Christine Moung

List of Publications by Year
in descending order

10 papers	339 citations	1684188 5 h-index	1872680 6 g-index
10 all docs	10 docs citations	10 times ranked	599 citing authors

#	Article	IF	Citations
1	Off-the-shelf EBV-specific T cell immunotherapy for rituximab-refractory EBV-associated lymphoma following transplantation. Journal of Clinical Investigation, 2020, 130, 733-747.	8.2	161
2	Establishment of Immunoglobulin Heavy (IGH) Chain Clonality Testing by Next-Generation Sequencing for Routine Characterization of B-Cell and Plasma Cell Neoplasms. Journal of Molecular Diagnostics, 2019, 21, 330-342.	2.8	69
3	Enhanced specificity of clinical high-sensitivity tumor mutation profiling in cell-free DNA via paired normal sequencing using MSK-ACCESS. Nature Communications, 2021, 12, 3770.	12.8	68
4	Routine Evaluation of Minimal Residual Disease in Myeloma Using Next-Generation Sequencing Clonality Testing. Journal of Molecular Diagnostics, 2021, 23, 181-199.	2.8	19
5	Rapid EGFR Mutation Detection Using the Idylla Platform. Journal of Molecular Diagnostics, 2021, 23, 310-322.	2.8	19
6	Quantitative Off-Target Detection of Epstein-Barr Virusâ€“Derived DNA in Routine Molecular Profiling of Hematopoietic Neoplasms by Panel-Based Hybrid-Capture Next-Generation Sequencing. Journal of Molecular Diagnostics, 2021, , .	2.8	2
7	The t(11;14)(q13;q32)/ CCND1â€“IGH translocation in chronic lymphocytic leukaemia/small lymphocytic lymphoma: an unusual genetic aberration during the natural clinical course. Histopathology, 2019, 75, 291-294.	2.9	1
8	Clonally-Related CD5+ CLL/SLL and CD10+ high grade B-cell lymphoma suggests common neoplastic progenitor with branched disease evolution, with therapeutic implications. Leukemia and Lymphoma, 2020, 61, 460-464.	1.3	0
9	Next-Generation Sequencing-Based Assay Shows High Clonal Characterization Success Rate for Plasma Cell Neoplasms, and Concordance with Flow Cytometry in Minimal Residual Disease Detection. Blood, 2018, 132, 4475-4475.	1.4	0
10	Plasma Cell Myeloma Residual Disease Quantitation Using a Next-Generation Sequencing-Based IGH Clonal Rearrangement Assay with the Aid of a "Spike-in" Clonal Sequence. Blood, 2019, 134, 3380-3380.	1.4	0