Hashim M Al-Hashimi

List of Publications by Year
in descending order

129	7,164	46918	66788
papers	citations	47 h-index	78 g-index

143	143	143	4332
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural basis for impaired 5â€² processing of a mutant tRNA associated with defects in neuronal homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119529119.	3.3	5
2	Measuring thermodynamic preferences to form non-native conformations in nucleic acids using ultraviolet melting. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	8
3	Understanding the characteristics of nonspecific binding of drug-like compounds to canonical stemâ€“loop RNAs and their implications for functional cellular assays. Rna, 2021, 27, 12-26.	1.6	13
4	A quantitative model predicts how m6A reshapes the kinetic landscape of nucleic acid hybridization and conformational transitions. Nature Communications, 2021, 12, 5201.	5.8	18
5	Rapid assessment of Watsonâ€“Crick to Hoogsteen exchange in unlabeled DNA duplexes using high-power SELOPE imino ¹H CEST. Magnetic Resonance, 2021, 2, 715-731.	0.8	9
6	Developments in solution-state NMR yield broader and deeper views of the dynamic ensembles of nucleic acids. Current Opinion in Structural Biology, 2021, 70, 16-25.	2.6	42
7	Revealing A-T and G-C Hoogsteen base pairs in stressed protein-bound duplex DNA. Nucleic Acids Research, 2021, 49, 12540-12555.	6.5	10
8	Exposing Hidden High-Affinity RNA Conformational States. Journal of the American Chemical Society, 2020, 142, 907-921.	6.6	21
9	Demonstration that Small Molecules can Bind and Stabilize Low-abundance Short-lived RNA Excited Conformational States. Journal of Molecular Biology, 2020, 432, 1297-1304.	2.0	16
10	DNA mismatches reveal conformational penalties in proteinâ€“DNA recognition. Nature, 2020, 587, 291-296.	13.7	74
11	Rapid and accurate determination of atomistic RNA dynamic ensemble models using NMR and structure prediction. Nature Communications, 2020, 11, 5531.	5.8	52
12	2â€²-O-Methylation can increase the abundance and lifetime of alternative RNA conformational states. Nucleic Acids Research, 2020, 48, 12365-12379.	6.5	59
13	Probing conformational transitions towards mutagenic Watsonâ€“Crick-like GÂ·T mismatches using off-resonance sugar carbon R1Ï•relaxation dispersion. Journal of Biomolecular NMR, 2020, 74, 457-471.	1.6	15
14	Extending the Sensitivity of CEST NMR Spectroscopy to Microâ€toâ€Millisecond Dynamics in Nucleic Acids Using Highâ€Power Radioâ€Frequency Fields. Angewandte Chemie, 2020, 132, 11358-11362.	1.6	1
15	Anomalous Reverse Transcription through Chemical Modifications in Polyadenosine Stretches. Biochemistry, 2020, 59, 2154-2170.	1.2	8
16	Environmental Effects on Guanine-Thymine Mispair Tautomerization Explored with Quantum Mechanical/Molecular Mechanical Free Energy Simulations. Journal of the American Chemical Society, 2020, 142, 11183-11191.	6.6	20
17	Extending the Sensitivity of CEST NMR Spectroscopy to Microâ€toâ€Millisecond Dynamics in Nucleic Acids Using Highâ€Power Radioâ€Frequency Fields. Angewandte Chemie - International Edition, 2020, 59, 11262-11266.	7.2	20
18	Probing RNA Conformational Equilibria within the Functional Cellular Context. Cell Reports, 2020, 30, 2472-2480.e4.	2.9	28

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19	Hoogsteen base pairs increase the susceptibility of double-stranded DNA to cytotoxic damage. Journal of Biological Chemistry, 2020, 295, 15933-15947.	1.6	20
20	Infrared Spectroscopic Observation of a Gâ€“C⁺ Hoogsteen Base Pair in the DNA:TATAâ€Box Binding Protein Complex Under Solution Conditions. Angewandte Chemie, 2019, 131, 12138-12141.	1.6	1
21	Infrared Spectroscopic Observation of a Gâ€“C⁺ Hoogsteen Base Pair in the DNA:TATAâ€Box Binding Protein Complex Under Solution Conditions. Angewandte Chemie - International Edition, 2019, 58, 12010-12013.	7.2	13
22	Direct evidence for (G)O6Â·Â·Â·H2-N4(C)+ hydrogen bonding in transient G(syn)-C+ and G(syn)-m5C+ Hoogsteen base pairs in duplex DNA from cytosine amino nitrogen off-resonance R1Ï•relaxation dispersion measurements. Journal of Magnetic Resonance, 2019, 308, 106589.	1.2	11
23	Dynamic ensemble of HIV-1 RRE stem IIB reveals non-native conformations that disrupt the Rev-binding site. Nucleic Acids Research, 2019, 47, 7105-7117.	6.5	31
24	The roles of structural dynamics in the cellular functions of RNAs. Nature Reviews Molecular Cell Biology, 2019, 20, 474-489.	16.1	322
25	Characterizing micro-to-millisecond chemical exchange in nucleic acids using off-resonance R1Ï• relaxation dispersion. Progress in Nuclear Magnetic Resonance Spectroscopy, 2019, 112-113, 55-102.	3.9	53
26	Characterizing Watsonâ€“Crick versus Hoogsteen Base Pairing in a DNAâ€“Protein Complex Using Nuclear Magnetic Resonance and Site-Specifically 13C- and 15N-Labeled DNA. Biochemistry, 2019, 58, 1963-1974.	1.2	17
27	Structural and Functional Characterization of Sulfonium Carbonâ€“Oxygen Hydrogen Bonding in the Deoxyamino Sugar Methyltransferase TylM1. Biochemistry, 2019, 58, 2152-2159.	1.2	0
28	NMR Chemical Exchange Measurements Reveal That N⁶-Methyladenosine Slows RNA Annealing. Journal of the American Chemical Society, 2019, 141, 19988-19993.	6.6	46
29	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. PLoS ONE, 2019, 14, e0224850.	1.1	15
30	The RRM of the kRNA-editing protein TbRGG2 uses multiple surfaces to bind and remodel RNA. Nucleic Acids Research, 2019, 47, 2130-2142.	6.5	8
31	Using Conformational Penalties to Assess the Structure Dependence of RNA Cellular Function. FASEB Journal, 2019, 33, 220.1.	0.2	0
32	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
33	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
34	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
35	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
36	Atomic structures of excited state Aâ€“T Hoogsteen base pairs in duplex DNA by combining NMR relaxation dispersion, mutagenesis, and chemical shift calculations. Journal of Biomolecular NMR, 2018, 70, 229-244.	1.6	30

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37	Modulation of Hoogsteen dynamics on DNA recognition. Nature Communications, 2018, 9, 1473.	5.8	38
38	Dynamic basis for dGâ€¢dT misincorporation via tautomerization and ionization. Nature, 2018, 554, 195-201.	13.7	117
39	High-performance virtual screening by targeting a high-resolution RNA dynamic ensemble. Nature Structural and Molecular Biology, 2018, 25, 425-434.	3.6	69
40	Hidden Structural Modules in a Cooperative RNA Folding Transition. Cell Reports, 2018, 22, 3240-3250.	2.9	20
41	The Mechanism of HdeA Unfolding and Chaperone Activation. Journal of Molecular Biology, 2018, 430, 33-40.	2.0	15
42	Why are Hoogsteen base pairs energetically disfavored in A-RNA compared to B-DNA?. Nucleic Acids Research, 2018, 46, 11099-11114.	6.5	23
43	5â€Oxyacetic Acid Modification Destabilizes Double Helical Stem Structures and Favors Anionic Watsonâ€“Crick like cmo⁵Uâ€G Base Pairs. Chemistry - A European Journal, 2018, 24, 18903-18906.	1.7	18
44	A potentially abundant junctional RNA motif stabilized by m6A and Mg2+. Nature Communications, 2018, 9, 2761.	5.8	66
45	Increasing the length of poly-pyrimidine bulges broadens RNA conformational ensembles with minimal impact on stacking energetics. Rna, 2018, 24, 1363-1376.	1.6	13
46	Water-Mediated Carbonâ€“Oxygen Hydrogen Bonding Facilitates S-Adenosylmethionine Recognition in the Reactivation Domain of Cobalamin-Dependent Methionine Synthase. Biochemistry, 2018, 57, 3733-3740.	1.2	16
47	Pseudouridine and N⁶-methyladenosine modifications weaken PUF protein/RNA interactions. Rna, 2017, 23, 611-618.	1.6	50
48	Resolving sugar puckers in RNA excited states exposes slow modes of repuckering dynamics. Nucleic Acids Research, 2017, 45, e134-e134.	6.5	33
49	Insights into Watsonâ€“Crick/Hoogsteen breathing dynamics and damage repair from the solution structure and dynamic ensemble of DNA duplexes containing m1A. Nucleic Acids Research, 2017, 45, 5586-5601.	6.5	57
50	Robust <scp>IR</scp>â€based detection of stable and fractionally populated Gâ€C⁺ and Aâ€T Hoogsteen base pairs in duplex <scp>DNA</scp>. FEBS Letters, 2017, 591, 1770-1784.	1.3	15
51	Direct NMR Evidence that Transient Tautomeric and Anionic States in dGÂ·dT Form Watsonâ€“Crick-like Base Pairs. Journal of the American Chemical Society, 2017, 139, 4326-4329.	6.6	47
52	Amiloride as a new RNA-binding scaffold with activity against HIV-1 TAR. MedChemComm, 2017, 8, 1022-1036.	3.5	60
53	Visualizing the formation of an RNA folding intermediate through a fast highly modular secondary structure switch. Nature Communications, 2016, 7, ncomms11768.	5.8	50
54	Secondary structure encodes a cooperative tertiary folding funnel in theAzoarcusribozyme. Nucleic Acids Research, 2016, 44, 402-412.	6.5	3

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55	Shortening the HIV-1 TAR RNA Bulge by a Single Nucleotide Preserves Motional Modes over a Broad Range of Time Scales. Biochemistry, 2016, 55, 4445-4456.	1.2	23
56	m1A and m1G disrupt A-RNA structure through the intrinsic instability of Hoogsteen base pairs. Nature Structural and Molecular Biology, 2016, 23, 803-810.	3.6	100
57	RNA Structural Modules Control the Rate and Pathway of RNA Folding and Assembly. Journal of Molecular Biology, 2016, 428, 3972-3985.	2.0	14
58	HIV-1 leader RNA dimeric interface revealed by NMR. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13263-13265.	3.3	4
59	Rapid Exchange Between Free and Bound States in RNAâ€“Dendrimer Polyplexes: Implications on the Mechanism of Delivery and Release. Biomacromolecules, 2016, 17, 154-164.	2.6	20
60	Inter-helical conformational preferences of HIV-1 TAR-RNA from maximum occurrence analysis of NMR data and molecular dynamics simulations. Physical Chemistry Chemical Physics, 2016, 18, 5743-5752.	1.3	15
61	Structural and Dynamic Basis for Low-Affinity, High-Selectivity Binding of L-Glutamine by the Glutamine Riboswitch. Cell Reports, 2015, 13, 1800-1813.	2.9	50
62	Dynamic Motions of the HIV-1 Frameshift Site RNA. Biophysical Journal, 2015, 108, 644-654.	0.2	4
63	Slowdown of Interhelical Motions Induces a Glass Transition in RNA. Biophysical Journal, 2015, 108, 2876-2885.	0.2	7
64	Unveiling Inherent Degeneracies in Determining Population-Weighted Ensembles of Interdomain Orientational Distributions Using NMR Residual Dipolar Couplings: Application to RNA Helix Junction Helix Motifs. Journal of Physical Chemistry B, 2015, 119, 9614-9626.	1.2	11
65	New insights into Hoogsteen base pairs in DNA duplexes from a structure-based survey. Nucleic Acids Research, 2015, 43, 3420-3433.	6.5	66
66	Characterizing RNA Excited States Using NMR Relaxation Dispersion. Methods in Enzymology, 2015, 558, 39-73.	0.4	55
67	Noncanonical Secondary Structure Stabilizes Mitochondrial tRNA^{Ser(UCN)} by Reducing the Entropic Cost of Tertiary Folding. Journal of the American Chemical Society, 2015, 137, 3592-3599.	6.6	15
68	Editorial overview: Nucleic acids and their protein complexes: Progress in nucleic acid structural biology: new technologies and discoveries. Current Opinion in Structural Biology, 2015, 30, vii-viii.	2.6	0
69	Visualizing transient Watsonâ€“Crick-like mispairs in DNA and RNA duplexes. Nature, 2015, 519, 315-320.	13.7	218
70	Modulating RNA Alignment Using Directional Dynamic Kinks: Application in Determining an Atomic-Resolution Ensemble for a Hairpin using NMR Residual Dipolar Couplings. Journal of the American Chemical Society, 2015, 137, 12954-12965.	6.6	31
71	Engineering a Therapeutic Lectin by Uncoupling Mitogenicity from Antiviral Activity. Cell, 2015, 163, 746-758.	13.5	89
72	Guanine to Inosine Substitution Leads to Large Increases in the Population of a Transient GÂ·C Hoogsteen Base Pair. Biochemistry, 2014, 53, 7145-7147.	1.2	9

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73	Evaluating the uncertainty in exchange parameters determined from off-resonance R1Ï•relaxation dispersion for systems in fast exchange. Journal of Magnetic Resonance, 2014, 244, 18-29.	1.2	30
74	Flipping of the Ribosomal A-Site Adenines Provides a Basis for tRNA Selection. Journal of Molecular Biology, 2014, 426, 3201-3213.	2.0	31
75	Measuring similarity between dynamic ensembles of biomolecules. Nature Methods, 2014, 11, 552-554.	9.0	29
76	Increasing occurrences and functional roles for high energy purine-pyrimidine base-pairs in nucleic acids. Current Opinion in Structural Biology, 2014, 24, 72-80.	2.6	13
77	Development and application of aromatic [13C, 1H] SOFAST-HMQC NMR experiment for nucleic acids. Journal of Biomolecular NMR, 2014, 60, 77-83.	1.6	34
78	An RNA tertiary switch by modifying how helices are tethered. Genome Biology, 2014, 15, 425.	3.8	3
79	Topological constraints are major determinants of tRNA tertiary structure and dynamics and provide basis for tertiary folding cooperativity. Nucleic Acids Research, 2014, 42, 11792-11804.	6.5	22
80	Invisible RNA state dynamically couples distant motifs. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9485-9490.	3.3	51
81	Widespread transient Hoogsteen base pairs in canonical duplex DNA with variable energetics. Nature Communications, 2014, 5, 4786.	5.8	113
82	Hierarchy of RNA Functional Dynamics. Annual Review of Biochemistry, 2014, 83, 441-466.	5.0	162
83	Advances in the Determination of Nucleic Acid Conformational Ensembles. Annual Review of Physical Chemistry, 2014, 65, 293-316.	4.8	84
84	Structural dynamics of a single-stranded RNAâ€“helix junction using NMR. Rna, 2014, 20, 782-791.	1.6	16
85	Coarse Grained Models Reveal Essential Contributions of Topological Constraints to the Conformational Free Energy of RNA Bulges. Journal of Physical Chemistry B, 2014, 118, 2615-2627.	1.2	53
86	NMR studies of nucleic acid dynamics. Journal of Magnetic Resonance, 2013, 237, 191-204.	1.2	40
87	Utility of 1H NMR Chemical Shifts in Determining RNA Structure and Dynamics. Journal of Physical Chemistry B, 2013, 117, 2045-2052.	1.2	31
88	Characterizing the Protonation State of Cytosine in Transient GÂ·C Hoogsteen Base Pairs in Duplex DNA. Journal of the American Chemical Society, 2013, 135, 6766-6769.	6.6	77
89	A General Method for Constructing Atomic-Resolution RNA Ensembles using NMR Residual Dipolar Couplings: The Basis for Interhelical Motions Revealed. Journal of the American Chemical Society, 2013, 135, 5457-5466.	6.6	94
90	A historical account of hoogsteen baseâ€pairs in duplex DNA. Biopolymers, 2013, 99, 955-968.	1.2	92

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91	Unraveling the structural complexity in a single-stranded RNA tail: implications for efficient ligand binding in the prequeuosine riboswitch. Nucleic Acids Research, 2012, 40, 1345-1355.	6.5	52
92	Visualizing transient low-populated structures of RNA. Nature, 2012, 491, 724-728.	13.7	184
93	New insights into the fundamental role of topological constraints as a determinant of two-way junction conformation. Nucleic Acids Research, 2012, 40, 892-904.	6.5	34
94	Probing Sequence-Specific DNA Flexibility in A-Tracts and Pyrimidine-Purine Steps by Nuclear Magnetic Resonance ¹³C Relaxation and Molecular Dynamics Simulations. Biochemistry, 2012, 51, 8654-8664.	1.2	44
95	Functional complexity and regulation through RNA dynamics. Nature, 2012, 482, 322-330.	13.7	286
96	Probing Transient Hoogsteen Hydrogen Bonds in Canonical Duplex DNA Using NMR Relaxation Dispersion and Single-Atom Substitution. Journal of the American Chemical Society, 2012, 134, 3667-3670.	6.6	83
97	Sequence-Specific B-DNA Flexibility Modulates Z-DNA Formation. Journal of the American Chemical Society, 2011, 133, 2016-2018.	6.6	28
98	Discovery of selective bioactive small molecules by targeting an RNA dynamic ensemble. Nature Chemical Biology, 2011, 7, 553-559.	3.9	232
99	Characterizing RNA dynamics at atomic resolution using solution-state NMR spectroscopy. Nature Methods, 2011, 8, 919-931.	9.0	131
100	Transient Hoogsteen base pairs in canonical duplex DNA. Nature, 2011, 470, 498-502.	13.7	291
101	Topological constraints: using RNA secondary structure to model 3D conformation, folding pathways, and dynamic adaptation. Current Opinion in Structural Biology, 2011, 21, 296-305.	2.6	58
102	3D maps of RNA interhelical junctions. Nature Protocols, 2011, 6, 1536-1545.	5.5	46
103	RNA Dynamics by Design: Biasing Ensembles Towards the Ligandâ€Bound State. Angewandte Chemie - International Edition, 2010, 49, 5731-5733.	7.2	44
104	Topology Links RNA Secondary Structure with Global Conformation, Dynamics, and Adaptation. Science, 2010, 327, 202-206.	6.0	177
105	Exciting Structures. Science, 2010, 329, 1295-1296.	6.0	6
106	Constructing RNA dynamical ensembles by combining MD and motionally decoupled NMR RDCs: new insights into RNA dynamics and adaptive ligand recognition. Nucleic Acids Research, 2009, 37, 3670-3679.	6.5	106
107	Extending the Range of Microsecond-to-Millisecond Chemical Exchange Detected in Labeled and Unlabeled Nucleic Acids by Selective Carbon R_{1Ï} NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 3818-3819.	6.6	109
108	RNA dynamics: it is about time. Current Opinion in Structural Biology, 2008, 18, 321-329.	2.6	279

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109	Characterizing Complex Dynamics in the Transactivation Response Element Apical Loop and Motional Correlations with the Bulge by NMR, Molecular Dynamics, and Mutagenesis. Biophysical Journal, 2008, 95, 3906-3915.	0.2	65
110	Resolving fast and slow motions in the internal loop containing stem-loop 1 of HIV-1 that are modulated by Mg2+ binding: role in the kissingâ€“duplex structural transition. Nucleic Acids Research, 2007, 35, 1698-1713.	6.5	51
111	Probing Na+-Induced Changes in the HIV-1 TAR Conformational Dynamics Using NMR Residual Dipolar Couplings:â€‰ New Insights into the Role of Counterions and Electrostatic Interactions in Adaptive Recognition. Biochemistry, 2007, 46, 6525-6535.	1.2	50
112	Dynamics of Large Elongated RNA by NMR Carbon Relaxation. Journal of the American Chemical Society, 2007, 129, 16072-16082.	6.6	85
113	iRED Analysis of TAR RNA Reveals Motional Coupling, Long-Range Correlations, and a Dynamical Hinge. Biophysical Journal, 2007, 93, 411-422.	0.2	31
114	Review NMR studies of RNA dynamics and structural plasticity using NMR residual dipolar couplings. Biopolymers, 2007, 86, 384-402.	1.2	95
115	Characterizing the relative orientation and dynamics of RNA A-form helices using NMR residual dipolar couplings. Nature Protocols, 2007, 2, 1536-1546.	5.5	56
116	Visualizing spatially correlated dynamics that directs RNA conformational transitions. Nature, 2007, 450, 1263-1267.	13.7	236
117	Impact of static and dynamic A-form heterogeneity on the determination of RNA global structural dynamics using NMR residual dipolar couplings. Journal of Biomolecular NMR, 2006, 36, 235-249.	1.6	54
118	Insight into the CSA tensors of nucleobase carbons in RNA polynucleotides from solution measurements of residual CSA: Towards new long-range orientational constraints. Journal of Magnetic Resonance, 2006, 179, 299-307.	1.2	56
119	Structural plasticity and Mg2+ binding properties of RNase P P4 from combined analysis of NMR residual dipolar couplings and motionally decoupled spin relaxation. Rna, 2006, 13, 251-266.	1.6	43
120	Resolving the Motional Modes That Code for RNA Adaptation. Science, 2006, 311, 653-656.	6.0	216
121	Evidence that Electrostatic Interactions Dictate the Ligand-Induced Arrest of RNA Global Flexibility. Angewandte Chemie - International Edition, 2005, 44, 3412-3415.	7.2	29
122	Dynamics-Based Amplification of RNA Function and Its Characterization by Using NMR Spectroscopy. ChemBioChem, 2005, 6, 1506-1519.	1.3	51
123	Argininamide Binding Arrests Global Motions in HIV-1 TAR RNA: Comparison with Mg2+-induced Conformational Stabilization. Journal of Molecular Biology, 2004, 338, 7-16.	2.0	76
124	Mg2+-induced Variations in the Conformation and Dynamics of HIV-1 TAR RNA Probed Using NMR Residual Dipolar Couplings. Journal of Molecular Biology, 2003, 329, 867-873.	2.0	67
125	NMR Studies of Biomolecular Dynamics and Structural Plasticity Using Residual Dipolar Couplings. Annual Reports on NMR Spectroscopy, 2003, 51, 105-166.	0.7	14
126	Concerted motions in HIV-1 TAR RNA may allow access to bound state conformations: RNA dynamics from NMR residual dipolar couplings 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2002, 315, 95-102.	2.0	141

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127	Towards Structural Genomics of RNA: Rapid NMR Resonance Assignment and Simultaneous RNA Tertiary Structure Determination Using Residual Dipolar Couplings. Journal of Molecular Biology, 2002, 318, 637-649.	2.0	63
128	Residual dipolar couplings: synergy between NMR and structural genomics. Journal of Biomolecular NMR, 2002, 22, 1-8.	1.6	26
129	Field- and Phage-Induced Dipolar Couplings in a Homodimeric DNA Quadruplex:â€‰ Relative Orientation of GÂ·(Câ˜A) Triad and G-Tetrad Motifs and Direct Determination of C2 Symmetry Axis Orientation. Journal of the American Chemical Society, 2001, 123, 633-640.	6.6	47