

# Karl-peter Hopfner

## List of Publications by Year in descending order

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193  
papers

19,040  
citations

12346

69  
h-index

13985

130  
g-index

223  
all docs

223  
docs citations

223  
times ranked

25764  
citing authors

#	ARTICLE	IF	CITATIONS
1	cGAS produces a 2'5'-linked cyclic dinucleotide second messenger that activates STING. <i>Nature</i> , 2013, 498, 380-384.	36.2	1,273
2	Molecular mechanisms and cellular functions of cGAS-STING signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 501-521.	37.3	1,001
3	Structural Biology of Rad50 ATPase. <i>Cell</i> , 2000, 101, 789-800.	27.8	894
4	Structural mechanism of cytosolic DNA sensing by cGAS. <i>Nature</i> , 2013, 498, 332-337.	36.2	666
5	Modulation of protein properties in living cells using nanobodies. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 133-138.	8.1	521
6	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. <i>Nature</i> , 2002, 418, 562-566.	36.2	488
7	The C-Terminal Regulatory Domain Is the RNA 5'-Triphosphate Sensor of RIG-I. <i>Molecular Cell</i> , 2008, 29, 169-179.	9.6	462
8	Structural Biochemistry and Interaction Architecture of the DNA Double-Strand Break Repair Mre11 Nuclease and Rad50-ATPase. <i>Cell</i> , 2001, 105, 473-485.	27.8	456
9	Structural Biochemistry of a Bacterial Checkpoint Protein Reveals Diadenylate Cyclase Activity Regulated by DNA Recombination Intermediates. <i>Molecular Cell</i> , 2008, 30, 167-178.	9.6	377
10	5'-triphosphate RNA requires base-paired structures to activate antiviral signaling via RIG-I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12067-12072.	7.6	353
11	Crosstalk between the cGAS DNA Sensor and Beclin-1 Autophagy Protein Shapes Innate Antimicrobial Immune Responses. <i>Cell Host and Microbe</i> , 2014, 15, 228-238.	11.0	303
12	Epitope interactions of monoclonal antibodies targeting CD20 and their relationship to functional properties. <i>MAbs</i> , 2013, 5, 22-33.	6.7	291
13	Structural basis for DNA duplex separation by a superfamily-2 helicase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 647-652.	8.1	287
14	Cytosolic RNA:DNA hybrids activate the cGAS-STING axis. <i>EMBO Journal</i> , 2014, 33, 2937-2946.	8.2	272
15	Establishment of Sister Chromatid Cohesion at the <i>S. cerevisiae</i> Replication Fork. <i>Molecular Cell</i> , 2006, 23, 787-799.	9.6	271
16	OAS proteins and cGAS: unifying concepts in sensing and responding to cytosolic nucleic acids. <i>Nature Reviews Immunology</i> , 2014, 14, 521-528.	22.5	266
17	Mutations affecting the secretory COPII coat component SEC23B cause congenital dyserythropoietic anemia type II. <i>Nature Genetics</i> , 2009, 41, 936-940.	20.4	260
18	Syk Kinase-Coupled C-type Lectin Receptors Engage Protein Kinase C $\beta$ to Elicit Card9 Adaptor-Mediated Innate Immunity. <i>Immunity</i> , 2012, 36, 32-42.	14.2	254

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19	X-Ray Structures of the <i>Sulfolobus solfataricus</i> SWI2/SNF2 ATPase Core and Its Complex with DNA. <i>Cell</i> , 2005, 121, 363-373.	27.8	233
20	Roles of RIG-I N-terminal tandem CARD and splice variant in TRIM25-mediated antiviral signal transduction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16743-16748.	7.6	223
21	Sequence-specific activation of the DNA sensor cGAS by Y-form DNA structures as found in primary HIV-1 cDNA. <i>Nature Immunology</i> , 2015, 16, 1025-1033.	13.9	214
22	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	36.2	212
23	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. <i>Nature</i> , 2018, 556, 386-390.	36.2	207
24	Crystal structure of a thermostable type B DNA polymerase from <i>Thermococcus gorgonarius</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 3600-3605.	7.6	206
25	Epitope characterization and crystal structure of GA101 provide insights into the molecular basis for type I/II distinction of CD20 antibodies. <i>Blood</i> , 2011, 118, 358-367.	1.4	203
26	Structure and Subunit Topology of the INO80 Chromatin Remodeler and Its Nucleosome Complex. <i>Cell</i> , 2013, 154, 1207-1219.	27.8	198
27	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. <i>Nature Immunology</i> , 2018, 19, 53-62.	13.9	196
28	Rad50/SMC proteins and ABC transporters: unifying concepts from high-resolution structures. <i>Current Opinion in Structural Biology</i> , 2003, 13, 249-255.	5.9	195
29	The Mre11:Rad50 Structure Shows an ATP-Dependent Molecular Clamp in DNA Double-Strand Break Repair. <i>Cell</i> , 2011, 145, 54-66.	27.8	186
30	Species-specific detection of the antiviral small-molecule compound CMA by STING. <i>EMBO Journal</i> , 2013, 32, 1440-1450.	8.2	172
31	Structural basis for sequestration and autoinhibition of cGAS by chromatin. <i>Nature</i> , 2020, 587, 678-682.	36.2	168
32	Structural Biochemistry of ATP-Driven Dimerization and DNA-Stimulated Activation of SMC ATPases. <i>Current Biology</i> , 2004, 14, 1778-1782.	4.0	157
33	RIG-I detects infection with live <i>Listeria</i> by sensing secreted bacterial nucleic acids. <i>EMBO Journal</i> , 2012, 31, 4153-4164.	8.2	157
34	Metabolism and Renal Effects of Enflurane in Man. <i>Anesthesiology</i> , 1976, 44, 44-53.	2.7	145
35	Structural Framework for the Mechanism of Archaeal Exosomes in RNA Processing. <i>Molecular Cell</i> , 2005, 20, 461-471.	9.6	145
36	GATA2 zinc finger 1 mutations associated with biallelic CEBPA mutations define a unique genetic entity of acute myeloid leukemia. <i>Blood</i> , 2012, 120, 395-403.	1.4	140

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37	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002, 12, 115-122.	5.9	136
38	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1 $\beta$ production. <i>Nature Immunology</i> , 2014, 15, 538-545.	13.9	135
39	The ternary microplasmin-staphylokinase-microplasmin complex is a proteinase-cofactor-substrate complex in action. <i>Nature Structural Biology</i> , 1998, 5, 917-923.	8.1	134
40	The regulatory domain of the RIG-I family ATPase LGP2 senses double-stranded RNA. <i>Nucleic Acids Research</i> , 2009, 37, 2014-2025.	14.0	133
41	Coagulation factor IXa: the relaxed conformation of Tyr99 blocks substrate binding. <i>Structure</i> , 1999, 7, 989-996.	3.4	126
42	Functional and biochemical dissection of the structure-specific nuclease ARTEMIS. <i>EMBO Journal</i> , 2004, 23, 1987-1997.	8.2	124
43	Mre11 and Rad50 from <i>Pyrococcus furiosus</i> : Cloning and Biochemical Characterization Reveal an Evolutionarily Conserved Multiprotein Machine. <i>Journal of Bacteriology</i> , 2000, 182, 6036-6041.	2.4	117
44	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004081.	4.1	116
45	MRE11/RAD50/NBS1: complex activities. <i>Chromosoma</i> , 2004, 113, 157-66.	2.1	115
46	Point mutations in the juxtamembrane domain of FLT3 define a new class of activating mutations in AML. <i>Blood</i> , 2006, 107, 3700-3707.	1.4	110
47	Dihydrofolate Reductase Deficiency Due to a Homozygous DHFR Mutation Causes Megaloblastic Anemia and Cerebral Folate Deficiency Leading to Severe Neurologic Disease. <i>American Journal of Human Genetics</i> , 2011, 88, 226-231.	6.1	110
48	Structure of Mre11-Nbs1 complex yields insights into ataxia-telangiectasia-like disease mutations and DNA damage signaling. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 693-700.	8.1	108
49	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014, 46, 901-904.	20.4	106
50	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. <i>Genes and Development</i> , 2016, 30, 337-354.	5.9	105
51	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. <i>Molecular Cell</i> , 2019, 76, 382-394.e6.	9.6	105
52	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. <i>Science Signaling</i> , 2021, 14, .	5.1	105
53	Measuring DNA mechanics on the genome scale. <i>Nature</i> , 2021, 589, 462-467.	36.2	103
54	RG7116, a Therapeutic Antibody That Binds the Inactive HER3 Receptor and Is Optimized for Immune Effector Activation. <i>Cancer Research</i> , 2013, 73, 5183-5194.	0.9	101

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55	Structural mechanism of ATP-dependent DNA binding and DNA end bridging by eukaryotic Rad50. <i>EMBO Journal</i> , 2016, 35, 759-772.	8.2	101
56	Human TGF- $\beta$ 1 deficiency causes severe inflammatory bowel disease and encephalopathy. <i>Nature Genetics</i> , 2018, 50, 344-348.	20.4	100
57	Snf2 family ATPases and DExx box helicases: differences and unifying concepts from high-resolution crystal structures. <i>Nucleic Acids Research</i> , 2006, 34, 4160-4167.	14.0	96
58	ATP driven structural changes of the bacterial Mre11:Rad50 catalytic head complex. <i>Nucleic Acids Research</i> , 2012, 40, 914-927.	14.0	96
59	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011, 25, 2093-2105.	5.9	88
60	The RIG-I ATPase domain structure reveals insights into ATP-dependent antiviral signalling. <i>EMBO Reports</i> , 2011, 12, 1127-1134.	5.1	87
61	The Rad50 Signature Motif: Essential to ATP Binding and Biological Function. <i>Journal of Molecular Biology</i> , 2004, 335, 937-951.	4.3	86
62	Structure and DNA binding activity of the mouse condensin hinge domain highlight common and diverse features of SMC proteins. <i>Nucleic Acids Research</i> , 2010, 38, 3454-3465.	14.0	84
63	X-ray Structure of the Complete ABC Enzyme ABCE1 from <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 7962-7971.	3.5	80
64	Bifunctional PD-1 $\beta$ -CD3 $\beta$ -CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. <i>Blood</i> , 2018, 132, 2484-2494.	1.4	80
65	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. <i>ELife</i> , 2015, 4, .	5.9	78
66	Crystal Structures of Uninhibited Factor VIIa Link its Cofactor and Substrate-assisted Activation to Specific Interactions. <i>Journal of Molecular Biology</i> , 2002, 322, 591-603.	4.3	76
67	Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. <i>Nature</i> , 2011, 475, 403-407.	36.2	74
68	Structural Analysis of Phenothiazine Derivatives as Allosteric Inhibitors of the MALT1 Paracaspase. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 10384-10387.	14.8	72
69	The nuclear actin-containing Arp8 module is a linker DNA sensor driving INO80 chromatin remodeling. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 823-832.	8.1	71
70	X-Ray Structure of RLI, an Essential Twin Cassette ABC ATPase Involved in Ribosome Biogenesis and HIV Capsid Assembly. <i>Structure</i> , 2005, 13, 649-659.	3.4	70
71	Bispecific digoxigenin-binding antibodies for targeted payload delivery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8194-8199.	7.6	69
72	Discrimination of cytosolic self and non-self RNA by RIG-I-like receptors. <i>Journal of Biological Chemistry</i> , 2017, 292, 9000-9009.	3.5	69

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73	Converting blood coagulation factor IXa into factor Xa: dramatic increase in amidolytic activity identifies important active site determinants. <i>EMBO Journal</i> , 1997, 16, 6626-6635.	8.2	68
74	Structural biochemistry of nuclear actin-related proteins 4 and 8 reveals their interaction with actin. <i>EMBO Journal</i> , 2011, 30, 2153-2166.	8.2	65
75	Activating FLT3 Mutants Show Distinct Gain-of-Function Phenotypes In Vitro and a Characteristic Signaling Pathway Profile Associated with Prognosis in Acute Myeloid Leukemia. <i>PLoS ONE</i> , 2014, 9, e89560.	2.5	65
76	Swi2/Snf2 remodelers: hybrid views on hybrid molecular machines. <i>Current Opinion in Structural Biology</i> , 2012, 22, 225-233.	5.9	64
77	Invited review: Architectures and mechanisms of ATP binding cassette proteins. <i>Biopolymers</i> , 2016, 105, 492-504.	2.6	64
78	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. <i>Molecular Cell</i> , 2016, 64, 951-966.	9.6	62
79	Structure of the Rad50 <scp>DNA</scp> double-strand break repair protein in complex with <scp>DNA</scp>. <i>EMBO Journal</i> , 2014, 33, 2847-2859.	8.2	57
80	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. <i>Cell Reports</i> , 2020, 31, 107522.	6.3	56
81	Differential Arrangements of Conserved Building Blocks among Homologs of the Rad50/Mre11 DNA Repair Protein Complex. <i>Journal of Molecular Biology</i> , 2004, 339, 937-949.	4.3	54
82	Molecular architecture and regulation of BCL10-MALT1 filaments. <i>Nature Communications</i> , 2018, 9, 4041.	13.2	52
83	New enzyme lineages by subdomain shuffling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 9813-9818.	7.6	49
84	Structure of Actin-related protein 8 and its contribution to nucleosome binding. <i>Nucleic Acids Research</i> , 2012, 40, 11036-11046.	14.0	49
85	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. <i>Blood</i> , 2013, 122, 1761-1769.	1.4	49
86	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021, 12, 3232.	13.2	49
87	Mechanisms of nucleic acid translocases: lessons from structural biology and single-molecule biophysics. <i>Current Opinion in Structural Biology</i> , 2007, 17, 87-95.	5.9	48
88	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. <i>Nature Communications</i> , 2016, 7, 11733.	13.2	47
89	Structural and functional analysis of Mre11-3. <i>Nucleic Acids Research</i> , 2004, 32, 1886-1893.	14.0	46
90	Theory of allosteric effects in serine proteases. <i>Biophysical Journal</i> , 1996, 70, 174-181.	0.5	43

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91	Correlating Calcium Binding, Förster Resonance Energy Transfer, and Conformational Change in the Biosensor TN-XXL. <i>Biophysical Journal</i> , 2012, 102, 2401-2410.	0.5	43
92	Structural Basis for Dodecameric Assembly States and Conformational Plasticity of the Full-Length AAA+ ATPases Rvb1-Rvb2. <i>Structure</i> , 2015, 23, 483-495.	3.4	43
93	PSMA Expression in Glioblastoma as a Basis for Theranostic Approaches: A Retrospective, Correlational Panel Study Including Immunohistochemistry, Clinical Parameters and PET Imaging. <i>Frontiers in Oncology</i> , 2021, 11, 646387.	2.9	43
94	Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle. <i>Nucleic Acids Research</i> , 2008, 36, 1881-1890.	14.0	41
95	Physiological fliXa Activation Involves a Cooperative Conformational Rearrangement of the 99-Loop. <i>Journal of Biological Chemistry</i> , 2003, 278, 4121-4126.	3.5	40
96	The exosome: a macromolecular cage for controlled RNA degradation. <i>Molecular Microbiology</i> , 2006, 61, 1372-1379.	2.5	40
97	Sensing of viral nucleic acids by RIG-I: From translocation to translation. <i>European Journal of Cell Biology</i> , 2012, 91, 78-85.	3.7	40
98	Nuclear cGAS: guard or prisoner?. <i>EMBO Journal</i> , 2021, 40, e108293.	8.2	40
99	MlaA, a hexameric ATPase linked to the Mre11 complex in archaeal genomes. <i>EMBO Reports</i> , 2004, 5, 54-59.	5.1	39
100	Mechanism of replication blocking and bypass of Y-family polymerase $\eta$ by bulky acetylaminofluorene DNA adducts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20720-20725.	7.6	39
101	Structural and biochemical characterization of the cell fate determining nucleotidyltransferase fold protein MAB21L1. <i>Scientific Reports</i> , 2016, 6, 27498.	3.4	38
102	Activity-Based Probes for Detection of Active MALT1 Paracaspase in Immune Cells and Lymphomas. <i>Chemistry and Biology</i> , 2015, 22, 129-138.	6.2	37
103	Challenges in eHealth: From Enabling to Enforcing Privacy. <i>Lecture Notes in Computer Science</i> , 2012, , 195-206.	1.0	34
104	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. <i>Nature Communications</i> , 2021, 12, 3231.	13.2	34
105	Molecular basis of human ATM kinase inhibition. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 789-798.	8.1	33
106	Impact of Heterogeneity and Lattice Bond Strength on DNA Triangle Crystal Growth. <i>ACS Nano</i> , 2016, 10, 9156-9164.	15.3	32
107	Structural Basis for Transcription-coupled Repair: the N Terminus of Mfd Resembles UvrB with Degenerate ATPase Motifs. <i>Journal of Molecular Biology</i> , 2006, 355, 675-683.	4.3	30
108	Crystal Structure of an Anti-Ang2 CrossFab Demonstrates Complete Structural and Functional Integrity of the Variable Domain. <i>PLoS ONE</i> , 2013, 8, e61953.	2.5	30

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109	Structural and biochemical characterization of human Schlafen 5. <i>Nucleic Acids Research</i> , 2022, 50, 1147-1161.	14.0	28
110	Structural Studies of DNA End Detection and Resection in Homologous Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a017962-a017962.	5.4	27
111	CD19-specific triplebody SPM-1 engages NK and $\gamma\delta$ T cells for rapid and efficient lysis of malignant B-lymphoid cells. <i>Oncotarget</i> , 2016, 7, 83392-83408.	2.1	27
112	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. <i>ELife</i> , 2018, 7, .	5.9	27
113	Mechanistic understanding of human SLFN11. <i>Nature Communications</i> , 2022, 13, .	13.2	27
114	Structure and DNA-binding activity of the <i>Pyrococcus furiosus</i> SMC protein hinge domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 558-568.	3.2	26
115	Near-Complete Structure and Model of Tel1ATM from <i>Chaetomium thermophilum</i> Reveals a Robust Autoinhibited ATP State. <i>Structure</i> , 2020, 28, 83-95.e5.	3.4	26
116	Megadalton chromatin remodelers: common principles for versatile functions. <i>Current Opinion in Structural Biology</i> , 2020, 64, 134-144.	5.9	26
117	A modular and controllable T cell therapy platform for acute myeloid leukemia. <i>Leukemia</i> , 2021, 35, 2243-2257.	7.5	26
118	Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017, 45, 12025-12038.	14.0	25
119	Cryo-EM structure of the Mre11-Rad50-Nbs1 complex reveals the molecular mechanism of scaffolding functions. <i>Molecular Cell</i> , 2023, 83, 167-185.e9.	9.6	25
120	Structural analysis of the diadenylate cyclase reaction of DNA-integrity scanning protein A (DisA) and its inhibition by $\gamma$ -dATP. <i>Biochemical Journal</i> , 2015, 469, 367-374.	3.8	24
121	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. <i>Nucleic Acids Research</i> , 2010, 38, 5166-5176.	14.0	23
122	Dual-targeting triplebody 33-16-123 (SPM-2) mediates effective redirected lysis of primary blasts from patients with a broad range of AML subtypes in combination with natural killer cells. <i>Oncolmmunology</i> , 2018, 7, e1472195.	4.8	23
123	Energetics of the thrombin-fibrinogen interaction. <i>Biochemistry</i> , 1992, 31, 11567-11571.	2.6	21
124	Chemical compensation in macromolecular bridge-binding to thrombin. <i>Biochemistry</i> , 1993, 32, 2947-2953.	2.6	21
125	DNA Mismatch Repair. <i>Structure</i> , 2000, 8, R237-R241.	3.4	21
126	OAS1/RNase L executes RIG-I ligand-dependent tumor cell apoptosis. <i>Science Immunology</i> , 2021, 6, .	13.1	21



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127	Crystal Structure of Human TWEAK in Complex with the Fab Fragment of a Neutralizing Antibody Reveals Insights into Receptor Binding. <i>PLoS ONE</i> , 2013, 8, e62697.	2.5	19
128	Structure of the catalytic domain of Mre11 from <i>Chaetomium thermophilum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 752-757.	0.9	19
129	The bacterial Mre11-Rad50 homolog SbcCD cleaves opposing strands of DNA by two chemically distinct nuclease reactions. <i>Nucleic Acids Research</i> , 2018, 46, 11303-11314.	14.0	19
130	Dual-targeting triplebody 33-3-19 mediates selective lysis of biphenotypic CD19+ CD33+ leukemia cells. <i>Oncotarget</i> , 2016, 7, 22579-22589.	2.1	19
131	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. <i>ELife</i> , 2015, 4, .	5.9	19
132	Energy model for contrast detection: spatiotemporal characteristics of threshold vision. <i>Biological Cybernetics</i> , 1999, 81, 61-71.	1.3	18
133	SIRP $\alpha$ -antibody fusion proteins stimulate phagocytosis and promote elimination of acute myeloid leukemia cells. <i>Oncotarget</i> , 2017, 8, 11284-11301.	2.1	18
134	A Click-Chemistry Linked 2 $\beta$ -3 $\beta$ -cGAMP Analogue. <i>Chemistry - A European Journal</i> , 2019, 25, 2089-2095.	3.9	17
135	Structural mechanism of extranucleosomal DNA readout by the INO80 complex. <i>Science Advances</i> , 2022, 8, .	10.9	17
136	Lessons from structural and biochemical studies on the archaeal exosome. <i>Biochemical Society Transactions</i> , 2009, 37, 83-87.	3.4	16
137	ATP puts the brake on DNA double-strand break repair. <i>BioEssays</i> , 2014, 36, 1170-1178.	2.6	16
138	SIRP $\alpha$ -CD123 fusion antibodies targeting CD123 in conjunction with CD47 blockade enhance the clearance of AML-initiating cells. <i>Journal of Hematology and Oncology</i> , 2021, 14, 155.	17.6	16
139	Novel Poxin Stable cGAMP-Derivatives Are Remarkable STING Agonists. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	14.8	16
140	Hexasome-INO80 complex reveals structural basis of noncanonical nucleosome remodeling. <i>Science</i> , 2023, 381, 313-319.	20.9	15
141	DNA Double-Strand Breaks Come into Focus. <i>Cell</i> , 2009, 139, 25-27.	27.8	14
142	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. <i>Nucleic Acids Research</i> , 2021, 49, 10166-10177.	14.0	14
143	Rustless translation. <i>Biological Chemistry</i> , 2012, 393, 1079-1088.	2.6	13
144	Monocyte-derived macrophages aggravate pulmonary vasculitis via cGAS/STING/IFN-mediated nucleic acid sensing. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.8	13

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145	Reversible and Controllable Nanolocomotion of an RNA-Processing Machinery. <i>Nano Letters</i> , 2010, 10, 5123-5130.	9.5	12
146	NK cells from an AML patient have recovered in remission and reached comparable cytolytic activity to that of a healthy monozygotic twin mediated by the single-chain triplebody SPM-2. <i>Journal of Translational Medicine</i> , 2013, 11, 289.	4.5	12
147	Response to: Monoclonal antibodies targeting CD20. <i>MAbs</i> , 2013, 5, 337-338.	6.7	12
148	Biochemical Characterization and Crystal Structure of a Dim1 Family Associated Protein: Dim2. <i>Biochemistry</i> , 2005, 44, 11997-12008.	2.6	11
149	Structural Basis for Adenylate Kinase Activity in ABC ATPases. <i>Journal of Molecular Biology</i> , 2010, 401, 265-273.	4.3	10
150	Mre11-Rad50: the DNA end game. <i>Biochemical Society Transactions</i> , 2023, 51, 527-538.	3.4	10
151	Structural basis of the (in)activity of the apical DNA damage response kinases ATM, ATR and DNA-PKcs. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 163, 120-129.	3.0	9
152	Accumulation of mutations in antibody and CD8 T cell epitopes in a B cell depleted lymphoma patient with chronic SARS-CoV-2 infection. <i>Nature Communications</i> , 2022, 13, .	13.2	9
153	Chromosome Biology: The Crux of the Ring. <i>Current Biology</i> , 2006, 16, R102-R105.	4.0	8
154	Structure-Function Analysis of SWI2/SNF2 Enzymes. <i>Methods in Enzymology</i> , 2006, 409, 375-388.	1.7	8
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