## Lawrence J Stern

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Phenylsulfamoyl Benzoic Acid Inhibitor of ERAP2 with a Novel Mode of Inhibition. ACS Chemical Biology, 2022, 17, 1756-1768.	3.4	2
2	Conformational dynamics linked to domain closure and substrate binding explain the ERAP1 allosteric regulation mechanism. Nature Communications, 2021, 12, 5302.	12.8	22
3	Discovery of Selective Inhibitors of Endoplasmic Reticulum Aminopeptidase 1. Journal of Medicinal Chemistry, 2020, 63, 103-121.	6.4	30
4	Structural Basis of Inhibition of Insulin-Regulated Aminopeptidase by a Macrocyclic Peptidic Inhibitor. ACS Medicinal Chemistry Letters, 2020, 11, 1429-1434.	2.8	11
5	Inactivating mutations and X-ray crystal structure of the tumor suppressor OPCML reveal cancer-associated functions. Nature Communications, 2019, 10, 3134.	12.8	9
6	A temporal thymic selection switch and ligand binding kinetics constrain neonatal Foxp3+ Treg cell development. Nature Immunology, 2019, 20, 1046-1058.	14.5	31
7	In vivo clonal expansion and phenotypes of hypocretin-specific CD4+ T cells in narcolepsy patients and controls. Nature Communications, 2019, 10, 5247.	12.8	39
8	CDR3αÂdrives selection of the immunodominant Epstein Barr virus (EBV) BRLF1-specific CD8 T cell receptor repertoire in primary infection. PLoS Pathogens, 2019, 15, e1008122.	4.7	21
9	HLA-DO Modulates the Diversity of the MHC-II Self-peptidome. Molecular and Cellular Proteomics, 2019, 18, 490-503.	3.8	33
10	Class II MHC antigen processing in immune tolerance and inflammation. Immunogenetics, 2019, 71, 171-187.	2.4	77
11	Molecular pathways for antigenic peptide generation by ER aminopeptidase 1. Molecular Immunology, 2019, 113, 50-57.	2.2	17
12	Recognition of Listeria Infection by Germline Elements of the Vγ1.1 Vδ6.3 TCR. ImmunoHorizons, 2019, 3, 341-351.	1.8	2
13	Quantitative Profiling of the Lymph Node Clearance Capacity. Scientific Reports, 2018, 8, 11253.	3.3	35
14	The N-terminal region of photocleavable peptides that bind HLA-DR1 determines the kinetics of fragment release. PLoS ONE, 2018, 13, e0199704.	2.5	5
15	Broad TCR repertoire and diverse structural solutions for recognition of an immunodominant CD8+ T cell epitope. Nature Structural and Molecular Biology, 2017, 24, 395-406.	8.2	87
16	<i>Shigella</i> depends on SepA to destabilize the intestinal epithelial integrity via cofilin activation. Gut Microbes, 2017, 8, 544-560.	9.8	46
17	The cytosolic domain of T-cell receptor ζ associates with membranes in a dynamic equilibrium and deeply penetrates the bilayer. Journal of Biological Chemistry, 2017, 292, 17746-17759.	3.4	14
18	The melting pot of the MHC II peptidome. Current Opinion in Immunology, 2016, 40, 70-77.	5.5	33

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19	A Simple Proteomics-Based Approach to Identification of Immunodominant Antigens from a Complex Pathogen: Application to the CD4 T Cell Response against Human Herpesvirus 6B. PLoS ONE, 2015, 10, e0142871.	2.5	9
20	Evaluating the Role of HLA-DM in MHC Class Il–Peptide Association Reactions. Journal of Immunology, 2015, 195, 706-716.	0.8	21
21	Susceptibility to HLA-DM Protein Is Determined by a Dynamic Conformation of Major Histocompatibility Complex Class II Molecule Bound with Peptide. Journal of Biological Chemistry, 2014, 289, 23449-23464.	3.4	49
22	A novel method to measure HLA-DM-susceptibility of peptides bound to MHC class II molecules based on peptide binding competition assay and differential IC50 determination. Journal of Immunological Methods, 2014, 406, 21-33.	1.4	10
23	HLA-DM and HLA-DO, key regulators of MHC-II processing and presentation. Current Opinion in Immunology, 2014, 26, 115-122.	5.5	119
24	HLA-DO acts as a substrate mimic to inhibit HLA-DM by a competitive mechanism. Nature Structural and Molecular Biology, 2013, 20, 90-98.	8.2	99
25	HLA-DM Constrains Epitope Selection in the Human CD4 T Cell Response to Vaccinia Virus by Favoring the Presentation of Peptides with Longer HLA-DM–Mediated Half-Lives. Journal of Immunology, 2012, 189, 3983-3994.	0.8	51
26	Conformational variation in structures of classical and non lassical <scp>MHCII</scp> proteins and functional implications. Immunological Reviews, 2012, 250, 144-157.	6.0	59
27	Antigen-specific T cell phenotyping microarrays using grating coupled surface plasmon resonance imaging and surface plasmon coupled emission. Biosensors and Bioelectronics, 2012, 31, 264-269.	10.1	35
28	Conformational lability in the class II MHC 3 <sub>10</sub> helix and adjacent extended strand dictate HLA-DM susceptibility and peptide exchange. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19329-19334.	7.1	70
29	HLA-DR: Molecular Insights and Vaccine Design. Current Pharmaceutical Design, 2009, 15, 3249-3261.	1.9	78
30	GMCSF in the absence of other cytokines sustains human dendritic cell precursors with T cell regulatory activity and capacity to differentiate into functional dendritic cells. Immunology Letters, 2008, 116, 41-54.	2.5	38
31	Model for the Peptide-Free Conformation of Class II MHC Proteins. PLoS ONE, 2008, 3, e2403.	2.5	60
32	Human CD4+ T Cell Epitopes from Vaccinia Virus Induced by Vaccination or Infection. PLoS Pathogens, 2007, 3, e144.	4.7	51
33	Structure Induction of the T-Cell Receptor ζ-Chain upon Lipid Binding Investigated by NMR Spectroscopy. ChemBioChem, 2007, 8, 820-827.	2.6	39
34	Enhanced Catalytic Action of HLA-DM on the Exchange of Peptides Lacking Backbone Hydrogen Bonds between their N-Terminal Region and the MHC Class II α-Chain. Journal of Immunology, 2004, 172, 1109-1117.	0.8	57
35	Exploration of the P6/P7 Region of the Peptide-binding Site of the Human Class II Major Histocompatability Complex Protein HLA-DR1. Journal of Biological Chemistry, 2003, 278, 44904-44912.	3.4	30
36	The kinetic basis of peptide exchange catalysis by HLA-DM. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 12450-12455.	7.1	67