

# Federico De Masi

## List of Publications by Year in Descending Order

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

34  
papers

1,464  
citations

15  
h-index

37  
g-index

37  
ext. papers

1,894  
ext. citations

11  
avg, IF

3.58  
L-index

#	Paper	IF	Citations
34	Four groups of type 2 diabetes contribute to the etiological and clinical heterogeneity in newly diagnosed individuals: An IMI DIRECT study.. <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100477	18	1
33	Processes Underlying Glycemic Deterioration in Type 2 Diabetes: An IMI DIRECT Study. <i>Diabetes Care</i> , <b>2021</b> , 44, 511-518	14.6	6
32	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. <i>Diabetes</i> , <b>2021</b> , 70, 2092-2106	0.9	4
31	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2021</b> , 106, 80-90	5.6	2
30	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. <i>PLoS Medicine</i> , <b>2020</b> , 17, e1003149	11.6	18
29	The role of physical activity in metabolic homeostasis before and after the onset of type 2 diabetes: an IMI DIRECT study. <i>Diabetologia</i> , <b>2020</b> , 63, 744-756	10.3	4
28	Post-load glucose subgroups and associated metabolic traits in individuals with type 2 diabetes: An IMI-DIRECT study. <i>PLoS ONE</i> , <b>2020</b> , 15, e0242360	3.7	2
27	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , <b>2020</b> , 2, 1135-1148	14.6	61
26	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , <b>2020</b> , 12, 109	14.4	3
25	Dietary metabolite profiling brings new insight into the relationship between nutrition and metabolic risk: An IMI DIRECT study. <i>EBioMedicine</i> , <b>2020</b> , 58, 102932	8.8	2
24	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
23	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
22	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
21	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
20	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts <b>2020</b> , 17, e1003149		
19	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. <i>Diabetologia</i> , <b>2019</b> , 62, 1601-1615	10.3	14
18	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. <i>Journal of Hepatology</i> , <b>2019</b> , 71, 594-602	13.4	10

17	Ibuprofen alters human testicular physiology to produce a state of compensated hypogonadism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E715-E724	11.5	67
16	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D354-D359	20.1	44
15	The governance structure for data access in the DIRECT consortium: an innovative medicines initiative (IMI) project. <i>Life Sciences, Society and Policy</i> , <b>2018</b> , 14, 20	3.2	5
14	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. <i>RNA Technologies</i> , <b>2018</b> , 229-238	0.2	
13	Cross-recognition of a pit viper (Crotalinae) polyspecific antivenom explored through high-density peptide microarray epitope mapping. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005768	4.8	14
12	High-throughput immuno-profiling of mamba (Dendroaspis) venom toxin epitopes using high-density peptide microarrays. <i>Scientific Reports</i> , <b>2016</b> , 6, 36629	4.9	26
11	Control of lysosomal biogenesis and Notch-dependent tissue patterning by components of the TFEB-V-ATPase axis in <i>Drosophila melanogaster</i> . <i>Autophagy</i> , <b>2016</b> , 12, 499-514	10.2	26
10	High-throughput sequencing enhanced phage display enables the identification of patient-specific epitope motifs in serum. <i>Scientific Reports</i> , <b>2015</b> , 5, 12913	4.9	46
9	A DNA-binding-site landscape and regulatory network analysis for NAC transcription factors in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 7681-93	20.1	61
8	ATAF1 transcription factor directly regulates abscisic acid biosynthetic gene NCED3 in <i>Arabidopsis thaliana</i> . <i>FEBS Open Bio</i> , <b>2013</b> , 3, 321-7	2.7	121
7	Using a structural and logics systems approach to infer bHLH-DNA binding specificity determinants. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 4553-63	20.1	54
6	Using protein design algorithms to understand the molecular basis of disease caused by protein-DNA interactions: the Pax6 example. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 7422-31	20.1	48
5	High-resolution DNA-binding specificity analysis of yeast transcription factors. <i>Genome Research</i> , <b>2009</b> , 19, 556-66	9.7	306
4	A multiparameter network reveals extensive divergence between <i>C. elegans</i> bHLH transcription factors. <i>Cell</i> , <b>2009</b> , 138, 314-27	56.2	196
3	High throughput production of mouse monoclonal antibodies using antigen microarrays. <i>Proteomics</i> , <b>2005</b> , 5, 4070-81	4.8	65
2	Systematic discovery of new recognition peptides mediating protein interaction networks. <i>PLoS Biology</i> , <b>2005</b> , 3, e405	9.7	257
1	Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study		1