Armand Valsesia

List of Publications by Year
in descending order

56 papers	10,470 citations	201575 27 h-index	149623 56 g-index
58 all docs	58 docs citations	58 times ranked	17683 citing authors

#	Article	IF	Citations
1	Global variation in copy number in the human genome. Nature, 2006, 444, 444-454.	13.7	3,831
2	Origins and functional impact of copy number variation in the human genome. Nature, 2010, 464, 704-712.	13.7	1,721
3	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
4	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	9.0	679
5	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. Nature, 2010, 463, 671-675.	13.7	476
6	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258.	2.4	476
7	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	13.7	394
8	Exome sequencing identifies recurrent somatic MAP2K1 and MAP2K2 mutations in melanoma. Nature Genetics, 2012, 44, 133-139.	9.4	369
9	Genome-wide association study identifies new HLA class II haplotypes strongly protective against narcolepsy. Nature Genetics, 2010, 42, 786-789.	9.4	170
10	Analysis of 1508 Plasma Samples by Capillary-Flow Data-Independent Acquisition Profiles Proteomics of Weight Loss and Maintenance. Molecular and Cellular Proteomics, 2019, 18, 1242-1254.	2.5	162
11	Accurate and reliable high-throughput detection of copy number variation in the human genome. Genome Research, 2006, 16, 1566-1574.	2.4	136
12	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. Genome Biology, 2007, 8, R228.	13.9	120
13	Proteomic Biomarker Discovery in 1000 Human Plasma Samples with Mass Spectrometry. Journal of Proteome Research, 2016, 15, 389-399.	1.8	77
14	Protein quantitative trait locus study in obesity during weight-loss identifies a leptin regulator. Nature Communications, 2017, 8, 2084.	5.8	66
15	Identification of ALK in Thinness. Cell, 2020, 181, 1246-1262.e22.	13.5	66
16	The complex SNP and CNV genetic architecture of the increased risk of congenital heart defects in Down syndrome. Genome Research, 2013, 23, 1410-1421.	2.4	65
17	Transcriptome profiling from adipose tissue during a low-calorie diet reveals predictors of weight and glycemic outcomes in obese, nondiabetic subjects. American Journal of Clinical Nutrition, 2017, 106, 736-746.	2.2	59
18	Genome-wide identification of circulating-miRNA expression quantitative trait loci reveals the role of several miRNAs in the regulation of cardiometabolic phenotypes. Cardiovascular Research, 2019, 115, 1629-1645.	1.8	55

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19	Network-Guided Analysis of Genes with Altered Somatic Copy Number and Gene Expression Reveals Pathways Commonly Perturbed in Metastatic Melanoma. PLoS ONE, 2011, 6, e18369.	1.1	51
20	The Growing Importance of CNVs: New Insights for Detection and Clinical Interpretation. Frontiers in Genetics, 2013, 4, 92.	1.1	49
21	Obesity shows preserved plasma proteome in large independent clinical cohorts. Scientific Reports, 2018, 8, 16981.	1.6	45
22	Metabolic profiling of tissue-specific insulin resistance in human obesity: results from the Diogenes study and the Maastricht Study. International Journal of Obesity, 2020, 44, 1376-1386.	1.6	36
23	Subcutaneous Adipose Tissue and Systemic Inflammation Are Associated With Peripheral but Not Hepatic Insulin Resistance in Humans. Diabetes, 2019, 68, 2247-2258.	0.3	35
24	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	1.4	33
25	Rare Genomic Structural Variants in Complex Disease: Lessons from the Replication of Associations with Obesity. PLoS ONE, 2013, 8, e58048.	1.1	33
26	Crosstalk between Drp1 phosphorylation sites during mitochondrial remodeling and their impact on metabolic adaptation. Cell Reports, 2021, 36, 109565.	2.9	32
27	Copy Number Variation. Methods in Molecular Biology, 2018, 1793, 231-258.	0.4	31
28	Endogenous nicotinamide riboside metabolism protects against diet-induced liver damage. Nature Communications, 2019, 10, 4291.	5.8	30
29	Apolipoprotein M: a novel adipokine decreasing with obesity and upregulated by calorie restriction. American Journal of Clinical Nutrition, 2019, 109, 1499-1510.	2.2	30
30	Molecular Biomarkers for Weight Control in Obese Individuals Subjected to a Multiphase Dietary Intervention. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2751-2761.	1.8	28
31	Distinct lipid profiles predict improved glycemic control in obese, nondiabetic patients after a low-caloric diet intervention: the Diet, Obesity and Genes randomized trial. American Journal of Clinical Nutrition, 2016, 104, 566-575.	2.2	27
32	Plasma lipid profiling of tissue-specific insulin resistance in human obesity. International Journal of Obesity, 2019, 43, 989-998.	1.6	27
33	Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans. BMC Biology, 2020, 18, 51.	1.7	26
34	Genome-wide gene-based analyses of weight loss interventions identify a potential role for NKX6.3 in metabolism. Nature Communications, 2019, 10, 540.	5.8	25
35	Augmented mitochondrial energy metabolism is an early response to chronic glucose stress in human pancreatic beta cells. Diabetologia, 2020, 63, 2628-2640.	2.9	24
36	Plasma metabolites and lipids predict insulin sensitivity improvement in obese, nondiabetic individuals after a 2-phase dietary intervention. American Journal of Clinical Nutrition, 2018, 108, 13-23.	2.2	20

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37	Variation in extracellular matrix genes is associated with weight regain after weight loss in a sex-specific manner. Genes and Nutrition, 2015, 10, 56.	1.2	19
38	A fully joint Bayesian quantitative trait locus mapping of human protein abundance in plasma. PLoS Computational Biology, 2020, 16, e1007882.	1.5	19
39	Diet-resistant obesity is characterized by a distinct plasma proteomic signature and impaired muscle fiber metabolism. International Journal of Obesity, 2018, 42, 353-362.	1.6	17
40	Integrative phenotyping of glycemic responders upon clinical weight loss using multi-omics. Scientific Reports, 2020, 10, 9236.	1.6	17
41	Identification and validation of copy number variants using SNP genotyping arrays from a large clinical cohort. BMC Genomics, 2012, 13, 241.	1.2	16
42	Rational and design of an overfeeding protocol in constitutional thinness: Understanding the physiology, metabolism and genetic background of resistance to weight gain. Annales D'Endocrinologie, 2016, 77, 563-569.	0.6	15
43	Analysis of circulating angiopoietin-like protein 3 and genetic variants in lipid metabolism and liver health: the DiOGenes study. Genes and Nutrition, 2018, 13, 7.	1.2	15
44	GH deficiency status combined with GH receptor polymorphism affects response to GH in children. European Journal of Endocrinology, 2015, 173, 777-789.	1.9	14
45	Sexual Dimorphism, Age, and Fat Mass Are Key Phenotypic Drivers of Proteomic Signatures. Journal of Proteome Research, 2017, 16, 4122-4133.	1.8	14
46	Differential Mitochondrial Gene Expression in Adipose Tissue Following Weight Loss Induced by Diet or Bariatric Surgery. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 1312-1324.	1.8	13
47	Network Analysis of Metabolite GWAS Hits: Implication of CPS1 and the Urea Cycle in Weight Maintenance. PLoS ONE, 2016, 11, e0150495.	1.1	11
48	Salivary Î±-amylase copy number is not associated with weight trajectories and glycemic improvements following clinical weight loss: results from a 2-phase dietary intervention study. American Journal of Clinical Nutrition, 2019, 109, 1029-1037.	2.2	10
49	Fast and Accurate Approaches for Large-Scale, Automated Mapping of Food Diaries on Food Composition Tables. Frontiers in Nutrition, 2018, 5, 38.	1.6	9
50	FADS1 genotype is distinguished by human subcutaneous adipose tissue fatty acids, but not inflammatory gene expression. International Journal of Obesity, 2019, 43, 1539-1548.	1.6	9
51	Untargeted Profiling of Bile Acids and Lysophospholipids Identifies the Lipid Signature Associated with Glycemic Outcome in an Obese Non-Diabetic Clinical Cohort. Biomolecules, 2020, 10, 1049.	1.8	8
52	Network Analyses Reveal Negative Link Between Changes in Adipose Tissue GDF15 and BMI During Dietary-induced Weight Loss. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e130-e142.	1.8	7
53	Multiple hot-deck imputation for network inference from RNA sequencing data. Bioinformatics, 2018, 34, 1726-1732.	1.8	5
54	AssociationViewer: a scalable and integrated software tool for visualization of large-scale variation data in genomic context. Bioinformatics, 2009, 25, 662-663.	1.8	3

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55	Increasing the discovery power of -omics studies. Systems Biomedicine (Austin, Tex), 2013, 1, 84-93.	0.7	2
56	Clinical- and omics-based models of subclinical atherosclerosis in healthy Chinese adults: a cross-sectional exploratory study. American Journal of Clinical Nutrition, 2021, 114, 1752-1762.	2.2	2