Francesca Nadalin

List of Publications by Year
in descending order

12 papers	**830** citations	1040056 **9** h-index	1372567 **10** g-index
15 all docs	**15** docs citations	**15** times ranked	**1946** citing authors

#	Article	IF	Citations
1	Single-cell analysis reveals divergent responses of human dendritic cells to the MVA vaccine. Science Signaling, 2021, 14, .	3.6	13
2	Coevolution analysis of amino-acids reveals diversified drug-resistance solutions in viral sequences: a case study of hepatitis B virus. Virus Evolution, 2020, 6, veaa006.	4.9	4
3	S100A7/Ran-binding protein 9 coevolution in mammals. Immunogenetics, 2020, 72, 155-164.	2.4	1
4	The N-Terminal Domain of cGAS Determines Preferential Association with Centromeric DNA and Innate Immune Activation in the Nucleus. Cell Reports, 2019, 26, 2377-2393.e13.	6.4	166
5	Protein–protein interaction specificity is captured by contact preferences and interface composition. Bioinformatics, 2018, 34, 459-468.	4.1	29
6	NONO Detects the Nuclear HIV Capsid to Promote cGAS-Mediated Innate Immune Activation. Cell, 2018, 175, 488-501.e22.	28.9	154
7	A protein coevolution method uncovers critical features of the Hepatitis C Virus fusion mechanism. PLoS Pathogens, 2018, 14, e1006908.	4.7	20
8	BIS2Analyzer: a server for co-evolution analysis of conserved protein families. Nucleic Acids Research, 2017, 45, W307-W314.	14.5	43
9	Chimera: a Bioconductor package for secondary analysis of fusion products. Bioinformatics, 2014, 30, 3556-3557.	4.1	18
10	A Multi-objective Optimisation Approach to the Design of Experiment in De Novo Assembly Projects. , 2012, , .		0
11	GapFiller: a de novo assembly approach to fill the gap within paired reads. BMC Bioinformatics, 2012, 13, S8.	2.6	324
12	iBIS2Analyzer: a web server for a phylogeny-driven coevolution analysis of protein families. Nucleic Acids Research, 0, , .	14.5	3