Alain J Van Gool

List of Publications by Year
in descending order

63	3,616	236925 25	133252 59
papers	citations	h-index	g-index

66	66	66	4052
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Site-Specific, Platform-Based Conjugation Strategy for the Synthesis of Dual-Labeled Immunoconjugates for Bimodal PET/NIRF Imaging of HER2-Positive Tumors. Bioconjugate Chemistry, 2022, 33, 530-540.	3.6	10
2	Fasting Proinsulin Independently Predicts Incident Type 2 Diabetes in the General Population. Journal of Personalized Medicine, 2022, 12, 1131.	2.5	1
3	Biomarker Research and Development for Coronavirus Disease 2019 (COVID-19): European Medical Research Infrastructures Call for Global Coordination. Clinical Infectious Diseases, 2021, 72, 1838-1842.	5.8	3
4	Clonotypic Features of Rearranged Immunoglobulin Genes Yield Personalized Biomarkers for Minimal Residual Disease Monitoring in Multiple Myeloma. Clinical Chemistry, 2021, 67, 867-875.	3.2	12
5	Data Sharing Under the General Data Protection Regulation. Hypertension, 2021, 77, 1029-1035.	2.7	47
6	Common Variants Associated With OSMR Expression Contribute to Carotid Plaque Vulnerability, but Not to Cardiovascular Disease in Humans. Frontiers in Cardiovascular Medicine, 2021, 8, 658915.	2.4	3
7	Metabolomics-Based Screening of Inborn Errors of Metabolism: Enhancing Clinical Application with a Robust Computational Pipeline. Metabolites, 2021, 11, 568.	2.9	11
8	Understanding the increased risk of infections in diabetes: innate and adaptive immune responses in type 1 diabetes. Metabolism: Clinical and Experimental, 2021, 121, 154795.	3.4	11
9	The funhouse mirror: the I in personalised healthcare. Life Sciences, Society and Policy, 2021, 17, 1.	3.2	10
10	Multiple Myeloma Minimal Residual Disease Detection: Targeted Mass Spectrometry in Blood vs Next-Generation Sequencing in Bone Marrow. Clinical Chemistry, 2021, 67, 1689-1698.	3.2	24
11	Semi-Quantitative Multiplex Profiling of the Complement System Identifies Associations of Complement Proteins with Genetic Variants and Metabolites in Age-Related Macular Degeneration. Journal of Personalized Medicine, 2021, 11, 1256.	2.5	5
12	Plasma C-Peptide and Risk of Developing Type 2 Diabetes in the General Population. Journal of Clinical Medicine, 2020, 9, 3001.	2.4	14
13	Evaluation of cyclooxygenase oxylipins as potential biomarker for obesity-associated adipose tissue inflammation and type 2 diabetes using targeted multiple reaction monitoring mass spectrometry. Prostaglandins Leukotrienes and Essential Fatty Acids, 2020, 160, 102157.	2.2	21
14	Cerebrospinal fluid monocyte chemoattractant protein 1 correlates with progression of Parkinsonâ€™s disease. Npj Parkinson's Disease, 2020, 6, 21.	5.3	17
15	Quantitative multiplex profiling of the complement system to diagnose complementâ€mediated diseases. Clinical and Translational Immunology, 2020, 9, e1225.	3.8	9
16	Limited impact of impaired awareness of hypoglycaemia and severe hypoglycaemia on the inflammatory profile of people with type 1 diabetes. Diabetes, Obesity and Metabolism, 2020, 22, 2427-2436.	4.4	5
17	Analytical techniques for multiplex analysis of protein biomarkers. Expert Review of Proteomics, 2020, 17, 257-273.	3.0	60
18	Affimers as an alternative to antibodies for protein biomarker enrichment. Protein Expression and Purification, 2020, 174, 105677.	1.3	13

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19	Proteomic profiling of striatal tissue of a rat model of Parkinson's disease after implantation of collagenâ€encapsulated human umbilical cord mesenchymal stem cells. Journal of Tissue Engineering and Regenerative Medicine, 2020, 14, 1077-1086.	2.7	4
20	Mass Spectrometry for Identification, Monitoring, and Minimal Residual Disease Detection of M-Proteins. Clinical Chemistry, 2020, 66, 421-433.	3.2	41
21	Sharing lessons learnt across European cardiovascular research consortia. Drug Discovery Today, 2020, 25, 787-792.	6.4	1
22	Inflammation biomarker discovery in Parkinsonâ€™s disease and atypical parkinsonisms. BMC Neurology, 2020, 20, 26.	1.8	51
23	Biosynthetic homeostasis and resilience of the complement system in health and infectious disease. EBioMedicine, 2019, 45, 303-313.	6.1	20
24	Clinical biomarker innovation: when is it worthwhile?. Clinical Chemistry and Laboratory Medicine, 2019, 57, 1712-1720.	2.3	2
25	Oncostatin M reduces atherosclerosis development in APOE*3Leiden.CETP mice and is associated with increased survival probability in humans. PLoS ONE, 2019, 14, e0221477.	2.5	10
26	The future of protein biomarker research in type 2 diabetes mellitus. Expert Review of Proteomics, 2019, 16, 105-115.	3.0	6
27	Evaluation of chitotriosidase as a biomarker for adipose tissue inflammation in overweight individuals and type 2 diabetic patients. International Journal of Obesity, 2019, 43, 1712-1723.	3.4	6
28	Uncovering a Predictive Molecular Signature for the Onset of NASH-Related Fibrosis in a Translational NASH Mouse Model. Cellular and Molecular Gastroenterology and Hepatology, 2018, 5, 83-98.e10.	4.5	44
29	Towards a routine application of Top-Down approaches for label-free discovery workflows. Journal of Proteomics, 2018, 175, 12-26.	2.4	17
30	Qualitative evaluation of coronary atherosclerosis in a large cohort of young and middle-aged Dutch tissue donors implies that coronary thrombo-embolic manifestations are stochastic. PLoS ONE, 2018, 13, e0207943.	2.5	3
31	Integrated Chemometrics and Statistics to Drive Successful Proteomics Biomarker Discovery. Proteomes, 2018, 6, 20.	3.5	19
32	Inflammatory cytokine oncostatin M induces endothelial activation in macro- and microvascular endothelial cells and in APOE*3Leiden.CETP mice. PLoS ONE, 2018, 13, e0204911.	2.5	15
33	Bridging the translational innovation gap through good biomarker practice. Nature Reviews Drug Discovery, 2017, 16, 587-588.	46.4	48
34	Alterations in the hepatic transcriptional landscape after RNAi mediated ApoB silencing in cynomolgus monkeys. Atherosclerosis, 2015, 242, 383-395.	0.8	5
35	Network signatures link hepatic effects of anti-diabetic interventions with systemic disease parameters. BMC Systems Biology, 2014, 8, 108.	3.0	5
36	Analysis of 953 Human Proteins from a Mitochondrial HEK293 Fraction by Complexome Profiling. PLoS ONE, 2013, 8, e68340.	2.5	51

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37	An integrated framework of personalized medicine: from individual genomes to participatory health care. Croatian Medical Journal, 2012, 53, 301-303.	0.7	25
38	Minocycline Effects on the Cerebrospinal Fluid Proteome of Experimental Autoimmune Encephalomyelitis Rats. Journal of Proteome Research, 2012, 11, 4315-4325.	3.7	19
39	The proteomic toolbox for studying cerebrospinal fluid. Expert Review of Proteomics, 2012, 9, 165-179.	3.0	20
40	NMR and Pattern Recognition Can Distinguish Neuroinflammation and Peripheral Inflammation. Journal of Proteome Research, 2011, 10, 4428-4438.	3.7	20
41	Genome sequencing and comparison of two nonhuman primate animal models, the cynomolgus and Chinese rhesus macaques. Nature Biotechnology, 2011, 29, 1019-1023.	17.5	284
42	The Impact of Delayed Storage on the Measured Proteome and Metabolome of Human Cerebrospinal Fluid. Clinical Chemistry, 2011, 57, 1703-1711.	3.2	59
43	From biomarker strategies to biomarker activities and back. Drug Discovery Today, 2010, 15, 121-126.	6.4	29
44	Quantitative Proteomics and Metabolomics Analysis of Normal Human Cerebrospinal Fluid Samples*. Molecular and Cellular Proteomics, 2010, 9, 2063-2075.	3.8	127
45	The Effect of Preanalytical Factors on Stability of the Proteome and Selected Metabolites in Cerebrospinal Fluid (CSF). Journal of Proteome Research, 2009, 8, 5511-5522.	3.7	102
46	Quantitative Matrix-Assisted Laser Desorption Ionizationâ^'Fourier Transform Ion Cyclotron Resonance (MALDIâ^'FT-ICR) Peptide Profiling and Identification of Multiple-Sclerosis-Related Proteins. Journal of Proteome Research, 2009, 8, 1404-1414.	3.7	51
47	Biomarkers in the drug development process: Report from workshop discussions. Regulatory Toxicology and Pharmacology, 2008, 52, 75-76.	2.7	1
48	Molecular Portrait of the Progestagenic and Estrogenic Actions of Tibolone: Behavior of Cellular Networks in Response to Tibolone. Journal of Clinical Endocrinology and Metabolism, 2005, 90, 973-983.	3.6	25
49	Functional interactions of Mycobacterium leprae RuvA with Escherichia coli RuvB and RuvC on holliday junctions 1 1Edited by M. Yaniv. Journal of Molecular Biology, 2000, 301, 839-850.	4.2	6
50	Escherichia coli RuvBL268S: a mutant RuvB protein that exhibits wild- type activities in vitro but confers a UV-sensitive ruv phenotype in vivo. Nucleic Acids Research, 1999, 27, 1275-1282.	14.5	7
51	Assembly of the Escherichia coli RuvABC resolvasome directs the orientation of Holliday junction resolution. Genes and Development, 1999, 13, 1861-1870.	5.9	85
52	Molecular Analysis of Mutations in the CSB(ERCC6) Gene in Patients with Cockayne Syndrome. American Journal of Human Genetics, 1998, 62, 77-85.	6.2	145
53	Functional interactions between the Holliday junction resolvase and the branch migration motor of Escherichia coli. EMBO Journal, 1998, 17, 1838-1845.	7.8	77
54	Biochemical and Biological Characterization of Wild-type and ATPase-deficient Cockayne Syndrome B Repair Protein. Journal of Biological Chemistry, 1998, 273, 11844-11851.	3.4	98

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55	Mammalian nucleotide excision repair and syndromes. Biochemical Society Transactions, 1997, 25, 309-315.	3.4	26
56	Phenotypic heterogeneity in nucleotide excision repair mutants of rodent complementation groups 1 and 4. Mutation Research DNA Repair, 1997, 383, 91-106.	3.7	25
57	Defective Transcription-Coupled Repair in Cockayne Syndrome B Mice Is Associated with Skin Cancer Predisposition. Cell, 1997, 89, 425-435.	28.9	301
58	Cockayne syndrome: defective repair of transcription?. EMBO Journal, 1997, 16, 4155-4162.	7.8	106
59	The Cockayne syndrome B protein, involved in transcription-coupled DNA repair, resides in an RNA polymerase II-containing complex. EMBO Journal, 1997, 16, 5955-5965.	7.8	232
60	A CHO mutant, UV40, that is sensitive to diverse mutagens and represents a new complementation group of mitomycin C sensitivity. Mutation Research DNA Repair, 1996, 363, 209-221.	3.7	34
61	UV-induced ubiquitination of RNA polymerase II: a novel modification deficient in Cockayne syndrome cells.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 11586-11590.	7.1	290
62	Double Mutants of Saccharomyces cerevisiae with Alterations in Global Genome and Transcription-Coupled Repair. Molecular and Cellular Biology, 1996, 16, 496-502.	2.3	99
63	ERCC6, a member of a subfamily of putative helicases, is involved in Cockayne's syndrome and preferential repair of active genes. Cell, 1992, 71, 939-953.	28.9	698