

James M Kovacs

List of Publications by Year in descending order

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17
papers

1,035
citations

623734

14
h-index

888059

17
g-index

17
all docs

17
docs citations

17
times ranked

1681
citing authors

#	ARTICLE	IF	CITATIONS
1	HIV-1 Neutralizing Antibody Signatures and Application to Epitope-Targeted Vaccine Design. <i>Cell Host and Microbe</i> , 2019, 25, 59-72.e8.	11.0	124
2	Neutralizing Antibody Responses following Long-Term Vaccination with HIV-1 Env gp140 in Guinea Pigs. <i>Journal of Virology</i> , 2018, 92, .	3.4	10
3	Effect of the cytoplasmic domain on antigenic characteristics of HIV-1 envelope glycoprotein. <i>Science</i> , 2015, 349, 191-195.	12.6	113
4	A Multivalent Clade C HIV-1 Env Trimer Cocktail Elicits a Higher Magnitude of Neutralizing Antibodies than Any Individual Component. <i>Journal of Virology</i> , 2015, 89, 2507-2519.	3.4	42
5	Characterization and Immunogenicity of a Novel Mosaic M HIV-1 gp140 Trimer. <i>Journal of Virology</i> , 2014, 88, 9538-9552.	3.4	30
6	Stable, uncleaved HIV-1 envelope glycoprotein gp140 forms a tightly folded trimer with a native-like structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18542-18547.	7.1	67
7	Design of Lipid Nanocapsule Delivery Vehicles for Multivalent Display of Recombinant Env Trimers in HIV Vaccination. <i>Bioconjugate Chemistry</i> , 2014, 25, 1470-1478.	3.6	38
8	Detection of complement activation using monoclonal antibodies against C3d. <i>Journal of Clinical Investigation</i> , 2013, 123, 2218-2230.	8.2	78
9	HIV-1 envelope trimer elicits more potent neutralizing antibody responses than monomeric gp120. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12111-12116.	7.1	163
10	Characterizing the complement receptor Type 2â€“C3d complex by site-directed mutagenesis and molecular modeling. <i>Molecular Immunology</i> , 2010, 47, 2258-2258.	2.2	1
11	Biophysical Investigations of Complement Receptor 2 (CD21 and CR2)-Ligand Interactions Reveal Amino Acid Contacts Unique to Each Receptor-Ligand Pair. <i>Journal of Biological Chemistry</i> , 2010, 285, 27251-27258.	3.4	10
12	Delineation of the Complement Receptor Type 2â€“C3d Complex by Site-Directed Mutagenesis and Molecular Docking. <i>Journal of Molecular Biology</i> , 2010, 404, 697-710.	4.2	24
13	Mapping of the C3d Ligand Binding Site on Complement Receptor 2 (CR2/CD21) Using Nuclear Magnetic Resonance and Chemical Shift Analysis. <i>Journal of Biological Chemistry</i> , 2009, 284, 9513-9520.	3.4	28
14	Intrinsic amino acid sideâ€“chain hydrophilicity/hydrophobicity coefficients determined by reversedâ€“phase highâ€“performance liquid chromatography of model peptides: Comparison with other hydrophilicity/hydrophobicity scales. <i>Biopolymers</i> , 2009, 92, 573-595.	2.4	114
15	Requirements for prediction of peptide retention time in reversed-phase high-performance liquid chromatography: Hydrophilicity/hydrophobicity of side-chains at the N- and C-termini of peptides are dramatically affected by the end-groups and location. <i>Journal of Chromatography A</i> , 2007, 1141, 212-225.	3.7	50
16	Quantitation of the nearest-neighbour effects of amino acid side-chains that restrict conformational freedom of the polypeptide chain using reversed-phase liquid chromatography of synthetic model peptides with l- and d-amino acid substitutions. <i>Journal of Chromatography A</i> , 2006, 1123, 212-224.	3.7	20
17	Determination of intrinsic hydrophilicity/hydrophobicity of amino acid side chains in peptides in the absence of nearest-neighbor or conformational effects. <i>Biopolymers</i> , 2006, 84, 283-297.	2.4	123