Christopher P Wardell

List of Publications by Citations

102 papers	4,103 citations	31 h-index	63 g-index
112 ext. papers	5,110 ext. citations	4.8 avg, IF	4.62 L-index

#	Paper	IF	Citations
102	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423
101	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. *Journal of Clinical Oncology*, **2015**, 33, 3911-20	2.2	348
100	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, 349-55	10.7	236
99	Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. *Leukemia*, **2014**, 28, 384-390	10.7	202
98	Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. *Blood*, **2012**, 120, 1077-86	2.2	200
97	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. *Blood*, **2018**, 132, 587-597	2.2	196
96	Aberrant global methylation patterns affect the molecular pathogenesis and prognosis of multiple myeloma. *Blood*, **2011**, 117, 553-62	2.2	182
95	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. *Nature Communications*, **2015**, 6, 6997	17.4	176
94	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. *Leukemia*, **2019**, 33, 159-170	10.7	176
93	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. *Nature Communications*, **2017**, 8, 268	17.4	170
92	Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. *Leukemia*, **2014**, 28, 1705-15	10.7	162
91	Genomic characterization of biliary tract cancers identifies driver genes and predisposing mutations. *Journal of Hepatology*, **2018**, 68, 959-969	13.4	149
90	Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. *Blood*, **2013**, 122, 219-26	2.2	128
89	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, 7776-84	12.9	122
88	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	7	114
87	Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. *Blood*, **2013**, 121, 3413-9	2.2	101
86	Cancer whole-genome sequencing: present and future. *Oncogene*, **2015**, 34, 5943-50	9.2	71

85	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. *Leukemia*, **2019**, 33, 1713-1722	10.7	66
84	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
83	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. *Clinical Cancer Research*, **2016**, 22, 5783-5794	12.9	56
82	The clinical impact and molecular biology of del(17p) in multiple myeloma treated with conventional or thalidomide-based therapy. *Genes Chromosomes and Cancer*, **2011**, 50, 765-74	5	52
81	Coexistent hyperdiploidy does not abrogate poor prognosis in myeloma with adverse cytogenetics and may precede IGH translocations. *Blood*, **2015**, 125, 831-40	2.2	48
80	Improved risk stratification in myeloma using a microRNA-based classifier. *British Journal of Haematology*, **2013**, 162, 348-59	4.5	44
79	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	6.6	42
78	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	6.6	39
77	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, 2186-202	4.8	39
76	Gender disparities in the tumor genetics and clinical outcome of multiple myeloma. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 1703-7	4	33
75	TCF12 is mutated in anaplastic oligodendroglioma. *Nature Communications*, **2015**, 6, 7207	17.4	32
74	MMSET is the key molecular target in t(4;14) myeloma. *Blood Cancer Journal*, **2013**, 3, e114	7	32
73	HSF1 Is Essential for Myeloma Cell Survival and A Promising Therapeutic Target. *Clinical Cancer Research*, **2018**, 24, 2395-2407	12.9	31
72	A TC classification-based predictor for multiple myeloma using multiplexed real-time quantitative PCR. *Leukemia*, **2013**, 27, 1754-7	10.7	31
71	A molecular diagnostic approach able to detect the recurrent genetic prognostic factors typical of presenting myeloma. *Genes Chromosomes and Cancer*, **2015**, 54, 91-8	5	26
70	A modified method for whole exome resequencing from minimal amounts of starting DNA. *PLoS ONE*, **2012**, 7, e32617	3.7	24
69	High expression levels of the mammalian target of rapamycin inhibitor DEPTOR are predictive of response to thalidomide in myeloma. *Leukemia and Lymphoma*, **2010**, 51, 2126-9	1.9	23
68	Microhomology-mediated end joining drives complex rearrangements and overexpression of and in multiple myeloma. *Haematologica*, **2020**, 105, 1055-1066	6.6	22

67	Genomewide profiling of copy-number alteration in monoclonal gammopathy of undetermined significance. *European Journal of Haematology*, **2016**, 97, 568-575	3.8	20
66	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. *Nature Communications*, **2021**, 12, 293	17.4	20
65	and Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. *Clinical Cancer Research*, **2020**, 26, 2422-2432	12.9	17
64	An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. *Blood Cancer Journal*, **2019**, 9, 62	7	17
63	Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. *Blood Cancer Journal*, **2020**, 10, 70	7	16
62	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. *Cell Reports*, **2017**, 20, 2556-2564	10.6	15
61	Neutral tumor evolution in myeloma is associated with poor prognosis. *Blood*, **2017**, 130, 1639-1643	2.2	14
60	Emerging Mutations in Cancer Progression and Their Possible Effects on Transcriptional Networks. *Genes*, **2020**, 11,	4.2	13
59	Daratumumab and dexamethasone is safe and effective for triple refractory myeloma patients: final results of the IFM 2014-04 (Etoile du Nord) trial. *British Journal of Haematology*, **2019**, 187, 319-327	4.5	12
58	The genomic landscape of plasma cells in systemic light chain amyloidosis. *Blood*, **2018**, 132, 2775-2777	2.2	10
57	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	3.7	9
56	Search for rare protein altering variants influencing susceptibility to multiple myeloma. *Oncotarget*, **2017**, 8, 36203-36210	3.3	9
55	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. *Haematologica*, **2021**, 106, 736-745	6.6	7
54	Identification of a novel t(7;14) translocation in multiple myeloma resulting in overexpression of EGFR. *Genes Chromosomes and Cancer*, **2013**, 52, 817-22	5	6
53	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of. *Oncotarget*, **2019**, 10, 732-737	3.3	5
52	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	2.2	4
51	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	3.7	4
50	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. *Blood*, **2010**, 116, 782-782	2.2	3

49	Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. *Leukemia*, **2021**, 35, 3017-3020	10.7	3
48	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*, **2021**,	10.7	3
47	The Mutational Landscape of Primary Plasma Cell Leukemia. *Blood*, **2018**, 132, 114-114	2.2	2
46	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. *Blood*, **2018**, 132, 408-408	2.2	2
45	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	2.2	2
44	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	2.2	2
43	Exome Sequencing To Define A Genetic Signature Of Plasma Cells In Systemic AL Amyloidosis. *Blood*, **2013**, 122, 3098-3098	2.2	2
42	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. *Blood*, **2016**, 128, 3278-3278	2.2	2
41	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	2.2	2
40	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	2.2	2
39	High-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	4.5	2
38	Hypermethylation Is A Key Feature of the Transition of Multiple Myeloma to Plasma Cell Leukemia. *Blood*, **2010**, 116, 535-535	2.2	1
37	Somatic Mutation Spectrum in Monoclonal Gammopathy of Undetermined Significance Compared to Multiple Myeloma. *Blood*, **2014**, 124, 3346-3346	2.2	1
36	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	2.2	1
35	Exome Sequencing to Define a Genetic Signature of Plasma Cells in Systemic AL Amyloidosis. *Blood*, **2014**, 124, 726-726	2.2	1
34	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. *Blood*, **2016**, 128, 196-196	2.2	1
33	Defining High Risk Myeloma Using Co-Segregating FISH Variables; Results of MRC Myeloma IX. *Blood*, **2010**, 116, 1907-1907	2.2	1
32	Proteogenomic analysis of melanoma brain metastases from distinct anatomical sites identifies pathways of metastatic progression. *Acta Neuropathologica Communications*, **2020**, 8, 157	7.3	1

31	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. *BMC Bioinformatics*, **2020**, 21, 144	3.6	1
30	FiNGS: high quality somatic mutations using filters for next generation sequencing. *BMC Bioinformatics*, **2021**, 22, 77	3.6	1
29	The Spectrum of Epigenetic Mutations in Myeloma and Their Clinical Impact. *Blood*, **2014**, 124, 2194-2194	2.2	0
28	An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. *Blood*, **2018**, 132, 4489-4489	2.2	0
27	MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. *Blood*, **2013**, 122, 274-274	2.2	0
26	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	2.6	
25	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	2.2	
24	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	2.2	
23	Primary glioblastoma of the cauda equina with molecular and histopathological characterization: Case report. *Neuro-Oncology Advances*, **2021**, 3, vdab154	0.9	
22	Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. *Blood*, **2018**, 132, 4457-4457	2.2	
21	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	2.2	
20	Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. *Blood*, **2018**, 132, 3185-3185	2.2	
19	Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. *Blood*, **2018**, 132, 1906-1906	2.2	
18	Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. *Blood*, **2018**, 132, 4454-4454	2.2	
17	The Translational Switch of MYC Protein Aliases in Myeloma Tumor Cells. *Blood*, **2019**, 134, 4390-4390	2.2	
16	Characterization of RAS Alterations in Myeloma: Why Direct Targeting of RAS May be the Most Appropriate Therapeutic Approach. *Blood*, **2014**, 124, 643-643	2.2	
15	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	2.2	
14	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	2.2	

List of Publications

13	Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. *Blood*, **2016**, 128, 3271-3271	2.2
12	Whole Genome Sequencing Illuminates the Genetic and Biological Features Underlying the Transition of SMM to MM. *Blood*, **2011**, 118, 296-296	2.2
11	The Interaction of Response and FISH-Based Risk Stratification to Better Define Clinical Outcome in Myeloma. *Blood*, **2011**, 118, 1823-1823	2.2
10	Exome Sequencing of the t(4;14) and t(11;14) Translocation Specific Subgroups of MM. *Blood*, **2011**, 118, 1817-1817	2.2
9	Improved Risk Stratification in Myeloma Using Microrna-Based Classifier. *Blood*, **2012**, 120, 932-932	2.2
8	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	2.2
7	Base-Pair Resolution Mapping of IGH Translocations in Multiple Myeloma Using Targeted Capture and Massively Parallel Sequencing. *Blood*, **2012**, 120, 3490-3490	2.2
6	High-Resolution, Genome Wide Analysis of DNA Methylation Provides Insights Into the Epigenetic Architecture of t(4;14) Myeloma.. *Blood*, **2012**, 120, 2385-2385	2.2
5	Genome-Wide Methylation and Gene Expression Analyses Identify Patients At High and Low Risk of Disease Progression. *Blood*, **2012**, 120, 319-319	2.2
4	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	2.2
3	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	2.2
2	Expression Quantitative Trait Loci Reveal Regulatory Regions Important In The Pathogenesis of Multiple Myeloma. *Blood*, **2013**, 122, 1847-1847	2.2
1	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	0.4