

Karl-peter Hopfner

List of Publications by Year in descending order

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193
papers

19,040
citations

12346

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h-index

13985

130
g-index

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all docs

223
docs citations

223
times ranked

25764
citing authors

#	ARTICLE	IF	CITATIONS
1	Energy-driven genome regulation by ATP-dependent chromatin remodellers. <i>Nature Reviews Molecular Cell Biology</i> , 2024, 25, 309-332.	37.3	8
2	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
3	Mre11-Rad50: the DNA end game. <i>Biochemical Society Transactions</i> , 2023, 51, 527-538.	3.4	10
4	Hexasome-INO80 complex reveals structural basis of noncanonical nucleosome remodeling. <i>Science</i> , 2023, 381, 313-319.	20.9	15
5	Structural basis for TBP displacement from TATA box DNA by the Swi2/Snf2 ATPase Mot1. <i>Nature Structural and Molecular Biology</i> , 2023, 30, 640-649.	8.1	3
6	A SAM-key domain required for enzymatic activity of the Fun30 nucleosome remodeler. <i>Life Science Alliance</i> , 2023, 6, e202201790.	2.9	0
7	Structural and biochemical characterization of human Schlafen 5. <i>Nucleic Acids Research</i> , 2022, 50, 1147-1161.	14.0	28
8	Chemical Synthesis of the Fluorescent, Cyclic Dinucleotides cGAMP. <i>ChemBioChem</i> , 2022, 23, .	2.8	7
9	Novel Poxin Stable cGAMP-Derivatives Are Remarkable STING Agonists. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	14.8	16
10	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
11	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
12	Mechanistic understanding of human SLFN11. <i>Nature Communications</i> , 2022, 13, .	13.2	27
13	Structural mechanism of extranucleosomal DNA readout by the INO80 complex. <i>Science Advances</i> , 2022, 8, .	10.9	17
14	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
15	Measuring DNA mechanics on the genome scale. <i>Nature</i> , 2021, 589, 462-467.	36.2	103
16	A modular and controllable T cell therapy platform for acute myeloid leukemia. <i>Leukemia</i> , 2021, 35, 2243-2257.	7.5	26
17	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
18	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. <i>Science Signaling</i> , 2021, 14, .	5.1	105

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19	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021, 12, 3232.	13.2	49
20	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. <i>Nature Communications</i> , 2021, 12, 3231.	13.2	34
21	Nuclear cGAS: guard or prisoner?. <i>EMBO Journal</i> , 2021, 40, e108293.	8.2	40
22	OAS1/RNase L executes RIG-I ligand-dependent tumor cell apoptosis. <i>Science Immunology</i> , 2021, 6, .	13.1	21
23	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. <i>Nucleic Acids Research</i> , 2021, 49, 10166-10177.	14.0	14
24	SIRP α -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
25	Molecular basis of human ATM kinase inhibition. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 789-798.	8.1	33
26	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
27	Megadalton chromatin remodelers: common principles for versatile functions. <i>Current Opinion in Structural Biology</i> , 2020, 64, 134-144.	5.9	26
28	Structural basis for sequestration and autoinhibition of cGAS by chromatin. <i>Nature</i> , 2020, 587, 678-682.	36.2	168
29	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. <i>Cell Reports</i> , 2020, 31, 107522.	6.3	56
30	Molecular mechanisms and cellular functions of cGAS-STING signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 501-521.	37.3	1,001
31	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. <i>Molecular Cell</i> , 2019, 76, 382-394.e6.	9.6	105
32	A Click-Chemistry Linked 2 β -GAMP Analogue. <i>Chemistry - A European Journal</i> , 2019, 25, 2089-2095.	3.9	17
33	Exploiting an Anti-CD3/CD33 Bispecific Antibody to Redirect Donor T Cells Against HLA Loss Leukemia Relapses. <i>Blood</i> , 2019, 134, 513-513.	1.4	2
34	Evaluation of a Bifunctional Sirp α -CD123 Fusion Antibody for the Elimination of Acute Myeloid Leukemia Stem Cells. <i>Blood</i> , 2019, 134, 2544-2544.	1.4	3
35	Aberrant Cathepsin S Induces a Supportive Immune Microenvironment in Follicular Lymphoma. <i>Blood</i> , 2019, 134, 657-657.	1.4	0
36	Human TGF β 1 deficiency causes severe inflammatory bowel disease and encephalopathy. <i>Nature Genetics</i> , 2018, 50, 344-348.	20.4	100

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37	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. <i>Nature</i> , 2018, 556, 386-390.	36.2	207
38	Mechanistic Insight into the Assembly of the HerA-NurA Helicase-Nuclease DNA End Resection Complex using Native Mass Spectrometry. <i>Biophysical Journal</i> , 2018, 114, 440a.	0.5	0
39	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. <i>Nature Immunology</i> , 2018, 19, 53-62.	13.9	196
40	Bifunctional PD-1 Δ CD3 Δ CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. <i>Blood</i> , 2018, 132, 2484-2494.	1.4	80
41	Molecular architecture and regulation of BCL10-MALT1 filaments. <i>Nature Communications</i> , 2018, 9, 4041.	13.2	52
42	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
43	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
44	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>Oncology</i> , 2018, 7, e1472195.	4.8	23
45	Crystal structure of the full Swi2/Snf2 remodeler Mot1 in the resting state. <i>ELife</i> , 2018, 7, .	5.9	4
46	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. <i>ELife</i> , 2018, 7, .	5.9	27
47	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
48	Dissecting the Mechanism of the HerA NurA DNA Break Resection Complex using Native Mass Spectrometry. <i>Biophysical Journal</i> , 2017, 112, 515a.	0.5	0
49	SIRP α -antibody fusion proteins stimulate phagocytosis and promote elimination of acute myeloid leukemia cells. <i>Oncotarget</i> , 2017, 8, 11284-11301.	2.1	18
50	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
51	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
52	Catalytic Mechanism of the INO80 Chromatin Remodeler Acting on the Nucleosome. <i>Biophysical Journal</i> , 2016, 110, 236a.	0.5	0
53	RIG-I-Like Receptors: One STREP Forward. <i>Trends in Microbiology</i> , 2016, 24, 517-519.	7.7	4
54	Editorial overview: Macromolecular machines and assemblies. <i>Current Opinion in Structural Biology</i> , 2016, 37, vi-viii.	5.9	0

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55	Impact of Heterogeneity and Lattice Bond Strength on DNA Triangle Crystal Growth. ACS Nano, 2016, 10, 9156-9164.	15.3	32
56	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. Molecular Cell, 2016, 64, 951-966.	9.6	62
57	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. Nature Communications, 2016, 7, 11733.	13.2	47
58	Structural and biochemical characterization of the cell fate determining nucleotidyltransferase fold protein MAB21L1. Scientific Reports, 2016, 6, 27498.	3.4	38
59	Invited review: Architectures and mechanisms of ATP binding cassette proteins. Biopolymers, 2016, 105, 492-504.	2.6	64
60	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. Genes and Development, 2016, 30, 337-354.	5.9	105
61	Chip-based platform for dynamic analysis of NK cell cytotoxicity mediated by a triplebody. Analyst, The, 2016, 141, 2284-2295.	3.5	7
62	CD19-specific triplebody SPM-1 engages NK and T cells for rapid and efficient lysis of malignant B-lymphoid cells. Oncotarget, 2016, 7, 83392-83408.	2.1	27
63	Dual-targeting triplebody 33-3-19 mediates selective lysis of biphenotypic CD19+ CD33+ leukemia cells. Oncotarget, 2016, 7, 22579-22589.	2.1	19
64	Structural analysis of the diadenylate cyclase reaction of DNA-integrity scanning protein A (DisA) and its inhibition by 3'-dATP. Biochemical Journal, 2015, 469, 367-374.	3.8	24
65	Activity-Based Probes for Detection of Active MALT1 Paracaspase in Immune Cells and Lymphomas. Chemistry and Biology, 2015, 22, 129-138.	6.2	37
66	Serendipitous crystallization and structure determination of cyanase (CynS) from <i>Serratia proteamaculans</i> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 471-476.	0.9	8
67	Structure of the catalytic domain of Mre11 from <i>Chaetomium thermophilum</i> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 752-757.	0.9	19
68	Structural Basis for Dodecameric Assembly States and Conformational Plasticity of the Full-Length AAA+ ATPases Rvb1-Rvb2. Structure, 2015, 23, 483-495.	3.4	43
69	Sequence-specific activation of the DNA sensor cGAS by Y-form DNA structures as found in primary HIV-1 cDNA. Nature Immunology, 2015, 16, 1025-1033.	13.9	214
70	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. ELife, 2015, 4, .	5.9	19
71	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. ELife, 2015, 4, .	5.9	78
72	Crystal and solution structure of the human RIG-I SF2 domain. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1027-1031.	0.9	4

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73	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004081.	4.1	116
74	Cytosolic RNA:DNA hybrids activate the cGAS-STING axis. <i>EMBO Journal</i> , 2014, 33, 2937-2946.	8.2	272
75	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
76	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1 β production. <i>Nature Immunology</i> , 2014, 15, 538-545.	13.9	135
77	Editorial overview: Theory and simulation: Macromolecular machines. <i>Current Opinion in Structural Biology</i> , 2014, 25, vi-viii.	5.9	0
78	Structure of the Rad50 DNA double-strand break repair protein in complex with DNA. <i>EMBO Journal</i> , 2014, 33, 2847-2859.	8.2	57
79	ATP puts the brake on DNA double-strand break repair. <i>BioEssays</i> , 2014, 36, 1170-1178.	2.6	16
80	RIG-I Holds the CARDS in a Game of Self versus Nonself. <i>Molecular Cell</i> , 2014, 55, 505-507.	9.6	7
81	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
82	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
83	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014, 46, 901-904.	20.4	106
84	Single-Molecule Choreography between Telomere Proteins and G Quadruplexes. <i>Structure</i> , 2014, 22, 801-802.	3.4	0
85	Crystallization of Mouse RIG-I ATPase Domain: In Situ Proteolysis. <i>Methods in Molecular Biology</i> , 2014, 1169, 27-35.	0.0	1
86	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
87	T cell-recruiting triplebody 19-3-19 mediates serial lysis of malignant B-lymphoid cells by a single T cell. <i>Oncotarget</i> , 2014, 5, 6466-6483.	2.1	6
88	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
89	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
90	Structure and Subunit Topology of the INO80 Chromatin Remodeler and Its Nucleosome Complex. <i>Cell</i> , 2013, 154, 1207-1219.	27.8	198

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91	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
92	Species-specific detection of the antiviral small-molecule compound CMA by STING. <i>EMBO Journal</i> , 2013, 32, 1440-1450.	8.2	172
93	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
94	Epitope interactions of monoclonal antibodies targeting CD20 and their relationship to functional properties. <i>MAbs</i> , 2013, 5, 22-33.	6.7	291
95	Structural mechanism of cytosolic DNA sensing by cGAS. <i>Nature</i> , 2013, 498, 332-337.	36.2	666
96	cGAS produces a 2â€²-5â€²-linked cyclic dinucleotide second messenger that activates STING. <i>Nature</i> , 2013, 498, 380-384.	36.2	1,273
97	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. <i>Blood</i> , 2013, 122, 1761-1769.	1.4	49
98	Response to: Monoclonal antibodies targeting CD20. <i>MAbs</i> , 2013, 5, 337-338.	6.7	12
99	Strukturelle Analyse von Phenothiazinâ€¦Derivaten als allosterische Inhibitoren der MALT1â€¦Paracaspase. <i>Angewandte Chemie</i> , 2013, 125, 10575-10579.	2.1	0
100	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
101	Rustless translation. <i>Biological Chemistry</i> , 2012, 393, 1079-1088.	2.6	13
102	ATP driven structural changes of the bacterial Mre11:Rad50 catalytic head complex. <i>Nucleic Acids Research</i> , 2012, 40, 914-927.	14.0	96
103	Structure of Actin-related protein 8 and its contribution to nucleosome binding. <i>Nucleic Acids Research</i> , 2012, 40, 11036-11046.	14.0	49
104	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
105	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	36.2	212
106	Syk Kinase-Coupled C-type Lectin Receptors Engage Protein Kinase C-Î³ to Elicit Card9 Adaptor-Mediated Innate Immunity. <i>Immunity</i> , 2012, 36, 32-42.	14.2	254
107	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
108	Structure of Mre11â€¦Nbs1 complex yields insights into ataxia-telangiectasiaâ€¦like disease mutations and DNA damage signaling. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 693-700.	8.1	108

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109	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
110	Challenges in eHealth: From Enabling to Enforcing Privacy. <i>Lecture Notes in Computer Science</i> , 2012, , 195-206.	1.0	34
111	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
112	Swi2/Snf2 remodelers: hybrid views on hybrid molecular machines. <i>Current Opinion in Structural Biology</i> , 2012, 22, 225-233.	5.9	64
113	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
114	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
115	The RIG-I ATPase domain structure reveals insights into ATP-dependent antiviral signalling. <i>EMBO Reports</i> , 2011, 12, 1127-1134.	5.1	87
116	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
117	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
118	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
119	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
120	Nuclear actin-related proteins take shape. <i>Bioarchitecture</i> , 2011, 1, 192-195.	1.5	7
121	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
122	Molecular basis of Rn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011, 25, 2093-2105.	5.9	88
123	Modulation of protein properties in living cells using nanobodies. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 133-138.	8.1	521
124	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
125	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. <i>Nucleic Acids Research</i> , 2010, 38, 5166-5176.	14.0	23
126	Mechanism of replication blocking and bypass of Y-family polymerase η 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

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127	Reversible and Controllable Nanolocomotion of an RNA-Processing Machinery. <i>Nano Letters</i> , 2010, 10, 5123-5130.	9.5	12
128	Structural Basis for Adenylate Kinase Activity in ABC ATPases. <i>Journal of Molecular Biology</i> , 2010, 401, 265-273.	4.3	10
129	RIG-I-Like RNA Helicases: Multidomain Proteins in Antiviral Innate Immunity and Processing of Small Regulatory RNAs. , 2010, , 121-148.		0
130	Insights into DNA damage signaling from the structure of an Mre11:Nbs1 complex. <i>FASEB Journal</i> , 2010, 24, 1b39.	0.5	0
131	5â€²-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
132	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
133	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
134	DNA Double-Strand Breaks Come into Focus. <i>Cell</i> , 2009, 139, 25-27.	27.8	14
135	Single Molecule Study Of the RNA Degradation and Polyadenylation Activities of the Archaeal Exosome. <i>Biophysical Journal</i> , 2009, 96, 367a.	0.5	0
136	Lessons from structural and biochemical studies on the archaeal exosome. <i>Biochemical Society Transactions</i> , 2009, 37, 83-87.	3.4	16
137	The C-Terminal Regulatory Domain Is the RNA 5â€²-Triphosphate Sensor of RIG-I. <i>Molecular Cell</i> , 2008, 29, 169-179.	9.6	462
138	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
139	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
140	Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle. <i>Nucleic Acids Research</i> , 2008, 36, 1881-1890.	14.0	41
141	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
142	The chemistry of transcription through damaged DNA and of translesion synthesis at atomic resolution. <i>Nucleic Acids Symposium Series</i> , 2007, 51, 103-103.	0.3	0
143	The exosome, plugged. <i>EMBO Reports</i> , 2007, 8, 456-457.	5.1	1
144	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

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145	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
146	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
147	Establishment of Sister Chromatid Cohesion at the <i>S. cerevisiae</i> Replication Fork. <i>Molecular Cell</i> , 2006, 23, 787-799.	9.6	271
148	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
149	The exosome: a macromolecular cage for controlled RNA degradation. <i>Molecular Microbiology</i> , 2006, 61, 1372-1379.	2.5	40
150	Chromosome Biology: The Crux of the Ring. <i>Current Biology</i> , 2006, 16, R102-R105.	4.0	8
151	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
152	Structure-Function Analysis of SWI2/SNF2 Enzymes. <i>Methods in Enzymology</i> , 2006, 409, 375-388.	1.7	8
153	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
154	Biochemical Characterization and Crystal Structure of a Dim1 Family Associated Protein: Dim2. <i>Biochemistry</i> , 2005, 44, 11997-12008.	2.6	11
155	Structural Framework for the Mechanism of Archaeal Exosomes in RNA Processing. <i>Molecular Cell</i> , 2005, 20, 461-471.	9.6	145
156	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
157	Structure and Function of Rad50/SMC Protein Complexes in Chromosome Biology. , 2005, , 201-218.		0
158	The Mre11/Rad50/Nbs1 Complex. , 2005, , .		0
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