Chris Sander

List of Publications by Citations

340 papers	**120,352** citations	**136** h-index	**346** g-index
366 ext. papers	**145,412** ext. citations	**15** avg, IF	**7.96** L-index

#	Paper	IF	Citations
340	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. *Cancer Discovery*, **2012**, 2, 401-4	24.4	8578
339	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. *Science Signaling*, **2013**, 6, pl1	8.8	7715
338	Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. *Science*, **2015**, 348, 124-8	33.3	5003
337	The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, **2013**, 45, 1113-20	36.3	3933
336	Protein structure comparison by alignment of distance matrices. *Journal of Molecular Biology*, **1993**, 233, 123-38	6.5	3573
335	A mammalian microRNA expression atlas based on small RNA library sequencing. *Cell*, **2007**, 129, 1401-14	46.2	3005
334	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
333	Human MicroRNA targets. *PLoS Biology*, **2004**, 2, e363	9.7	2746
332	Integrative genomic profiling of human prostate cancer. *Cancer Cell*, **2010**, 18, 11-22	24.3	2666
331	Prediction of protein secondary structure at better than 70% accuracy. *Journal of Molecular Biology*, **1993**, 232, 584-99	6.5	2597
330	MicroRNA targets in Drosophila. *Genome Biology*, **2003**, 5, R1	18.3	2206
329	The microRNA.org resource: targets and expression. *Nucleic Acids Research*, **2008**, 36, D149-53	20.1	1892
328	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
327	Integration of biological networks and gene expression data using Cytoscape. *Nature Protocols*, **2007**, 2, 2366-82	18.8	1798
326	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
325	Errors in protein structures. *Nature*, **1996**, 381, 272	50.4	1730
324	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713

323	Global mapping of the yeast genetic interaction network. *Science*, **2004**, 303, 808-13	33.3	1700
322	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
321	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
320	Database of homology-derived protein structures and the structural meaning of sequence alignment. *Proteins: Structure, Function and Bioinformatics*, **1991**, 9, 56-68	4.2	1411
319	Combining evolutionary information and neural networks to predict protein secondary structure. *Proteins: Structure, Function and Bioinformatics*, **1994**, 19, 55-72	4.2	1319
318	Identification of virus-encoded microRNAs. *Science*, **2004**, 304, 734-6	33.3	1293
317	Dali: a network tool for protein structure comparison. *Trends in Biochemical Sciences*, **1995**, 20, 478-80	10.3	1275
316	Predicting the functional impact of protein mutations: application to cancer genomics. *Nucleic Acids Research*, **2011**, 39, e118	20.1	1237
315	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites. *Genome Biology*, **2010**, 11, R90	18.3	1143
314	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
313	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
312	A novel class of small RNAs bind to MILI protein in mouse testes. *Nature*, **2006**, 442, 203-7	50.4	1099
311	Precision microbiome reconstitution restores bile acid mediated resistance to Clostridium difficile. *Nature*, **2015**, 517, 205-8	50.4	1064
310	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
309	Identification of microRNAs of the herpesvirus family. *Nature Methods*, **2005**, 2, 269-76	21.6	962
308	Emerging landscape of oncogenic signatures across human cancers. *Nature Genetics*, **2013**, 45, 1127-33	36.3	889
307	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
306	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854

305	Direct-coupling analysis of residue coevolution captures native contacts across many protein families. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E1293-301	11.5	837
304	Evaluating cell lines as tumour models by comparison of genomic profiles. *Nature Communications*, **2013**, 4, 2126	17.4	831
303	Pathway Commons, a web resource for biological pathway data. *Nucleic Acids Research*, **2011**, 39, D685-90	20.1	786
302	Protein 3D structure computed from evolutionary sequence variation. *PLoS ONE*, **2011**, 6, e28766	3.7	709
301	Correlated mutations and residue contacts in proteins. *Proteins: Structure, Function and Bioinformatics*, **1994**, 18, 309-17	4.2	662
300	The Systems Biology Graphical Notation. *Nature Biotechnology*, **2009**, 27, 735-41	44.5	651
299	miR-122, a mammalian liver-specific microRNA, is processed from hcr mRNA and may downregulate the high affinity cationic amino acid transporter CAT-1. *RNA Biology*, **2004**, 1, 106-13	4.8	642
298	Selection of representative protein data sets. *Protein Science*, **1992**, 1, 409-17	6.3	639
297	The double cubic lattice method: Efficient approaches to numerical integration of surface area and volume and to dot surface contouring of molecular assemblies. *Journal of Computational Chemistry*, **1995**, 16, 273-284	3.5	632
296	Enlarged representative set of protein structures. *Protein Science*, **1994**, 3, 522-4	6.3	610
295	Genomic and transcriptomic hallmarks of poorly differentiated and anaplastic thyroid cancers. *Journal of Clinical Investigation*, **2016**, 126, 1052-66	15.9	576
294	Transmembrane helices predicted at 95% accuracy. *Protein Science*, **1995**, 4, 521-33	6.3	551
293	Genome sequencing identifies a basis for everolimus sensitivity. *Science*, **2012**, 338, 221	33.3	546
292	Conservation and prediction of solvent accessibility in protein families. *Proteins: Structure, Function and Bioinformatics*, **1994**, 20, 216-26	4.2	523
291	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. *Nature Genetics*, **2010**, 42, 715-21	36.3	521
290	The ras protein family: evolutionary tree and role of conserved amino acids. *Biochemistry*, **1991**, 30, 4637-48	3.1	517
289	The nuclear deubiquitinase BAP1 is commonly inactivated by somatic mutations and 3p21.1 losses in malignant pleural mesothelioma. *Nature Genetics*, **2011**, 43, 668-72	36.3	512
288	The HUPO PSI molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504

287	The BioPAX community standard for pathway data sharing. *Nature Biotechnology*, **2010**, 28, 935-42	44.5	499
286	A series of PDB related databases for everyday needs. *Nucleic Acids Research*, **2011**, 39, D411-9	20.1	487
285	Cellular cofactors affecting hepatitis C virus infection and replication. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 12884-9	11.5	478
284	Mutual exclusivity analysis identifies oncogenic network modules. *Genome Research*, **2012**, 22, 398-406	9.7	452
283	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
282	(V600E)BRAF is associated with disabled feedback inhibition of RAF-MEK signaling and elevated transcriptional output of the pathway. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 4519-24	11.5	444
281	PredictProtein--an open resource for online prediction of protein structural and functional features. *Nucleic Acids Research*, **2014**, 42, W337-43	20.1	433
280	Protein structure prediction from sequence variation. *Nature Biotechnology*, **2012**, 30, 1072-80	44.5	432
279	Quantitative technologies establish a novel microRNA profile of chronic lymphocytic leukemia. *Blood*, **2007**, 109, 4944-51	2.2	422
278	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
277	A role for neuronal piRNAs in the epigenetic control of memory-related synaptic plasticity. *Cell*, **2012**, 149, 693-707	56.2	399
276	Three-dimensional structures of membrane proteins from genomic sequencing. *Cell*, **2012**, 149, 1607-21	56.2	395
275	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. *Nature Biotechnology*, **2009**, 27, 549-55	44.5	393
274	Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. *Genome Biology*, **2016**, 17, 231	18.3	391
273	Cooperativity of TMPRSS2-ERG with PI3-kinase pathway activation in prostate oncogenesis. *Nature Genetics*, **2009**, 41, 524-6	36.3	386
272	Dali/FSSP classification of three-dimensional protein folds. *Nucleic Acids Research*, **1997**, 25, 231-4	20.1	381
271	Characterizing gene sets with FuncAssociate. *Bioinformatics*, **2003**, 19, 2502-4	7.2	380
270	Genetic dissection of the miR-17~92 cluster of microRNAs in Myc-induced B-cell lymphomas. *Genes and Development*, **2009**, 23, 2806-11	12.6	379

251	Antisense-mediated depletion reveals essential and specific functions of microRNAs in Drosophila development. *Cell*, **2005**, 121, 1097-108	56.2	276
250	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. *Cancer Cell*, **2018**, 33, 706-720.e9	24.3	275
249	Mutation effects predicted from sequence co-variation. *Nature Biotechnology*, **2017**, 35, 128-135	44.5	273
248	Automated network analysis identifies core pathways in glioblastoma. *PLoS ONE*, **2010**, 5, e8918	3.7	268
247	Target mRNA abundance dilutes microRNA and siRNA activity. *Molecular Systems Biology*, **2010**, 6, 363	12.2	264
246	A large domain common to sperm receptors (Zp2 and Zp3) and TGF-beta type III receptor. *FEBS Letters*, **1992**, 300, 237-40	3.8	264
245	The developmental miRNA profiles of zebrafish as determined by small RNA cloning. *Genes and Development*, **2005**, 19, 1288-93	12.6	258
244	Redefining the goals of protein secondary structure prediction. *Journal of Molecular Biology*, **1994**, 235, 13-26	6.5	257
243	PHD--an automatic mail server for protein secondary structure prediction. *Bioinformatics*, **1994**, 10, 53-60	7.2	257
242	Positioning hydrogen atoms by optimizing hydrogen-bond networks in protein structures. *Proteins: Structure, Function and Bioinformatics*, **1996**, 26, 363-76	4.2	256
241	Mitochondrial DNA copy number variation across human cancers. *ELife*, **2016**, 5,	8.9	255
240	Pattern discovery and cancer gene identification in integrated cancer genomic data. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 4245-50	11.5	250
239	An Effective Solvation Term Based on Atomic Occupancies for Use in Protein Simulations. *Molecular Simulation*, **1993**, 10, 97-120	2	243
238	Protein fold recognition by prediction-based threading. *Journal of Molecular Biology*, **1997**, 270, 471-80	6.5	238
237	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. *Cell*, **2016**, 166, 766-778	56.2	236
236	Pathway and network analysis of cancer genomes. *Nature Methods*, **2015**, 12, 615-621	21.6	235
235	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
234	Adverse outcomes in clear cell renal cell carcinoma with mutations of 3p21 epigenetic regulators BAP1 and SETD2: a report by MSKCC and the KIRC TCGA research network. *Clinical Cancer Research*, **2013**, 19, 3259-67	12.9	233

233 Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. *Cell Reports*, **2016**, 14, 2476-89 10.6 228

232 Prevalence and co-occurrence of actionable genomic alterations in high-grade bladder cancer. *Journal of Clinical Oncology*, **2013**, 31, 3133-40 2.2 226

231 Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111 50.4 220

230 Searching protein structure databases has come of age. *Proteins: Structure, Function and Bioinformatics*, **1994**, 19, 165-73 4.2 220

229 Copy number alteration burden predicts prostate cancer relapse. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 11139-44 11.5 218

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227 The tyrosine phosphatase PTPRD is a tumor suppressor that is frequently inactivated and mutated in glioblastoma and other human cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 9435-40 11.5 196

226 DGCR8-dependent microRNA biogenesis is essential for skin development. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 498-502 11.5 190

225 Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4 10.6 188

224 Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. *Genome Research*, **2014**, 24, 1740-50 9.7 187

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222 Evaluation of protein models by atomic solvation preference. *Journal of Molecular Biology*, **1992**, 225, 93-105 6.5 186

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217 Detection of common three-dimensional substructures in proteins. *Proteins: Structure, Function and Bioinformatics*, **1991**, 11, 52-8 4.2 170

216 A sequence property approach to searching protein databases. *Journal of Molecular Biology*, **1995**, 251, 390-9 6.5 161

215	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
214	Molecular modelling of the Norrie disease protein predicts a cystine knot growth factor tertiary structure. *Nature Genetics*, **1993**, 5, 376-80	36.3	154
213	Analysis of microRNA-target interactions across diverse cancer types. *Nature Structural and Molecular Biology*, **2013**, 20, 1325-32	17.6	153
212	Distinct patterns of dysregulated expression of enzymes involved in androgen synthesis and metabolism in metastatic prostate cancer tumors. *Cancer Research*, **2012**, 72, 6142-52	10.1	152
211	Models from experiments: combinatorial drug perturbations of cancer cells. *Molecular Systems Biology*, **2008**, 4, 216	12.2	151
210	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
209	Genome-wide identification of microRNA targets in human ES cells reveals a role for miR-302 in modulating BMP response. *Genes and Development*, **2011**, 25, 2173-86	12.6	143
208	CancerGenes: a gene selection resource for cancer genome projects. *Nucleic Acids Research*, **2007**, 35, D721-6	20.1	143
207	Dictionary of recurrent domains in protein structures. *Proteins: Structure, Function and Bioinformatics*, **1998**, 33, 88-96	4.2	142
206	Integrative subtype discovery in glioblastoma using iCluster. *PLoS ONE*, **2012**, 7, e35236	3.7	140
205	Prediction of protein structure by evaluation of sequence-structure fitness. Aligning sequences to contact profiles derived from three-dimensional structures. *Journal of Molecular Biology*, **1993**, 232, 805-25	6.5	138
204	The amino-acid mutational spectrum of human genetic disease. *Genome Biology*, **2003**, 4, R72	18.3	136
203	Applications of targeted proteomics in systems biology and translational medicine. *Proteomics*, **2015**, 15, 3193-208	4.8	134
202	Fast and simple Monte Carlo algorithm for side chain optimization in proteins: application to model building by homology. *Proteins: Structure, Function and Bioinformatics*, **1992**, 14, 213-23	4.2	133
201	Identification of PHLPP1 as a tumor suppressor reveals the role of feedback activation in PTEN-mutant prostate cancer progression. *Cancer Cell*, **2011**, 20, 173-86	24.3	131
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199	Functional copy-number alterations in cancer. *PLoS ONE*, **2008**, 3, e3179	3.7	129
198	Objectively judging the quality of a protein structure from a Ramachandran plot. *Bioinformatics*, **1997**, 13, 425-30	7.2	122

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192 3D RNA and Functional Interactions from Evolutionary Couplings. *Cell*, **2016**, 165, 963-75 — 56.2 — 108

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187 Perturbation biology: inferring signaling networks in cellular systems. *PLoS Computational Biology*, **2013**, 9, e1003290 — 5 — 98

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183 Structured States of Disordered Proteins from Genomic Sequences. *Cell*, **2016**, 167, 158-170.e12 — 56.2 — 90

182 miR-34a repression in proneural malignant gliomas upregulates expression of its target PDGFRA and promotes tumorigenesis. *PLoS ONE*, **2012**, 7, e33844 — 3.7 — 90

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179	Modeling of transmembrane seven helix bundles. *Protein Engineering, Design and Selection*, **1993**, 6, 59-64	1.9	89
178	Frequent alterations and epigenetic silencing of differentiation pathway genes in structurally rearranged liposarcomas. *Cancer Discovery*, **2011**, 1, 587-97	24.4	88
177	Progress of 1D protein structure prediction at last. *Proteins: Structure, Function and Bioinformatics*, **1995**, 23, 295-300	4.2	84
176	cPath: open source software for collecting, storing, and querying biological pathways. *BMC Bioinformatics*, **2006**, 7, 497	3.6	83
175	Pathway information for systems biology. *FEBS Letters*, **2005**, 579, 1815-20	3.8	83
174	TFIIB, an evolutionary link between the transcription machineries of archaebacteria and eukaryotes. *Cell*, **1992**, 71, 189-90	56.2	83
173	The cytidylyltransferase superfamily: identification of the nucleotide-binding site and fold prediction. *Proteins: Structure, Function and Bioinformatics*, **1995**, 22, 259-66	4.2	81
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171	mRNA turnover rate limits siRNA and microRNA efficacy. *Molecular Systems Biology*, **2010**, 6, 433	12.2	78
170	CellMinerCDB for Integrative Cross-Database Genomics and Pharmacogenomics Analyses of Cancer Cell Lines. *IScience*, **2018**, 10, 247-264	6.1	78
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168	TCEB1-mutated renal cell carcinoma: a distinct genomic and morphological subtype. *Modern Pathology*, **2015**, 28, 845-853	9.8	76
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165	Structural similarity of plant chitinase and lysozymes from animals and phage. An evolutionary connection. *FEBS Letters*, **1994**, 340, 129-32	3.8	76
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156   Computational analysis of mouse piRNA sequence and biogenesis. *PLoS Computational Biology*, **2007**, 3, e222   5   71

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150   Off-target effects dominate a large-scale RNAi screen for modulators of the TGF-β pathway and reveal microRNA regulation of TGFBR2. *Silence: A Journal of RNA Regulation*, **2011**, 2, 3   67

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140	Inferring Pairwise Interactions from Biological Data Using Maximum-Entropy Probability Models. *PLoS Computational Biology*, **2015**, 11, e1004182	5	59
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138	Evaluation of annotation strategies using an entire genome sequence. *Bioinformatics*, **2003**, 19, 717-26	7.2	58
137	How to determine protein secondary structure in solution by Raman spectroscopy: practical guide and test case DNase I. *Biochemistry*, **1989**, 28, 4271-4277	3.2	58
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135	Protein structure determination by combining sparse NMR data with evolutionary couplings. *Nature Methods*, **2015**, 12, 751-4	21.6	56
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