

# Pauline Lanting

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5883509/publications.pdf>

Version: 2024-02-01

10  
papers

241  
citations

1477746

6  
h-index

1372195

10  
g-index

16  
all docs

16  
docs citations

16  
times ranked

457  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gender differences in the mental health impact of the COVID-19 lockdown: Longitudinal evidence from the Netherlands. <i>SSM - Population Health</i> , 2021, 15, 100878.	1.3	53
2	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. <i>BMJ Open</i> , 2021, 11, e044474.	0.8	49
3	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. <i>Frontiers in Genetics</i> , 2020, 11, 613.	1.1	45
4	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. <i>Journal of Women's Health</i> , 2021, 30, 1686-1692.	1.5	20
5	Predicted efficacy of a pharmacogenetic passport for inflammatory bowel disease. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 51, 1105-1115.	1.9	17
6	Practical Barriers and Facilitators Experienced by Patients, Pharmacists and Physicians to the Implementation of Pharmacogenomic Screening in Dutch Outpatient Hospital Care—An Explorative Pilot Study. <i>Journal of Personalized Medicine</i> , 2020, 10, 293.	1.1	15
7	Impact of Drug-Gene-Interaction, Drug-Drug-Interaction, and Drug-Drug-Gene-Interaction on (es)Citalopram Therapy: The PharmLines Initiative. <i>Journal of Personalized Medicine</i> , 2020, 10, 256.	1.1	10
8	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. <i>PLoS ONE</i> , 2021, 16, e0255402.	1.1	6
9	Increased genetic contribution to wellbeing during the COVID-19 pandemic. <i>PLoS Genetics</i> , 2022, 18, e1010135.	1.5	3
10	IdFix: identifying accidental sample mix-ups in biobanks using polygenic scores. <i>Bioinformatics</i> , 2022, 38, 1059-1066.	1.8	1