

Peter H Von Hippel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

176 papers	22,192 citations	68 h-index	148 g-index
181 ext. papers	23,105 ext. citations	7.9 avg, IF	6.65 L-index

#	Paper	IF	Citations
176	Temperature-dependent local conformations and conformational distributions of cyanine dimer labeled single-stranded-double-stranded DNA junctions by 2D fluorescence spectroscopy.. <i>Journal of Chemical Physics</i> , 2022 , 156, 045101	3.9	4
175	Mapping DNA conformations and interactions within the binding cleft of bacteriophage T4 single-stranded DNA binding protein (gp32) at single nucleotide resolution. <i>Nucleic Acids Research</i> , 2021 , 49, 916-927	20.1	2
174	Dinucleotides as simple models of the base stacking-unstacking component of DNA breathing mechanisms. <i>Nucleic Acids Research</i> , 2021 , 49, 1872-1885	20.1	3
173	Submillisecond Conformational Transitions of Short Single-Stranded DNA Lattices by Photon Correlation Single-Molecule FRET Resonance Energy Transfer. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 9426-9440	3.4	5
172	Measuring local conformations and conformational disorder of (Cy3) dimer labeled DNA fork junctions using absorbance, circular dichroism and two-dimensional fluorescence spectroscopy. <i>Faraday Discussions</i> , 2019 , 216, 211-235	3.6	14
171	Local DNA Base Conformations and Ligand Intercalation in DNA Constructs Containing Optical Probes. <i>Biophysical Journal</i> , 2019 , 117, 1101-1115	2.9	2
170	The Many Roles of Binding Cooperativity in the Control of DNA Replication. <i>Biophysical Journal</i> , 2019 , 117, 2043-2046	2.9	4
169	Using microsecond single-molecule FRET to determine the assembly pathways of T4 ssDNA binding protein onto model DNA replication forks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E3612-E3621	11.5	11
168	Changing the Stability of Macromolecular Surfaces by Manipulating the Aqueous Environment. <i>Biophysical Journal</i> , 2016 , 111, 1817-1820	2.9	2
167	Using Multiorder Time-Correlation Functions (TCFs) To Elucidate Biomolecular Reaction Pathways from Microsecond Single-Molecule Fluorescence Experiments. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 13003-13016	3.4	9
166	Single-molecule FRET studies of the cooperative and non-cooperative binding kinetics of the bacteriophage T4 single-stranded DNA binding protein (gp32) to ssDNA lattices at replication fork junctions. <i>Nucleic Acids Research</i> , 2016 , 44, 10691-10710	20.1	6
165	John Schellman and the birth of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6776-7	11.5	
164	Sequence-Dependent Conformational Heterogeneity and Proton-Transfer Reactivity of the Fluorescent Guanine Analogue 6-Methyl Isoxanthopterin (6-MI) in DNA. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 12798-807	3.4	3
163	Mapping the interactions of the single-stranded DNA binding protein of bacteriophage T4 (gp32) with DNA lattices at single nucleotide resolution: gp32 monomer binding. <i>Nucleic Acids Research</i> , 2015 , 43, 9276-90	20.1	15
162	Mapping the interactions of the single-stranded DNA binding protein of bacteriophage T4 (gp32) with DNA lattices at single nucleotide resolution: polynucleotide binding and cooperativity. <i>Nucleic Acids Research</i> , 2015 , 43, 9291-305	20.1	8
161	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. <i>PLoS ONE</i> , 2015 , 10, e0126420	3.7	55
160	Increased subtlety of transcription factor binding increases complexity of genome regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17344-5	11.5	7

159	Internally labeled Cy3/Cy5 DNA constructs show greatly enhanced photo-stability in single-molecule FRET experiments. <i>Nucleic Acids Research</i> , 2014 , 42, 5967-77	20.1	34
158	Old and new approaches to DNA breathing: Comments on "Fluctuations in the DNA double helix: A critical review" by M.D. Frank-Kamenetskii and S. Prakash. <i>Physics of Life Reviews</i> , 2014 , 11, 176-7	2.1	2
157	Fifty years of DNA "breathing": Reflections on old and new approaches. <i>Biopolymers</i> , 2013 , 99, 923-54	2.2	72
156	A single-molecule view of the assembly pathway, subunit stoichiometry, and unwinding activity of the bacteriophage T4 primosome (helicase-primase) complex. <i>Biochemistry</i> , 2013 , 52, 3157-70	3.2	22
155	Single-molecule FRET and linear dichroism studies of DNA breathing and helicase binding at replication fork junctions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17320-5	11.5	62
154	Solution conformation of 2-aminopurine (2-AP) dinucleotide determined by ultraviolet 2D fluorescence spectroscopy (UV-2D FS). <i>New Journal of Physics</i> , 2013 , 15,	2.9	44
153	Electronic transition moments of 6-methyl isoxanthopterin--a fluorescent analogue of the nucleic acid base guanine. <i>Nucleic Acids Research</i> , 2013 , 41, 995-1004	20.1	8
152	Probing the nucleic acid binding modes of the single-stranded DNA binding protein of the bacteriophage T4 replication complex. <i>FASEB Journal</i> , 2013 , 27, 541.2	0.9	
151	Breathing fluctuations in position-specific DNA base pairs are involved in regulating helicase movement into the replication fork. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14428-33	11.5	29
150	Characterization of the 6-methyl isoxanthopterin (6-MI) base analog dimer, a spectroscopic probe for monitoring guanine base conformations at specific sites in nucleic acids. <i>Nucleic Acids Research</i> , 2012 , 40, 1191-202	20.1	26
149	Assembly and subunit stoichiometry of the functional helicase-primase (primosome) complex of bacteriophage T4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13596-601	11.5	13
148	Development of a "modular" scheme to describe the kinetics of transcript elongation by RNA polymerase. <i>Biophysical Journal</i> , 2011 , 101, 1155-65	2.9	9
147	Fitting experimental transcription data with a comprehensive template-dependent modular kinetic model. <i>Biophysical Journal</i> , 2011 , 101, 1166-74	2.9	4
146	DNA conformational changes at the primer-template junction regulate the fidelity of replication by DNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17980-5	11.5	27
145	Local conformations and competitive binding affinities of single- and double-stranded primer-template DNA at the polymerization and editing active sites of DNA polymerases. <i>Journal of Biological Chemistry</i> , 2009 , 284, 17180-17193	5.4	19
144	The protein factors MBNL1 and U2AF65 bind alternative RNA structures to regulate splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 9203-8	11.5	103
143	Spectroscopic studies of position-specific DNA "breathing" fluctuations at replication forks and primer-template junctions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 4231-6	11.5	65
142	DNA models of trinucleotide frameshift deletions: the formation of loops and bulges at the primer-template junction. <i>Nucleic Acids Research</i> , 2009 , 37, 1682-9	20.1	18

141	Solution conformations of primer DNA shuttling between the polymerase and 3'-5' exonuclease sites of DNA polymerase I. <i>FASEB Journal</i> , 2009 , 23, 481.7	0.9	
140	The antitermination activity of bacteriophage lambda N protein is controlled by the kinetics of an RNA-looping-facilitated interaction with the transcription complex. <i>Journal of Molecular Biology</i> , 2008 , 384, 87-108	6.5	8
139	Monitoring RNA transcription in real time by using surface plasmon resonance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 3315-20	11.5	25
138	Multiple ATP binding is required to stabilize the "activated" (clamp open) clamp loader of the T4 DNA replication complex. <i>Journal of Biological Chemistry</i> , 2008 , 283, 28338-53	5.4	20
137	Direct spectroscopic study of reconstituted transcription complexes reveals that intrinsic termination is driven primarily by thermodynamic destabilization of the nucleic acid framework. <i>Journal of Biological Chemistry</i> , 2008 , 283, 3537-3549	5.4	25
136	From "simple" DNA-protein interactions to the macromolecular machines of gene expression. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007 , 36, 79-105		146
135	Transcriptional pausing caught in the act. <i>Cell</i> , 2006 , 125, 1027-8	56.2	3
134	Mapping the conformation of the nucleic acid framework of the T7 RNA polymerase elongation complex in solution using low-energy CD and fluorescence spectroscopy. <i>Journal of Molecular Biology</i> , 2006 , 360, 800-13	6.5	24
133	A fluorescent assay to compare the effect of NTP concentration and temperature on transcript elongation by E. coli RNA polymerase.. <i>FASEB Journal</i> , 2006 , 20, A68	0.9	
132	Mechanistic studies of the T4 DNA (gp41) replication helicase: functional interactions of the C-terminal Tails of the helicase subunits with the T4 (gp59) helicase loader protein. <i>Journal of Molecular Biology</i> , 2005 , 347, 257-75	6.5	11
131	A quantitative description of the binding states and in vitro function of antitermination protein N of bacteriophage lambda. <i>Journal of Molecular Biology</i> , 2005 , 348, 1039-57	6.5	5
130	Thinking quantitatively about transcriptional regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 221-32	48.7	131
129	Investigating local conformations of double-stranded DNA by low-energy circular dichroism of pyrrolo-cytosine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7169-73	11.5	24
128	Low energy CD of RNA hairpin unveils a loop conformation required for lambdaN antitermination activity. <i>Journal of Biological Chemistry</i> , 2005 , 280, 32177-83	5.4	20
127	Assembly of an RNA-protein complex. Binding of NusB and NusE (S10) proteins to boxA RNA nucleates the formation of the antitermination complex involved in controlling rRNA transcription in Escherichia coli. <i>Journal of Biological Chemistry</i> , 2005 , 280, 36397-408	5.4	54
126	Low-energy circular dichroism of 2-aminopurine dinucleotide as a probe of local conformation of DNA and RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 3426-31	11.5	52
125	Graduate student days at MIT. <i>Biophysical Chemistry</i> , 2004 , 108, 17-22	3.5	0
124	Biochemistry. Completing the view of transcriptional regulation. <i>Science</i> , 2004 , 305, 350-2	33.3	46

123	Function and assembly of the bacteriophage T4 DNA replication complex: interactions of the T4 polymerase with various model DNA constructs. <i>Journal of Biological Chemistry</i> , 2003 , 278, 25435-47	5.4	19
122	Helicase mechanisms and the coupling of helicases within macromolecular machines. Part II: Integration of helicases into cellular processes. <i>Quarterly Reviews of Biophysics</i> , 2003 , 36, 1-69	7	115
121	Macromolecular complexes that unwind nucleic acids. <i>BioEssays</i> , 2003 , 25, 1168-77	4.1	29
120	Reaction pathways in transcript elongation. <i>Biophysical Chemistry</i> , 2002 , 101-102, 401-23	3.5	25
119	Helicase mechanisms and the coupling of helicases within macromolecular machines. Part I: Structures and properties of isolated helicases. <i>Quarterly Reviews of Biophysics</i> , 2002 , 35, 431-78	7	132
118	Active Escherichia coli transcription elongation complexes are functionally homogeneous. <i>Journal of Molecular Biology</i> , 2002 , 322, 505-19	6.5	16
117	Dissection of the ATP-driven reaction cycle of the bacteriophage T4 DNA replication processivity clamp loading system. <i>Journal of Molecular Biology</i> , 2001 , 309, 869-91	6.5	36
116	A general model for nucleic acid helicases and their "coupling" within macromolecular machines. <i>Cell</i> , 2001 , 104, 177-90	56.2	167
115	Molecular mechanisms of the functional coupling of the helicase (gp41) and polymerase (gp43) of bacteriophage T4 within the DNA replication fork. <i>Biochemistry</i> , 2001 , 40, 4459-77	3.2	71
114	Quantitative dissection of transcriptional control system: N-dependent antitermination complex of phage lambda as regulatory paradigm. <i>Methods in Enzymology</i> , 2000 , 323, 1-31	1.7	8
113	Regulation of rho-dependent transcription termination by NusG is specific to the Escherichia coli elongation complex. <i>Biochemistry</i> , 2000 , 39, 5573-85	3.2	72
112	Interactions of bacteriophage T4-coded primase (gp61) with the T4 replication helicase (gp41) and DNA in primosome formation. <i>Journal of Biological Chemistry</i> , 1999 , 274, 27287-98	5.4	29
111	Proposed changes for NIH Center for Scientific Review. Panel on Scientific Boundaries for Review. Center for Scientific Review Advisory Committee, National Institutes of Health. <i>Science</i> , 1999 , 285, 666-733	33.3	6
110	Determinants of the stability of transcription elongation complexes: interactions of the nascent RNA with the DNA template and the RNA polymerase. <i>Journal of Molecular Biology</i> , 1999 , 289, 1179-94	6.5	29
109	Rho-dependent termination within the trp t _Q terminator. I. Effects of rho loading and template sequence. <i>Biochemistry</i> , 1998 , 37, 11202-14	3.2	26
108	Rho-dependent termination within the trp t _Q terminator. II. Effects of kinetic competition and rho processivity. <i>Biochemistry</i> , 1998 , 37, 11215-22	3.2	20
107	Effects of reaction conditions on RNA secondary structure and on the helicase activity of Escherichia coli transcription termination factor Rho. <i>Journal of Molecular Biology</i> , 1998 , 279, 713-26	6.5	15
106	Structural analyses of gp45 sliding clamp interactions during assembly of the bacteriophage T4 DNA polymerase holoenzyme. II. The Gp44/62 clamp loader interacts with a single defined face of the sliding clamp ring. <i>Journal of Biological Chemistry</i> , 1997 , 272, 31677-84	5.4	31

105	Structural analyses of gp45 sliding clamp interactions during assembly of the bacteriophage T4 DNA polymerase holoenzyme. I. Conformational changes within the gp44/62-gp45-ATP complex during clamp loading. <i>Journal of Biological Chemistry</i> , 1997 , 272, 31666-76	5.4	41
104	Structural analyses of gp45 sliding clamp interactions during assembly of the bacteriophage T4 DNA polymerase holoenzyme. III. The Gp43 DNA polymerase binds to the same face of the sliding clamp as the clamp loader. <i>Journal of Biological Chemistry</i> , 1997 , 272, 31685-92	5.4	30
103	Kinetics of the RNA-DNA helicase activity of Escherichia coli transcription termination factor rho. 2. Processivity, ATP consumption, and RNA binding. <i>Biochemistry</i> , 1997 , 36, 7993-8004	3.2	46
102	Complexes of N antitermination protein of phage lambda with specific and nonspecific RNA target sites on the nascent transcript. <i>Biochemistry</i> , 1997 , 36, 1514-24	3.2	66
101	Kinetics of the RNA-DNA helicase activity of Escherichia coli transcription termination factor rho. 1. Characterization and analysis of the reaction. <i>Biochemistry</i> , 1997 , 36, 7980-92	3.2	34
100	Transcriptional activation via DNA-looping: visualization of intermediates in the activation pathway of E. coli RNA polymerase x sigma 54 holoenzyme by scanning force microscopy. <i>Journal of Molecular Biology</i> , 1997 , 270, 125-38	6.5	138
99	Regulation of the elongation-termination decision at intrinsic terminators by antitermination protein N of phage lambda. <i>Journal of Molecular Biology</i> , 1997 , 273, 797-813	6.5	50
98	Assembly of the N-dependent antitermination complex of phage lambda: NusA and RNA bind independently to different unfolded domains of the N protein. <i>Journal of Molecular Biology</i> , 1997 , 274, 160-73	6.5	33
97	Fluorescence monitoring of T4 polymerase holoenzyme accessory protein interactions during loading of the sliding clamp onto the template-primer junction. <i>Journal of Molecular Biology</i> , 1996 , 264, 426-39	6.5	31
96	The kinetic mechanism of formation of the bacteriophage T4 DNA polymerase sliding clamp. <i>Journal of Molecular Biology</i> , 1996 , 264, 440-52	6.5	36
95	Components of multiprotein-RNA complex that controls transcription elongation in Escherichia coli phage lambda. <i>Methods in Enzymology</i> , 1996 , 274, 374-402	1.7	19
94	Specificity mechanisms in the control of transcription. <i>Biophysical Chemistry</i> , 1996 , 59, 231-46	3.5	30
93	The ATP-activated hexameric helicase of bacteriophage T4 (gp41) forms a stable primosome with a single subunit of T4-coded primase (gp61). <i>Journal of Biological Chemistry</i> , 1996 , 271, 19625-31	5.4	37
92	The phage T4-coded DNA replication helicase (gp41) forms a hexamer upon activation by nucleoside triphosphate. <i>Journal of Biological Chemistry</i> , 1995 , 270, 7462-73	5.4	111
91	Using macromolecular crowding agents to identify weak interactions within DNA replication complexes. <i>Methods in Enzymology</i> , 1995 , 262, 466-76	1.7	17
90	Action at a distance: DNA-looping and initiation of transcription. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 500-6	10.3	255
89	Template copying. Passing lanes for polymerases?. <i>Current Biology</i> , 1994 , 4, 333-6	6.3	3
88	Kinetic theory of ATP-driven translocases on one-dimensional polymer lattices. <i>Journal of Molecular Biology</i> , 1994 , 235, 1436-46	6.5	60

87	Kinetic parameters of the translocation of bacteriophage T4 gene 41 protein helicase on single-stranded DNA. <i>Journal of Molecular Biology</i> , 1994 , 235, 1447-58	6.5	76
86	Stability of Escherichia coli transcription complexes near an intrinsic terminator. <i>Journal of Molecular Biology</i> , 1994 , 244, 36-51	6.5	52
85	RNA displacement pathways during transcription from synthetic RNA-DNA bubble duplexes. <i>Biochemistry</i> , 1994 , 33, 340-7	3.2	53
84	Mass Spectrometric Protocol for the Analysis of UV-Crosslinked Protein-Nucleic Acid Complexes. <i>Techniques in Protein Chemistry</i> , 1994 , 27-37		1
83	Betaine can eliminate the base pair composition dependence of DNA melting. <i>Biochemistry</i> , 1993 , 32, 137-44	3.2	245
82	Direct observation of UV-crosslinked protein-nucleic acid complexes by matrix-assisted laser desorption ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1993 , 7, 496-501	2.2	53
81	The elongation-termination decision in transcription. <i>Science</i> , 1992 , 255, 809-12	33.3	76
80	The single-nucleotide addition cycle in transcription: a biophysical and biochemical perspective. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1992 , 21, 379-415		99
79	Structure and function of the bacteriophage T4 DNA polymerase holoenzyme. <i>Biochemistry</i> , 1992 , 31, 8675-90	3.2	105
78	Physical properties of the Escherichia coli transcription termination factor rho. 2. Quaternary structure of the rho hexamer. <i>Biochemistry</i> , 1992 , 31, 121-32	3.2	60
77	Physical properties of the Escherichia coli transcription termination factor rho. 1. Association states and geometry of the rho hexamer. <i>Biochemistry</i> , 1992 , 31, 111-21	3.2	77
76	Cryoelectron microscopic visualization of functional subassemblies of the bacteriophage T4 DNA replication complex. <i>Journal of Molecular Biology</i> , 1992 , 224, 395-412	6.5	67
75	Functional interactions of ligand cofactors with Escherichia coli transcription termination factor rho. I. Binding of ATP. <i>Protein Science</i> , 1992 , 1, 850-60	6.3	56
74	Functional interactions of ligand cofactors with Escherichia coli transcription termination factor rho. II. Binding of RNA. <i>Protein Science</i> , 1992 , 1, 861-73	6.3	41
73	A thermodynamic analysis of RNA transcript elongation and termination in Escherichia coli. <i>Biochemistry</i> , 1991 , 30, 1097-118	3.2	179
72	Structure and assembly of the Escherichia coli transcription termination factor rho and its interaction with RNA. I. Cryoelectron microscopic studies. <i>Journal of Molecular Biology</i> , 1991 , 221, 1127-38	6.5	100
71	Structure and assembly of the Escherichia coli transcription termination factor rho and its interactions with RNA. II. Physical chemical studies. <i>Journal of Molecular Biology</i> , 1991 , 221, 1139-51	6.5	23
70	Escherichia coli sigma 70 and NusA proteins. I. Binding interactions with core RNA polymerase in solution and within the transcription complex. <i>Journal of Molecular Biology</i> , 1991 , 220, 307-24	6.5	120

69	Escherichia coli sigma 70 and NusA proteins. II. Physical properties and self-association states. <i>Journal of Molecular Biology</i> , 1991 , 220, 325-33	6.5	17
68	Laser cross-linking of protein-nucleic acid complexes. <i>Methods in Enzymology</i> , 1991 , 208, 211-36	1.7	71
67	Thermodynamic analysis of the transcription cycle in E. coli. <i>Biophysical Chemistry</i> , 1990 , 37, 239-50	3.5	19
66	Calculation of protein extinction coefficients from amino acid sequence data. <i>Analytical Biochemistry</i> , 1989 , 182, 319-26	3.1	5029
65	UV laser crosslinking of proteins with nucleic acids. <i>Zeitschrift Fur Elektrotechnik Und Elektrochemie</i> , 1989 , 93, 406-410		2
64	Interactions of Escherichia coli transcription termination factor rho with RNA. I. Binding stoichiometries and free energies. <i>Journal of Molecular Biology</i> , 1988 , 199, 609-22	6.5	99
63	Selection of DNA binding sites by regulatory proteins. II. The binding specificity of cyclic AMP receptor protein to recognition sites. <i>Journal of Molecular Biology</i> , 1988 , 200, 709-23	6.5	264
62	Selection of DNA binding sites by regulatory proteins. <i>Trends in Biochemical Sciences</i> , 1988 , 13, 207-11	10.3	98
61	Interactions of Escherichia coli transcription termination factor rho with RNA. II. Electron microscopy and nuclease protection experiments. <i>Journal of Molecular Biology</i> , 1988 , 199, 623-35	6.5	88
60	Selection of DNA binding sites by regulatory proteins. Statistical-mechanical theory and application to operators and promoters. <i>Journal of Molecular Biology</i> , 1987 , 193, 723-50	6.5	554
59	Kinetics of protein-nucleic acid interactions: use of salt effects to probe mechanisms of interaction. <i>Critical Reviews in Biochemistry</i> , 1986 , 19, 191-245		159
58	Cooperative and noncooperative binding of protein ligands to nucleic acid lattices: experimental approaches to the determination of thermodynamic parameters. <i>Biochemistry</i> , 1986 , 25, 1226-40	3.2	177
57	RNA sequence and secondary structure requirements for rho-dependent transcription termination. <i>Nucleic Acids Research</i> , 1985 , 13, 3739-54	20.1	99
56	Diffusion-controlled macromolecular interactions. <i>Annual Review of Biophysics and Biophysical Chemistry</i> , 1985 , 14, 131-60		609
55	Protein-nucleic acid interactions in transcription: a molecular analysis. <i>Annual Review of Biochemistry</i> , 1984 , 53, 389-446	29.1	610
54	On the determination of deoxyribonucleic acid-protein interaction parameters using the nitrocellulose filter-binding assay. <i>Biochemistry</i> , 1983 , 22, 4730-7	3.2	92
53	On the processivity of DNA replication. <i>Journal of Biomolecular Structure and Dynamics</i> , 1983 , 1, 715-27	3.6	43
52	How do genome-regulatory proteins locate their DNA target sites?. <i>Trends in Biochemical Sciences</i> , 1982 , 7, 52-55	10.3	117

51	Autoregulation of gene expression. Quantitative evaluation of the expression and function of the bacteriophage T4 gene 32 (single-stranded DNA binding) protein system. <i>Journal of Molecular Biology</i> , 1982 , 162, 795-818	6.5	98
50	Interactions of bacteriophage T4-coded gene 32 protein with nucleic acids. I. Characterization of the binding interactions. <i>Journal of Molecular Biology</i> , 1981 , 145, 75-104	6.5	310
49	Interactions of bacteriophage T4-coded gene 32 protein with nucleic acids. II. Specificity of binding to DNA and RNA. <i>Journal of Molecular Biology</i> , 1981 , 145, 105-21	6.5	151
48	Interactions of bacteriophage T4-coded gene 32 protein with nucleic acids. III. Binding properties of two specific proteolytic digestion products of the protein (G32P*I and G32P*III). <i>Journal of Molecular Biology</i> , 1981 , 145, 123-38	6.5	90
47	Diffusion-driven mechanisms of protein translocation on nucleic acids. 3. The Escherichia coli lac repressor--operator interaction: kinetic measurements and conclusions. <i>Biochemistry</i> , 1981 , 20, 6961-77	3.2	514
46	Diffusion-driven mechanisms of protein translocation on nucleic acids. 2. The Escherichia coli repressor--operator interaction: equilibrium measurements. <i>Biochemistry</i> , 1981 , 20, 6948-60	3.2	269
45	Diffusion-driven mechanisms of protein translocation on nucleic acids. 1. Models and theory. <i>Biochemistry</i> , 1981 , 20, 6929-48	3.2	1014
44	21 Single-Stranded DNA Binding Proteins. <i>The Enzymes</i> , 1981 , 373-444	2.3	68
43	Physical chemical studies of the structure and function of DNA binding (helix-destabilizing) proteins. <i>Critical Reviews in Biochemistry</i> , 1980 , 7, 247-89		100
42	Nucleic acid binding properties of Escherichia coli ribosomal protein S1. I. Structure and interactions of binding site I. <i>Journal of Molecular Biology</i> , 1978 , 122, 321-38	6.5	99
41	Nucleic acid binding properties of Escherichia coli ribosomal protein S1. II. Co-operativity and specificity of binding site II. <i>Journal of Molecular Biology</i> , 1978 , 122, 339-59	6.5	30
40	The role of DNA structure in genetic regulation. <i>CRC Critical Reviews in Biochemistry</i> , 1977 , 4, 305-40		137
39	Direct measurement of association constants for the binding of Escherichia coli lac repressor to non-operator DNA. <i>Biochemistry</i> , 1977 , 16, 4769-76	3.2	145
38	Formaldehyde as a probe of DNA structure. 3. Equilibrium denaturation of DNA and synthetic polynucleotides. <i>Biochemistry</i> , 1977 , 16, 3267-76	3.2	76
37	Formaldehyde as a probe of DNA structure. r. Mechanism of the initial reaction of Formaldehyde with DNA. <i>Biochemistry</i> , 1977 , 16, 3276-93	3.2	114
36	A boundary sedimentation velocity method for determining nonspecific nucleic acid-protein interaction binding parameters. <i>Analytical Biochemistry</i> , 1977 , 80, 267-81	3.1	25
35	Formaldehyde as a probe of DNA structure. II. Reaction with endocyclic imino groups of DNA bases. <i>Biochemistry</i> , 1975 , 14, 1297-303	3.2	95
34	Formaldehyde as a probe of DNA structure. I. Reaction with exocyclic amino groups of DNA bases. <i>Biochemistry</i> , 1975 , 14, 1281-96	3.2	182

33	Effects of methylation on the stability of nucleic acid conformations: studies at the monomer level. <i>Biochemistry</i> , 1974 , 13, 4143-58	3.2	174
32	Theoretical aspects of DNA-protein interactions: co-operative and non-co-operative binding of large ligands to a one-dimensional homogeneous lattice. <i>Journal of Molecular Biology</i> , 1974 , 86, 469-89	6.5	2609
31	Native collagen has a two-banded structure. <i>Journal of Molecular Biology</i> , 1974 , 83, 1-16	6.5	56
30	Model studies on the effects of neutral salts on the conformational stability of biological macromolecules. I. Ion binding to polyacrylamide and polystyrene columns. <i>Biochemistry</i> , 1973 , 12, 1256-64	3.2	129
29	Model studies on the effects of neutral salts on the conformational stability of biological macromolecules. II. Effects of vicinal hydrophobic groups on the specificity of binding of ions to amide groups. <i>Biochemistry</i> , 1973 , 12, 1264-71	3.2	68
28	Model studies on the effects of neutral salts on the conformational stability of biological macromolecules. 3. Solubility of fatty acid amides in ionic solutions. <i>Biochemistry</i> , 1973 , 12, 1271-8	3.2	27
27	Model studies on the effects of neutral salts on the conformational stability of biological macromolecules. IV. Properties of fatty acid amide micelles. <i>Biochemistry</i> , 1973 , 12, 1278-82	3.2	10
26	DNA-protein interactions. <i>Annual Review of Biochemistry</i> , 1972 , 41, 231-300	29.1	252
25	Equilibrium and kinetic studies of Escherichia coli lac repressor-inducer interactions. <i>Journal of Molecular Biology</i> , 1972 , 66, 143-55	6.5	101
24	Dynamic aspects of native DNA structure: kinetics of the formaldehyde reaction with calf thymus DNA. <i>Journal of Molecular Biology</i> , 1971 , 61, 587-613	6.5	84
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