

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	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	13.5	788
2	Fundamental Aspects of Protein-Protein Association Kinetics. <i>Chemical Reviews</i> , 2009, 109, 839-860.	23.0	637
3	Rapid, electrostatically assisted association of proteins. <i>Nature Structural Biology</i> , 1996, 3, 427-431.	9.7	523
4	Energetics of protein-protein interactions: Analysis of the Barnase-Barstar interface by single mutations and double mutant cycles. <i>Journal of Molecular Biology</i> , 1995, 248, 478-486.	2.0	428
5	Type I interferon responses in rhesus macaques prevent SIV infection and slow disease progression. <i>Nature</i> , 2014, 511, 601-605.	13.7	422
6	SARS-CoV-2 spike L452R variant evades cellular immunity and increases infectivity. <i>Cell Host and Microbe</i> , 2021, 29, 1124-1136.e11.	5.1	421
7	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
8	Assessing computational methods for predicting protein stability upon mutation: good on average but not in the details. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 553-560.	1.0	325
9	SARS-CoV-2 variant prediction and antiviral drug design are enabled by RBD in vitro evolution. <i>Nature Microbiology</i> , 2021, 6, 1188-1198.	5.9	314
10	Structural Linkage between Ligand Discrimination and Receptor Activation by Type I Interferons. <i>Cell</i> , 2011, 146, 621-632.	13.5	310
11	Kinetic studies of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2002, 12, 41-47.	2.6	296
12	Interaction of barnase with its polypeptide inhibitor barstar studied by protein engineering. <i>Biochemistry</i> , 1993, 32, 5145-5150.	1.2	288
13	Rational design of faster associating and tighter binding protein complexes. <i>Nature Structural Biology</i> , 2000, 7, 537-541.	9.7	282
14	Virological characteristics of the SARS-CoV-2 Omicron BA.2 spike. <i>Cell</i> , 2022, 185, 2103-2115.e19.	13.5	273
15	Inquiring into the Differential Action of Interferons (IFNs): an IFN- γ 2 Mutant with Enhanced Affinity to IFNAR1 Is Functionally Similar to IFN- γ 2. <i>Molecular and Cellular Biology</i> , 2006, 26, 1888-1897.	1.1	217
16	Protein binding specificity versus promiscuity. <i>Current Opinion in Structural Biology</i> , 2011, 21, 50-61.	2.6	209
17	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
18	Electrostatic enhancement of diffusion-controlled protein-protein association: comparison of theory and experiment on barnase and barstar 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1998, 278, 1015-1024.	2.0	199

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19	Protein-Protein Association in Polymer Solutions: From Dilute to Semidilute to Concentrated. <i>Biophysical Journal</i> , 2007, 92, 2139-2149.	0.2	193
20	The molecular architecture of protein-protein binding sites. <i>Current Opinion in Structural Biology</i> , 2007, 17, 67-76.	2.6	182
21	The molecular basis for functional plasticity in type I interferon signaling. <i>Trends in Immunology</i> , 2015, 36, 139-149.	2.9	179
22	The molecular basis for differential type I interferon signaling. <i>Journal of Biological Chemistry</i> , 2017, 292, 7285-7294.	1.6	171
23	Binding and activity of all human alpha interferon subtypes. <i>Cytokine</i> , 2011, 56, 282-289.	1.4	169
24	Stability and function: two constraints in the evolution of barnase and other proteins. <i>Structure</i> , 1994, 2, 945-951.	1.6	165
25	The SARS-CoV-2 Lambda variant exhibits enhanced infectivity and immune resistance. <i>Cell Reports</i> , 2022, 38, 110218.	2.9	148
26	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
27	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
28	Thermodynamics of the interaction of barnase and barstar: changes in free energy versus changes in enthalpy on mutation 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 267, 696-706.	2.0	125
29	Predicting the rate enhancement of protein complex formation from the electrostatic energy of interaction 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1999, 287, 409-419.	2.0	120
30	Biophysical analysis of the interaction of human ifnar2 expressed in E. coli with IFN-2 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 289, 57-67.	2.0	119
31	Common Crowding Agents Have Only a Small Effect on Protein-Protein Interactions. <i>Biophysical Journal</i> , 2009, 97, 875-885.	0.2	119
32	ppGpp-mediated regulation of DNA replication and cell division in Escherichia coli. <i>Current Microbiology</i> , 1995, 30, 27-32.	1.0	116
33	Expression of the genes coding for the Escherichia coli integration host factor are controlled by growth phase, rpoS, ppGpp and by autoregulation. <i>Molecular Microbiology</i> , 1994, 14, 1021-1031.	1.2	113
34	New insights into the mechanism of protein-protein association. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 45, 190-198.	1.5	113
35	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
36	Formation of protein complexes in crowded environments - From in vitro to in vivo. <i>FEBS Letters</i> , 2013, 587, 1046-1052.	1.3	111

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37	PyInteraph: 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
38	The Stability of the Ternary Interferon-Receptor Complex Rather than the Affinity to the Individual Subunits Dictates Differential Biological Activities. <i>Journal of Biological Chemistry</i> , 2008, 283, 32925-32936.	1.6	105
39	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
40	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
41	Experimental assignment of the structure of the transition state for the association of barnase and barstar11 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 2001, 308, 69-77.	2.0	101
42	Biophysical Characterization of the Interaction of the \hat{I}^2 -Lactamase TEM-1 with Its Protein Inhibitor BLIP. <i>Biochemistry</i> , 1999, 38, 11-21.	1.2	100
43	Mutational and structural analysis of the binding interface between type I interferons and their receptor ifnar2 1 1 Edited by J. A. Wells. <i>Journal of Molecular Biology</i> , 1999, 294, 223-237.	2.0	96
44	Stochastic Receptor Expression Determines Cell Fate upon Interferon Treatment. <i>Molecular and Cellular Biology</i> , 2011, 31, 3252-3266.	1.1	96
45	Multifaceted Activities of Type I Interferon Are Revealed by a Receptor Antagonist. <i>Science Signaling</i> , 2014, 7, ra50.	1.6	94
46	An Interferon \hat{I}^2 Mutant Optimized by Phage Display for IFNAR1 Binding Confers Specifically Enhanced Antitumor Activities. <i>Journal of Biological Chemistry</i> , 2007, 282, 11602-11611.	1.6	92
47	Receptor Density Is Key to the Alpha2/Beta Interferon Differential Activities. <i>Molecular and Cellular Biology</i> , 2009, 29, 4778-4787.	1.1	91
48	The Role of Type I Interferons in the Pathogenesis and Treatment of COVID-19. <i>Frontiers in Immunology</i> , 2020, 11, 595739.	2.2	90
49	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
50	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
51	Mutational Analysis of the IFNAR1 Binding Site on IFN \hat{I}^2 Reveals the Architecture of a Weak Ligand-Receptor Binding-site. <i>Journal of Molecular Biology</i> , 2005, 353, 271-281.	2.0	80
52	The Human Type I Interferon Receptor. <i>Structure</i> , 2003, 11, 791-802.	1.6	79
53	SARS-CoV-2 suppresses IFN \hat{I}^2 production mediated by NSP1, 5, 6, 15, ORF6 and ORF7b but does not suppress the effects of added interferon. <i>PLoS Pathogens</i> , 2021, 17, e1009800.	2.1	74
54	On the Contribution of Water-Mediated Interactions to Protein-Complex Stability. <i>Biochemistry</i> , 2008, 47, 1051-1060.	1.2	70

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55	Quantifying enzyme activity in living cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 15838-15848.	1.6	67
56	Reversible PEGylation: A Novel Technology To Release Native Interferon β over a Prolonged Time Period. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 4897-4904.	2.9	63
57	Noncovalent, Site-Specific Biotinylation of Histidine-Tagged Proteins. <i>Analytical Chemistry</i> , 2007, 79, 8590-8600.	3.2	60
58	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
59	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
60	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
61	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
62	Fast Transient Cytokine-Receptor Interactions Monitored in Real Time by Reflectometric Interference Spectroscopy. <i>Analytical Biochemistry</i> , 2001, 289, 173-186.	1.1	54
63	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
64	Computational design of protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 903-910.	2.6	53
65	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
66	Fruitful and Futile Encounters along the Association Reaction between Proteins. <i>Biophysical Journal</i> , 2009, 96, 4237-4248.	0.2	47
67	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
68	Cytokine-receptor interactions as drug targets. <i>Current Opinion in Chemical Biology</i> , 2010, 14, 511-519.	2.8	46
69	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
70	The Human Interferon Receptor: NMR-Based Modeling, Mapping of the IFN β Binding Site, and Observed Ligand-Induced Tightening. <i>Biochemistry</i> , 2002, 41, 3575-3585.	1.2	42
71	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
72	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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73	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
74	Similar chemistry, but different bond preferences in inter versus intra-protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 741-753.	1.5	37
75	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
76	Mutation of the IFNAR-1 Receptor Binding Site of Human IFN- β Generates Type I IFN Competitive Antagonists. <i>Biochemistry</i> , 2008, 47, 12018-12027.	1.2	34
77	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
78	Upregulation of a Small Subset of Genes Drives Type I Interferon-Induced Antiviral Memory. <i>Journal of Interferon and Cytokine Research</i> , 2007, 27, 653-664.	0.5	33
79	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
80	Electrostatic Design of Protein-Protein Association Rates. , 2006, 340, 235-250.		31
81	Four Distances between Pairs of Amino Acids Provide a Precise Description of their Interaction. <i>PLoS Computational Biology</i> , 2009, 5, e1000470.	1.5	29
82	Bridging the Species Divide: Transgenic Mice Humanized for Type-I Interferon Response. <i>PLoS ONE</i> , 2014, 9, e84259.	1.1	28
83	A Protein-Engineered, Enhanced Yeast Display Platform for Rapid Evolution of Challenging Targets. <i>ACS Synthetic Biology</i> , 2021, 10, 3445-3460.	1.9	28
84	eMovie: a storyboard-based tool for making molecular movies. <i>Trends in Biochemical Sciences</i> , 2007, 32, 199-204.	3.7	27
85	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
86	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
87	ProMateus—an open research approach to protein-binding sites analysis. <i>Nucleic Acids Research</i> , 2007, 35, W543-W548.	6.5	24
88	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
89	CRISPR/Cas9-based Knockout Strategy Elucidates Components Essential for Type 1 Interferon Signaling in Human HeLa Cells. <i>Journal of Molecular Biology</i> , 2019, 431, 3324-3338.	2.0	24
90	IFNAR1 and IFNAR2 play distinct roles in initiating type I interferon-induced JAK-STAT signaling and activating STATs. <i>Science Signaling</i> , 2021, 14, eabe4627.	1.6	24

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91	Promiscuous Protein Binding as a Function of Protein Stability. <i>Structure</i> , 2017, 25, 1867-1874.e3.	1.6	23
92	Optimizing the Binding Affinity of a Carrier Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 18046-18053.	1.6	19
93	Understanding hydrogen-bond patterns in proteins using network motifs. <i>Bioinformatics</i> , 2009, 25, 2921-2928.	1.8	19
94	Docking of Antizyme to Ornithine Decarboxylase and Antizyme Inhibitor using Experimental Mutant and Double-Mutant Cycle Data. <i>Journal of Molecular Biology</i> , 2009, 390, 503-515.	2.0	19
95	Cluster conservation as a novel tool for studying proteinâ€“protein interactions evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 621-630.	1.5	15
96	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
97	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
98	Dose-Dependent Differences in HIV Inhibition by Different Interferon Alpha Subtypes While Having Overall Similar Biologic Effects. <i>MSphere</i> , 2019, 4, .	1.3	14
99	Line-FRAP, A Versatile Method to Measure Diffusion Rates In Vitro and In Vivo. <i>Journal of Molecular Biology</i> , 2021, 433, 166898.	2.0	14
100	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
101	Perspectives: SARS-CoV-2 Spike Convergent Evolution as a Guide to Explore Adaptive Advantage. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	1.8	12
102	A robust type I interferon gene signature from blood RNA defines quantitative but not qualitative differences between three major IFN α drugs in the treatment of multiple sclerosis. <i>Human Molecular Genetics</i> , 2015, 24, 3192-3205.	1.4	11
103	Fine Tuning of a Type 1 Interferon Antagonist. <i>PLoS ONE</i> , 2015, 10, e0130797.	1.1	10
104	Gelatin Stabilizes Nebulized Proteins in Pulmonary Drug Delivery against COVID-19. <i>ACS Biomaterials Science and Engineering</i> , 2022, 8, 2553-2563.	2.6	9
105	Selecting for Fast Proteinâ€“Protein Association As Demonstrated on a Random TEM1 Yeast Library Binding BLIP. <i>Biochemistry</i> , 2018, 57, 4644-4650.	1.2	8
106	The ProteOn XPR36 μ s Array Systemâ€“High Throughput Kinetic Binding Analysis of Biomolecular Interactions. <i>Cellular and Molecular Bioengineering</i> , 2008, 1, 216-228.	1.0	7
107	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
108	<i>De novo</i> developed protein binders mimicking Interferon lambda signaling. <i>FEBS Journal</i> , 2022, 289, 2672-2684.	2.2	4

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109	Protein Engineering in the Design of Protein-Protein Interactions: SARS-CoV-2 Inhibitors as a Test Case. <i>Biochemistry</i> , 2021, 60, 3429-3435.	1.2	3
110	Understanding Hydrogen-Bond Patterns in Proteins using a Novel Statistical Model. <i>Nature Precedings</i> , 2008, , .	0.1	0
111	Free Energy Landscapes in Protein-Protein Interactions. , 2010, , 15-21.		0
112	Editorial overview: Folding and binding. <i>Current Opinion in Structural Biology</i> , 2014, 24, viii-x.	2.6	0
113	Competing Ligands Can Both Obstruct and Enhance Protein-Complex Formation. <i>Biophysical Journal</i> , 2019, 117, 1552-1553.	0.2	0
114	In vitro Evolution of Uracil Glycosylase Towards DnaKJ and GroEL Binding Evolves Different Misfolded States. <i>Journal of Molecular Biology</i> , 2022, 434, 167627.	2.0	0