

# Gideon Schreiber

## List of Publications by Year in descending order

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114  
papers

12,764  
citations

26567

56  
h-index

27345

106  
g-index

168  
all docs

168  
docs citations

168  
times ranked

14024  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>De novo</i> developed protein binders mimicking Interferon lambda signaling. FEBS Journal, 2022, 289, 2672-2684.	2.2	4
2	The SARS-CoV-2 Lambda variant exhibits enhanced infectivity and immune resistance. Cell Reports, 2022, 38, 110218.	2.9	148
3	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. Cell, 2022, 185, 467-484.e15.	13.5	788
4	Virological characteristics of the SARS-CoV-2 Omicron BA.2 spike. Cell, 2022, 185, 2103-2115.e19.	13.5	273
5	In vitro Evolution of Uracil Glycosylase Towards DnaKJ and GroEL Binding Evolves Different Misfolded States. Journal of Molecular Biology, 2022, 434, 167627.	2.0	0
6	Gelatin Stabilizes Nebulized Proteins in Pulmonary Drug Delivery against COVID-19. ACS Biomaterials Science and Engineering, 2022, 8, 2553-2563.	2.6	9
7	Line-FRAP, A Versatile Method to Measure Diffusion Rates In Vitro and In Vivo. Journal of Molecular Biology, 2021, 433, 166898.	2.0	14
8	SARS-CoV-2 spike L452R variant evades cellular immunity and increases infectivity. Cell Host and Microbe, 2021, 29, 1124-1136.e11.	5.1	421
9	Protein Engineering in the Design of Protein-Protein Interactions: SARS-CoV-2 Inhibitors as a Test Case. Biochemistry, 2021, 60, 3429-3435.	1.2	3
10	SARS-CoV-2 variant prediction and antiviral drug design are enabled by RBD in vitro evolution. Nature Microbiology, 2021, 6, 1188-1198.	5.9	314
11	SARS-CoV-2 suppresses IFN $\gamma$ production mediated by NSP1, 5, 6, 15, ORF6 and ORF7b but does not suppress the effects of added interferon. PLoS Pathogens, 2021, 17, e1009800.	2.1	74
12	IFNAR1 and IFNAR2 play distinct roles in initiating type I interferon-induced JAK-STAT signaling and activating STATs. Science Signaling, 2021, 14, eabe4627.	1.6	24
13	A Protein-Engineered, Enhanced Yeast Display Platform for Rapid Evolution of Challenging Targets. ACS Synthetic Biology, 2021, 10, 3445-3460.	1.9	28
14	The Role of Type I Interferons in the Pathogenesis and Treatment of COVID-19. Frontiers in Immunology, 2020, 11, 595739.	2.2	90
15	Competing Ligands Can Both Obstruct and Enhance Protein-Complex Formation. Biophysical Journal, 2019, 117, 1552-1553.	0.2	0
16	CRISPR/Cas9-based Knockout Strategy Elucidates Components Essential for Type 1 Interferon Signaling in Human HeLa Cells. Journal of Molecular Biology, 2019, 431, 3324-3338.	2.0	24
17	Dose-Dependent Differences in HIV Inhibition by Different Interferon Alpha Subtypes While Having Overall Similar Biologic Effects. MSphere, 2019, 4, .	1.3	14
18	Selecting for Fast Protein-Protein Association As Demonstrated on a Random TEM1 Yeast Library Binding BLIP. Biochemistry, 2018, 57, 4644-4650.	1.2	8

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19	Human-Specific Adaptations in Vpu Conferring Anti-tetherin Activity Are Critical for Efficient Early HIV-1 Replication In Vivo. <i>Cell Host and Microbe</i> , 2018, 23, 110-120.e7.	5.1	43
20	Type I IFN signaling blockade by a PASylated antagonist during chronic SIV infection suppresses specific inflammatory pathways but does not alter T cell activation or virus replication. <i>PLoS Pathogens</i> , 2018, 14, e1007246.	2.1	33
21	The molecular basis for differential type I interferon signaling. <i>Journal of Biological Chemistry</i> , 2017, 292, 7285-7294.	1.6	171
22	Quantifying enzyme activity in living cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 15838-15848.	1.6	67
23	Promiscuous Protein Binding as a Function of Protein Stability. <i>Structure</i> , 2017, 25, 1867-1874.e3.	1.6	23
24	Dynamic Modulation of Binding Affinity as a Mechanism for Regulating Interferon Signaling. <i>Journal of Molecular Biology</i> , 2017, 429, 2571-2589.	2.0	14
25	Low-stringency selection of TEM1 for BLIP shows interface plasticity and selection for faster binders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14982-14987.	3.3	25
26	Spatiotemporal control of interferon-induced JAK/STAT signalling and gene transcription by the retromer complex. <i>Nature Communications</i> , 2016, 7, 13476.	5.8	50
27	Direct determination of enzyme kinetic parameters from single reactions using a new progress curve analysis tool. <i>Protein Engineering, Design and Selection</i> , 2016, 30, 149-156.	1.0	6
28	Type I Interferon Signaling Is Decoupled from Specific Receptor Orientation through Lenient Requirements of the Transmembrane Domain. <i>Journal of Biological Chemistry</i> , 2016, 291, 3371-3384.	1.6	15
29	Fine Tuning of a Type 1 Interferon Antagonist. <i>PLoS ONE</i> , 2015, 10, e0130797.	1.1	10
30	The molecular basis for functional plasticity in type I interferon signaling. <i>Trends in Immunology</i> , 2015, 36, 139-149.	2.9	179
31	A robust type I interferon gene signature from blood RNA defines quantitative but not qualitative differences between three major IFN $\alpha$ drugs in the treatment of multiple sclerosis. <i>Human Molecular Genetics</i> , 2015, 24, 3192-3205.	1.4	11
32	Bridging the Species Divide: Transgenic Mice Humanized for Type-I Interferon Response. <i>PLoS ONE</i> , 2014, 9, e84259.	1.1	28
33	Multifaceted Activities of Type I Interferon Are Revealed by a Receptor Antagonist. <i>Science Signaling</i> , 2014, 7, ra50.	1.6	94
34	PyInterph: A Framework for the Analysis of Interaction Networks in Structural Ensembles of Proteins. <i>Journal of Chemical Information and Modeling</i> , 2014, 54, 1537-1551.	2.5	107
35	Enhanced in Vivo Efficacy of a Type I Interferon Superagonist with Extended Plasma Half-life in a Mouse Model of Multiple Sclerosis. <i>Journal of Biological Chemistry</i> , 2014, 289, 29014-29029.	1.6	55
36	Type I interferon responses in rhesus macaques prevent SIV infection and slow disease progression. <i>Nature</i> , 2014, 511, 601-605.	13.7	422

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37	Editorial overview: Folding and binding. <i>Current Opinion in Structural Biology</i> , 2014, 24, viii-x.	2.6	0
38	Computational design of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 903-910.	2.6	53
39	Type I Interferons Induce Apoptosis by Balancing cFLIP and Caspase-8 Independent of Death Ligands. <i>Molecular and Cellular Biology</i> , 2013, 33, 800-814.	1.1	54
40	Formation of protein complexes in crowded environments - From in vitro to in vivo. <i>FEBS Letters</i> , 2013, 587, 1046-1052.	1.3	111
41	Protein-binding dynamics imaged in a living cell. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1461-1466.	3.3	105
42	FRETex: a FRET-based, high-throughput technique to analyze protein-protein interactions. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 681-687.	1.0	12
43	Structural and dynamic determinants of type I interferon receptor assembly and their functional interpretation. <i>Immunological Reviews</i> , 2012, 250, 317-334.	2.8	201
44	Contrasting Factors on the Kinetic Path to Protein Complex Formation Diminish the Effects of Crowding Agents. <i>Biophysical Journal</i> , 2012, 103, 1011-1019.	0.2	39
45	Structural Linkage between Ligand Discrimination and Receptor Activation by Type I Interferons. <i>Cell</i> , 2011, 146, 621-632.	13.5	310
46	Binding and activity of all human alpha interferon subtypes. <i>Cytokine</i> , 2011, 56, 282-289.	1.4	169
47	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	2.0	131
48	Protein binding specificity versus promiscuity. <i>Current Opinion in Structural Biology</i> , 2011, 21, 50-61.	2.6	209
49	A Quantitative, Real-Time Assessment of Binding of Peptides and Proteins to Gold Surfaces. <i>Chemistry - A European Journal</i> , 2011, 17, 1327-1336.	1.7	35
50	Stochastic Receptor Expression Determines Cell Fate upon Interferon Treatment. <i>Molecular and Cellular Biology</i> , 2011, 31, 3252-3266.	1.1	96
51	Protein structure modelling and evaluation based on a 4-distance description of side-chain interactions. <i>BMC Bioinformatics</i> , 2010, 11, 374.	1.2	24
52	Cytokine-receptor interactions as drug targets. <i>Current Opinion in Chemical Biology</i> , 2010, 14, 511-519.	2.8	46
53	Free Energy Landscapes in Protein-Protein Interactions. , 2010, , 15-21.		0
54	Improved Binding of Raf to Ras-GDP Is Correlated with Biological Activity. <i>Journal of Biological Chemistry</i> , 2009, 284, 31893-31902.	1.6	41

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55	Four Distances between Pairs of Amino Acids Provide a Precise Description of their Interaction. PLoS Computational Biology, 2009, 5, e1000470.	1.5	29
56	Understanding hydrogen-bond patterns in proteins using network motifs. Bioinformatics, 2009, 25, 2921-2928.	1.8	19
57	Receptor Density Is Key to the Alpha2/Beta Interferon Differential Activities. Molecular and Cellular Biology, 2009, 29, 4778-4787.	1.1	91
58	Assessing computational methods for predicting protein stability upon mutation: good on average but not in the details. Protein Engineering, Design and Selection, 2009, 22, 553-560.	1.0	325
59	Docking of Antizyme to Ornithine Decarboxylase and Antizyme Inhibitor using Experimental Mutant and Double-Mutant Cycle Data. Journal of Molecular Biology, 2009, 390, 503-515.	2.0	19
60	Fruitful and Futile Encounters along the Association Reaction between Proteins. Biophysical Journal, 2009, 96, 4237-4248.	0.2	47
61	Common Crowding Agents Have Only a Small Effect on Protein-Protein Interactions. Biophysical Journal, 2009, 97, 875-885.	0.2	119
62	Fundamental Aspects of Protein-Protein Association Kinetics. Chemical Reviews, 2009, 109, 839-860.	23.0	637
63	The ProteOn XPR36 Array System—High Throughput Kinetic Binding Analysis of Biomolecular Interactions. Cellular and Molecular Bioengineering, 2008, 1, 216-228.	1.0	7
64	Cluster conservation as a novel tool for studying protein-protein interactions evolution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 621-630.	1.5	15
65	Similar chemistry, but different bond preferences in inter versus intra-protein interactions. Proteins: Structure, Function and Bioinformatics, 2008, 72, 741-753.	1.5	37
66	On the Contribution of Water-Mediated Interactions to Protein-Complex Stability. Biochemistry, 2008, 47, 1051-1060.	1.2	70
67	Mutation of the IFNAR-1 Receptor Binding Site of Human IFN- $\alpha$ 2 Generates Type I IFN Competitive Antagonists. Biochemistry, 2008, 47, 12018-12027.	1.2	34
68	The Stability of the Ternary Interferon-Receptor Complex Rather than the Affinity to the Individual Subunits Dictates Differential Biological Activities. Journal of Biological Chemistry, 2008, 283, 32925-32936.	1.6	105
69	Understanding Hydrogen-Bond Patterns in Proteins using a Novel Statistical Model. Nature Precedings, 2008, , .	0.1	0
70	An Interferon $\alpha$ 2 Mutant Optimized by Phage Display for IFNAR1 Binding Confers Specifically Enhanced Antitumor Activities. Journal of Biological Chemistry, 2007, 282, 11602-11611.	1.6	92
71	Upregulation of a Small Subset of Genes Drives Type I Interferon-Induced Antiviral Memory. Journal of Interferon and Cytokine Research, 2007, 27, 653-664.	0.5	33
72	ProMateus—an open research approach to protein-binding sites analysis. Nucleic Acids Research, 2007, 35, W543-W548.	6.5	24

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73	The fast release of sticky protons: Kinetics of substrate binding and proton release in a multidrug transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17989-17994.	3.3	58
74	Binding Hot Spots in the TEM1-BLIP Interface in Light of its Modular Architecture. <i>Journal of Molecular Biology</i> , 2007, 365, 663-679.	2.0	81
75	On the Dynamic Nature of the Transition State for Protein-Protein Association as Determined by Double-mutant Cycle Analysis and Simulation. <i>Journal of Molecular Biology</i> , 2007, 371, 180-196.	2.0	42
76	Protein-Protein Association in Polymer Solutions: From Dilute to Semidilute to Concentrated. <i>Biophysical Journal</i> , 2007, 92, 2139-2149.	0.2	193
77	Noncovalent, Site-Specific Biotinylation of Histidine-Tagged Proteins. <i>Analytical Chemistry</i> , 2007, 79, 8590-8600.	3.2	60
78	The molecular architecture of protein-protein binding sites. <i>Current Opinion in Structural Biology</i> , 2007, 17, 67-76.	2.6	182
79	eMovie: a storyboard-based tool for making molecular movies. <i>Trends in Biochemical Sciences</i> , 2007, 32, 199-204.	3.7	27
80	Variations in the Unstructured C-terminal Tail of Interferons Contribute to Differential Receptor Binding and Biological Activity. <i>Journal of Molecular Biology</i> , 2006, 360, 1019-1030.	2.0	55
81	Electrostatic Design of Protein-Protein Association Rates. , 2006, 340, 235-250.		31
82	Inquiring into the Differential Action of Interferons (IFNs): an IFN- $\beta$ Mutant with Enhanced Affinity to IFNAR1 Is Functionally Similar to IFN- $\gamma$ . <i>Molecular and Cellular Biology</i> , 2006, 26, 1888-1897.	1.1	217
83	Exploring the charge space of protein-protein association: A proteomic study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 341-352.	1.5	58
84	Separating the Contribution of Translational and Rotational Diffusion to Protein Association. <i>Journal of the American Chemical Society</i> , 2005, 127, 15138-15144.	6.6	81
85	Mutational Analysis of the IFNAR1 Binding Site on IFN- $\beta$ Reveals the Architecture of a Weak Ligand-Receptor Binding-site. <i>Journal of Molecular Biology</i> , 2005, 353, 271-281.	2.0	80
86	Optimizing the Binding Affinity of a Carrier Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 18046-18053.	1.6	19
87	A novel method for scoring of docked protein complexes using predicted protein-protein binding sites. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 183-189.	1.0	26
88	Reversible PEGylation: A Novel Technology To Release Native Interferon $\beta$ over a Prolonged Time Period. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 4897-4904.	2.9	63
89	Effect of Crowding on Protein-Protein Association Rates: Fundamental Differences between Low and High Mass Crowding Agents. <i>Journal of Molecular Biology</i> , 2004, 336, 763-774.	2.0	112
90	ProMate: A Structure Based Prediction Program to Identify the Location of Protein-Protein Binding Sites. <i>Journal of Molecular Biology</i> , 2004, 338, 181-199.	2.0	420

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91	The Human Type I Interferon Receptor. <i>Structure</i> , 2003, 11, 791-802.	1.6	79
92	The Human Interferon Receptor: NMR-Based Modeling, Mapping of the IFN- $\beta$ Binding Site, and Observed Ligand-Induced Tightening. <i>Biochemistry</i> , 2002, 41, 3575-3585.	1.2	42
93	Kinetic studies of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2002, 12, 41-47.	2.6	296
94	Experimental assignment of the structure of the transition state for the association of barnase and barstar. Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2001, 308, 69-77.	2.0	101
95	New insights into the mechanism of protein-protein association. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 190-198.	1.5	113
96	Fast Transient Cytokine Receptor Interactions Monitored in Real Time by Reflectometric Interference Spectroscopy. <i>Analytical Biochemistry</i> , 2001, 289, 173-186.	1.1	54
97	Rational design of faster associating and tighter binding protein complexes. <i>Nature Structural Biology</i> , 2000, 7, 537-541.	9.7	282
98	New Structural and Functional Aspects of the Type I Interferon-Receptor Interaction Revealed by Comprehensive Mutational Analysis of the Binding Interface. <i>Journal of Biological Chemistry</i> , 2000, 275, 40425-40433.	1.6	137
99	Evaluation of direct and cooperative contributions towards the strength of buried hydrogen bonds and salt bridges. <i>Journal of Molecular Biology</i> , 2000, 298, 503-520.	2.0	102
100	Biophysical Characterization of the Interaction of the $\beta$ -Lactamase TEM-1 with Its Protein Inhibitor BLIP. <i>Biochemistry</i> , 1999, 38, 11-21.	1.2	100
101	Predicting the rate enhancement of protein complex formation from the electrostatic energy of interaction. Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1999, 287, 409-419.	2.0	120
102	Biophysical analysis of the interaction of human ifnar2 expressed in <i>E. coli</i> with IFN- $\beta$ . Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 289, 57-67.	2.0	119
103	Mutational and structural analysis of the binding interface between type I interferons and their receptor ifnar2. Edited by J. A. Wells. <i>Journal of Molecular Biology</i> , 1999, 294, 223-237.	2.0	96
104	Electrostatic enhancement of diffusion-controlled protein-protein association: comparison of theory and experiment on barnase and barstar. Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1998, 278, 1015-1024.	2.0	199
105	Thermodynamics of the interaction of barnase and barstar: changes in free energy versus changes in enthalpy on mutation. Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 267, 696-706.	2.0	125
106	Fluorescence properties of a tryptophan residue in an aromatic core of the protein subunit of ribonuclease P from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1997, 267, 765-769.	2.0	33
107	The role of glu73 of barnase in catalysis and the binding of barstar. <i>Journal of Molecular Biology</i> , 1997, 270, 111-122.	2.0	46
108	Rapid, electrostatically assisted association of proteins. <i>Nature Structural Biology</i> , 1996, 3, 427-431.	9.7	523

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109	ppGpp-mediated regulation of DNA replication and cell division in Escherichia coli. Current Microbiology, 1995, 30, 27-32.	1.0	116
110	Energetics of protein-protein interactions: Analysis of the Barnase-Barstar interface by single mutations and double mutant cycles. Journal of Molecular Biology, 1995, 248, 478-486.	2.0	428
111	Expression of the genes coding for the Escherichia coli integration host factor are controlled by growth phase, rpoS, ppGpp and by autoregulation. Molecular Microbiology, 1994, 14, 1021-1031.	1.2	113
112	Stability and function: two constraints in the evolution of barstar and other proteins. Structure, 1994, 2, 945-951.	1.6	165
113	Interaction of barnase with its polypeptide inhibitor barstar studied by protein engineering. Biochemistry, 1993, 32, 5145-5150.	1.2	288
114	Perspectives: SARS-CoV-2 Spike Convergent Evolution as a Guide to Explore Adaptive Advantage. Frontiers in Cellular and Infection Microbiology, 0, 12, .	1.8	12