Andrea S Llera

List of Publications by Year
in descending order

13 papers	705 citations	1040056 9 h-index	1125743 13 g-index
13 all docs	13 docs citations	13 times ranked	1061 citing authors

#	Article	IF	Citations
1	The role of the matricellular protein SPARC in the dynamic interaction between the tumor and the host. Cancer and Metastasis Reviews, 2008, 27, 691-705.	5.9	172
2	Structure of the VÎ´ domain of a human Î³Î´ T-cell antigen receptor. Nature, 1998, 391, 502-506.	27.8	121
3	Structures of Two Streptococcal Superantigens Bound to TCR Î² Chains Reveal Diversity in the Architecture of T Cell Signaling Complexes. Structure, 2002, 10, 687-699.	3.3	116
4	The role of the matricellular protein SPARC in the dynamic interaction between the tumor and the host. Cancer and Metastasis Reviews, 2008, 27, 523-537.	5.9	97
5	SPARC Promotes Cathepsin B-Mediated Melanoma Invasiveness through a Collagen I/Î±2Î²1 Integrin Axis. Journal of Investigative Dermatology, 2011, 131, 2438-2447.	0.7	61
6	Functional Analysis of the TCR Binding Domain of Toxic Shock Syndrome Toxin-1 Predicts Further Diversity in MHC Class II/Superantigen/TCR Ternary Complexes. Journal of Immunology, 2003, 171, 1385-1392.	0.8	44
7	SPARC modulates the proliferation of stromal but not melanoma cells unless endogenous SPARC expression is downregulated. International Journal of Cancer, 2008, 122, 1465-1475.	5.1	28
8	Cloning, expression and interaction of human Tâ€cell receptors with the bacterial superantigen SSA. FEBS Journal, 2004, 271, 4075-4083.	0.2	23
9	Predictive Outcomes for HER2-enriched Cancer Using Growth and Metastasis Signatures Driven By SPARC. Molecular Cancer Research, 2017, 15, 304-316.	3.4	21
10	Improving information retrieval in functional analysis. Computers in Biology and Medicine, 2016, 79, 10-20.	7.0	9
11	Massive integrative gene set analysis enables functional characterization of breast cancer subtypes. Journal of Biomedical Informatics, 2019, 93, 103157.	4.3	6
12	The multi-reference contrast method: Facilitating set enrichment analysis. Computers in Biology and Medicine, 2012, 42, 188-194.	7.0	5
13	Improving 2D-DIGE protein expression analysis by two-stage linear mixed models: assessing experimental effects in a melanoma cell study. Bioinformatics, 2008, 24, 2706-2712.	4.1	2