With Poor Response to Therapy. Clinical Lymphoma, Myeloma and Leukemia, 2017, 17, e10. | 0.2 | 0 |
| 88 | Long-term Analysis Of Multiple Sequential Samples Reveals Patterns Of Progression In Smoldering Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e59-e60. | 0.2 | 0 |
| 89 | Primary glioblastoma of the cauda equina with molecular and histopathological characterization: case report. Neuro-Oncology Advances, 2021, 3, vdab154. | 0.4 | 0 |
| 90 | The Interaction of Response and FISH-Based Risk Stratification to Better Define Clinical Outcome in Myeloma. Blood, 2011, 118, 1823-1823. | 0.6 | 0 |

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|---|---|---|---|
| 91 | Exome Sequencing of the t(4;14) and t(11;14) Translocation Specific Subgroups of MM. Blood, 2011, 118, 1817-1817. | 0.6 | 0 |
| 92 | Intra-Clonal Heterogeneity Is a Critical Early Event in the Preclinical Stages of Multiple Myeloma and Is Subject to Darwinian Fluctuation throughout the Disease. Blood, 2012, 120, 3941-3941. | 0.6 | 0 |
| 93 | Base-Pair Resolution Mapping of IGH Translocations in Multiple Myeloma Using Targeted Capture and Massively Parallel Sequencing. Blood, 2012, 120, 3490-3490. | 0.6 | 0 |
| 94 | High-Resolution, Genome Wide Analysis of DNA Methylation Provides Insights Into the Epigenetic Architecture of t(4;14) Myeloma.. Blood, 2012, 120, 2385-2385. | 0.6 | 0 |
| 95 | Genome-Wide Methylation and Gene Expression Analyses Identify Patients At High and Low Risk of Disease Progression. Blood, 2012, 120, 319-319. | 0.6 | 0 |
| 96 | Discovery Of Genome Wide Epigenetic Programming In t(4;14) Multiple Myeloma and In The Progression From Myeloma To Plasma Cell Leukemia Via Methyl Binding Domain Protein Capture and Sequencing. Blood, 2013, 122, 599-599. | 0.6 | 0 |
| 97 | Single-Cell Genetic Analysis Reveals The Genetic Composition Of Founder Clones, Phylogenetic Patterns Of Branching and Parallel Evolution, and Clonal Fluctuations Following Patient Treatment In Multiple Myeloma. Blood, 2013, 122, 398-398. | 0.6 | 0 |
| 98 | Characterization of RAS Alterations in Myeloma: Why Direct Targeting of RAS May be the Most Appropriate Therapeutic Approach. Blood, 2014, 124, 643-643. | 0.6 | 0 |
| 99 | The Extent of Intra-Clonal Genetic Diversity within the Myeloma Clone Is a Predictive Biomarker of Progression and Outcome after Treatment. Blood, 2014, 124, 640-640. | 0.6 | 0 |
| 100 | High Resolution Genome Wide DNA Methylation Analysis in a Large Trial Group Reveals a Novel Epigenetically Defined Subgroup of Myeloma Patients Characterized By Developmental Gene Hypermethylation. Blood, 2014, 124, 2189-2189. | 0.6 | 0 |
| 101 | Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. Blood, 2018, 132, 4457-4457. | 0.6 | 0 |
| 102 | Mutations and Copy Number Changes Predict Progression from Smoldering Myeloma to Symptomatic Myeloma in the Era of Novel IMWG Criteria. Blood, 2018, 132, 4456-4456. | 0.6 | 0 |
| 103 | Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. Blood, 2018, 132, 3185-3185. | 0.6 | 0 |
| 104 | Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. Blood, 2018, 132, 4454-4454. | 0.6 | 0 |
| 105 | The Translational Switch of MYC Protein Aliases in Myeloma Tumor Cells. Blood, 2019, 134, 4390-4390. | 0.6 | 0 |
| 106 | Genomic and Transcriptomic Profiling of Brain Metastases. Cancers, 2021, 13, 5598. | 1.7 | 0 |
| 107 | The Impact of gain1q on Mutational Structure and Clonal Evolution in a Uniformly Treated High-Risk Series of Patients at First Relapse. Blood, 2021, 138, 2683-2683. | 0.6 | 0 |
| 108 | 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. Blood, 2020, 136, 6-7. | 0.6 | 0 |

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|---|---|---|---|
| 109 | 323 Generation of a functional precision medicine pipeline which combines comparative transcriptomics and tumor organoid modeling to identify bespoke treatment strategies for glioblastoma. Journal of Clinical and Translational Science, 2022, 6, 58-58. | 0.3 | 0 |