

# Petr Smirnov

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/2105565/petr-smirnov-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

31  
papers

606  
citations

12  
h-index

24  
g-index

41  
ext. papers

948  
ext. citations

12.5  
avg, IF

3.83  
L-index

#	Paper	IF	Citations
31	Evaluation of statistical approaches for association testing in noisy drug screening data.. <i>BMC Bioinformatics</i> , <b>2022</b> , 23, 188	3.6	1
30	Orchestrating and sharing large multimodal data for transparent and reproducible research. <i>Nature Communications</i> , <b>2021</b> , 12, 5797	17.4	0
29	Consistency of in vitro drug sensitivities within pharmacological classes. <i>University of Toronto Journal of Undergraduate Life Sciences</i> , <b>2021</b> , 15, 12	0	
28	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. <i>Leukemia</i> , <b>2021</b> , 35, 796-808	10.7	6
27	Drug sensitivity prediction from cell line-based pharmacogenomics data: guidelines for developing machine learning models. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	3
26	ToxicoDB: an integrated database to mine and visualize large-scale toxicogenomic datasets. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W455-W462	20.1	3
25	Machine learning approaches to drug response prediction: challenges and recent progress. <i>Npj Precision Oncology</i> , <b>2020</b> , 4, 19	9.8	50
24	Assessment of Genetic Drift in Large Pharmacogenomic Studies. <i>Cell Systems</i> , <b>2020</b> , 11, 393-401.e2	10.6	3
23	Creating reproducible pharmacogenomic analysis pipelines. <i>Scientific Data</i> , <b>2019</b> , 6, 166	8.2	1
22	Modeling Cellular Response in Large-Scale Radiogenomic Databases to Advance Precision Radiotherapy. <i>Cancer Research</i> , <b>2019</b> , 79, 6227-6237	10.1	15
21	Integrative Pharmacogenomics Analysis of Patient-Derived Xenografts. <i>Cancer Research</i> , <b>2019</b> , 79, 4539-4550	15.0	18
20	Dr.VAE: improving drug response prediction via modeling of drug perturbation effects. <i>Bioinformatics</i> , <b>2019</b> , 35, 3743-3751	7.2	55
19	Disruption of the anaphase-promoting complex confers resistance to TTK inhibitors in triple-negative breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E1570-E1577	11.5	32
18	Tissue specificity of in vitro drug sensitivity. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2018</b> , 25, 158-166	8.6	15
17	PharmacODB: an integrative database for mining in vitro anticancer drug screening studies. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D994-D1002	20.1	82
16	Design of a HIFU array for the treatment of deep venous thrombosis: a simulation study. <i>Physics in Medicine and Biology</i> , <b>2017</b> , 62, 6108-6125	3.8	7
15	Gene isoforms as expression-based biomarkers predictive of drug response in vitro. <i>Nature Communications</i> , <b>2017</b> , 8, 1126	17.4	34

14	PharmacGx: an R package for analysis of large pharmacogenomic datasets. <i>Bioinformatics</i> , <b>2016</b> , 32, 1244-6	7.2	127
13	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , <b>2016</b> , 5, 825	3.6	25
12	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , <b>2016</b> , 5, 2333	3.6	49
11	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , <b>2016</b> , 5, 2333	3.6	35
10	Safikhani et al. reply. <i>Nature</i> , <b>2016</b> , 540, E6-E8	50.4	9
9	Safikhani et al. reply. <i>Nature</i> , <b>2016</b> , 540, E11-E12	50.4	8
8	Personalized diagnosis of medulloblastoma subtypes across patients and model systems. <i>Genomics</i> , <b>2015</b> , 106, 96-106	4.3	7
7	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 5, 2333	3.6	5
6	Revisiting inconsistency in large pharmacogenomic studies		4
5	Integrative pharmacogenomics to infer large-scale drug taxonomy		3
4	Tissue specificity of in vitro drug sensitivity		1
3	Gene isoforms as expression-based biomarkers predictive of drug response in vitro		3
2	Orchestrating and sharing large multimodal data for transparent and reproducible research		2
1	Integrative Pharmacogenomics Analysis of Patient Derived Xenografts		1