Christopher P Wardell

List of Publications by Year
in descending order

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109 papers	5,788 citations	126708 33 h-index	79541 73 g-index
112 all docs	112 docs citations	112 times ranked	8034 citing authors

#	Article	IF	Citations
1	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
2	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
3	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
4	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. Blood Cancer Journal, 2022, 12, .	2.8	7
5	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. Haematologica, 2021, 106, 736-745.	1.7	20
6	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. Nature Communications, 2021, 12, 293.	5.8	54
7	FiNGS: high quality somatic mutations using filters for next generation sequencing. BMC Bioinformatics, 2021, 22, 77.	1.2	7
8	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
9	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
10	Primary glioblastoma of the cauda equina with molecular and histopathological characterization: case report. Neuro-Oncology Advances, 2021, 3, vdab154.	0.4	0
11	Genomic and Transcriptomic Profiling of Brain Metastases. Cancers, 2021, 13, 5598.	1.7	0
12	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
13	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
14	Microhomology-mediated end joining drives complex rearrangements and overexpression of MYC and PVT1 in multiple myeloma. Haematologica, 2020, 105, 1055-1066.	1.7	42
15	Emerging BRAF Mutations in Cancer Progression and Their Possible Effects on Transcriptional Networks. Genes, 2020, 11, 1342.	1.0	58
16	Proteogenomic analysis of melanoma brain metastases from distinct anatomical sites identifies pathways of metastatic progression. Acta Neuropathologica Communications, 2020, 8, 157.	2.4	5
17	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
18	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

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19	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. BMC Bioinformatics, 2020, 21, 144.	1.2	2
20	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
21	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. Leukemia, 2019, 33, 159-170.	3.3	313
22	An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. Blood Cancer Journal, 2019, 9, 62.	2.8	23
23	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
24	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
25	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
26	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
27	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. Leukemia, 2019, 33, 1713-1722.	3.3	112
28	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
29	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
30	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
31	The Translational Switch of MYC Protein Aliases in Myeloma Tumor Cells. Blood, 2019, 134, 4390-4390.	0.6	0
32	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. Journal of Hepatology, 2018, 68, 959-969.	1.8	254
33	HSF1 Is Essential for Myeloma Cell Survival and A Promising Therapeutic Target. Clinical Cancer Research, 2018, 24, 2395-2407.	3.2	46
34	The genomic landscape of plasma cells in systemic light chain amyloidosis. Blood, 2018, 132, 2775-2777.	0.6	12
35	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. Blood, 2018, 132, 587-597.	0.6	335
36	The Mutational Landscape of Primary Plasma Cell Leukemia. Blood, 2018, 132, 114-114.	0.6	2

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37	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. Blood, 2018, 132, 408-408.	0.6	3
38	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
39	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
40	Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. Blood, 2018, 132, 3185-3185.	0.6	0
41	Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. Blood, 2018, 132, 1906-1906.	0.6	1
42	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
43	An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. Blood, 2018, 132, 4489-4489.	0.6	1
44	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
45	Neutral tumor evolution in myeloma is associated with poor prognosis. Blood, 2017, 130, 1639-1643.	0.6	20
46	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	2.9	17
47	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. Nature Communications, 2017, 8, 268.	5.8	277
48	Neutral Tumor Evolution in Myeloma is Associated With Poor Response to Therapy. Clinical Lymphoma, Myeloma and Leukemia, 2017, 17, e10.	0.2	0
49	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	1.8	81
50	Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget, 2017, 8, 36203-36210.	0.8	11
51	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
52	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	9.4	596
53	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794.	3.2	81
54	Genomewide profiling of copyâ€number alteration in monoclonal gammopathy of undetermined significance. European Journal of Haematology, 2016, 97, 568-575.	1.1	24

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55	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278.	0.6	2
56	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
57	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
58	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
59	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
60	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
61	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
62	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Nature Communications, 2015, 6, 6997.	5.8	261
63	Cancer whole-genome sequencing: present and future. Oncogene, 2015, 34, 5943-5950.	2.6	87
64	TCF12 is mutated in anaplastic oligodendroglioma. Nature Communications, 2015, 6, 7207.	5.8	42
65	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
66	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
67	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
68	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
69	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
70	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
71	The Spectrum of Epigenetic Mutations in Myeloma and Their Clinical Impact. Blood, 2014, 124, 2194-2194.	0.6	2
72	Somatic Mutation Spectrum in Monoclonal Gammopathy of Undetermined Significance Compared to Multiple Myeloma. Blood, 2014, 124, 3346-3346.	0.6	1

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73	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
74	Exome Sequencing to Define a Genetic Signature of Plasma Cells in Systemic AL Amyloidosis. Blood, 2014, 124, 726-726.	0.6	1
75	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
76	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
77	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
78	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
79	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
80	Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. Blood, 2013, 122, 219-226.	0.6	147
81	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
82	A TC classification-based predictor for multiple myeloma using multiplexed real-time quantitative PCR. Leukemia, 2013, 27, 1754-1757.	3.3	36
83	MMSET is the key molecular target in t(4;14) myeloma. Blood Cancer Journal, 2013, 3, e114-e114.	2.8	40
84	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
85	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
86	Exome Sequencing To Define A Genetic Signature Of Plasma Cells In Systemic AL Amyloidosis. Blood, 2013, 122, 3098-3098.	0.6	2
87	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
88	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
89	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
90	Expression Quantitative Trait Loci Reveal Regulatory Regions Important In The Pathogenesis of Multiple Myeloma. Blood, 2013, 122, 1847-1847.	0.6	1

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91	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
92	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
93	A Modified Method for Whole Exome Resequencing from Minimal Amounts of Starting DNA. PLoS ONE, 2012, 7, e32617.	1.1	24
94	Improved Risk Stratification in Myeloma Using Microrna-Based Classifier. Blood, 2012, 120, 932-932.	0.6	1
95	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
96	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
97	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
98	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
99	Aberrant global methylation patterns affect the molecular pathogenesis and prognosis of multiple myeloma. Blood, 2011, 117, 553-562.	0.6	217
100	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
101	Gender Disparities in the Tumor Genetics and Clinical Outcome of Multiple Myeloma. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1703-1707.	1.1	39
102	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
103	Whole Genome Sequencing Illuminates the Genetic and Biological Features Underlying the Transition of SMM to MM. Blood, 2011, 118, 296-296.	0.6	1
104	The Interaction of Response and FISH-Based Risk Stratification to Better Define Clinical Outcome in Myeloma. Blood, 2011, 118, 1823-1823.	0.6	0
105	Exome Sequencing of the t(4;14) and t(11;14) Translocation Specific Subgroups of MM. Blood, 2011, 118, 1817-1817.	0.6	0
106	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
107	Hypermethylation Is A Key Feature of the Transition of Multiple Myeloma to Plasma Cell Leukemia. Blood, 2010, 116, 535-535.	0.6	1
108	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. Blood, 2010, 116, 782-782.	0.6	3

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109	Defining High Risk Myeloma Using Co-Segregating FISH Variables; Results of MRC Myeloma IX. Blood, 2010, 116, 1907-1907.	0.6	1