

# Josep Gregori Font

## List of Publications by Year in descending order

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77  
papers

1,749  
citations

318942

23  
h-index

371746

37  
g-index

83  
all docs

83  
docs citations

83  
times ranked

2746  
citing authors

#	ARTICLE	IF	CITATIONS
1	Inspecting the Ribozyme Region of Hepatitis Delta Virus Genotype 1: Conservation and Variability. <i>Viruses</i> , 2022, 14, 215.	1.5	4
2	Dynamics of SARS-CoV-2 Alpha (B.1.1.7) variant spread: The wastewater surveillance approach. <i>Environmental Research</i> , 2022, 208, 112720.	3.7	16
3	Characteristics of hepatitis C virus resistance in an international cohort after a decade of direct-acting antivirals. <i>JHEP Reports</i> , 2022, 4, 100462.	2.6	10
4	Hepatitis B Virus Variants with Multiple Insertions and/or Deletions in the X Open Reading Frame 3â€² End: Common Members of Viral Quasispecies in Chronic Hepatitis B Patients. <i>Biomedicines</i> , 2022, 10, 1194.	1.4	1
5	Host-dependent editing of SARS-CoV-2 in COVID-19 patients. <i>Emerging Microbes and Infections</i> , 2021, 10, 1777-1789.	3.0	13
6	Sophisticated viral quasispecies with a genotype-related pattern of mutations in the hepatitis B X gene of HBsAg-ve chronically infected patients. <i>Scientific Reports</i> , 2021, 11, 4215.	1.6	3
7	Resistance-associated substitutions after sofosbuvir/velpatasvir/voxilaprevir triple therapy failure. <i>Journal of Viral Hepatitis</i> , 2021, 28, 1319-1324.	1.0	7
8	Population Disequilibrium as Promoter of Adaptive Explorations in Hepatitis C Virus. <i>Viruses</i> , 2021, 13, 616.	1.5	7
9	Monitoring Emergence of the SARS-CoV-2 B.1.1.7 Variant through the Spanish National SARS-CoV-2 Wastewater Surveillance System (VATar COVID-19). <i>Environmental Science &amp; Technology</i> , 2021, 55, 11756-11766.	4.6	39
10	Study of Quasispecies Complexity and Liver Damage Progression after Liver Transplantation in Hepatitis C Virus Infected Patients. <i>Genes</i> , 2021, 12, 1731.	1.0	0
11	Cross-sectional evaluation of circulating hepatitis B virus RNA and DNA: Different quasispecies?. <i>World Journal of Gastroenterology</i> , 2021, 27, 7144-7158.	1.4	1
12	Deep-sequencing reveals broad subtype-specific HCV resistance mutations associated with treatment failure. <i>Antiviral Research</i> , 2020, 174, 104694.	1.9	39
13	Amino Acid Substitutions Associated with Treatment Failure for Hepatitis C Virus Infection. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	15
14	Naturally occurring SARS-CoV-2 gene deletions close to the spike S1/S2 cleavage site in the viral quasispecies of COVID19 patients. <i>Emerging Microbes and Infections</i> , 2020, 9, 1900-1911.	3.0	57
15	Dissimilar Conservation Pattern in Hepatitis C Virus Mutant Spectra, Consensus Sequences, and Data Banks. <i>Journal of Clinical Medicine</i> , 2020, 9, 3450.	1.0	12
16	Broad and Dynamic Diversification of Infectious Hepatitis C Virus in a Cell Culture Environment. <i>Journal of Virology</i> , 2020, 94, .	1.5	20
17	A new implication of quasispecies dynamics: Broad virus diversification in absence of external perturbations. <i>Infection, Genetics and Evolution</i> , 2020, 82, 104278.	1.0	20
18	Conservation and variability of hepatitis B core at different chronic hepatitis stages. <i>World Journal of Gastroenterology</i> , 2020, 26, 2584-2598.	1.4	8

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19	The Critical Role of Codon Composition on the Translation Efficiency Robustness of the Hepatitis A Virus Capsid. <i>Genome Biology and Evolution</i> , 2019, 11, 2439-2456.	1.1	12
20	<p></p>Deep-sequencing study of HCV G4a resistance-associated substitutions in Egyptian patients failing DAA treatment</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 2799-2807.	1.1	5
21	SAT-472-Massive sequencing of circulating DNA as a potential tool for diagnosis and follow-up in patients with hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2019, 70, e841-e842.	1.8	1
22	SAT-163-HBeAg-negative chronic infection: more complex and conserved quasispecies in Hepatitis B X gene. <i>Journal of Hepatology</i> , 2019, 70, e701.	1.8	0
23	<p></p>Whole-genome characterization and resistance-associated substitutions in a new HCV genotype 1 subtype</p>. <i>Infection and Drug Resistance</i> , 2019, Volume 12, 947-955.	1.1	5
24	The increasing impact of lethal mutagenesis of viruses. <i>Future Medicinal Chemistry</i> , 2019, 11, 1645-1657.	1.1	30
25	Evidence for positive selection of hepatitis A virus antigenic variants in vaccinated men-having-sex-with men patients: Implications for immunization policies. <i>EBioMedicine</i> , 2019, 39, 348-357.	2.7	22
26	Synergistic Lethal Mutagenesis of Hepatitis C Virus. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	10
27	Characterization of hepatitis B virus X gene quasispecies complexity in mono-infection and hepatitis delta virus superinfection. <i>World Journal of Gastroenterology</i> , 2019, 25, 1566-1579.	1.4	7
28	Hepatitis C virus intrinsic molecular determinants may contribute to the development of cholestatic hepatitis after liver transplantation. <i>Journal of General Virology</i> , 2019, 100, 63-68.	1.3	1
29	Hepatitis C virus deep sequencing for sub-genotype identification in mixed infections: A real-life experience. <i>International Journal of Infectious Diseases</i> , 2018, 67, 114-117.	1.5	23
30	Quantitative characterization of hepatitis delta virus genome edition by next-generation sequencing. <i>Virus Research</i> , 2018, 243, 52-59.	1.1	11
31	Detection of hyper-conserved regions in hepatitis B virus X gene potentially useful for gene therapy. <i>World Journal of Gastroenterology</i> , 2018, 24, 2095-2107.	1.4	17
32	Pipeline for specific subtype amplification and drug resistance detection in hepatitis C virus. <i>BMC Infectious Diseases</i> , 2018, 18, 446.	1.3	29
33	Baseline hepatitis C virus resistance-associated substitutions present at frequencies lower than 15% may be clinically significant. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 2207-2210.	1.1	26
34	Thrombotic thrombocytopenic purpura relapse induced by acute hepatitis E transmitted by cryosupernatant plasma and successfully controlled with ribavirin. <i>Transfusion</i> , 2018, 58, 2501-2505.	0.8	14
35	Rare haplotype load as marker for lethal mutagenesis. <i>PLoS ONE</i> , 2018, 13, e0204877.	1.1	8
36	Hepatitis C virus early kinetics and resistance-associated substitution dynamics during antiviral therapy with direct-acting antivirals. <i>Journal of Viral Hepatitis</i> , 2018, 25, 1515-1525.	1.0	10

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37	Resistance of high fitness hepatitis C virus to lethal mutagenesis. <i>Virology</i> , 2018, 523, 100-109.	1.1	30
38	Characterization of intra- and inter-host norovirus P2 genetic variability in linked individuals by amplicon sequencing. <i>PLoS ONE</i> , 2018, 13, e0201850.	1.1	10
39	Extracellular HMGA1 Promotes Tumor Invasion and Metastasis in Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 6367-6382.	3.2	52
40	HIV-1 Protease Evolvability Is Affected by Synonymous Nucleotide Recoding. <i>Journal of Virology</i> , 2018, 92, .	1.5	9
41	New hepatitis C virus genotype 1 subtype naturally harbouring resistance-associated mutations to NS5A inhibitors. <i>Journal of General Virology</i> , 2018, 99, 97-102.	1.3	6
42	Analysis of hepatitis B virus preS1 variability and prevalence of the rs2296651 polymorphism in a Spanish population. <i>World Journal of Gastroenterology</i> , 2018, 24, 680-692.	1.4	10
43	Internal Disequilibria and Phenotypic Diversification during Replication of Hepatitis C Virus in a Noncoevolving Cellular Environment. <i>Journal of Virology</i> , 2017, 91, .	1.5	42
44	High HCV subtype heterogeneity in a chronically infected general population revealed by high-resolution hepatitis C virus subtyping. <i>Clinical Microbiology and Infection</i> , 2017, 23, 775.e1-775.e6.	2.8	11
45	Selection of the highly replicative and partially multidrug resistant rtS78T HBV polymerase mutation during TDF-ETV combination therapy. <i>Journal of Hepatology</i> , 2017, 67, 246-254.	1.8	52
46	Phylogenetic analysis of an epidemic outbreak of acute hepatitis C in HIV-infected patients by ultra-deep pyrosequencing. <i>Journal of Clinical Virology</i> , 2017, 92, 42-47.	1.6	17
47	Deep sequencing in the management of hepatitis virus infections. <i>Virus Research</i> , 2017, 239, 115-125.	1.1	23
48	Assessment of a Novel Automatic Real-Time PCR Assay on the Cobas 4800 Analyzer as a Screening Platform for Hepatitis C Virus Genotyping in Clinical Practice: Comparison with Massive Sequencing. <i>Journal of Clinical Microbiology</i> , 2017, 55, 504-509.	1.8	15
49	Epidemiological trends of HIV-1 infection in blood donors from Catalonia, Spain (2005-2014). <i>Transfusion</i> , 2017, 57, 2164-2173.	0.8	11
50	Red blood cell transfusion-transmitted acute hepatitis E in an immunocompetent subject in Europe: a case report. <i>Transfusion</i> , 2017, 57, 244-247.	0.8	41
51	Lethal Mutagenesis of Hepatitis C Virus Induced by Favipiravir. <i>PLoS ONE</i> , 2016, 11, e0164691.	1.1	63
52	Identification of hepatitis C virus genotype 3 by a commercial assay challenged by natural polymorphisms detected in Spain from patients with diverse origins. <i>Journal of Clinical Virology</i> , 2016, 78, 14-19.	1.6	2
53	Barrier-Independent, Fitness-Associated Differences in Sofosbuvir Efficacy against Hepatitis C Virus. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3786-3793.	1.4	42
54	Viral quasispecies complexity measures. <i>Virology</i> , 2016, 493, 227-237.	1.1	109

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55	Improving virus production through quasispecies genomic selection and molecular breeding. <i>Scientific Reports</i> , 2016, 6, 35962.	1.6	12
56	Evidence of an Exponential Decay Pattern of the Hepatitis Delta Virus Evolution Rate and Fluctuations in Quasispecies Complexity in Long-Term Studies of Chronic Delta Infection. <i>PLoS ONE</i> , 2016, 11, e0158557.	1.1	19
57	New real-time-PCR method to identify single point mutations in hepatitis C virus. <i>World Journal of Gastroenterology</i> , 2016, 22, 9604.	1.4	5
58	Resistance of Hepatitis C Virus to Inhibitors: Complexity and Clinical Implications. <i>Viruses</i> , 2015, 7, 5746-5766.	1.5	44
59	Complex Genotype Mixtures Analyzed by Deep Sequencing in Two Different Regions of Hepatitis B Virus. <i>PLoS ONE</i> , 2015, 10, e0144816.	1.1	9
60	Deep-sequencing analysis demonstrates the persistence of pre-transplant HCV dominant variants within a more homogeneous quasispecies after liver transplantation (LT) in cholestatic hepatitis C patients. <i>Digestive and Liver Disease</i> , 2015, 47, e44.	0.4	0
61	High-Resolution Hepatitis C Virus Subtyping Using NS5B Deep Sequencing and Phylogeny, an Alternative to Current Methods. <i>Journal of Clinical Microbiology</i> , 2015, 53, 219-226.	1.8	74
62	Quasispecies dynamics in hepatitis C liver transplant recipients receiving grafts from hepatitis C virus infected donors. <i>Journal of General Virology</i> , 2015, 96, 3493-3498.	1.3	9
63	Clinical Application of Estimating Hepatitis B Virus Quasispecies Complexity by Massive Sequencing: Correlation between Natural Evolution and On-Treatment Evolution. <i>PLoS ONE</i> , 2014, 9, e112306.	1.1	26
64	Identification of host and viral factors involved in a dissimilar resolution of a hepatitis C virus infection. <i>Liver International</i> , 2014, 34, 896-906.	1.9	10
65	Inference with viral quasispecies diversity indices: clonal and NGS approaches. <i>Bioinformatics</i> , 2014, 30, 1104-1111.	1.8	56
66	Circulating pEGFR Is a Candidate Response Biomarker of Cetuximab Therapy in Colorectal Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 6346-6356.	3.2	24
67	Enhancing the Biological Relevance of Secretome-Based Proteomics by Linking Tumor Cell Proliferation and Protein Secretion. <i>Journal of Proteome Research</i> , 2014, 13, 3706-3721.	1.8	7
68	Increased Replicative Fitness Can Lead to Decreased Drug Sensitivity of Hepatitis C Virus. <i>Journal of Virology</i> , 2014, 88, 12098-12111.	1.5	74
69	An effect size filter improves the reproducibility in spectral counting-based comparative proteomics. <i>Journal of Proteomics</i> , 2013, 95, 55-65.	1.2	17
70	A comparative study of ultra-deep pyrosequencing and cloning to quantitatively analyze the viral quasispecies using hepatitis B virus infection as a model. <i>Antiviral Research</i> , 2013, 98, 273-283.	1.9	53
71	Unconventional Secretion is a Major Contributor of Cancer Cell Line Secretomes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1046-1060.	2.5	69
72	Extinction of Hepatitis C Virus by Ribavirin in Hepatoma Cells Involves Lethal Mutagenesis. <i>PLoS ONE</i> , 2013, 8, e71039.	1.1	60

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73	Ultra-Deep Pyrosequencing (UDPS) Data Treatment to Study Amplicon HCV Minor Variants. PLoS ONE, 2013, 8, e83361.	1.1	54
74	Molecular epidemiology and putative origin of hepatitis C virus in random volunteers from Argentina. World Journal of Gastroenterology, 2013, 19, 5813.	1.4	15
75	Batch effects correction improves the sensitivity of significance tests in spectral counting-based comparative discovery proteomics. Journal of Proteomics, 2012, 75, 3938-3951.	1.2	37
76	SCFTheory of multiplet states. International Journal of Quantum Chemistry, 1980, 17, 725-736.	1.0	9
77	Average fock operators. International Journal of Quantum Chemistry, 1980, 18, 1207-1221.	1.0	8