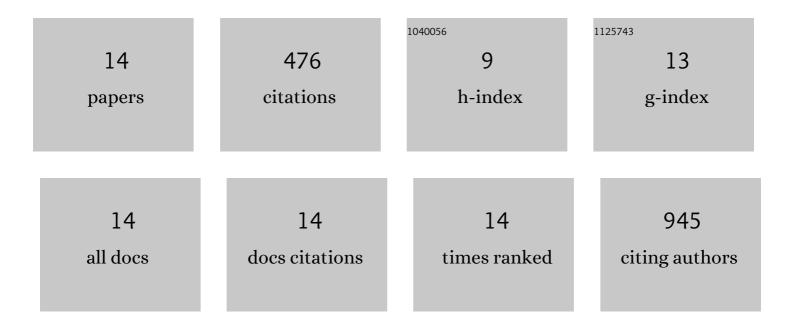
Hernando Escobar

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Development of UHPLC/Q-TOF Analysis Method to Screen Glycerin for Direct Detection of Process Contaminants 3-Monochloropropane-1,2-diol Esters (3-MCPDEs) and Glycidyl Esters (GEs). Molecules, 2021, 26, 2449.	3.8	5
2	Peptidomic analysis of type 1 diabetes associated HLAâ€DQ molecules and the impact of HLAâ€DM on peptide repertoire editing. European Journal of Immunology, 2017, 47, 314-326.	2.9	22
3	Type 1 diabetes associated HLAâ€ĐQ2 and DQ8 molecules are relatively resistant to HLAâ€DM mediated release of invariant chainâ€derived CLIP peptides. European Journal of Immunology, 2016, 46, 834-845.	2.9	21
4	High Sensitivity Measurement of Pancreatic Polypeptide and Its Variant in Serum and Plasma by LC-MS/MS. Methods in Molecular Biology, 2016, 1378, 199-210.	0.9	5
5	Measurement of Pancreatic Polypeptide ans Its Peptide Variant in Human Serum and Plasma by Immunocapture-Liquid-Chromatography-Tandem Mass Spectrometry. Reference Intervals and Practical Assay Considerations Biochemistry & Physiology, 2014, 03, .	0.2	4
6	Expression of the Mouse MHC Class Ib H2-T11 Gene Product, a Paralog of H2-T23 (Qa-1) with Shared Peptide-Binding Specificity. Journal of Immunology, 2014, 193, 1427-1439.	0.8	10
7	ERAAP and Tapasin Independently Edit the Amino and Carboxyl Termini of MHC Class I Peptides. Journal of Immunology, 2013, 191, 1547-1555.	0.8	29
8	Regulation of HLA-DR peptide occupancy by histone deacetylase inhibitors. Human Vaccines and Immunotherapeutics, 2013, 9, 784-789.	3.3	13
9	Mice completely lacking immunoproteasomes show major changes in antigen presentation. Nature Immunology, 2012, 13, 129-135.	14.5	222
10	Utility of Characteristic QTOF MS/MS Fragmentation for MHC Class I Peptides. Journal of Proteome Research, 2011, 10, 2494-2507.	3.7	18
11	Endoplasmic Reticulum Aminopeptidase Associated with Antigen Processing Defines the Composition and Structure of MHC Class I Peptide Repertoire in Normal and Virus-Infected Cells. Journal of Immunology, 2010, 184, 3033-3042.	0.8	79
12	Identification of naturally processed ligands in the C57BL/6 mouse using large-scale mass spectrometric peptide sequencing and bioinformatics prediction. Immunogenetics, 2009, 61, 241-246.	2.4	12
13	Large Scale Mass Spectrometric Profiling of Peptides Eluted from HLA Molecules Reveals N-Terminal-Extended Peptide Motifs. Journal of Immunology, 2008, 181, 4874-4882.	0.8	36
14	Large Scale Mass Spectrometric Sequencing of Peptides Eluted from HLAâ€B35 Molecules Revealed Broad and Nâ€ŧerminal Extended Peptide Motifs. FASEB Journal, 2008, 22, 423-423.	0.5	0