

Philip E Johnson

List of Publications by Year in descending order

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55
papers

1,789
citations

304743

22
h-index

276875

41
g-index

55
all docs

55
docs citations

55
times ranked

1768
citing authors

#	ARTICLE	IF	CITATIONS
1	The pKa of the General Acid/Base Carboxyl Group of a Glycosidase Cycles during Catalysis: A 13C-NMR Study of <i>Bacillus circulans</i> Xylanase. <i>Biochemistry</i> , 1996, 35, 9958-9966.	2.5	269
2	Structure of the N-Terminal Cellulose-Binding Domain of <i>Cellulomonas fimi</i> CenC Determined by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1996, 35, 14381-14394.	2.5	138
3	A Mechanism for Plus-Strand Transfer Enhancement by the HIV-1 Nucleocapsid Protein during Reverse Transcription. <i>Biochemistry</i> , 2000, 39, 9084-9091.	2.5	94
4	Defining the secondary structural requirements of a cocaine-binding aptamer by a thermodynamic and mutation study. <i>Biophysical Chemistry</i> , 2010, 153, 9-16.	2.8	89
5	Interaction of Soluble Cellooligosaccharides with the N-Terminal Cellulose-Binding Domain of <i>Cellulomonas fimi</i> CenC. 2. NMR and Ultraviolet Absorption Spectroscopy. <i>Biochemistry</i> , 1996, 35, 13895-13906.	2.5	88
6	Defining a Stem Length-Dependent Binding Mechanism for the Cocaine-Binding Aptamer. A Combined NMR and Calorimetry Study. <i>Biochemistry</i> , 2010, 49, 8478-8487.	2.5	85
7	Assembly PCR oligo maker: a tool for designing oligodeoxynucleotides for constructing long DNA molecules for RNA production. <i>Nucleic Acids Research</i> , 2005, 33, W521-W525.	14.5	69
8	Quinine Binding by the Cocaine-Binding Aptamer. Thermodynamic and Hydrodynamic Analysis of High-Affinity Binding of an Off-Target Ligand. <i>Biochemistry</i> , 2013, 52, 8652-8662.	2.5	69
9	RNA recognition by the Vts1p SAM domain. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 177-178.	8.2	61
10	Probing the role of tryptophan residues in a cellulose-binding domain by chemical modification. <i>Protein Science</i> , 1996, 5, 2311-2318.	7.6	55
11	Structure and Binding Specificity of the Second N-Terminal Cellulose-Binding Domain from <i>Cellulomonas fimi</i> Endoglucanase C. <i>Biochemistry</i> , 2000, 39, 2445-2458.	2.5	54
12	The cellulose-binding domains from <i>Cellulomonas fimi</i> β -1,4-glucanase CenC bind nitroxide spin-labeled cellooligosaccharides in multiple orientations. <i>Journal of Molecular Biology</i> , 1999, 287, 609-625.	4.2	49
13	Label-Free Solution-Based Kinetic Study of Aptamer-Small Molecule Interactions by Kinetic Capillary Electrophoresis with UV Detection Revealing How Kinetics Control Equilibrium. <i>Analytical Chemistry</i> , 2011, 83, 8387-8390.	6.5	46
14	Binding Site Analysis of Cellulose Binding Domain CBDN1 from Endoglucanase C of <i>Cellulomonas fimi</i> by Site-Directed Mutagenesis. <i>Biochemistry</i> , 2000, 39, 8844-8852.	2.5	42
15	Structure-affinity relationship of the cocaine-binding aptamer with quinine derivatives. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 2593-2597.	3.0	42
16	The NMR Structure of the Nucleocapsid Protein from the Mouse Mammary Tumor Virus Reveals Unusual Folding of the C-Terminal Zinc Knuckle. <i>Biochemistry</i> , 2000, 39, 1604-1612.	2.5	36
17	Salt-mediated two-site ligand binding by the cocaine-binding aptamer. <i>Nucleic Acids Research</i> , 2017, 45, gkx1294.	14.5	35
18	Optimizing Stem Length To Improve Ligand Selectivity in a Structure-Switching Cocaine-Binding Aptamer. <i>ACS Sensors</i> , 2017, 2, 1539-1545.	7.8	33

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19	Analysis of the interaction between the cocaine-binding aptamer and its ligands using fluorescence spectroscopy. Canadian Journal of Chemistry, 2017, 95, 1253-1260.	1.1	27
20	Engineering a Structure Switching Mechanism into a Steroid-Binding Aptamer and Hydrodynamic Analysis of the Ligand Binding Mechanism. Biochemistry, 2011, 50, 9368-9376.	2.5	25
21	Thermodynamic analysis of cooperative ligand binding by the ATP-binding DNA aptamer indicates a population-shift binding mechanism. Scientific Reports, 2020, 10, 18944.	3.3	25
22	Identification of a novel non-carbohydrate molecule that binds to the ribosomal A-site RNA. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 5987-5990.	2.2	23
23	Kinetic Capillary Electrophoresis with Mass Spectrometry Detection (KCE-MS) Facilitates Label-Free Solution-Based Kinetic Analysis of Protein-Small Molecule Binding. ChemBioChem, 2011, 12, 2551-2554.	2.6	21
24	Calcium Binding by the N-Terminal Cellulose-Binding Domain from Cellulomonas fimi ² -1,4-Glucanase CenC. Biochemistry, 1998, 37, 12772-12781.	2.5	20
25	Kinetic Size-Exclusion Chromatography with Mass Spectrometry Detection: An Approach for Solution-Based Label-Free Kinetic Analysis of Protein-Small Molecule Interactions. Analytical Chemistry, 2014, 86, 10016-10020.	6.5	20
26	Aptamer facilitated purification of functional proteins. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2018, 1073, 201-206.	2.3	20
27	The NMR and X-ray Structures of the Saccharomyces cerevisiae Vts1 SAM Domain Define a Surface for the Recognition of RNA Hairpins. Journal of Molecular Biology, 2006, 356, 274-279.	4.2	19
28	Nanomolar binding affinity of quinine-based antimalarial compounds by the cocaine-binding aptamer. Bioorganic and Medicinal Chemistry, 2018, 26, 5427-5434.	3.0	18
29	Stability and Oligosaccharide Binding of the N1 Cellulose-Binding Domain of Cellulomonas fimi Endoglucanase CenC. Biochemistry, 1998, 37, 3529-3537.	2.5	17
30	Structure of the cytosine-cytosine mismatch in the thymidylate synthase mRNA binding site and analysis of its interaction with the aminoglycoside paromomycin. Rna, 2009, 15, 911-922.	3.5	17
31	Comparison of the free and ligand-bound imino hydrogen exchange rates for the cocaine-binding aptamer. Journal of Biomolecular NMR, 2017, 68, 33-39.	2.8	17
32	Development of a thermal-stable structure-switching cocaine-binding aptamer. Biochimie, 2018, 145, 137-144.	2.6	16
33	Colorimetric detection of catalase and catalase-positive bacteria (E. coli) using silver nanoprisms. Analytical Methods, 2016, 8, 6625-6630.	2.7	13
34	Rapid characterization of folding and binding interactions with thermolabile ligands by DSC. Chemical Communications, 2016, 52, 13471-13474.	4.1	13
35	Cellulose-binding Domains.. Annals of the New York Academy of Sciences, 1996, 799, 418-424.	3.8	12
36	A proof of concept application of aptachain: ligand-induced self-assembly of a DNA aptamer. RSC Advances, 2019, 9, 1690-1695.	3.6	12

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37	A Unique Conformational Distortion Mechanism Drives Lipocalin 2 Binding to Bacterial Siderophores. <i>ACS Chemical Biology</i> , 2020, 15, 234-242.	3.4	12
38	Specific (15)N, NH correlations for residues in (15) N, (13)C and fractionally deuterated proteins that immediately follow methyl-containing amino acids. <i>Journal of Biomolecular NMR</i> , 1997, 10, 283-288.	2.8	11
39	Pre-equilibration kinetic size-exclusion chromatography with mass spectrometry detection (peKSEC-MS) for label-free solution-based kinetic analysis of protein–small molecule interactions. <i>Analyst</i> , 2015, 140, 990-994.	3.5	9
40	Analysis of the role played by ligand-induced folding of the cocaine-binding aptamer in the photochrome aptamer switch assay. <i>Talanta</i> , 2020, 217, 121022.	5.5	9
41	How to Develop and Prove High-Efficiency Selection of Ligands from Oligonucleotide Libraries: A Universal Framework for Aptamers and DNA-Encoded Small-Molecule Ligands. <i>Analytical Chemistry</i> , 2021, 93, 5343-5354.	6.5	9
42	Designed Alteration of Binding Affinity in Structure-Switching Aptamers through the Use of Dangling Nucleotides. <i>Biochemistry</i> , 2020, 59, 663-670.	2.5	8
43	Reduction in Dynamics of Base pair Opening upon Ligand Binding by the Cocaine-Binding Aptamer. <i>Biophysical Journal</i> , 2020, 119, 1147-1156.	0.5	8
44	Visible Fluorescent Light-up Probe for DNA Three-Way Junctions Provides Host–Guest Biosensing Applications. <i>ACS Applied Bio Materials</i> , 2021, 4, 6732-6741.	4.6	8
45	DNA binding by the antimalarial compound artemisinin. <i>Scientific Reports</i> , 2022, 12, 133.	3.3	6
46	Thermodynamic and NMR analysis of inhibitor binding to dihydrofolate reductase. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 8485-8492.	3.0	5
47	The three-dimensional structure of the <i>Moorella thermoacetica</i> selenocysteine insertion sequence RNA hairpin and its interaction with the elongation factor SelB. <i>Rna</i> , 2007, 13, 1948-1956.	3.5	4
48	Enhanced NMR signal detection of imino protons in RNA molecules containing 3' dangling nucleotides. <i>Journal of Biomolecular NMR</i> , 2008, 40, 183-188.	2.8	3
49	HACS1 signaling adaptor protein recognizes a motif in the paired immunoglobulin receptor B cytoplasmic domain. <i>Communications Biology</i> , 2020, 3, 672.	4.4	3
50	Identification of RNA–ligand interactions by affinity electrophoresis. <i>Analytical Biochemistry</i> , 2011, 409, 54-58.	2.4	2
51	Weak Binding of Levamisole by the Cocaine-Binding Aptamer Does Not Interfere with an Aptamer-Based Detection Assay. <i>ACS Omega</i> , 2021, 6, 24209-24217.	3.5	2
52	Quantitative affinity electrophoresis of RNA–small molecule interactions by cross-linking the ligand to acrylamide. <i>Analytical Biochemistry</i> , 2013, 442, 231-236.	2.4	1
53	Identification of a Novel Non-Carbohydrate Molecule that Binds to the Ribosomal A-Site RNA. <i>ChemInform</i> , 2005, 36, no.	0.0	0
54	Finding the Path in an RNA Folding Landscape. <i>Structure</i> , 2010, 18, 1550-1551.	3.3	0

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55	Measuring Biomolecular DSC Profiles with Thermolabile Ligands to Rapidly Characterize Folding and Binding Interactions. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	0