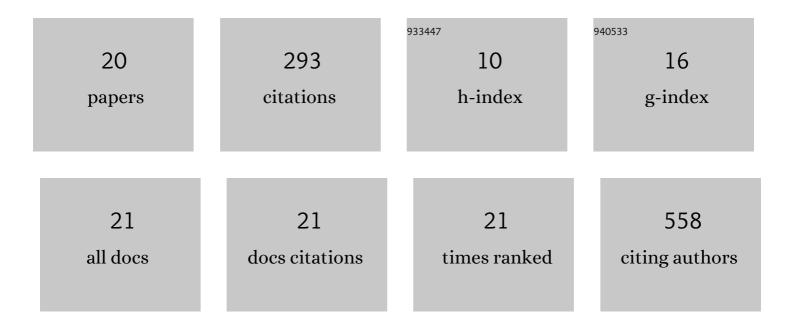
## Carmen F Manso

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/722346/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Real world SOF/VEL/VOX retreatment outcomes and viral resistance analysis for HCV patients with prior failure to DAA therapy. Journal of Viral Hepatitis, 2021, 28, 1256-1264.	2.0	16
2	Clinical evaluation of a Hepatitis C Virus whole-genome sequencing pipeline for genotyping and resistance testing. Clinical Microbiology and Infection, 2021, , .	6.0	1
3	Technical Validation of a Hepatitis C Virus Whole Genome Sequencing Assay for Detection of Genotype and Antiviral Resistance in the Clinical Pathway. Frontiers in Microbiology, 2020, 11, 576572.	3.5	13
4	Surveillance of HIV-1 transmitted integrase strand transfer inhibitor resistance in the UK. Journal of Antimicrobial Chemotherapy, 2020, 75, 3311-3318.	3.0	15
5	Enhanced Detection of DNA Viruses in the Cerebrospinal Fluid of Encephalitis Patients Using Metagenomic Next-Generation Sequencing. Frontiers in Microbiology, 2020, 11, 1879.	3.5	10
6	Real-world retreatment of HCV-infected patients with prior failure to direct acting antiviral therapy using sofosbuvir, velpatasvir and voxilaprevir. Journal of Hepatology, 2020, 73, S336.	3.7	3
7	LBP-34-Effect of Resistance Associated Substitutions on Retreatment of HCV infected patients with prior failure to Direct Acting Antiviral Therapy. Journal of Hepatology, 2019, 70, e158-e159.	3.7	0
8	Interpreting Viral Deep Sequencing Data with GLUE. Viruses, 2019, 11, 323.	3.3	29
9	Clinical evaluation of herPHEgen®: a herpesvirus genotype-to-phenotype antiviral resistance database and testing service. Access Microbiology, 2019, 1, .	0.5	0
10	The Effect of Nucleic Acid Extraction Platforms and Sample Storage on the Integrity of Viral RNA for Use in Whole Genome Sequencing. Journal of Molecular Diagnostics, 2017, 19, 303-312.	2.8	15
11	Efficient and unbiased metagenomic recovery of RNA virus genomes from human plasma samples. Scientific Reports, 2017, 7, 4173.	3.3	31
12	Molecular epidemiology of norovirus from patients with acute gastroenteritis in northwestern Spain. Epidemiology and Infection, 2015, 143, 316-324.	2.1	10
13	Efficiency of hepatitis A virus removal in six sewage treatment plants from central Tunisia. Applied Microbiology and Biotechnology, 2015, 99, 10759-10769.	3.6	20
14	Bioaccumulation and Removal Dynamics of Murine Norovirus in Manila Clams (Venerupis) Tj ETQq0 0 0 rgBT /Ov	erlock 10 T	rf 50 222 Td
15	Detection and Characterization of Hepatitis A Virus and Norovirus in Mussels from Galicia (NW) Tj ETQq1 1 0.784	4314 rgBT	/Gyerlock 1
16	Role of norovirus in acute gastroenteritis in the Northwest of Spain during 2010–2011. Journal of Medical Virology, 2013, 85, 2009-2015.	5.0	10
17	Norovirus, hepatitis A virus and enterovirus presence in shellfish from high quality harvesting areas in Portugal. Food Microbiology, 2011, 28, 936-941.	4.2	48

18Genotyping of hepatitis A virus detected in bivalve shellfish in Galicia (NW Spain). Water Science and<br/>Technology, 2010, 61, 15-24.2.516

#	Article	IF	CITATIONS
19	Imported Mollusks and Dissemination of Human Enteric Viruses. Emerging Infectious Diseases, 2010, 16, 1036-1038.	4.3	25
20	Detection and quantification of Hepatitis A and E vÃrus in wastewater from Tunisia. Frontiers in Marine Science, 0, 1, .	2.5	0