

# Simon C Lovell

## List of Publications by Year in descending order

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69  
papers

13,170  
citations

172457

29  
h-index

98798

67  
g-index

74  
all docs

74  
docs citations

74  
times ranked

21219  
citing authors

#	ARTICLE	IF	CITATIONS
1	EVI1 phosphorylation at S436 regulates interactions with CtBP1 and DNMT3A and promotes self-renewal. <i>Cell Death and Disease</i> , 2020, 11, 878.	6.3	4
2	Variability in Gene Expression is Associated with Incomplete Penetrance in Inherited Eye Disorders. <i>Genes</i> , 2020, 11, 179.	2.4	14
3	Using an integrative machine learning approach utilising homology modelling to clinically interpret genetic variants: CACNA1F as an exemplar. <i>European Journal of Human Genetics</i> , 2020, 28, 1274-1282.	2.8	11
4	Reliable Generation of Native-Like Decoys Limits Predictive Ability in Fragment-Based Protein Structure Prediction. <i>Biomolecules</i> , 2019, 9, 612.	4.0	0
5	Mutations in PCYT2 disrupt etherlipid biosynthesis and cause a complex hereditary spastic paraplegia. <i>Brain</i> , 2019, 142, 3382-3397.	7.6	76
6	Biochemical and structural analyses suggest that plasminogen activators coevolved with their cognate protein substrates and inhibitors. <i>Journal of Biological Chemistry</i> , 2019, 294, 3794-3805.	3.4	5
7	MolProbity: More and better reference data for improved all-atom structure validation. <i>Protein Science</i> , 2018, 27, 293-315.	7.6	2,776
8	Improved fragment-based protein structure prediction by redesign of search heuristics. <i>Scientific Reports</i> , 2018, 8, 13694.	3.3	12
9	EVI1 carboxy-terminal phosphorylation is ATM-mediated and sustains transcriptional modulation and self-renewal via enhanced CtBP1 association. <i>Nucleic Acids Research</i> , 2018, 46, 7662-7674.	14.5	11
10	Rapid functional and evolutionary changes follow gene duplication in yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20171393.	2.6	41
11	On heuristic bias in fragment-assembly methods for protein structure prediction. , 2017, , .		0
12	Adaptive HIV-1 evolutionary trajectories are constrained by protein stability. <i>Virus Evolution</i> , 2017, 3, vex019.	4.9	10
13	Non-muscle myosin IIB (Myh10) is required for epicardial function and coronary vessel formation during mammalian development. <i>PLoS Genetics</i> , 2017, 13, e1007068.	3.5	22
14	Toward a detailed understanding of search trajectories in fragment assembly approaches to protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 411-426.	2.6	18
15	Binding interface change and cryptic variation in the evolution of protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2016, 16, 40.	3.2	7
16	Generating, Maintaining, and Exploiting Diversity in a Memetic Algorithm for Protein Structure Prediction. <i>Evolutionary Computation</i> , 2016, 24, 577-607.	3.0	38
17	DupliPHY-Web: a web server for DupliPHY and DupliPHY-ML. <i>Bioinformatics</i> , 2015, 31, 416-417.	4.1	4
18	Abrogation of HMX1 Function Causes Rare Oculoauricular Syndrome Associated With Congenital Cataract, Anterior Segment Dysgenesis, and Retinal Dystrophy. <i>Investigative Ophthalmology and Visual Science</i> , 2015, 56, 883-891.	3.3	22

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19	Agnathia-otocephaly complex and asymmetric velopharyngeal insufficiency due to an in-frame duplication in OTX2. <i>Journal of Human Genetics</i> , 2015, 60, 199-202.	2.3	25
20	Ebolavirus is evolving but not changing: No evidence for functional change in EBOV from 1976 to the 2014 outbreak. <i>Virology</i> , 2015, 482, 202-207.	2.4	31
21	Covariation Is a Poor Measure of Molecular Coevolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 2456-2468.	8.9	49
22	Using Machine Learning to Explore the Relevance of Local and Global Features During Conformational Search in Rosetta. , 2015, , .		1
23	Sequencing and Characterisation of Rearrangements in Three <i>S. pastorianus</i> Strains Reveals the Presence of Chimeric Genes and Gives Evidence of Breakpoint Reuse. <i>PLoS ONE</i> , 2014, 9, e92203.	2.5	71
24	Erb2 Is Required for Cardiac Atrial Electrical Activity during Development. <i>PLoS ONE</i> , 2014, 9, e107041.	2.5	7
25	Constraints from protein structure and intra-molecular coevolution influence the fitness of HIV-1 recombinants. <i>Virology</i> , 2014, 454-455, 34-39.	2.4	12
26	Inferring Gene Family Histories in Yeast Identifies Lineage Specific Expansions. <i>PLoS ONE</i> , 2014, 9, e99480.	2.5	6
27	Alternative splicing and protein interaction data sets. <i>Nature Biotechnology</i> , 2013, 31, 292-293.	17.5	10
28	Modular Biological Function Is Most Effectively Captured by Combining Molecular Interaction Data Types. <i>PLoS ONE</i> , 2013, 8, e62670.	2.5	16
29	Mutations in Non-Acid Patch Residues Disrupt H2A.Z's Association with Chromatin through Multiple Mechanisms. <i>PLoS ONE</i> , 2013, 8, e76394.	2.5	6
30	Analysis of Genetic Interaction Networks Shows That Alternatively Spliced Genes Are Highly Versatile. <i>PLoS ONE</i> , 2013, 8, e55671.	2.5	1
31	The Role of Protein Interactions in Mediating Essentiality and Synthetic Lethality. <i>PLoS ONE</i> , 2013, 8, e62866.	2.5	9
32	Phosphorylation of the Leukemic Oncoprotein EVI1 on Serine 196 Modulates DNA Binding, Transcriptional Repression and Transforming Ability. <i>PLoS ONE</i> , 2013, 8, e66510.	2.5	14
33	Determining the evolutionary history of gene families. <i>Bioinformatics</i> , 2012, 28, 48-55.	4.1	48
34	Evolvability of Yeast Protein-Protein Interaction Interfaces. <i>Journal of Molecular Biology</i> , 2012, 419, 387-396.	4.2	4
35	The origins of the evolutionary signal used to predict protein-protein interactions. <i>BMC Evolutionary Biology</i> , 2012, 12, 238.	3.2	8
36	Mutations in CTC1, encoding conserved telomere maintenance component 1, cause Coats plus. <i>Nature Genetics</i> , 2012, 44, 338-342.	21.4	234

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37	Mutations in ADAR1 cause Aicardi-Goutières syndrome associated with a type I interferon signature. <i>Nature Genetics</i> , 2012, 44, 1243-1248.	21.4	712
38	The dual role of fragments in fragmentâ€ assembly methods for de novo protein structure prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 490-504.	2.6	42
39	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	7.6	188
40	Using Knowledge of Protein Structural Constraints to Predict the Evolution of HIV-1. <i>Journal of Molecular Biology</i> , 2011, 410, 1023-1034.	4.2	4
41	Tartrate-resistant acid phosphatase deficiency causes a bone dysplasia with autoimmunity and a type I interferon expression signature. <i>Nature Genetics</i> , 2011, 43, 127-131.	21.4	214
42	Diversification at Transcription Factor Binding Sites within a Species and the Implications for Environmental Adaptation. <i>Molecular Biology and Evolution</i> , 2011, 28, 3331-3344.	8.9	5
43	Characterization of Protein-Protein Interaction Interfaces from a Single Species. <i>PLoS ONE</i> , 2011, 6, e21053.	2.5	43
44	Gene Duplication and Environmental Adaptation within Yeast Populations. <i>Genome Biology and Evolution</i> , 2010, 2, 591-601.	2.5	44
45	Interactions between Kar2p and Its Nucleotide Exchange Factors Sil1p and Lhs1p Are Mechanistically Distinct. <i>Journal of Biological Chemistry</i> , 2010, 285, 21600-21606.	3.4	27
46	Constraints on HIV-1 Diversity from Protein Structure. <i>Journal of Virology</i> , 2010, 84, 12995-13003.	3.4	25
47	An Integrated View of Molecular Coevolution in Protein-Protein Interactions. <i>Molecular Biology and Evolution</i> , 2010, 27, 2567-2575.	8.9	119
48	The Effect of Sequence Evolution on Protein Structural Divergence. <i>Molecular Biology and Evolution</i> , 2009, 26, 1055-1065.	8.9	30
49	Analysis of Synthetic Lethality Reveals Genetic Interactions Between the GTPase Snu114p and snRNAs in the Catalytic Core of the <i>Saccharomyces cerevisiae</i> Spliceosome. <i>Genetics</i> , 2009, 183, 497-515.	2.9	12
50	Correlation of microsynteny conservation and disease gene distribution in mammalian genomes. <i>BMC Genomics</i> , 2009, 10, 521.	2.8	5
51	Quantitative analysis and prediction of curvature in leucineâ€ rich repeat proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 342-358.	2.6	16
52	Evolution in protein interaction networks: co-evolution, rewiring and the role of duplication. <i>Biochemical Society Transactions</i> , 2009, 37, 768-771.	3.4	9
53	Protein-protein interaction networks and biologyâ€ what's the connection?. <i>Nature Biotechnology</i> , 2008, 26, 69-72.	17.5	175
54	Specificity in protein interactions and its relationship with sequence diversity and coevolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7999-8004.	7.1	114

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55	All duplicates are not equal: the difference between small-scale and genome duplication. <i>Genome Biology</i> , 2007, 8, R209.	9.6	163
56	ERp57 is essential for efficient folding of glycoproteins sharing common structural domains. <i>EMBO Journal</i> , 2007, 26, 28-40.	7.8	177
57	An algorithm for predicting protein-protein interaction sites: Abnormally exposed amino acid residues and secondary structure elements. <i>Protein Science</i> , 2006, 15, 1017-1029.	7.6	61
58	Secondary structure assignment that accurately reflects physical and evolutionary characteristics. <i>BMC Bioinformatics</i> , 2005, 6, S8.	2.6	53
59	Human glutamyl cyclase and bacterial zinc aminopeptidase share a common fold and active site. <i>BMC Biology</i> , 2004, 2, 2.	3.8	26
60	Distinguishing Structural and Functional Restraints in Evolution in Order to Identify Interaction Sites. <i>Journal of Molecular Biology</i> , 2004, 342, 1487-1504.	4.2	89
61	Ab initio construction of polypeptide fragments: Efficient generation of accurate, representative ensembles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 41-55.	2.6	134
62	Structure validation by C $\alpha$ geometry: $\overline{\delta}$ , $\overline{\gamma}$ and C $\beta$ deviation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 437-450.	2.6	4,134
63	Are non-functional, unfolded proteins ("junk proteins") common in the genome?. <i>FEBS Letters</i> , 2003, 554, 237-239.	2.8	22
64	Crystal Structures of Engrailed Homeodomain Mutants. <i>Journal of Biological Chemistry</i> , 2003, 278, 43699-43708.	3.4	39
65	The penultimate rotamer library. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 389-408.	2.6	977
66	Exploring steric constraints on protein mutations using MAGE/PROBE. <i>Protein Science</i> , 2000, 9, 2251-2259.	7.6	68
67	Visualizing and quantifying molecular goodness-of-fit: small-probe contact dots with explicit hydrogen atoms 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 1999, 285, 1711-1733.	4.2	511
68	Asparagine and glutamine: using hydrogen atom contacts in the choice of side-chain amide orientation 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 1999, 285, 1735-1747.	4.2	1,264
69	Cooperativity in <i>Bacillus stearothermophilus</i> pyruvate kinase. <i>Journal of Molecular Biology</i> , 1998, 276, 839-851.	4.2	16