Elvezia M Paraboschi

List of Publications by Year
in descending order

45 papers	3,198 citations	394421 19 h-index	243625 44 g-index
50 all docs	50 docs citations	50 times ranked	7976 citing authors

#	Article	IF	Citations
1	Recognition and inhibition of SARS-CoV-2 by humoral innate immunity pattern recognition molecules. Nature Immunology, 2022, 23, 275-286.	14.5	95
2	Impact of chronic exposure to 5-alpha reductase inhibitors on the risk of hospitalization for COVID-19: a case-control study in male population from two COVID-19 regional centers of Lombardy, Italy. Minerva Urology and Nephrology, 2022, 74, .	2.5	4
3	Needles in Haystacks: Understanding the Success of Selective Pairing of Nucleic Acids. International Journal of Molecular Sciences, 2022, 23, 3072.	4.1	1
4	OxDNA to Study Species Interactions. Entropy, 2022, 24, 458.	2.2	1
5	The Role of Epigenetics in Primary Biliary Cholangitis. International Journal of Molecular Sciences, 2022, 23, 4873.	4.1	11
6	Reply to: HultstrÃ¶m et al., Genetic determinants of mannose-binding lectin activity predispose to thromboembolic complications in critical COVID-19. Mannose-binding lectin genetics in COVID-19. Nature Immunology, 2022, 23, 865-867.	14.5	4
7	Detailed stratified GWAS analysis for severe COVID-19 in four European populations. Human Molecular Genetics, 2022, 31, 3945-3966.	2.9	46
8	Functional and clinical implications of genetic structure in 1686 Italian exomes. Human Mutation, 2021, 42, 272-289.	2.5	5
9	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. Gastroenterology, 2021, 160, 2483-2495.e26.	1.3	27
10	MEDTEC Students against Coronavirus: Investigating the Role of Hemostatic Genes in the Predisposition to COVID-19 Severity. Journal of Personalized Medicine, 2021, 11, 1166.	2.5	7
11	The first case of the TARDBP p.G294V mutation in a homozygous state: is a single pathogenic allele sufficient to cause ALS?. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2020, 21, 273-279.	1.7	10
12	Saposin D variants are not a common cause of familial Parkinsonâ€™s disease among Italians. Brain, 2020, 143, e71-e71.	7.6	7
13	Hereditary Hypofibrinogenemia with Hepatic Storage. International Journal of Molecular Sciences, 2020, 21, 7830.	4.1	15
14	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. New England Journal of Medicine, 2020, 383, 1522-1534.	27.0	1,548
15	Profiling the mutational landscape of coagulation factor V deficiency. Haematologica, 2020, 105, e180-e185.	3.5	10
16	Rare variants lowering the levels of coagulation factor X are protective against ischemic heart disease. Haematologica, 2020, 105, e365-e369.	3.5	9
17	ACE2 and TMPRSS2 variants and expression as candidates to sex and country differences in COVID-19 severity in Italy. Aging, 2020, 12, 10087-10098.	3.1	331
18	Understanding the Impact of Aberrant Splicing in Coagulation Factor V Deficiency. International Journal of Molecular Sciences, 2019, 20, 910.	4.1	5

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19	Sighting acute myocardial infarction through platelet gene expression. Scientific Reports, 2019, 9, 19574.	3.3	19
20	Mycobacterium tuberculosis Drives Expansion of Low-Density Neutrophils Equipped With Regulatory Activities. Frontiers in Immunology, 2019, 10, 2761.	4.8	23
21	Characterisation of a DNA hydrogel viscosity by an integrated optofluidic microrheometer. , 2019, , .		0
22	Not only cancer: the long non-coding RNA MALAT1 affects the repertoire of alternatively spliced transcripts and circular RNAs in multiple sclerosis. Human Molecular Genetics, 2019, 28, 1414-1428.	2.9	56
23	Newtonian to non-newtonian fluid transition of a model transient network. Soft Matter, 2018, 14, 3288-3295.	2.7	17
24	Molecular investigation of 41 patients affected by coagulation factor <scp>XI</scp> deficiency. Haemophilia, 2018, 24, e50-e55.	2.1	6
25	Genetic Association and Altered Gene Expression of CYBB in Multiple Sclerosis Patients. Biomedicines, 2018, 6, 117.	3.2	10
26	Interpreting Non-coding Genetic Variation in Multiple Sclerosis Genome-Wide Associated Regions. Frontiers in Genetics, 2018, 9, 647.	2.3	25
27	Nonenzymatic Polymerization into Long Linear RNA Templated by Liquid Crystal Self-Assembly. ACS Nano, 2018, 12, 9750-9762.	14.6	35
28	Gene-gene interactions among coding genes of iron-homeostasis proteins and APOE-alleles in cognitive impairment diseases. PLoS ONE, 2018, 13, e0193867.	2.5	40
29	miR-634 is a Pol III-dependent intronic microRNA regulating alternative-polyadenylated isoforms of its host gene PRKCA. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 1046-1056.	2.4	7
30	A frequent oligogenic involvement in congenital hypothyroidism. Human Molecular Genetics, 2017, 26, 2507-2514.	2.9	107
31	Exploring the global landscape of genetic variation in coagulation factor XI deficiency. Blood, 2017, 130, e1-e6.	1.4	41
32	Fibrinogen as a Pleiotropic Protein Causing Human Diseases: The Mutational Burden of AÎ±, BÎ², and Î³ Chains. International Journal of Molecular Sciences, 2017, 18, 2711.	4.1	36
33	The Characterization of GSDMB Splicing and Backsplicing Profiles Identifies Novel Isoforms and a Circular RNA That Are Dysregulated in Multiple Sclerosis. International Journal of Molecular Sciences, 2017, 18, 576.	4.1	81
34	Meta-Analysis of Multiple Sclerosis Microarray Data Reveals Dysregulation in RNA Splicing Regulatory Genes. International Journal of Molecular Sciences, 2015, 16, 23463-23481.	4.1	22
35	Identification of a novel large deletion in a patient with severe factor V deficiency using an inâ€house F5 <scp>MLPA</scp> assay. Haemophilia, 2015, 21, 140-147.	2.1	6
36	Abiotic ligation of DNA oligomers templated by their liquid crystal ordering. Nature Communications, 2015, 6, 6424.	12.8	42

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37	Genetic background and risk of postpartum haemorrhage: results from an Italian cohort of 3219 women. Haemophilia, 2014, 20, e377-83.	2.1	12
38	Functional variations modulating PRKCA expression and alternative splicing predispose to multiple sclerosis. Human Molecular Genetics, 2014, 23, 6746-6761.	2.9	32
39	Phase behavior and critical activated dynamics of limited-valence DNA nanostars. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15633-15637.	7.1	156
40	Notch1 regulates chemotaxis and proliferation by controlling the CCâ€chemokine receptors 5 and 9 in T cell acute lymphoblastic leukaemia. Journal of Pathology, 2012, 226, 713-722.	4.5	54
41	Functional characterization of a novel missense mutation identified in a Turkish patient affected by severe coagulation factor V deficiency. Haemophilia, 2012, 18, 205-210.	2.1	4
42	Identification of a new susceptibility variant for multiple sclerosis in OAS1 by population genetics analysis. Human Genetics, 2012, 131, 87-97.	3.8	20
43	Identification of the first Alu-mediated large deletion involving the F5 gene in a compound heterozygous patient with severe factor V deficiency. Thrombosis and Haemostasis, 2011, 106, 296-303.	3.4	10
44	Genetic Association and Altered Gene Expression of Mir-155 in Multiple Sclerosis Patients. International Journal of Molecular Sciences, 2011, 12, 8695-8712.	4.1	93
45	Molecular characterization of three novel splicing mutations causing factor V deficiency and analysis of the F5 gene splicing pattern. Haematologica, 2008, 93, 1505-1513.	3.5	23