Pantelis G Bagos

List of Publications by Year in Descending Order

133 papers	4,139 citations	35 h-index	60 g-index
147 ext. papers	4,927 ext. citations	4.6 avg, IF	5.79 L-index

#	Paper	IF	Citations
133	Meta-analysis of gene expression data in adipose tissue reveals new obesity associated genes.. *Gene*, **2022**, 818, 146223	3.8	0
132	Prediction and Optimization of the Cost of Energy Resources in Greek Public Hospitals. *Energies*, **2022**, 15, 381	3.1	1
131	Meta-Analysis Methods of Diagnostic Test Accuracy Studies. *Methods in Molecular Biology*, **2022**, 2345, 173-185	1.4	
130	Hidden neural networks for transmembrane protein topology prediction. *Computational and Structural Biotechnology Journal*, **2021**, 19, 6090-6097	6.8	2
129	OMPdb: A Global Hub of Beta-Barrel Outer Membrane Proteins. *Frontiers in Bioinformatics*, **2021**, 1,		1
128	Improved strategies to counter the COVID-19 pandemic: Lockdowns vs. primary and community healthcare. *Toxicology Reports*, **2021**, 8, 1-9	4.8	38
127	The human GPCR signal transduction network. *Network Modeling Analysis in Health Informatics and Bioinformatics*, **2021**, 10, 1	1.6	1
126	Effect of early application of social distancing interventions on COVID-19 mortality over the first pandemic wave: An analysis of longitudinal data from 37 countries. *Journal of Infection*, **2021**, 82, 133-142	18.9	32
125	Smoking prevalence among hospitalized COVID-19 patients and its association with disease severity and mortality: an expanded re-analysis of a recent publication. *Harm Reduction Journal*, **2021**, 18, 9	4.6	13
124	Meta-analysis of BCOR rearranged sarcomas: challenging the therapeutic approach. *Acta Oncologica*, **2021**, 60, 721-726	3.2	2
123	VICTOR: A visual analytics web application for comparing cluster sets. *Computers in Biology and Medicine*, **2021**, 135, 104557	7	2
122	Staphylococcus aureus Carriage in Hidradenitis Suppurativa: Impact on Response to Adalimumab. *Dermatology*, **2021**, 237, 372-377	4.4	1
121	Urinary N-Acetyl-ß-glucosaminidase (uNAG) as an Indicative Biomarker of Early Diabetic Nephropathy in Patients with Diabetes Mellitus (T1DM, T2DM): A Systematic Review and Meta-Analysis. *International Journal of Diabetology*, **2021**, 2, 272-285	1	0
120	Season of birth and multiple sclerosis: a systematic review and multivariate meta-analysis. *Journal of Neurology*, **2020**, 267, 2815-2822	5.5	7
119	Methods for multiple outcome meta-analysis of gene-expression data. *MethodsX*, **2020**, 7, 100834	1.9	1
118	Landscape of Eukaryotic Transmembrane Beta Barrel Proteins. *Journal of Proteome Research*, **2020**, 19, 1209-1221	5.6	2
117	Antibody Tests in Detecting SARS-CoV-2 Infection: A Meta-Analysis. *Diagnostics*, **2020**, 10,	3.8	143

116	Multiple outcome meta-analysis of gene-expression data in inflammatory bowel disease. *Genomics*, **2020**, 112, 1761-1767	4.3	5
115	Meta-analysis of gene expression profiles in preeclampsia. *Pregnancy Hypertension*, **2020**, 19, 52-60	2.6	3
114	Diagnostic Performance of Biomarkers Urinary KIM-1 and YKL-40 for Early Diabetic Nephropathy, in Patients with Type 2 Diabetes: A Systematic Review and Meta-Analysis. *Diagnostics*, **2020**, 10,	3.8	4
113	Susceptibility to leishmaniasis is affected by host SLC11A1 gene polymorphisms: a systematic review and meta-analysis. *Parasitology Research*, **2019**, 118, 2329-2342	2.4	11
112	Diagnostic Accuracy of Neutrophil Gelatinase-Associated Lipocalin for Predicting Early Diabetic Nephropathy in Patients with Type 1 and Type 2 Diabetes Mellitus: A Systematic Review and Meta-analysis. *journal of applied laboratory medicine, The*, **2019**, 4, 78-94	2	10
111	JUCHMME: a Java Utility for Class Hidden Markov Models and Extensions for biological sequence analysis. *Bioinformatics*, **2019**, 35, 5309-5312	7.2	2
110	Semi-supervised learning of Hidden Markov Models for biological sequence analysis. *Bioinformatics*, **2019**, 35, 2208-2215	7.2	8
109	Bipartite graphs in systems biology and medicine: a survey of methods and applications. *GigaScience*, **2018**, 7, 1-31	7.6	64
108	Interleukin gene polymorphisms and susceptibility to HIV-1 infection: a meta-analysis. *Journal of Genetics*, **2018**, 97, 235-251	1.2	9
107	Extending hidden Markov models to allow conditioning on previous observations. *Journal of Bioinformatics and Computational Biology*, **2018**, 16, 1850019	1	5
106	Multivariate Methods for Meta-Analysis of Genetic Association Studies. *Methods in Molecular Biology*, **2018**, 1793, 157-182	1.4	2
105	Methods of Analysis and Meta-Analysis for Identifying Differentially Expressed Genes. *Methods in Molecular Biology*, **2018**, 1793, 183-210	1.4	6
104	Identification of gene expression profiles in myocardial infarction: a systematic review and meta-analysis. *BMC Medical Genomics*, **2018**, 11, 109	3.7	6
103	ECCB 2018: The 17th European Conference on Computational Biology. *Bioinformatics*, **2018**, 34, i595-i598	7.2	1
102	Predicting Beta Barrel Transmembrane Proteins Using HMMs. *Methods in Molecular Biology*, **2017**, 1552, 43-61	1.4	2
101	Predicting Alpha Helical Transmembrane Proteins Using HMMs. *Methods in Molecular Biology*, **2017**, 1552, 63-82	1.4	1
100	GWAR: robust analysis and meta-analysis of genome-wide association studies. *Bioinformatics*, **2017**, 33, 1521-1527	7.2	3
99	The impact of pneumatic tube system on routine laboratory parameters: a systematic review and meta-analysis. *Clinical Chemistry and Laboratory Medicine*, **2017**, 55, 1834-1844	5.9	17

98	Molecular determinants of radiosensitivity in normal and tumor tissue: A bioinformatic approach. *Cancer Letters*, **2017**, 403, 37-47	9.9	31
97	NAP: The Network Analysis Profiler, a web tool for easier topological analysis and comparison of medium-scale biological networks. *BMC Research Notes*, **2017**, 10, 278	2.3	23
96	Apolipoprotein E Polymorphism and Left Ventricular Failure in Beta-Thalassemia: A Multivariate Meta-Analysis. *Annals of Human Genetics*, **2017**, 81, 213-223	2.2	4
95	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. *Nature Communications*, **2017**, 8, 121	17.4	52
94	Discriminating membrane proteins using the joint distribution of length sums of success and failure runs. *Statistical Methods and Applications*, **2017**, 26, 251-272	0.8	
93	A meta-analysis of FZD3 gene polymorphisms and their association with schizophrenia. *Psychiatric Genetics*, **2016**, 26, 272-280	2.9	6
92	Network analysis of genes and their association with diseases. *Gene*, **2016**, 590, 68-78	3.8	21
91	Unraveling the mechanisms of extreme radioresistance in prokaryotes: Lessons from nature. *Mutation Research - Reviews in Mutation Research*, **2016**, 767, 92-107	7	28
90	Effects of Yeast and Bacterial Commensals and Pathogens of the Female Genital Tract on the Transepithelial Electrical Resistance of HeLa Cells. *Open Microbiology Journal*, **2016**, 10, 90-6	0.8	4
89	PRED-TMBB2: improved topology prediction and detection of beta-barrel outer membrane proteins. *Bioinformatics*, **2016**, 32, i665-i671	7.2	47
88	Vitamin C for the Prevention of Postoperative Atrial Fibrillation after Cardiac Surgery: A Meta-Analysis. *Advanced Pharmaceutical Bulletin*, **2016**, 6, 243-50	4.5	18
87	A multivariate method for meta-analysis and comparison of diagnostic tests. *Statistics in Medicine*, **2016**, 35, 3509-23	2.3	12
86	Data and programs in support of network analysis of genes and their association with diseases. *Data in Brief*, **2016**, 8, 1036-9	1.2	3
85	Emerging molecular networks common in ionizing radiation, immune and inflammatory responses by employing bioinformatics approaches. *Cancer Letters*, **2015**, 368, 164-72	9.9	40
84	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015, bav063	5	5
83	Meta-analysis in Stata using gllamm. *Research Synthesis Methods*, **2015**, 6, 310-32	7.2	14
82	Polymorphisms of the CD24 Gene Are Associated with Risk of Multiple Sclerosis: A Meta-Analysis. *International Journal of Molecular Sciences*, **2015**, 16, 12368-81	6.3	4
81	Multivariate meta-analysis of the association of G-protein beta 3 gene (GNB3) haplotypes with cardiovascular phenotypes. *Molecular Biology Reports*, **2014**, 41, 3113-25	2.8	5

80	The role of genetic polymorphisms of the Renin-Angiotensin System in renal diseases: A meta-analysis. *Computational and Structural Biotechnology Journal*, **2014**, 10, 1-7	6.8	14
79	The association between plasminogen activator inhibitor type 1 (PAI-1) levels, PAI-1 4G/5G polymorphism, and myocardial infarction: a Mendelian randomization meta-analysis. *Clinical Chemistry and Laboratory Medicine*, **2014**, 52, 937-50	5.9	26
78	An approach for modelling multiple correlated outcomes in a network of interventions using odds ratios. *Statistics in Medicine*, **2014**, 33, 2275-87	2.3	30
77	HMMpTM: improving transmembrane protein topology prediction using phosphorylation and glycosylation site prediction. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 316-22	4	11
76	Are sample sizes clear and justified in RCTs published in dental journals?. *PLoS ONE*, **2014**, 9, e85949	3.7	33
75	Interpreting the Omics Gra Data. *Smart Innovation, Systems and Technologies*, **2013**, 79-100	0.5	7
74	Multilocus sequence typing (and phylogenetic analysis) of Campylobacter jejuni and Campylobacter coli strains isolated from clinical cases in Greece. *BMC Research Notes*, **2013**, 6, 359	2.3	10
73	Effect of hepatitis C virus on immunological and virological responses in HIV-infected patients initiating highly active antiretroviral therapy: a meta-analysis. *Journal of Viral Hepatitis*, **2013**, 20, 715-24	3.4	17
72	Percutaneous coronary intervention versus optimal medical therapy for prevention of spontaneous myocardial infarction in subjects with stable ischemic heart disease. *Circulation*, **2013**, 127, 769-81	16.7	71
71	Genetic model selection in genome-wide association studies: robust methods and the use of meta-analysis. *Statistical Applications in Genetics and Molecular Biology*, **2013**, 12, 285-308	1.2	27
70	Meeting report: the seventh conference of the hellenic society for computational biology and bioinformatics. *Computational and Structural Biotechnology Journal*, **2013**, 6, e201303006	6.8	1
69	The association between apolipoprotein E gene polymorphisms and essential hypertension: a meta-analysis of 45 studies including 13,940 cases and 16,364 controls. *Journal of Human Hypertension*, **2013**, 27, 245-55	2.6	16
68	Efficacy of emergency department-initiated tobacco control--systematic review and meta-analysis of randomized controlled trials. *Nicotine and Tobacco Research*, **2013**, 15, 643-55	4.9	21
67	Bisphosphonate use and risk of colorectal cancer: a systematic review and meta-analysis. *British Journal of Clinical Pharmacology*, **2013**, 76, 329-37	3.8	11
66	Impact of HIV type 1 DNA levels on spontaneous disease progression: a meta-analysis. *AIDS Research and Human Retroviruses*, **2012**, 28, 366-73	1.6	15
65	Use of fibrates and cancer risk: a systematic review and meta-analysis of 17 long-term randomized placebo-controlled trials. *PLoS ONE*, **2012**, 7, e45259	3.7	31
64	On the covariance of two correlated log-odds ratios. *Statistics in Medicine*, **2012**, 31, 1418-31	2.3	18
63	Methylene tetrahydrofolate reductase gene polymorphisms and their association with methotrexate toxicity: a meta-analysis. *Pharmacogenetics and Genomics*, **2012**, 22, 117-33	1.9	52

62	CW-PRED: A HMM-Based Method for the Classification of Cell Wall-Anchored Proteins of Gram-Positive Bacteria. *Lecture Notes in Computer Science*, **2012**, 285-290	0.9	9
61	Meta-analysis of haplotype-association studies: comparison of methods and empirical evaluation of the literature. *BMC Genetics*, **2011**, 12, 8	2.6	10
60	An ecological study of the determinants of differences in 2009 pandemic influenza mortality rates between countries in Europe. *PLoS ONE*, **2011**, 6, e19432	3.7	19
59	Developing the evidence base for cancer chemoprevention: use of meta-analysis. *Current Drug Targets*, **2011**, 12, 1989-97	3	7
58	Cytokine gene polymorphisms in multiple sclerosis: a meta-analysis of 45 studies including 7379 cases and 8131 controls. *European Journal of Neurology*, **2011**, 18, 944-51	6	7
57	Using graph theory to analyze biological networks. *BioData Mining*, **2011**, 4, 10	4.3	357
56	Phoenix 100 versus Vitek 2 in the identification of gram-positive and gram-negative bacteria: a comprehensive meta-analysis. *Journal of Clinical Microbiology*, **2011**, 49, 3284-91	9.7	42
55	Meta-Analysis of Family-Based and Case-Control Genetic Association Studies that Use the Same Cases. *Statistical Applications in Genetics and Molecular Biology*, **2011**, 10,	1.2	6
54	OMPdb: a database of {beta}-barrel outer membrane proteins from Gram-negative bacteria. *Nucleic Acids Research*, **2011**, 39, D324-31	20.1	49
53	Fcgamma receptor polymorphisms and their association with periodontal disease: a meta-analysis. *Journal of Clinical Periodontology*, **2010**, 37, 255-65	7.7	35
52	ExTopoDB: a database of experimentally derived topological models of transmembrane proteins. *Bioinformatics*, **2010**, 26, 2490-2	7.2	14
51	GPCRs, G-proteins, effectors and their interactions: human-gpDB, a database employing visualization tools and data integration techniques. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq019	5	18
50	Combined prediction of Tat and Sec signal peptides with hidden Markov models. *Bioinformatics*, **2010**, 26, 2811-7	7.2	165
49	Polymorphisms of the insulin receptor and the insulin receptor substrates genes in polycystic ovary syndrome: a Mendelian randomization meta-analysis. *Molecular Genetics and Metabolism*, **2010**, 99, 174-83	3.7	42
48	Apolipoprotein E polymorphisms and type 2 diabetes: a meta-analysis of 30 studies including 5423 cases and 8197 controls. *Molecular Genetics and Metabolism*, **2010**, 100, 283-91	3.7	57
47	Can statin therapy reduce the risk of melanoma? A meta-analysis of randomized controlled trials. *European Journal of Epidemiology*, **2010**, 25, 29-35	12.1	38
46	A multipoint method for meta-analysis of genetic association studies. *Genetic Epidemiology*, **2010**, 34, 702-15	2.6	6
45	Plasminogen activator inhibitor-1 4G/5G and 5,10-methylene-tetrahydrofolate reductase C677T polymorphisms in polycystic ovary syndrome. *Molecular Human Reproduction*, **2009**, 15, 19-26	4.4	25

44	Generalized least squares for assessing trends in cumulative meta-analysis with applications in genetic epidemiology. *Journal of Clinical Epidemiology*, **2009**, 62, 1037-44	5.7	32
43	How many 3D structures do we need to train a predictor?. *Genomics, Proteomics and Bioinformatics*, **2009**, 7, 128-37	6.5	4
42	Mixed-Effects Poisson Regression Models for Meta-Analysis of Follow-Up Studies with Constant or Varying Durations. *International Journal of Biostatistics*, **2009**, 5,	1.3	33
41	The effect of plasma homocysteine levels on clinical outcomes of patients with acute lung injury/acute respiratory distress syndrome. *American Journal of the Medical Sciences*, **2009**, 338, 474-7	2.2	3
40	Prediction of signal peptides in archaea. *Protein Engineering, Design and Selection*, **2009**, 22, 27-35	1.9	66
39	Computational Methods for the Prediction of GPCRs Coupling Selectivity **2009**, 167-181		
38	Bacterial Barrel Outer Membrane Proteins **2009**, 182-207		
37	Prediction of lipoprotein signal peptides in Gram-positive bacteria with a Hidden Markov Model. *Journal of Proteome Research*, **2008**, 7, 5082-93	5.6	101
36	The effect of the plasminogen activator inhibitor-1 4G/5G polymorphism on the thrombotic risk. *Thrombosis Research*, **2008**, 122, 736-42	8.2	70
35	Prediction of cell wall sorting signals in gram-positive bacteria with a hidden markov model: application to complete genomes. *Journal of Bioinformatics and Computational Biology*, **2008**, 6, 387-401[1]		21
34	gpDB: a database of GPCRs, G-proteins, effectors and their interactions. *Bioinformatics*, **2008**, 24, 1471-2	7.2	25
33	A unification of multivariate methods for meta-analysis of genetic association studies. *Statistical Applications in Genetics and Molecular Biology*, **2008**, 7, Article31	1.2	34
32	Cytokine gene polymorphisms in periodontal disease: a meta-analysis of 53 studies including 4178 cases and 4590 controls. *Journal of Clinical Periodontology*, **2008**, 35, 754-67	7.7	135
31	A method for meta-analysis of case-control genetic association studies using logistic regression. *Statistical Applications in Genetics and Molecular Biology*, **2007**, 6, Article17	1.2	44
30	Association between the plasminogen activator inhibitor-1 4G/5G polymorphism and venous thrombosis. *Thrombosis and Haemostasis*, **2007**, 97, 907-913	7	75
29	Vitamin B12 and hepatic enzyme serum levels correlate with interleukin-6 in alcohol-dependent individuals without liver disease. *Clinical Biochemistry*, **2007**, 40, 781-6	3.5	4
28	No evidence for association of CTLA-4 gene polymorphisms with the risk of developing multiple sclerosis: a meta-analysis. *Multiple Sclerosis Journal*, **2007**, 13, 156-68	5	22
27	The GNB3 C825T polymorphism and essential hypertension: a meta-analysis of 34 studies including 14,094 cases and 17,760 controls. *Journal of Hypertension*, **2007**, 25, 487-500	1.9	49

26	Plasminogen activator inhibitor-1 4G/5G polymorphism and risk of ischemic stroke: a meta-analysis. *Blood Coagulation and Fibrinolysis*, **2007**, 18, 497-504	1	30
25	Integrin, alpha 2 gene C807T polymorphism and risk of ischemic stroke: a meta-analysis. *Thrombosis Research*, **2007**, 119, 501-10	8.2	39
24	Lack of association between the platelet glycoprotein Ia C807T gene polymorphism and coronary artery disease: a meta-analysis. *International Journal of Cardiology*, **2007**, 118, 189-96	3.2	25
23	Association between the plasminogen activator inhibitor-1 4G/5G polymorphism and venous thrombosis. A meta-analysis. *Thrombosis and Haemostasis*, **2007**, 97, 907-13	7	24
22	Algorithms for incorporating prior topological information in HMMs: application to transmembrane proteins. *BMC Bioinformatics*, **2006**, 7, 189	3.6	57
21	Chlamydia pneumoniae infection and the risk of multiple sclerosis: a meta-analysis. *Multiple Sclerosis Journal*, **2006**, 12, 397-411	5	49
20	Correlation of liver dysfunction biological markers to the mood status of alcohol-dependent individuals. *International Journal of Psychiatry in Clinical Practice*, **2006**, 10, 166-73	2.4	
19	PredSL: a tool for the N-terminal sequence-based prediction of protein subcellular localization. *Genomics, Proteomics and Bioinformatics*, **2006**, 4, 48-55	6.5	98
18	beta-Barrel transmembrane proteins: Geometric modelling, detection of transmembrane region, and structural properties. *Computational Biology and Chemistry*, **2006**, 30, 416-24	3.6	9
17	Association between the Plasminogen Activator Inhibitor-1 4G/5G Gene Polymorphism and Ischemic Stroke; a Meta-Analysis.. *Blood*, **2006**, 108, 4010-4010	2.2	
16	Serum albumin: a late-reacting negative acute-phase protein in clinically evident inflammation in dialysis patients. *Nephrology Dialysis Transplantation*, **2005**, 20, 658-9; author reply 659-60	4.3	15
15	A method for the prediction of GPCRs coupling specificity to G-proteins using refined profile Hidden Markov Models. *BMC Bioinformatics*, **2005**, 6, 104	3.6	37
14	Evaluation of methods for predicting the topology of beta-barrel outer membrane proteins and a consensus prediction method. *BMC Bioinformatics*, **2005**, 6, 7	3.6	99
13	N-terminal sequence-based prediction of subcellular location. *BMC Bioinformatics*, **2005**, 6, S11	3.6	3
12	Prediction of the coupling specificity of GPCRs to four families of G-proteins using hidden Markov models and artificial neural networks. *Bioinformatics*, **2005**, 21, 4101-6	7.2	41
11	Exploring inflammation in hemodialysis patients: persistent and superimposed inflammation. A longitudinal study. *Kidney and Blood Pressure Research*, **2004**, 27, 63-70	3.1	25
10	TMRPres2D: high quality visual representation of transmembrane protein models. *Bioinformatics*, **2004**, 20, 3258-60	7.2	110
9	The variability and accurate assessment of microinflammation in haemodialysis patients. *Nephrology Dialysis Transplantation*, **2004**, 19, 150-7	4.3	60

List of Publications

8	PRED-GPCR: GPCR recognition and family classification server. *Nucleic Acids Research*, **2004**, 32, W380-2	20.1	41
7	PRED-TMBB: a web server for predicting the topology of beta-barrel outer membrane proteins. *Nucleic Acids Research*, **2004**, 32, W400-4	20.1	281
6	A database for G proteins and their interaction with GPCRs. *BMC Bioinformatics*, **2004**, 5, 208	3.6	31
5	A Hidden Markov Model method, capable of predicting and discriminating beta-barrel outer membrane proteins. *BMC Bioinformatics*, **2004**, 5, 29	3.6	131
4	Faster Gradient Descent Training of Hidden Markov Models, Using Individual Learning Rate Adaptation. *Lecture Notes in Computer Science*, **2004**, 40-52	0.9	7
3	The effect of viable Chlamydia pneumoniae on serum cytokines and adhesion molecules in hemodialysis patients. *Kidney International*, **2003**, S72-5	9.9	9
2	A novel method for GPCR recognition and family classification from sequence alone using signatures derived from profile hidden Markov models. *SAR and QSAR in Environmental Research*, **2003**, 14, 413-20	3.5	31
1	Antibody tests in detecting SARS-CoV-2 infection: a meta-analysis		13