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	The roles of structural dynamics in the cellular functions of RNAs. Nature Reviews Molecular Cell Biology, 2019, 20, 474-489.	16.1	322
2	Transient Hoogsteen base pairs in canonical duplex DNA. Nature, 2011, 470, 498-502.	13.7	291
3	Functional complexity and regulation through RNA dynamics. Nature, 2012, 482, 322-330.	13.7	286
4	RNA dynamics: it is about time. Current Opinion in Structural Biology, 2008, 18, 321-329.	2.6	279
5	Visualizing spatially correlated dynamics that directs RNA conformational transitions. Nature, 2007, 450, 1263-1267.	13.7	236
6	Discovery of selective bioactive small molecules by targeting an RNA dynamic ensemble. Nature Chemical Biology, 2011, 7, 553-559.	3.9	232
7	Visualizing transient Watsonâ€“Crick-like mispairs in DNA and RNA duplexes. Nature, 2015, 519, 315-320.	13.7	218
8	Resolving the Motional Modes That Code for RNA Adaptation. Science, 2006, 311, 653-656.	6.0	216
9	Visualizing transient low-populated structures of RNA. Nature, 2012, 491, 724-728.	13.7	184
10	Topology Links RNA Secondary Structure with Global Conformation, Dynamics, and Adaptation. Science, 2010, 327, 202-206.	6.0	177
11	Hierarchy of RNA Functional Dynamics. Annual Review of Biochemistry, 2014, 83, 441-466.	5.0	162
12	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
13	Characterizing RNA dynamics at atomic resolution using solution-state NMR spectroscopy. Nature Methods, 2011, 8, 919-931.	9.0	131
14	Dynamic basis for dGâ€¢dT misincorporation via tautomerization and ionization. Nature, 2018, 554, 195-201.	13.7	117
15	Widespread transient Hoogsteen base pairs in canonical duplex DNA with variable energetics. Nature Communications, 2014, 5, 4786.	5.8	113
16	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
17	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
18	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

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19	Review NMR studies of RNA dynamics and structural plasticity using NMR residual dipolar couplings. Biopolymers, 2007, 86, 384-402.	1.2	95
20	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
21	A historical account of hoogsteen baseâ€pairs in duplex DNA. Biopolymers, 2013, 99, 955-968.	1.2	92
22	Engineering a Therapeutic Lectin by Uncoupling Mitogenicity from Antiviral Activity. Cell, 2015, 163, 746-758.	13.5	89
23	Dynamics of Large Elongated RNA by NMR Carbon Relaxation. Journal of the American Chemical Society, 2007, 129, 16072-16082.	6.6	85
24	Advances in the Determination of Nucleic Acid Conformational Ensembles. Annual Review of Physical Chemistry, 2014, 65, 293-316.	4.8	84
25	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
26	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
27	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
28	DNA mismatches reveal conformational penalties in proteinâ€“DNA recognition. Nature, 2020, 587, 291-296.	13.7	74
29	High-performance virtual screening by targeting a high-resolution RNA dynamic ensemble. Nature Structural and Molecular Biology, 2018, 25, 425-434.	3.6	69
30	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
31	New insights into Hoogsteen base pairs in DNA duplexes from a structure-based survey. Nucleic Acids Research, 2015, 43, 3420-3433.	6.5	66
32	A potentially abundant junctional RNA motif stabilized by m6A and Mg2+. Nature Communications, 2018, 9, 2761.	5.8	66
33	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
34	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
35	Amiloride as a new RNA-binding scaffold with activity against HIV-1 TAR. MedChemComm, 2017, 8, 1022-1036.	3.5	60
36	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

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37	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
38	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
39	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
40	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
41	Characterizing RNA Excited States Using NMR Relaxation Dispersion. Methods in Enzymology, 2015, 558, 39-73.	0.4	55
42	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
43	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
44	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
45	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
46	Rapid and accurate determination of atomistic RNA dynamic ensemble models using NMR and structure prediction. Nature Communications, 2020, 11, 5531.	5.8	52
47	Dynamics-Based Amplification of RNA Function and Its Characterization by Using NMR Spectroscopy. ChemBioChem, 2005, 6, 1506-1519.	1.3	51
48	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
49	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
50	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
51	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
52	Visualizing the formation of an RNA folding intermediate through a fast highly modular secondary structure switch. Nature Communications, 2016, 7, ncomms11768.	5.8	50
53	Pseudouridine and N⁶-methyladenosine modifications weaken PUF protein/RNA interactions. Rna, 2017, 23, 611-618.	1.6	50
54	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

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55	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
56	3D maps of RNA interhelical junctions. Nature Protocols, 2011, 6, 1536-1545.	5.5	46
57	NMR Chemical Exchange Measurements Reveal That N⁶-Methyladenosine Slows RNA Annealing. Journal of the American Chemical Society, 2019, 141, 19988-19993.	6.6	46
58	RNA Dynamics by Design: Biasing Ensembles Towards the Ligandâ€Bound State. Angewandte Chemie - International Edition, 2010, 49, 5731-5733.	7.2	44
59	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
60	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
61	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
62	NMR studies of nucleic acid dynamics. Journal of Magnetic Resonance, 2013, 237, 191-204.	1.2	40
63	Modulation of Hoogsteen dynamics on DNA recognition. Nature Communications, 2018, 9, 1473.	5.8	38
64	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
65	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
66	Resolving sugar puckers in RNA excited states exposes slow modes of repuckering dynamics. Nucleic Acids Research, 2017, 45, e134-e134.	6.5	33
67	iRED Analysis of TAR RNA Reveals Motional Coupling, Long-Range Correlations, and a Dynamical Hinge. Biophysical Journal, 2007, 93, 411-422.	0.2	31
68	Utility of 1H NMR Chemical Shifts in Determining RNA Structure and Dynamics. Journal of Physical Chemistry B, 2013, 117, 2045-2052.	1.2	31
69	Flipping of the Ribosomal A-Site Adenines Provides a Basis for tRNA Selection. Journal of Molecular Biology, 2014, 426, 3201-3213.	2.0	31
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	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
72	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

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73	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
74	Evidence that Electrostatic Interactions Dictate the Ligand-Induced Arrest of RNA Global Flexibility. Angewandte Chemie - International Edition, 2005, 44, 3412-3415.	7.2	29
75	Measuring similarity between dynamic ensembles of biomolecules. Nature Methods, 2014, 11, 552-554.	9.0	29
76	Sequence-Specific B-DNA Flexibility Modulates Z-DNA Formation. Journal of the American Chemical Society, 2011, 133, 2016-2018.	6.6	28
77	Probing RNA Conformational Equilibria within the Functional Cellular Context. Cell Reports, 2020, 30, 2472-2480.e4.	2.9	28
78	Residual dipolar couplings: synergy between NMR and structural genomics. Journal of Biomolecular NMR, 2002, 22, 1-8.	1.6	26
79	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
80	Why are Hoogsteen base pairs energetically disfavored in A-RNA compared to B-DNA?. Nucleic Acids Research, 2018, 46, 11099-11114.	6.5	23
81	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
82	Exposing Hidden High-Affinity RNA Conformational States. Journal of the American Chemical Society, 2020, 142, 907-921.	6.6	21
83	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
84	Hidden Structural Modules in a Cooperative RNA Folding Transition. Cell Reports, 2018, 22, 3240-3250.	2.9	20
85	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
86	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
87	Hoogsteen base pairs increase the susceptibility of double-stranded DNA to cytotoxic damage. Journal of Biological Chemistry, 2020, 295, 15933-15947.	1.6	20
88	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
89	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
90	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

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91	Structural dynamics of a single-stranded RNAâ€“helix junction using NMR. Rna, 2014, 20, 782-791.	1.6	16
92	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
93	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
94	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
95	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
96	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
97	The Mechanism of HdeA Unfolding and Chaperone Activation. Journal of Molecular Biology, 2018, 430, 33-40.	2.0	15
98	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
99	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
100	NMR Studies of Biomolecular Dynamics and Structural Plasticity Using Residual Dipolar Couplings. Annual Reports on NMR Spectroscopy, 2003, 51, 105-166.	0.7	14
101	RNA Structural Modules Control the Rate and Pathway of RNA Folding and Assembly. Journal of Molecular Biology, 2016, 428, 3972-3985.	2.0	14
102	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
103	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
104	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
105	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
106	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
107	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
108	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

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109	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
110	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
111	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
112	Anomalous Reverse Transcription through Chemical Modifications in Polyadenosine Stretches. Biochemistry, 2020, 59, 2154-2170.	1.2	8
113	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
114	Slowdown of Interhelical Motions Induces a Glass Transition in RNA. Biophysical Journal, 2015, 108, 2876-2885.	0.2	7
115	Exciting Structures. Science, 2010, 329, 1295-1296.	6.0	6
116	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
117	Dynamic Motions of the HIV-1 Frameshift Site RNA. Biophysical Journal, 2015, 108, 644-654.	0.2	4
118	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
119	An RNA tertiary switch by modifying how helices are tethered. Genome Biology, 2014, 15, 425.	3.8	3
120	Secondary structure encodes a cooperative tertiary folding funnel in theAzoarcusribozyme. Nucleic Acids Research, 2016, 44, 402-412.	6.5	3
121	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
122	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
123	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
124	Structural and Functional Characterization of Sulfonium Carbonâ€“Oxygen Hydrogen Bonding in the Deoxyamino Sugar Methyltransferase TylM1. Biochemistry, 2019, 58, 2152-2159.	1.2	0
125	Using Conformational Penalties to Assess the Structure Dependence of RNA Cellular Function. FASEB Journal, 2019, 33, 220.1.	0.2	0
126	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0

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127	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
128	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0
129	m6A minimally impacts the structure, dynamics, and Rev ARM binding properties of HIV-1 RRE stem IIB. , 2019, 14, e0224850.		0