

# Simon J Cockell

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

2,651  
citations

318942

23  
h-index

232693

48  
g-index

59  
all docs

59  
docs citations

59  
times ranked

5057  
citing authors

#	ARTICLE	IF	CITATIONS
1	Increased serum miR-193a-5p during non-alcoholic fatty liver disease progression: Diagnostic and mechanistic relevance. <i>JHEP Reports</i> , 2022, 4, 100409.	2.6	20
2	Mechanical-Stress-Related Epigenetic Regulation of ZIC1 Transcription Factor in the Etiology of Postmenopausal Osteoporosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2957.	1.8	5
3	NASH limits anti-tumour surveillance in immunotherapy-treated HCC. <i>Nature</i> , 2021, 592, 450-456.	13.7	649
4	Therapeutic wavelengths of ultraviolet B radiation activate apoptotic, circadian rhythm, redox signalling and key canonical pathways in psoriatic epidermis. <i>Redox Biology</i> , 2021, 41, 101924.	3.9	10
5	Regional Differences in Gene Expression of Proliferating Human Choroidal Endothelial Cells. <i>International Journal of Translational Medicine</i> , 2021, 1, 83-100.	0.1	0
6	Transcriptomics Identify Thrombospondin-2 as a Biomarker for NASH and Advanced Liver Fibrosis. <i>Hepatology</i> , 2021, 74, 2452-2466.	3.6	71
7	Diagnostic accuracy of elastography and magnetic resonance imaging in patients with NAFLD: A systematic review and meta-analysis. <i>Journal of Hepatology</i> , 2021, 75, 770-785.	1.8	149
8	Network medicine for disease module identification and drug repurposing with the NeDRex platform. <i>Nature Communications</i> , 2021, 12, 6848.	5.8	39
9	Correlation of Infinium HumanMethylation450K and MethylationEPIC BeadChip arrays in cartilage. <i>Epigenetics</i> , 2020, 15, 594-603.	1.3	10
10	Understanding the complexity of retina and pluripotent stem cell derived retinal organoids with single cell RNA sequencing: current progress, remaining challenges and future prospective. <i>Current Eye Research</i> , 2020, 45, 385-396.	0.7	22
11	Transcriptomic profiling across the nonalcoholic fatty liver disease spectrum reveals gene signatures for steatohepatitis and fibrosis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	205
12	Genome-wide association study of non-alcoholic fatty liver and steatohepatitis in a histologically characterised cohort. <i>Journal of Hepatology</i> , 2020, 73, 505-515.	1.8	279
13	Epigenetic modifiers DNMT3A and BCOR are recurrently mutated in CYLD cutaneous syndrome. <i>Nature Communications</i> , 2019, 10, 4717.	5.8	20
14	An ancient germ cell-specific RNA-binding protein protects the germline from cryptic splice site poisoning. <i>ELife</i> , 2019, 8, .	2.8	22
15	High-throughput sequencing identifies aetiology-dependent differences in ductular reaction in human chronic liver disease. <i>Journal of Pathology</i> , 2019, 248, 66-76.	2.1	37
16	<i>Pax9</i> is required for cardiovascular development and interacts with <i>Tbx1</i> in the pharyngeal endoderm to control 4th pharyngeal arch artery morphogenesis. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	19
17	Deconstructing Retinal Organoids: Single Cell RNA-Seq Reveals the Cellular Components of Human Pluripotent Stem Cell-Derived Retina. <i>Stem Cells</i> , 2019, 37, 593-598.	1.4	106
18	Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer. <i>ELife</i> , 2019, 8, .	2.8	56

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19	Pro-inflammatory cytokine and high doses of ionizing radiation have similar effects on the expression of NF-kappaB-dependent genes. <i>Cellular Signalling</i> , 2018, 46, 23-31.	1.7	28
20	B-cell activity markers are associated with different disease activity domains in primary Sjögren's syndrome. <i>Rheumatology</i> , 2018, 57, 1222-1227.	0.9	23
21	RRAD, IL4I1, CDKN1A, and SERPINE1 genes are potentially co-regulated by NF- $\kappa$ B and p53 transcription factors in cells exposed to high doses of ionizing radiation. <i>BMC Genomics</i> , 2018, 19, 813.	1.2	20
22	Cross platform analysis of transcriptomic data identifies ageing has distinct and opposite effects on tendon in males and females. <i>Scientific Reports</i> , 2017, 7, 14443.	1.6	20
23	Influence of Genetic Variations in Selenoprotein Genes on the Pattern of Gene Expression after Supplementation with Brazil Nuts. <i>Nutrients</i> , 2017, 9, 739.	1.7	15
24	An Integrated Data Driven Approach to Drug Repositioning Using Gene-Disease Associations. <i>PLoS ONE</i> , 2016, 11, e0155811.	1.1	39
25	Misincorporation by RNA polymerase is a major source of transcription pausing in vivo. <i>Nucleic Acids Research</i> , 2016, 45, gkw969.	6.5	31
26	Transcriptomics and proteomics show that selenium affects inflammation, cytoskeleton, and cancer pathways in human rectal biopsies. <i>FASEB Journal</i> , 2016, 30, 2812-2825.	0.2	39
27	Zinc sensing by metal-responsive transcription factor 1 (MTF1) controls metallothionein and ZnT1 expression to buffer the sensitivity of the transcriptome response to zinc. <i>Metallomics</i> , 2016, 8, 337-343.	1.0	74
28	The NF- $\kappa$ B subunit c-Rel regulates Bach2 tumour suppressor expression in B-cell lymphoma. <i>Oncogene</i> , 2016, 35, 3476-3484.	2.6	32
29	Mining integrated semantic networks for drug repositioning opportunities. <i>PeerJ</i> , 2016, 4, e1558.	0.9	22
30	Genetic Networks Required to Coordinate Chromosome Replication by DNA Polymerases $\delta$ , $\epsilon$ , and $\mu$ in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2187-2197.	0.8	16
31	The Zinc Finger Protein ZNF658 Regulates the Transcription of Genes Involved in Zinc Homeostasis and Affects Ribosome Biogenesis through the Zinc Transcriptional Regulatory Element. <i>Molecular and Cellular Biology</i> , 2015, 35, 977-987.	1.1	34
32	Genome-wide ChIP-seq analysis of human TOP2B occupancy in MCF7 breast cancer epithelial cells. <i>Biology Open</i> , 2015, 4, 1436-1447.	0.6	42
33	A Transcriptional Signature of Fatigue Derived from Patients with Primary Sjögren's Syndrome. <i>PLoS ONE</i> , 2015, 10, e0143970.	1.1	45
34	Regulation of p53 and Rb Links the Alternative NF- $\kappa$ B Pathway to EZH2 Expression and Cell Senescence. <i>PLoS Genetics</i> , 2014, 10, e1004642.	1.5	83
35	Utility of B-13 Progenitor-Derived Hepatocytes in Hepatotoxicity and Genotoxicity Studies. <i>Toxicological Sciences</i> , 2014, 137, 350-370.	1.4	17
36	Contribution of natural antisense transcription to an endogenous siRNA signature in human cells. <i>BMC Genomics</i> , 2014, 15, 19.	1.2	40

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37	A distributed computational search strategy for the identification of diagnostics targets: Application to finding aptamer targets for methicillin-resistant staphylococci. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 80-92.	1.0	2
38	Bayesian integration of networks without gold standards. <i>Bioinformatics</i> , 2012, 28, 1495-1500.	1.8	11
39	MRE11 facilitates the removal of human topoisomerase II complexes from genomic DNA. <i>Biology Open</i> , 2012, 1, 863-873.	0.6	58
40	Three Steps to Heaven: Semantic Publishing in a Real World Workflow. <i>Future Internet</i> , 2012, 4, 1004-1015.	2.4	1
41	Customizable views on semantically integrated networks for systems biology. <i>Bioinformatics</i> , 2011, 27, 1299-1306.	1.8	9
42	Structure-function studies of an engineered scaffold protein derived from Stefin A. II: Development and applications of the SQT variant. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 751-763.	1.0	43
43	BioStar: An Online Question & Answer Resource for the Bioinformatics Community. <i>PLoS Computational Biology</i> , 2011, 7, e1002216.	1.5	82
44	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010, 28, 655-656.	9.4	22
45	An integrated dataset for in silico drug discovery. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	19
46	Changes in Protein Expression Profiles between a Low Phytic Acid Rice ( <i>Oryza sativa</i> L. Ssp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 T Agricultural and Food Chemistry, 2010, 58, 6912-6922.	2.4	16
47	An integrated dataset for in silico drug discovery. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	9
48	Structure-based evaluation of in silico predictions of protein-protein interactions using Comparative Docking. <i>Bioinformatics</i> , 2007, 23, 573-581.	1.8	18