Gregory L Verdine

List of Publications by Year
in descending order

178 papers	21,772 citations	11651 70 h-index	9103 144 g-index
182 all docs	182 docs citations	182 times ranked	16515 citing authors

#	Article	IF	Citations
1	Structure of a Covalently Trapped Catalytic Complex of HIV-1 Reverse Transcriptase: Implications for Drug Resistance. Science, 1998, 282, 1669-1675.	12.6	1,317
2	Activation of Apoptosis in Vivo by a Hydrocarbon-Stapled BH3 Helix. Science, 2004, 305, 1466-1470.	12.6	1,236
3	Structural basis for recognition and repair of the endogenous mutagen 8-oxoguanine in DNA. Nature, 2000, 403, 859-866.	27.8	894
4	An All-Hydrocarbon Cross-Linking System for Enhancing the Helicity and Metabolic Stability of Peptides. Journal of the American Chemical Society, 2000, 122, 5891-5892.	13.7	892
5	The T-cell transcription factor NFATp is a substrate for calcineurin and interacts with Fos and Jun. Nature, 1993, 365, 352-355.	27.8	746
6	Direct inhibition of the NOTCH transcription factor complex. Nature, 2009, 462, 182-188.	27.8	712
7	Regulation of MLL1 H3K4 methyltransferase activity by its core components. Nature Structural and Molecular Biology, 2006, 13, 713-719.	8.2	657
8	Structure of the NF-Î°B p50 homodimer bound to DNA. Nature, 1995, 373, 311-317.	27.8	531
9	Reactivation of the p53 Tumor Suppressor Pathway by a Stapled p53 Peptide. Journal of the American Chemical Society, 2007, 129, 2456-2457.	13.7	498
10	Cloning of a yeast 8-oxoguanine DNA glycosylase reveals the existence of a base-excision DNA-repair protein superfamily. Current Biology, 1996, 6, 968-980.	3.9	447
11	A base-excision DNA-repair protein finds intrahelical lesion bases by fast sliding in contact with DNA. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5752-5757.	7.1	441
12	The crystal structure of Haelll methyltransferase covalently complexed to DNA: An extrahelical cytosine and rearranged base pairing. Cell, 1995, 82, 143-153.	28.9	399
13	Stapled Peptides for Intracellular Drug Targets. Methods in Enzymology, 2012, 503, 3-33.	1.0	370
14	A Stapled BID BH3 Helix Directly Binds and Activates BAX. Molecular Cell, 2006, 24, 199-210.	9.7	347
15	Molecular cloning and overexpression of the human FK506-binding protein FKBP. Nature, 1990, 346, 671-674.	27.8	330
16	The Challenge of Drugging Undruggable Targets in Cancer: Lessons Learned from Targeting BCL-2 Family Members. Clinical Cancer Research, 2007, 13, 7264-7270.	7.0	330
17	Synthesis of all-hydrocarbon stapled Î±-helical peptides by ring-closing olefin metathesis. Nature Protocols, 2011, 6, 761-771.	12.0	328
18	DNA (cytosine-5)-methyltransferases in mouse cells and tissues. studies with a mechanism-based probe. Journal of Molecular Biology, 1997, 270, 385-395.	4.2	321

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19	A mammalian DNA repair enzyme that excises oxidatively damaged guanines maps to a locus frequently lost in lung cancer. Current Biology, 1997, 7, 397-407.	3.9	318
20	Structure of a repair enzyme interrogating undamaged DNA elucidates recognition of damaged DNA. Nature, 2005, 434, 612-618.	27.8	316
21	Nonspecifically bound proteins spin while diffusing along DNA. Nature Structural and Molecular Biology, 2009, 16, 1224-1229.	8.2	297
22	Induced Helix in the VP16 Activation Domain upon Binding to a Human TAF. Science, 1997, 277, 1310-1313.	12.6	293
23	Structural basis for removal of adenine mispaired with 8-oxoguanine by MutY adenine DNA glycosylase. Nature, 2004, 427, 652-656.	27.8	293
24	Crystal Structure of a Human Alkylbase-DNA Repair Enzyme Complexed to DNA. Cell, 1998, 95, 249-258.	28.9	284
25	Structural Basis for the Excision Repair of Alkylation-Damaged DNA. Cell, 1996, 86, 321-329.	28.9	258
26	DNA methyltransferases. Current Opinion in Cell Biology, 1994, 6, 380-389.	5.4	251
27	Control of phosphorothioate stereochemistry substantially increases the efficacy of antisense oligonucleotides. Nature Biotechnology, 2017, 35, 845-851.	17.5	246
28	Structure of the Stapled p53 Peptide Bound to Mdm2. Journal of the American Chemical Society, 2012, 134, 103-106.	13.7	222
29	Inhibition of oncogenic Wnt signaling through direct targeting of Î²-catenin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17942-17947.	7.1	221
30	Histone H3 recognition and presentation by the WDR5 module of the MLL1 complex. Nature Structural and Molecular Biology, 2006, 13, 704-712.	8.2	217
31	Identification of a new uracil-DNA glycosylase family by expression cloning using synthetic inhibitors. Current Biology, 1999, 9, 174-185.	3.9	200
32	Nucleotide-dependent Domain Movement in the ATPase Domain of a Human Type IIA DNA Topoisomerase. Journal of Biological Chemistry, 2005, 280, 37041-37047.	3.4	191
33	Towards understanding cell penetration by stapled peptides. MedChemComm, 2015, 6, 111-119.	3.4	183
34	Structure of a DNA Glycosylase Searching for Lesions. Science, 2006, 311, 1153-1157.	12.6	180
35	Structure of a trapped endonuclease III-DNA covalent intermediate. EMBO Journal, 2003, 22, 3461-3471.	7.8	177
36	Non-genotoxic conditioning for hematopoietic stem cell transplantation using a hematopoietic-cell-specific internalizing immunotoxin. Nature Biotechnology, 2016, 34, 738-745.	17.5	176

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37	DNA glycosylase recognition and catalysis. Current Opinion in Structural Biology, 2004, 14, 43-49.	5.7	172
38	DNA Lesion Recognition by the Bacterial Repair Enzyme MutM. Journal of Biological Chemistry, 2003, 278, 51543-51548.	3.4	169
39	Crystal structure of Staphylococcus aureus tRNA adenosine deaminase TadA in complex with RNA. Nature Structural and Molecular Biology, 2006, 13, 153-159.	8.2	151
40	Product-assisted catalysis in base-excision DNA repair. Nature Structural and Molecular Biology, 2003, 10, 204-211.	8.2	148
41	Stitched Î±-Helical Peptides via Bis Ring-Closing Metathesis. Journal of the American Chemical Society, 2014, 136, 12314-12322.	13.7	137
42	Encounter and extrusion of an intrahelical lesion by a DNA repair enzyme. Nature, 2009, 462, 762-766.	27.8	129
43	Structure and Specificity of the Vertebrate Anti-Mutator Uracil-DNA Glycosylase SMUG1. Molecular Cell, 2003, 11, 1647-1659.	9.7	127
44	Synthesis of functionally tethered oligodeoxynucleotides by the convertible nucleoside approach. Journal of Organic Chemistry, 1990, 55, 5931-5933.	3.2	122
45	A Chemical Method for Site-Specific Modification of RNA:Â The Convertible Nucleoside Approach. Journal of the American Chemical Society, 1997, 119, 7423-7433.	13.7	118
46	The leucine zipper domain controls the orientation of AP-1 in the NFATÂ·AP-1Â·DNA complex. Chemistry and Biology, 1996, 3, 981-991.	6.0	117
47	Covalent Trapping of Protein-DNA Complexes. Annual Review of Biochemistry, 2003, 72, 337-366.	11.1	113
48	Base Excision Repair. Advances in Protein Chemistry, 2004, 69, 1-41.	4.4	112
49	Disulfide-crosslinked oligonucleotides. Journal of the American Chemical Society, 1991, 113, 4000-4002.	13.7	108
50	Engineering tethered DNA molecules by the convertible nucleoside approach. Tetrahedron, 1991, 47, 2603-2616.	1.9	108
51	Introduction of All-Hydrocarbon <i>i</i>,<i>i</i>+3 Staples into Î±-Helices via Ring-Closing Olefin Metathesis. Organic Letters, 2010, 12, 3046-3049.	4.6	106
52	All-Atom Model for Stabilization of Î±-Helical Structure in Peptides by Hydrocarbon Staples. Journal of the American Chemical Society, 2009, 131, 4622-4627.	13.7	104
53	Unusual Rel-like architecture in the DNA-binding domain of the transcription factor NFATc. Nature, 1997, 385, 172-176.	27.8	103
54	Structural and Biochemical Exploration of a Critical Amino Acid in Human 8-Oxoguanine Glycosylaseâ€,â€¡. Biochemistry, 2003, 42, 1564-1572.	2.5	103

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55	Solution Structure of the Core NFATC1/DNA Complex. Cell, 1998, 92, 687-696.	28.9	101
56	Structural insights into lesion recognition and repair by the bacterial 8-oxoguanine DNA glycosylase MutM. , 2002, 9, 544-52.		100
57	Direct Visualization of a DNA Glycosylase Searching for Damage. Chemistry and Biology, 2002, 9, 345-350.	6.0	95
58	Specific Binding of a Designed Pyrrolidine Abasic Site Analog to Multiple DNA Glycosylases. Journal of Biological Chemistry, 1998, 273, 8592-8597.	3.4	93
59	Molecular basis of bacterial resistance to organomercurial and inorganic mercuric salts. FASEB Journal, 1988, 2, 124-130.	0.5	92
60	How do DNA repair proteins locate damaged bases in the genome?. Chemistry and Biology, 1997, 4, 329-334.	6.0	90
61	Synthesis and characterization of disulfide cross-linked oligonucleotides. Journal of the American Chemical Society, 1993, 115, 9006-9014.	13.7	86
62	DNA methylation through a locally unpaired intermediate. Journal of the American Chemical Society, 1993, 115, 12583-12584.	13.7	85
63	A Superhelical Spiral in the Escherichia coli DNA Gyrase A C-terminal Domain Imparts Unidirectional Supercoiling Bias. Journal of Biological Chemistry, 2005, 280, 26177-26184.	3.4	83
64	A Synthetic Library of Cell-Permeable Molecules. Journal of the American Chemical Society, 2001, 123, 398-408.	13.7	82
65	Crystal Structure of Bacillus stearothermophilus UvrA Provides Insight into ATP-Modulated Dimerization, UvrB Interaction, and DNA Binding. Molecular Cell, 2008, 29, 122-133.	9.7	82
66	Atomic substitution reveals the structural basis for substrate adenine recognition and removal by adenine DNA glycosylase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18497-18502.	7.1	82
67	Repair of oxidatively damaged guanine in Saccharomyces cerevisiae by an alternative pathway. Current Biology, 1998, 8, 393-404.	3.9	79
68	Coupling of Substrate Recognition and Catalysis by a Human Base-Excision DNA Repair Protein. Journal of the American Chemical Society, 2001, 123, 359-360.	13.7	79
69	The flip side of DNA methylation. Cell, 1994, 76, 197-200.	28.9	73
70	A Methylation-Dependent Electrostatic Switch Controls DNA Repair and Transcriptional Activation by E. coli Ada. Molecular Cell, 2005, 20, 117-129.	9.7	73
71	Stereochemical effects of all-hydrocarbon tethers in i,i+4 stapled peptides. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 2533-2536.	2.2	73
72	Integration Requires a Specific Interaction of the Donor DNA Terminal 5â€²-Cytosine with Glutamine 148 of the HIV-1 Integrase Flexible Loop. Journal of Biological Chemistry, 2006, 281, 461-467.	3.4	69

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73	The amazing demethylase. Nature, 1999, 397, 568-569.	27.8	68
74	Structure of Human Cytidine Deaminase Bound to a Potent Inhibitor. Journal of Medicinal Chemistry, 2005, 48, 658-660.	6.4	67
75	All-hydrocarbon stapled peptides as Synthetic Cell-Accessible Mini-Proteins. Drug Discovery Today: Technologies, 2012, 9, e41-e47.	4.0	65
76	Mutational separation of DNA binding from catalysis in a DNA cytosine methyltransferase. Journal of the American Chemical Society, 1993, 115, 5318-5319.	13.7	64
77	Only one of the two DNA-bound orientations of AP-1 found in solution cooperates with NFATp. Current Biology, 1995, 5, 882-889.	3.9	63
78	Trapping of a catalytic HIV reverse transcriptaseÂ·template:primer complex through a disulfide bond. Chemistry and Biology, 2000, 7, 355-364.	6.0	63
79	Structural Characterization of Human 8-Oxoguanine DNA Glycosylase Variants Bearing Active Site Mutations. Journal of Biological Chemistry, 2007, 282, 9182-9194.	3.4	63
80	Modifying the helical structure of DNA by design: recruitment of an architecture-specific protein to an enforced DNA bend. Chemistry and Biology, 1995, 2, 213-221.	6.0	58
81	A Designed Inhibitor of Base-Excision DNA Repair. Journal of the American Chemical Society, 1995, 117, 10781-10782.	13.7	58
82	Unusually Strong Binding of a Designed Transition-State Analog to a Base-Excision DNA Repair Protein. Journal of the American Chemical Society, 1997, 119, 7865-7866.	13.7	58
83	Specific binding of the DNA repair enzyme AlkA to a pyrrolidine-based inhibitor. Journal of the American Chemical Society, 1995, 117, 6623-6624.	13.7	54
84	Synthesis and Structure of Duplex DNA Containing the Genotoxic Nucleobase Lesion N7-Methylguanine. Journal of the American Chemical Society, 2008, 130, 11570-11571.	13.7	54
85	Subunit-specific Protein Footprinting Reveals Significant Structural Rearrangements and a Role for N-terminal Lys-14 of HIV-1 Integrase during Viral DNA Binding. Journal of Biological Chemistry, 2008, 283, 5632-5641.	3.4	52
86	A nucleobase lesion remodels the interaction of its normal neighbor in a DNA glycosylase complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15020-15025.	7.1	51
87	High-Affinity Mu Opioid Receptor Ligands Discovered by the Screening of an Exhaustively Stereodiversified Library of 1,5-Enediols. Journal of the American Chemical Society, 2002, 124, 13352-13353.	13.7	49
88	A Structural Model for the Damage-sensing Complex in Bacterial Nucleotide Excision Repair. Journal of Biological Chemistry, 2009, 284, 12837-12844.	3.4	48
89	Enforced Presentation of an Extrahelical Guanine to the Lesion Recognition Pocket of Human 8-Oxoguanine Glycosylase, hOGG1. Journal of Biological Chemistry, 2012, 287, 24916-24928.	3.4	48
90	Circular dichroism spectroscopy as a probe for the stereochemistry of aziridine cleavage reactions of mitomycin C. Application to adducts of mitomycin with DNA constituents. Journal of the American Chemical Society, 1984, 106, 7367-7370.	13.7	47

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91	A multifunctional plasmid for protein expression by ECPCR: overproduction of the p50 subunit of NF-Î°B. Bioorganic and Medicinal Chemistry Letters, 1993, 3, 1089-1094.	2.2	44
92	Entrapment and Structure of an Extrahelical Guanine Attempting to Enter the Active Site of a Bacterial DNA Glycosylase, MutM. Journal of Biological Chemistry, 2010, 285, 1468-1478.	3.4	44
93	Stapled peptide inhibitors of RAB25 target context-specific phenotypes in cancer. Nature Communications, 2017, 8, 660.	12.8	44
94	Limited proteolysis and site-directed mutagenesis of the NF-Î°B p50 DNA-binding subunit. Bioorganic and Medicinal Chemistry Letters, 1993, 3, 1095-1100.	2.2	42
95	The Synthesis of an Exhaustively Stereodiversified Library ofcis-1,5 Enediols by Silyl-Tethered Ring-Closing Metathesis. Organic Letters, 2001, 3, 2157-2159.	4.6	42
96	A Modular Synthetic Approach toward Exhaustively Stereodiversified Ligand Libraries. Organic Letters, 2000, 2, 3999-4002.	4.6	41
97	IMPDH2 Is an Intracellular Target of the Cyclophilin A and Sanglifehrin A Complex. Cell Reports, 2017, 18, 432-442.	6.4	41
98	Total Chemical Synthesis and Folding of All-<scp>l</scp> and All-<scp>d</scp> Variants of Oncogenic KRas(G12V). Journal of the American Chemical Society, 2017, 139, 7632-7639.	13.7	41
99	Metal-coordination sphere in the methylated Ada protein-DNA co-complex. Chemistry and Biology, 1994, 1, 91-97.	6.0	40
100	Genomic discovery of an evolutionarily programmed modality for small-molecule targeting of an intractable protein surface. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17195-17203.	7.1	40
101	Metal Dependence of Transcriptional Switching in Escherichia coli Ada. Journal of Biological Chemistry, 1995, 270, 6664-6670.	3.4	38
102	Deconstruction of GCN4/GCRE into a monomeric peptide-DNA complex. Nature Structural and Molecular Biology, 1995, 2, 450-457.	8.2	38
103	Concise enantio- and diastereoselective synthesis of Î±-hydroxy-Î±-methyl-Î²-amino acids. Tetrahedron Letters, 2001, 42, 3563-3565.	1.4	37
104	The Positively Charged Surface of Herpes Simplex Virus UL42 Mediates DNA Binding. Journal of Biological Chemistry, 2008, 283, 6154-6161.	3.4	36
105	A New <i>i</i>,<i> i</i>Â+Â3 Peptide Stapling System for Î±â€Helix Stabilization. Chemical Biology and Drug Design, 2013, 82, 635-642.	3.2	34
106	Strandwise translocation of a DNA glycosylase on undamaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1086-1091.	7.1	33
107	Exceptionally high-affinity Ras binders that remodel its effector domain. Journal of Biological Chemistry, 2018, 293, 3265-3280.	3.4	33
108	The effects of N7-methylguanine on duplex DNA structure. Chemistry and Biology, 1994, 1, 235-240.	6.0	32

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109	The Human Cytomegalovirus UL44 C Clamp Wraps around DNA. Structure, 2008, 16, 1214-1225.	3.3	31
110	A Small Region in HMG I(Y) Is Critical for Cooperation with NF-Î°B on DNA. Journal of Biological Chemistry, 1999, 274, 20235-20243.	3.4	30
111	Trapping Distinct Structural States of a Protein/DNA Interaction through Disulfide Crosslinking. Chemistry and Biology, 2002, 9, 1297-1303.	6.0	30
112	Ratcheting torsional stress in duplex DNA. Journal of the American Chemical Society, 1993, 115, 12585-12586.	13.7	29
113	Structures of End Products Resulting from Lesion Processing by a DNA Glycosylase/Lyase. Chemistry and Biology, 2004, 11, 1643-1649.	6.0	29
114	Structure of the E. coli DNA Glycosylase AlkA Bound to the Ends of Duplex DNA: A System for the Structure Determination of Lesion-Containing DNA. Structure, 2008, 16, 1166-1174.	3.3	29
115	A Concise Synthesis of 4â€˜-Fluoro Nucleosides. Organic Letters, 2007, 9, 5007-5009.	4.6	28
116	Structural Determinants for Specific Recognition by T4 Endonuclease V. Journal of Biological Chemistry, 1996, 271, 32147-32152.	3.4	27
117	A genotyping strategy based on incorporation and cleavage of chemically modified nucleotides. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11073-11078.	7.1	27
118	Trapping and Structural Elucidation of a Very Advanced Intermediate in the Lesion-Extrusion Pathway of hOGG1. Journal of the American Chemical Society, 2008, 130, 7784-7785.	13.7	27
119	Aberrantly methylated DNA: site-specific introduction of N-7-methyl-2'-deoxyguanosine into the Dickerson/Drew dodecamer.. Journal of the American Chemical Society, 1992, 114, 6562-6563.	13.7	26
120	[7] Overproduction of proteins using expression-cassette polymerase chain reaction. Methods in Enzymology, 1993, 217, 79-102.	1.0	26
121	Immobilized metal affinity chromatography of DNA. Nucleic Acids Research, 1996, 24, 3806-3810.	14.5	26
122	A high-capacity column for affinity purification of sequence-specific DNA-binding proteins. Nucleic Acids Research, 1992, 20, 3525-3525.	14.5	25
123	Synthesis of an oligonucleotide suicide substrate for DNA methyltransferases. Journal of Organic Chemistry, 1992, 57, 2989-2991.	3.2	25
124	Extensively Stereodiversified Scaffolds for Use in Diversity-Oriented Library Synthesis. Organic Letters, 2003, 5, 621-624.	4.6	25
125	Unpredictable Stereochemical Preferences for Mu Opioid Receptor Activity in an Exhaustively Stereodiversified Library of 1,4-Enediols. Organic Letters, 2003, 5, 633-636.	4.6	25
126	Template-directed interference footprinting of protein-thymine contacts. Journal of the American Chemical Society, 1993, 115, 373-374.	13.7	24

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127	Structural and Biochemical Analysis of DNA Helix Invasion by the Bacterial 8-Oxoguanine DNA Glycosylase MutM. Journal of Biological Chemistry, 2013, 288, 10012-10023.	3.4	24
128	Nature of the destruction of deoxyguanosine residues by mitomycin C. Journal of the American Chemical Society, 1985, 107, 6120-6121.	13.7	23
129	Aminolysis of 2â€²-Deoxyinosine Aryl Ethers: Nucleoside Model Studies for the Synthesis of Functionally Tethered Oligonucleotides. Nucleosides & Nucleotides, 1992, 11, 1749-1763.	0.5	23
130	Molecular dynamics simulations of disulfide cross-linked DNA decamers. Journal of the American Chemical Society, 1993, 115, 7569-7583.	13.7	23
131	The trajectory of intrahelical lesion recognition and extrusion by the human 8-oxoguanine DNA glycosylase. Nature Communications, 2020, 11, 4437.	12.8	23
132	Template-directed interference footprinting of protein-guanine contacts in DNA. Journal of the American Chemical Society, 1991, 113, 5104-5106.	13.7	22
133	2,6-Dimethyltyrosine Analogues of a Stereodiversified Ligand Library:Â Highly Potent, Selective, Non-Peptidic Î¼ Opioid Receptor Agonists. Journal of Medicinal Chemistry, 2003, 46, 677-680.	6.4	22
134	Structural Basis for Avoidance of Promutagenic DNA Repair by MutY Adenine DNA Glycosylase. Journal of Biological Chemistry, 2015, 290, 17096-17105.	3.4	22
135	Use of differential second-derivative UV and FTIR spectroscopy in structural studies of multichromophoric compounds. Journal of the American Chemical Society, 1985, 107, 6118-6120.	13.7	21
136	Protein overproduction for organic chemists. Tetrahedron, 1991, 47, 2543-2562.	1.9	21
137	Disulfide Cross-linking as a Mechanistic Probe for the B â†” Z Transition in DNA. Journal of the American Chemical Society, 1997, 119, 6927-6928.	13.7	21
138	Direct Activation of the Methyl Chemosensor Protein N-Ada by CH3I. Journal of the American Chemical Society, 1995, 117, 10749-10750.	13.7	20
139	Construction of an overproduction vector containing the novel <i>srp</i> (sterically repressed) promoter. Protein Science, 1994, 3, 132-138.	7.6	19
140	Structure of Escherichia coli AlkA in Complex with Undamaged DNA. Journal of Biological Chemistry, 2010, 285, 35783-35791.	3.4	19
141	Sequence-dependent Structural Variation in DNA Undergoing Intrahelical Inspection by the DNA glycosylase MutM. Journal of Biological Chemistry, 2012, 287, 18044-18054.	3.4	19
142	Structural Basis for the Lesion-scanning Mechanism of the MutY DNA Glycosylase. Journal of Biological Chemistry, 2017, 292, 5007-5017.	3.4	19
143	Analysis of an Anomalous Mutant of MutM DNA Glycosylase Leads to New Insights into the Catalytic Mechanism. Journal of the American Chemical Society, 2009, 131, 18208-18209.	13.7	18
144	The base promoted oligomerization of 15-dehydro-prostaglandin B1: dimer formation and structural implications for a complex mixture termed PGBx. Tetrahedron Letters, 1983, 24, 991-994.	1.4	17

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145	Direct observation of a specific contact in the .lambda. repressor-OL1 complex by isotope-edited NMR. Journal of the American Chemical Society, 1993, 115, 4921-4922.	13.7	17
146	Converting the Sacrificial DNA Repair Protein N-Ada into a Catalytic Methyl Phosphotriester Repair Enzyme. Journal of the American Chemical Society, 2003, 125, 1450-1451.	13.7	17
147	Template-Directed Interference Footprinting of Proteinâˆ'Adenine Contacts. Journal of the American Chemical Society, 1996, 118, 6116-6120.	13.7	16
148	DNA binding by an amino acid residue in the C-terminal half of the Rel homology region. Chemistry and Biology, 1994, 1, 47-55.	6.0	15
149	Mammalian DNA cytosine-5 methyltransferase interacts with p23 protein. FEBS Letters, 1996, 392, 179-183.	2.8	15
150	Chemical approaches toward understanding base excision DNA repair. Current Opinion in Chemical Biology, 1997, 1, 526-531.	6.1	15
151	High-resolution footprinting of sequence-specific proteinâ€"DNA contacts. Nature Biotechnology, 2002, 20, 183-186.	17.5	15
152	Identification of cyclosporin C from Amphichorda felina using a Cryptococcus neoformans differential temperature sensitivity assay. Applied Microbiology and Biotechnology, 2018, 102, 2337-2350.	3.6	15
153	Synthesis of photoactive DNA: incorporation of 8-bromo-2â€²-deoxyadenosine into synthetic oligodeoxynucleotides. Tetrahedron Letters, 1992, 33, 4265-4268.	1.4	13
154	In vitro selection of RNA aptamers against a composite small molecule-protein surface. Nucleic Acids Research, 2005, 33, 5602-5610.	14.5	13
155	Crystallization and Preliminary Crystallographic Analysis of a DNA (Cytosine-5)-Methyltransferase from Haemophilus aegyptius Bound Covalently to DNA. Journal of Molecular Biology, 1994, 238, 626-629.	4.2	12
156	Mapping Targetable Sites on Human Telomerase RNA Pseudoknot/Template Domain Using 2â€²-OMe RNA-interacting Polynucleotide (RIPtide) Microarrays. Journal of Biological Chemistry, 2012, 287, 18843-18853.	3.4	12
157	Differentiation Induction In Acute Myeloid Leukemia Using Site-Specific DNA-Targeting. Blood, 2013, 122, 3940-3940.	1.4	12
158	5-Amino-2â€˜-deoxyuridine, a Novel Thymidine Analogue for High-Resolution Footprinting of Proteinâˆ'DNA Complexes. Organic Letters, 2002, 4, 3867-3869.	4.6	11
159	Conformational Analysis of a Stereochemically Complete Set of Cis-enediol Peptide Analogues. Journal of the American Chemical Society, 2002, 124, 11131-11141.	13.7	11
160	Mechanism of DNA Lesion Homing and Recognition by the Uvr Nucleotide Excision Repair System. Research, 2019, 2019, 5641746.	5.7	10
161	The base promoted oligomerization of a 15-dehydro-PGB1 analog: Structural insights into the complex oligomeric mixture termed PGBX. Tetrahedron Letters, 1982, 23, 1967-1970.	1.4	9
162	Selective base-pair destabilization enhances binding of a DNA methyltransferase. Tetrahedron, 1997, 53, 12041-12056.	1.9	9

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163	Cilia and Hedgehog Signaling in the Mouse Embryo. , 2010, 102, 103-115.		9
164	Tracking the Road from Inflammation to Cancer: the Critical Role of IÎºB Kinase (IKK). , 2010, 102, 133-151.		8
165	Direct Inhibition of the Notch Transactivation Complex with Synthetic Constrained Peptides in T-Cell Acute Lymphoblastic Leukemia.. Blood, 2007, 110, 2819-2819.	1.4	7
166	Targeted Î²â€catenin ubiquitination and degradation by multifunctional stapled peptides. Journal of Peptide Science, 2022, 28, e3389.	1.4	7
167	Falling out of the fold: tumorigenic mutations and p53. Chemistry and Biology, 1994, 1, 79-84.	6.0	6
168	A stapled POL Îº peptide targets REV1 to inhibit mutagenic translesion synthesis. Environmental and Molecular Mutagenesis, 2020, 61, 830-836.	2.2	5
169	Anti-Leukemic Potency of Stapled BH3 Helices Correlates with Their Capacity for Bifunctional Activation of Apoptotic Pathways.. Blood, 2006, 108, 711-711.	1.4	4
170	Structural Origins of DNA Target Selection and Nucleobase Extrusion by a DNA Cytosine Methyltransferase. Journal of Biological Chemistry, 2012, 287, 40099-40105.	3.4	3
171	Template-Directed Interference Footprinting of Proteinâ˘'Phosphate Contacts in DNA. Organic Letters, 2001, 3, 71-74.	4.6	1
172	Signaling Networks that Control Synapse Development and Cognitive Function. , 2010, 102, 73-102.		1
173	Basal Bodies: Their Roles in Generating Asymmetry. , 2010, 102, 17-50.		1
174	Drugging the "undruggable". Harvey Lectures, 2006, 102, 1-15.	0.2	1
175	A Stapled p53 Helix Targets HDMX to Overcome Nutlin-3 Resistance and Reactivate the p53 Tumor Suppressor Pathway in Cancer. Blood, 2008, 112, 2645-2645.	1.4	0
176	Protein Transport in and out of the Endoplasmic Reticulum. , 2010, 102, 51-72.		0
177	Active Members. , 0, , 179-189.		0
178	Former Officers of the Harvey Society. , 0, , 153-168.		0