Lawrence Shapiro

List of Publications by Year
in descending order

152 papers	23,533 citations	16411 64 h-index	9839 141 g-index
175 all docs	175 docs citations	175 times ranked	22623 citing authors

#	Article	IF	Citations
1	Contributions of single-particle cryoelectron microscopy toward fighting COVID-19. Trends in Biochemical Sciences, 2022, 47, 117-123.	3.7	6
2	A monoclonal antibody that neutralizes SARS-CoV-2 variants, SARS-CoV, and other sarbecoviruses. Emerging Microbes and Infections, 2022, 11, 147-157.	3.0	25
3	Cryo-EM structure of the SARS-CoV-2 Omicron spike. Cell Reports, 2022, 38, 110428.	2.9	82
4	How clustered protocadherin binding specificity is tuned for neuronal self-/nonself-recognition. ELife, 2022, 11, .	2.8	18
5	Affinity requirements for control of synaptic targeting and neuronal cell survival by heterophilic IgSF cell adhesion molecules. Cell Reports, 2022, 39, 110618.	2.9	9
6	Structural basis for llama nanobody recognition and neutralization of HIV-1 at the CD4-binding site. Structure, 2022, 30, 862-875.e4.	1.6	4
7	An antibody class with a common CDRH3 motif broadly neutralizes sarbecoviruses. Science Translational Medicine, 2022, 14, eabn6859.	5.8	31
8	Functional properties of the spike glycoprotein of the emerging SARS-CoV-2 variant B.1.1.529. Cell Reports, 2022, 39, 110924.	2.9	20
9	Vaccination induces maturation in a mouse model of diverse unmutated VRC01-class precursors to HIV-neutralizing antibodies with >50% breadth. Immunity, 2021, 54, 324-339.e8.	6.6	36
10	Antibody resistance of SARS-CoV-2 variants B.1.351 and B.1.1.7. Nature, 2021, 593, 130-135.	13.7	1,904
11	Modular basis for potent SARS-CoV-2 neutralization by a prevalent VH1-2-derived antibody class. Cell Reports, 2021, 35, 108950.	2.9	54
12	Increased resistance of SARS-CoV-2 variant P.1 to antibody neutralization. Cell Host and Microbe, 2021, 29, 747-751.e4.	5.1	504
13	Potent SARS-CoV-2 neutralizing antibodies directed against spike N-terminal domain target a single supersite. Cell Host and Microbe, 2021, 29, 819-833.e7.	5.1	444
14	Dimerization of Cadherin-11 involves multi-site coupled unfolding and strand swapping. Structure, 2021, 29, 1105-1115.e6.	1.6	3
15	Structural basis for accommodation of emerging B.1.351 and B.1.1.7 variants by two potent SARS-CoV-2 neutralizing antibodies. Structure, 2021, 29, 655-663.e4.	1.6	52
16	Visualizing cadherin intermembrane adhesion assemblies using cryo-electron tomography. Microscopy and Microanalysis, 2021, 27, 284-287.	0.2	0
17	CIB2 and CIB3 are auxiliary subunits of the mechanotransduction channel of hair cells. Neuron, 2021, 109, 2131-2149.e15.	3.8	35
18	Sorting of cadherinâ€"catenin-associated proteins into individual clusters. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14

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19	Antibody screening at reduced <scp>pH</scp> enables preferential selection of potently neutralizing antibodies targeting <scp>SARSâ€CoV</scp>â€2. AIChE Journal, 2021, 67, e17440.	1.8	4
20	Paired heavy- and light-chain signatures contribute to potent SARS-CoV-2 neutralization in public antibody responses. Cell Reports, 2021, 37, 109771.	2.9	38
21	Neutralizing antibody 5-7 defines a distinct site of vulnerability in SARS-CoV-2 spike N-terminal domain. Cell Reports, 2021, 37, 109928.	2.9	52
22	Synaptogenic activity of the axon guidance molecule Robo2 underlies hippocampal circuit function. Cell Reports, 2021, 37, 109828.	2.9	18
23	Structural basis of glycan276-dependent recognition by HIV-1 broadly neutralizing antibodies. Cell Reports, 2021, 37, 109922.	2.9	5
24	Extended antibody-framework-to-antigen distance observed exclusively with broad HIV-1-neutralizing antibodies recognizing glycan-dense surfaces. Nature Communications, 2021, 12, 6470.	5.8	3
25	Extensive dissemination and intraclonal maturation of HIV Env vaccine-induced B cell responses. Journal of Experimental Medicine, 2020, 217, .	4.2	23
26	Structure-Based Design with Tag-Based Purification and In-Process Biotinylation Enable Streamlined Development of SARS-CoV-2 Spike Molecular Probes. Cell Reports, 2020, 33, 108322.	2.9	59
27	DIP/Dpr interactions and the evolutionary design of specificity in protein families. Nature Communications, 2020, 11, 2125.	5.8	26
28	Cryo-EM Structures of SARS-CoV-2 Spike without and with ACE2 Reveal a pH-Dependent Switch to Mediate Endosomal Positioning of Receptor-Binding Domains. Cell Host and Microbe, 2020, 28, 867-879.e5.	5.1	316
29	Antibody Isotype Switching as a Mechanism to Counter HIV Neutralization Escape. Cell Reports, 2020, 33, 108430.	2.9	16
30	Potent neutralizing antibodies against multiple epitopes on SARS-CoV-2 spike. Nature, 2020, 584, 450-456.	13.7	1,337
31	Immune Monitoring Reveals Fusion Peptide Priming to Imprint Cross-Clade HIV-Neutralizing Responses with a Characteristic Early B Cell Signature. Cell Reports, 2020, 32, 107981.	2.9	15
32	Identification and Structure of a Multidonor Class of Head-Directed Influenza-Neutralizing Antibodies Reveal the Mechanism for Its Recurrent Elicitation. Cell Reports, 2020, 32, 108088.	2.9	13
33	The covalent SNAP tag for protein display quantification and low-pH protein engineering. Journal of Biotechnology, 2020, 320, 50-56.	1.9	4
34	VRC34-Antibody Lineage Development Reveals How a Required Rare Mutation Shapes the Maturation of a Broad HIV-Neutralizing Lineage. Cell Host and Microbe, 2020, 27, 531-543.e6.	5.1	23
35	Sensing Actin Dynamics through Adherens Junctions. Cell Reports, 2020, 30, 2820-2833.e3.	2.9	22
36	Family-wide Structural and Biophysical Analysis of Binding Interactions among Non-clustered Î´-Protocadherins. Cell Reports, 2020, 30, 2655-2671.e7.	2.9	35

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37	Adhesion Protein Structure, Molecular Affinities, and Principles of Cell-Cell Recognition. Cell, 2020, 181, 520-535.	13.5	108
38	Structure of Super-Potent Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. Cell Reports, 2020, 31, 107488.	2.9	53
39	VSV-Displayed HIV-1 Envelope Identifies Broadly Neutralizing Antibodies Class-Switched to IgG and IgA. Cell Host and Microbe, 2020, 27, 963-975.e5.	5.1	23
40	Lipocalin-2 is an anorexigenic signal in primates. ELife, 2020, 9, .	2.8	27
41	Ubiquitin-dependent regulation of a conserved DMRT protein controls sexually dimorphic synaptic connectivity and behavior. ELife, 2020, 9, .	2.8	21
42	Trans-endocytosis elicited by nectins transfers cytoplasmic cargo including infectious material between cells. Journal of Cell Science, 2019, 132, .	1.2	25
43	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. Cell, 2019, 178, 567-584.e19.	13.5	106
44	cAb-Rep: A Database of Curated Antibody Repertoires for Exploring Antibody Diversity and Predicting Antibody Prevalence. Frontiers in Immunology, 2019, 10, 2365.	2.2	67
45	TOPAZ: A Positive-Unlabeled Convolutional Neural Network CryoEM Particle Picker that can Pick Any Size and Shape Particle. Microscopy and Microanalysis, 2019, 25, 986-987.	0.2	14
46	Isolation and Structure of an Antibody that Fully Neutralizes Isolate SIVmac239 Reveals Functional Similarity of SIV and HIV Glycan Shields. Immunity, 2019, 51, 724-734.e4.	6.6	13
47	Elasticity of individual protocadherin 15 molecules implicates tip links as the gating springs for hearing. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11048-11056.	3.3	55
48	Consistent elicitation of cross-clade HIV-neutralizing responses achieved in guinea pigs after fusion peptide priming by repetitive envelope trimer boosting. PLoS ONE, 2019, 14, e0215163.	1.1	41
49	Prolonged evolution of the memory B cell response induced by a replicating adenovirus-influenza H5 vaccine. Science Immunology, 2019, 4, .	5.6	40
50	Visualization of clustered protocadherin neuronal self-recognition complexes. Nature, 2019, 569, 280-283.	13.7	86
51	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. Nature Methods, 2019, 16, 1153-1160.	9.0	693
52	Structural Survey of Broadly Neutralizing Antibodies Targeting the HIV-1 Env Trimer Delineates Epitope Categories and Characteristics of Recognition. Structure, 2019, 27, 196-206.e6.	1.6	69
53	Spatial and temporal organization of cadherin in punctate adherens junctions. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4406-E4415.	3.3	46
54	Surface-Matrix Screening Identifies Semi-specific Interactions that Improve Potency of a Near Pan-reactive HIV-1-Neutralizing Antibody. Cell Reports, 2018, 22, 1798-1809.	2.9	52

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55	Pathogenic IgG4 autoantibodies from endemic pemphigus foliaceus recognize a desmoglein-1 conformational epitope. Journal of Autoimmunity, 2018, 89, 171-185.	3.0	19
56	A Neutralizing Antibody Recognizing Primarily N-Linked Glycan Targets the Silent Face of the HIV Envelope. Immunity, 2018, 48, 500-513.e6.	6.6	66
57	Neuron-Subtype-Specific Expression, Interaction Affinities, and Specificity Determinants of DIP/Dpr Cell Recognition Proteins. Neuron, 2018, 100, 1385-1400.e6.	3.8	65
58	Interactions between the Ig-Superfamily Proteins DIP-Î± and Dpr6/10 Regulate Assembly of Neural Circuits. Neuron, 2018, 100, 1369-1384.e6.	3.8	64
59	V2-Directed Vaccine-like Antibodies from HIV-1 Infection Identify an Additional K169-Binding Light Chain Motif with Broad ADCC Activity. Cell Reports, 2018, 25, 3123-3135.e6.	2.9	23
60	Intrinsic DNA Shape Accounts for Affinity Differences between Hox-Cofactor Binding Sites. Cell Reports, 2018, 24, 2221-2230.	2.9	31
61	Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. Neuron, 2018, 99, 480-492.e5.	3.8	43
62	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. Nature Medicine, 2018, 24, 857-867.	15.2	256
63	Homophilic and Heterophilic Interactions of Type II Cadherins Identify Specificity Groups Underlying Cell-Adhesive Behavior. Cell Reports, 2018, 23, 1840-1852.	2.9	54
64	Routine single particle CryoEM sample and grid characterization by tomography. ELife, 2018, 7, .	2.8	216
65	Positive-unlabeled convolutional neural networks for particle picking in cryo-electron micrographs. , 2018, 10812, 245-247.		12
66	Antibodyomics: bioinformatics technologies for understanding Bâ€cell immunity to <scp>HIV</scp>â€1. Immunological Reviews, 2017, 275, 108-128.	2.8	32
67	Quantification of the Impact of the HIV-1-Glycan Shield on Antibody Elicitation. Cell Reports, 2017, 19, 719-732.	2.9	160
68	Mammalian O-mannosylation of cadherins and plexins is independent of protein O-mannosyltransferases 1 and 2. Journal of Biological Chemistry, 2017, 292, 11586-11598.	1.6	39
69	Free Energy Perturbation Calculation of Relative Binding Free Energy between Broadly Neutralizing Antibodies and the gp120 Glycoprotein of HIV-1. Journal of Molecular Biology, 2017, 429, 930-947.	2.0	82
70	Discovery of an O-mannosylation pathway selectively serving cadherins and protocadherins. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11163-11168.	3.3	83
71	Protocadherin <i>cis</i> -dimer architecture and recognition unit diversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9829-E9837.	3.3	55
72	Structural origins of clustered protocadherin-mediated neuronal barcoding. Seminars in Cell and Developmental Biology, 2017, 69, 140-150.	2.3	36

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73	Gene-Specific Substitution Profiles Describe the Types and Frequencies of Amino Acid Changes during Antibody Somatic Hypermutation. Frontiers in Immunology, 2017, 8, 537.	2.2	82
74	SONAR: A High-Throughput Pipeline for Inferring Antibody Ontogenies from Longitudinal Sequencing of B Cell Transcripts. Frontiers in Immunology, 2016, 7, 372.	2.2	67
75	Effects of Darwinian Selection and Mutability on Rate of Broadly Neutralizing Antibody Evolution during HIV-1 Infection. PLoS Computational Biology, 2016, 12, e1004940.	1.5	35
76	Targeted Isolation of Antibodies Directed against Major Sites of SIV Env Vulnerability. PLoS Pathogens, 2016, 12, e1005537.	2.1	51
77	Structural Basis of Diverse Homophilic Recognition by Clustered Î±- and Î²-Protocadherins. Neuron, 2016, 90, 709-723.	3.8	87
78	Induction of HIV Neutralizing Antibody Lineages in Mice with Diverse Precursor Repertoires. Cell, 2016, 166, 1471-1484.e18.	13.5	198
79	Structure of the STRA6 receptor for retinol uptake. Science, 2016, 353, .	6.0	103
80	Vaccine-Induced Antibodies that Neutralize Group 1 and Group 2 Influenza A Viruses. Cell, 2016, 166, 609-623.	13.5	270
81	Identification of a CD4-Binding-Site Antibody to HIV that Evolved Near-Pan Neutralization Breadth. Immunity, 2016, 45, 1108-1121.	6.6	304
82	Structural basis of adhesive binding by desmocollins and desmogleins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7160-7165.	3.3	137
83	Structure and Function of Cadherin Extracellular Regions. , 2016, , 71-91.		2
84	Structure of the polyisoprenyl-phosphate glycosyltransferase GtrB and insights into the mechanism of catalysis. Nature Communications, 2016, 7, 10175.	5.8	33
85	Structures of aminoarabinose transferase ArnT suggest a molecular basis for lipid A glycosylation. Science, 2016, 351, 608-612.	6.0	94
86	Maturation Pathway from Germline to Broad HIV-1 Neutralizer of a CD4-Mimic Antibody. Cell, 2016, 165, 449-463.	13.5	305
87	New Member of the V1V2-Directed CAP256-VRC26 Lineage That Shows Increased Breadth and Exceptional Potency. Journal of Virology, 2016, 90, 76-91.	1.5	205
88	Molecular basis of sidekick-mediated cell-cell adhesion and specificity. ELife, 2016, 5, .	2.8	36
89	Î³-Protocadherin structural diversity and functional implications. ELife, 2016, 5, .	2.8	54
90	Structural Repertoire of HIV-1-Neutralizing Antibodies Targeting the CD4 Supersite in 14 Donors. Cell, 2015, 161, 1280-1292.	13.5	305

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91	E-cadherin junction formation involves an active kinetic nucleation process. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10932-10937.	3.3	84
92	Structural basis for phosphatidylinositol-phosphate biosynthesis. Nature Communications, 2015, 6, 8505.	5.8	43
93	Quality and quantity of T _{FH} cells are critical for broad antibody development in SHIV _{AD8} infection. Science Translational Medicine, 2015, 7, 298ra120.	5.8	119
94	Crystal structure, conformational fixation and entry-related interactions of mature ligand-free HIV-1 Env. Nature Structural and Molecular Biology, 2015, 22, 522-531.	3.6	333
95	Analysis of immunoglobulin transcripts and hypermutation following SHIVAD8 infection and protein-plus-adjuvant immunization. Nature Communications, 2015, 6, 6565.	5.8	77
96	Maturation and Diversity of the VRC01-Antibody Lineage over 15 Years of Chronic HIV-1 Infection. Cell, 2015, 161, 470-485.	13.5	226
97	Î±-Cateninâ€“mediated cadherin clustering couples cadherin and actin dynamics. Journal of Cell Biology, 2015, 210, 647-661.	2.3	42
98	Molecular Logic of Neuronal Self-Recognition through Protocadherin Domain Interactions. Cell, 2015, 163, 629-642.	13.5	141
99	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. Nature, 2014, 509, 55-62.	13.7	681
100	Strain Specific Anti-HIV Antibody Evolution during Acute Infection and Viral Escape. AIDS Research and Human Retroviruses, 2014, 30, A210-A210.	0.5	1
101	Enhanced Potency of a Broadly Neutralizing HIV-1 Antibody <i>In Vitro</i> Improves Protection against Lentiviral Infection <i>In Vivo</i>. Journal of Virology, 2014, 88, 12669-12682.	1.5	248
102	Structural and energetic determinants of adhesive binding specificity in type I cadherins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4175-84.	3.3	78
103	Single-Cell Identity Generated by Combinatorial Homophilic Interactions between Î±, Î², and Î³ Protocadherins. Cell, 2014, 158, 1045-1059.	13.5	190
104	Structural basis for catalysis in a CDP-alcohol phosphotransferase. Nature Communications, 2014, 5, 4068.	5.8	42
105	Cadherin-11 in poor prognosis malignancies and rheumatoid arthritis: common target, common therapies. Oncotarget, 2014, 5, 1458-1474.	0.8	52
106	Multidonor Analysis Reveals Structural Elements, Genetic Determinants, and Maturation Pathway for HIV-1 Neutralization by VRC01-Class Antibodies. Immunity, 2013, 39, 245-258.	6.6	332
107	Co-evolution of a broadly neutralizing HIV-1 antibody and founder virus. Nature, 2013, 496, 469-476.	13.7	961
108	Delineating Antibody Recognition in Polyclonal Sera from Patterns of HIV-1 Isolate Neutralization. Science, 2013, 340, 751-756.	6.0	213

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109	De novo identification of VRC01 class HIV-1â€“neutralizing antibodies by next-generation sequencing of B-cell transcripts. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4088-97.	3.3	105
110	Crystal structures of <i>Drosophila</i> N-cadherin ectodomain regions reveal a widely used class of Ca ²⁺ -free interdomain linkers. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E127-34.	3.3	40
111	Nectin ectodomain structures reveal a canonical adhesive interface. Nature Structural and Molecular Biology, 2012, 19, 906-915.	3.6	104
112	Complementary Chimeric Isoforms Reveal Dscam1 Binding Specificity InÂVivo. Neuron, 2012, 74, 261-268.	3.8	32
113	Somatic populations of PGT135â€“137 HIV-1-neutralizing antibodies identified by 454 pyrosequencing and bioinformatic. Frontiers in Microbiology, 2012, 3, 315.	1.5	70
114	Structures from Anomalous Diffraction of Native Biological Macromolecules. Science, 2012, 336, 1033-1037.	6.0	154
115	Thinking outside the cell: how cadherins drive adhesion. Trends in Cell Biology, 2012, 22, 299-310.	3.6	296
116	Focused Evolution of HIV-1 Neutralizing Antibodies Revealed by Structures and Deep Sequencing. Science, 2011, 333, 1593-1602.	6.0	788
117	Structure and Binding Mechanism of Vascular Endothelial Cadherin: A Divergent Classical Cadherin. Journal of Molecular Biology, 2011, 408, 57-73.	2.0	76
118	Crystal Structure of the Ligand Binding Domain of Netrin G2. Journal of Molecular Biology, 2011, 414, 723-734.	2.0	19
119	Molecular design principles underlying Î²-strand swapping in the adhesive dimerization of cadherins. Nature Structural and Molecular Biology, 2011, 18, 693-700.	3.6	101
120	The Extracellular Architecture of Adherens Junctions Revealed by Crystal Structures of Type I Cadherins. Structure, 2011, 19, 244-256.	1.6	347
121	Transforming binding affinities from three dimensions to two with application to cadherin clustering. Nature, 2011, 475, 510-513.	13.7	204
122	T-cadherin structures reveal a novel adhesive binding mechanism. Nature Structural and Molecular Biology, 2010, 17, 339-347.	3.6	118
123	Two-step adhesive binding by classical cadherins. Nature Structural and Molecular Biology, 2010, 17, 348-357.	3.6	184
124	Cooperativity between <i>trans</i> and <i>cis</i> interactions in cadherin-mediated junction formation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17592-17597.	3.3	128
125	Structural Basis for Broad and Potent Neutralization of HIV-1 by Antibody VRC01. Science, 2010, 329, 811-817.	6.0	1,050
126	Structure and Biochemistry of Cadherins and Catenins. Cold Spring Harbor Perspectives in Biology, 2009, 1, a003053-a003053.	2.3	373

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127	Tâ€cadherin, an Adiponectin Receptor in the Cardiovascular System. FASEB Journal, 2009, 23, 506.8.	0.2	2
128	Dynamic Properties of a Type II Cadherin Adhesive Domain: Implications for the Mechanism of Strand-Swapping of Classical Cadherins. Structure, 2008, 16, 1195-1205.	1.6	55
129	Sequence and Structural Determinants of Strand Swapping in Cadherin Domains: Do All Cadherins Bind Through the Same Adhesive Interface?. Journal of Molecular Biology, 2008, 378, 954-968.	2.0	52
130	Adhesion Molecules in the Nervous System: Structural Insights into Function and Diversity. Annual Review of Neuroscience, 2007, 30, 451-474.	5.0	175
131	Self-Recognition at the Atomic Level: Understanding the Astonishing Molecular Diversity of Homophilic Dscams. Neuron, 2007, 56, 10-13.	3.8	8
132	Adiposeâ€Selective Overexpression of CGIâ€58 Does Not Alter Lipolysis or Protect Against Dietâ€Induced Obesity. FASEB Journal, 2007, 21, A704.	0.2	0
133	Type II Cadherin Ectodomain Structures: Implications for Classical Cadherin Specificity. Cell, 2006, 124, 1255-1268.	13.5	252
134	Identification of a transiently exposed VE-cadherin epitope that allows for specific targeting of an antibody to the tumor neovasculature. Blood, 2005, 105, 4337-4344.	0.6	91
135	Crystal structures of the tryptophan repressor binding protein WrbA and complexes with flavin mononucleotide. Protein Science, 2005, 14, 3004-3012.	3.1	23
136	Specificity of cell-cell adhesion by classical cadherins: Critical role for low-affinity dimerization through Â-strand swapping. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8531-8536.	3.3	126
137	ADAM and Eph: How Ephrin-Signaling Cells Become Detached. Cell, 2005, 123, 185-187.	13.5	18
138	Laura Mgrdichian National Synchrotron Light Source, Brookhaven National Laboratory. Synchrotron Radiation News, 2004, 17, 13-29.	0.2	0
139	Cadherin-mediated cellâ€"cell adhesion: sticking together as a family. Current Opinion in Structural Biology, 2003, 13, 690-698.	2.6	195
140	Practical aspects of membrane protein crystallography: From overexpression to crystallization. Synchrotron Radiation News, 2002, 15, 17-18.	0.2	2
141	C-Cadherin Ectodomain Structure and Implications for Cell Adhesion Mechanisms. Science, 2002, 296, 1308-1313.	6.0	616
142	Functional Cis-Heterodimers of N- and R-Cadherins. Journal of Cell Biology, 2000, 148, 579-590.	2.3	178
143	Molecular Modification of N-Cadherin in Response to Synaptic Activity. Neuron, 2000, 25, 93-107.	3.8	301
144	The adhesive binding site of cadherins revisited. Biophysical Chemistry, 1999, 82, 157-163.	1.5	36

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145	The Diversity of Cadherins and Implications for a Synaptic Adhesive Code in the CNS. Neuron, 1999, 23, 427-430.	3.8	206
146	Structure-Function Analysis of Cell Adhesion by Neural (N-) Cadherin. Neuron, 1998, 20, 1153-1163.	3.8	312
147	Crystal Structure of the Extracellular Domain from P0, the Major Structural Protein of Peripheral Nerve Myelin. Neuron, 1996, 17, 435-449.	3.8	404
148	Structural basis of cell-cell adhesion by cadherins. Nature, 1995, 374, 327-337.	13.7	1,124
149	DNA and RNA: NMR studies of conformations and dynamics in solution. Quarterly Reviews of Biophysics, 1987, 20, 35-112.	2.4	177
150	Sequence-dependent conformations of DNA duplexes: The TATA segment of the d(G-G-T-A-T-A-C-C) duplex in aqueous solution. Biopolymers, 1986, 25, 693-706.	1.2	24
151	Sequence-dependent recognition of DNA duplexes: Netropsin complexation to the TATA site of the d(G-G-T-A-T-A-C-C) duplex in aqueous solution. Biopolymers, 1986, 25, 707-727.	1.2	34
152	Paired Heavy and Light Chain Signatures Contribute to Potent SARS-CoV-2 Neutralization in Public Antibody Responses. SSRN Electronic Journal, 0, , .	0.4	1