

# Karl-Peter Hopfner

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4563729/publications.pdf>

Version: 2024-02-01

188  
papers

18,255  
citations

13865

67  
h-index

14208

128  
g-index

208  
all docs

208  
docs citations

208  
times ranked

22955  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and biochemical characterization of human Schlafen 5. <i>Nucleic Acids Research</i> , 2022, 50, 1147-1161.	14.5	23
2	Chemical Synthesis of the Fluorescent, Cyclic Dinucleotides c <sup>th</sup> GAMP. <i>ChemBioChem</i> , 2022, 23, .	2.6	7
3	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.	2.9	8
4	Measuring DNA mechanics on the genome scale. <i>Nature</i> , 2021, 589, 462-467.	27.8	81
5	A modular and controllable T cell therapy platform for acute myeloid leukemia. <i>Leukemia</i> , 2021, 35, 2243-2257.	7.2	24
6	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. <i>Science Signaling</i> , 2021, 14, .	3.6	87
7	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021, 12, 3232.	12.8	34
8	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. <i>Nature Communications</i> , 2021, 12, 3231.	12.8	27
9	Nuclear cGAS: guard or prisoner?. <i>EMBO Journal</i> , 2021, 40, e108293.	7.8	36
10	OAS1/RNase L executes RIG-I ligandâ€“dependent tumor cell apoptosis. <i>Science Immunology</i> , 2021, 6, .	11.9	19
11	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. <i>Nucleic Acids Research</i> , 2021, 49, 10166-10177.	14.5	11
12	SIRPÎ±-Î±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.	17.0	13
13	Molecular basis of human ATM kinase inhibition. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 789-798.	8.2	26
14	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.	3.3	24
15	Megadalton chromatin remodelers: common principles for versatile functions. <i>Current Opinion in Structural Biology</i> , 2020, 64, 134-144.	5.7	22
16	Structural basis for sequestration and autoinhibition of cGAS by chromatin. <i>Nature</i> , 2020, 587, 678-682.	27.8	146
17	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. <i>Cell Reports</i> , 2020, 31, 107522.	6.4	50
18	Molecular mechanisms and cellular functions of cGASâ€“STING signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 501-521.	37.0	846

#	ARTICLE	IF	CITATIONS
19	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. <i>Molecular Cell</i> , 2019, 76, 382-394.e6.	9.7	100
20	DuoMab: a novel CrossMab-based IgG-derived antibody format for enhanced antibody-dependent cell-mediated cytotoxicity. <i>MAbs</i> , 2019, 11, 1402-1414.	5.2	8
21	A Click-Chemistry Linked 2'-5'-GAMP Analogue. <i>Chemistry - A European Journal</i> , 2019, 25, 2089-2095.	3.3	16
22	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	1
23	Evaluation of a Bifunctional Sirp1±-CD123 Fusion Antibody for the Elimination of Acute Myeloid Leukemia Stem Cells. <i>Blood</i> , 2019, 134, 2544-2544.	1.4	3
24	Aberrant Cathepsin S Induces a Supportive Immune Microenvironment in Follicular Lymphoma. <i>Blood</i> , 2019, 134, 657-657.	1.4	0
25	Human TGF-Î²1 deficiency causes severe inflammatory bowel disease and encephalopathy. <i>Nature Genetics</i> , 2018, 50, 344-348.	21.4	95
26	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. <i>Nature</i> , 2018, 556, 386-390.	27.8	188
27	Single-molecule nucleosome remodeling by <sc>INO</sc>80 and effects of histone tails. <i>FEBS Letters</i> , 2018, 592, 318-331.	2.8	12
28	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
29	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. <i>Nature Immunology</i> , 2018, 19, 53-62.	14.5	179
30	Bifunctional PD-1 Å— Î±CD3 Å— Î±CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. <i>Blood</i> , 2018, 132, 2484-2494.	1.4	73
31	Molecular architecture and regulation of BCL10-MALT1 filaments. <i>Nature Communications</i> , 2018, 9, 4041.	12.8	47
32	The bacterial Mre11â€“Rad50 homolog SbcCD cleaves opposing strands of DNA by two chemically distinct nuclease reactions. <i>Nucleic Acids Research</i> , 2018, 46, 11303-11314.	14.5	19
33	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.	8.2	63
34	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>OncImmunology</i> , 2018, 7, e1472195.	4.6	21
35	Crystal structure of the full Swi2/Snf2 remodeler Mot1 in the resting state. <i>ELife</i> , 2018, 7, .	6.0	4
36	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. <i>ELife</i> , 2018, 7, .	6.0	26

#	ARTICLE	IF	CITATIONS
37	Discrimination of cytosolic self and non-self RNA by RIG-I-like receptors. <i>Journal of Biological Chemistry</i> , 2017, 292, 9000-9009.	3.4	68
38	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
39	cGAS senses long and HMGB/TFAM-bound U-turn DNA by forming proteinâ€“DNA ladders. <i>Nature</i> , 2017, 549, 394-398.	27.8	346
40	SIRPÎ±-antibody fusion proteins stimulate phagocytosis and promote elimination of acute myeloid leukemia cells. <i>Oncotarget</i> , 2017, 8, 11284-11301.	1.8	17
41	Mechanistic insight into the assembly of the HerAâ€“NurA helicaseâ€“nuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017, 45, 12025-12038.	14.5	23
42	Structural mechanism of <scp>ATP</scp>-dependent <scp>DNA</scp> binding and <scp>DNA</scp> end bridging by eukaryotic Rad50. <i>EMBO Journal</i> , 2016, 35, 759-772.	7.8	99
43	Catalytic Mechanism of the INO80 Chromatin Remodeler Acting on the Nucleosome. <i>Biophysical Journal</i> , 2016, 110, 236a.	0.5	0
44	RIG-I-Like Receptors: One STREP Forward. <i>Trends in Microbiology</i> , 2016, 24, 517-519.	7.7	4
45	Editorial overview: Macromolecular machines and assemblies. <i>Current Opinion in Structural Biology</i> , 2016, 37, vi-viii.	5.7	0
46	Impact of Heterogeneity and Lattice Bond Strength on DNA Triangle Crystal Growth. <i>ACS Nano</i> , 2016, 10, 9156-9164.	14.6	31
47	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. <i>Molecular Cell</i> , 2016, 64, 951-966.	9.7	57
48	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. <i>Nature Communications</i> , 2016, 7, 11733.	12.8	45
49	Structural and biochemical characterization of the cell fate determining nucleotidyltransferase fold protein MAB21L1. <i>Scientific Reports</i> , 2016, 6, 27498.	3.3	36
50	Invited review: Architectures and mechanisms of ATP binding cassette proteins. <i>Biopolymers</i> , 2016, 105, 492-504.	2.4	62
51	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	103
52	Chip-based platform for dynamic analysis of NK cell cytotoxicity mediated by a triplebody. <i>Analyst</i> , The, 2016, 141, 2284-2295.	3.5	7
53	CD19-specific triplebody SPM-1 engages NK and Î³Î´ T cells for rapid and efficient lysis of malignant B-lymphoid cells. <i>Oncotarget</i> , 2016, 7, 83392-83408.	1.8	25
54	Dual-targeting triplebody 33-3-19 mediates selective lysis of biphenotypic CD19+ CD33+ leukemia cells. <i>Oncotarget</i> , 2016, 7, 22579-22589.	1.8	19

#	ARTICLE	IF	CITATIONS
55	Structural analysis of the diadenylate cyclase reaction of DNA-integrity scanning protein A (DisA) and its inhibition by 3 <sup>â€²</sup> -dATP. <i>Biochemical Journal</i> , 2015, 469, 367-374.	3.7	22
56	Activity-Based Probes for Detection of Active MALT1 Paracaspase in Immune Cells and Lymphomas. <i>Chemistry and Biology</i> , 2015, 22, 129-138.	6.0	36
57	Serendipitous crystallization and structure determination of cyanase (CynS) from <i>Serratia proteamaculans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 471-476.	0.8	8
58	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.	0.8	19
59	Structural Basis for Dodecameric Assembly States and Conformational Plasticity of the Full-Length AAA+ ATPases Rvb1 $\hat{A}$ -Rvb2. <i>Structure</i> , 2015, 23, 483-495.	3.3	39
60	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.	14.5	202
61	cAMP recognition by <i>Staphylococcus aureus</i> PstA. <i>FEBS Letters</i> , 2015, 589, 45-51.	2.8	52
62	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. <i>ELife</i> , 2015, 4, .	6.0	19
63	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. <i>ELife</i> , 2015, 4, .	6.0	75
64	Crystal and solution structure of the human RIG-I SF2 domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1027-1031.	0.8	4
65	In Vivo Ligands of MDA5 and RIG-I in Measles Virus-Infected Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004081.	4.7	111
66	Cytosolic RNA:DNA hybrids activate the cGAS $\hat{A}$ STING axis. <i>EMBO Journal</i> , 2014, 33, 2937-2946.	7.8	257
67	Molecular architecture of the HerA $\hat{A}$ NurA DNA double-strand break resection complex. <i>FEBS Letters</i> , 2014, 588, 4637-4644.	2.8	15
68	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	291
69	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1 $\hat{2}$ production. <i>Nature Immunology</i> , 2014, 15, 538-545.	14.5	132
70	Editorial overview: Theory and simulation: Macromolecular machines. <i>Current Opinion in Structural Biology</i> , 2014, 25, vi-viii.	5.7	0
71	Structure of the Rad50 DNA double-strand break repair protein in complex with DNA. <i>EMBO Journal</i> , 2014, 33, 2847-2859.	7.8	55
72	ATP puts the brake on DNA double-strand break repair. <i>BioEssays</i> , 2014, 36, 1170-1178.	2.5	16

#	ARTICLE	IF	CITATIONS
73	RIG-I Holds the CARDs in a Game of Self versus Nonself. <i>Molecular Cell</i> , 2014, 55, 505-507.	9.7	7
74	Structural Studies of DNA End Detection and Resection in Homologous Recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a017962-a017962.	5.5	25
75	OAS proteins and cGAS: unifying concepts in sensing and responding to cytosolic nucleic acids. <i>Nature Reviews Immunology</i> , 2014, 14, 521-528.	22.7	246
76	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014, 46, 901-904.	21.4	104
77	Single-Molecule Choreography between Telomere Proteins and G Quadruplexes. <i>Structure</i> , 2014, 22, 801-802.	3.3	0
78	Crystallization of Mouse RIG-I ATPase Domain: In Situ Proteolysis. <i>Methods in Molecular Biology</i> , 2014, 1169, 27-35.	0.9	1
79	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	60
80	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.	1.8	6
81	Structural Analysis of Phenothiazine Derivatives as Allosteric Inhibitors of the MALT1 Paracaspase. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 10384-10387.	13.8	70
82	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.	4.4	12
83	Structure and Subunit Topology of the INO80 Chromatin Remodeler and Its Nucleosome Complex. <i>Cell</i> , 2013, 154, 1207-1219.	28.9	192
84	Paramyxovirus V Proteins Disrupt the Fold of the RNA Sensor MDA5 to Inhibit Antiviral Signaling. <i>Science</i> , 2013, 339, 690-693.	12.6	107
85	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	96
86	Species-specific detection of the antiviral small-molecule compound CMA by STING. <i>EMBO Journal</i> , 2013, 32, 1440-1450.	7.8	162
87	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
88	Epitope interactions of monoclonal antibodies targeting CD20 and their relationship to functional properties. <i>MAbs</i> , 2013, 5, 22-33.	5.2	280
89	Structural mechanism of cytosolic DNA sensing by cGAS. <i>Nature</i> , 2013, 498, 332-337.	27.8	608
90	cGAS produces a 2'-5'-linked cyclic dinucleotide second messenger that activates STING. <i>Nature</i> , 2013, 498, 380-384.	27.8	1,193

#	ARTICLE	IF	CITATIONS
91	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. <i>Blood</i> , 2013, 122, 1761-1769.	1.4	48
92	Search for narrow resonances using the dijet mass spectrum in $\langle \text{mml:math} \text{xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \rangle \langle \text{mml:mi} \rangle \text{p} \langle \text{mml:mi} \rangle \langle \text{mml:mi} \rangle \text{p} \langle \text{mml:mi} \rangle \langle \text{mml:math} \text{xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \rangle \langle \text{mml:msqrt} \rangle \langle \text{mml:mi} \rangle \text{s} \langle \text{mml:mi} \rangle \langle \text{mml:msqrt} \rangle \langle \text{mml:mo} \text{mathvariant="bold"} \rangle = \langle \text{mml:mo} \rangle \langle \text{mml:mn} \rangle 8 \langle \text{mml:mn} \rangle \langle \text{mml:mtext} \rangle \hat{\text{a}} \langle \text{mml:mtext} \rangle \hat{\text{a}} \langle \text{mml:mtext} \rangle \hat{\text{a}} \langle \text{mml:mi} \rangle \text{Te}$ collisions at	4.7	71
93	Response to: Monoclonal antibodies targeting CD20. <i>MAbs</i> , 2013, 5, 337-338.	5.2	12
94	Strukturelle Analyse von Phenothiazin- $\hat{\text{a}}$ Derivaten als allosterische Inhibitoren der MALT1- $\hat{\text{a}}$ Paracaspase. <i>Angewandte Chemie</i> , 2013, 125, 10575-10579.	2.0	0
95	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
96	Rustless translation. <i>Biological Chemistry</i> , 2012, 393, 1079-1088.	2.5	13
97	ATP driven structural changes of the bacterial Mre11:Rad50 catalytic head complex. <i>Nucleic Acids Research</i> , 2012, 40, 914-927.	14.5	94
98	Structure of Actin-related protein 8 and its contribution to nucleosome binding. <i>Nucleic Acids Research</i> , 2012, 40, 11036-11046.	14.5	48
99	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	137
100	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	27.8	210
101	Syk Kinase-Coupled C-type Lectin Receptors Engage Protein Kinase C- $\hat{\text{I}}$ to Elicit Card9 Adaptor-Mediated Innate Immunity. <i>Immunity</i> , 2012, 36, 32-42.	14.3	249
102	RIG-I detects infection with live <i>Listeria</i> by sensing secreted bacterial nucleic acids. <i>EMBO Journal</i> , 2012, 31, 4153-4164.	7.8	153
103	Structure of Mre11- $\hat{\text{a}}$ Nbs1 complex yields insights into ataxia-telangiectasia- $\hat{\text{a}}$ like disease mutations and DNA damage signaling. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 693-700.	8.2	108
104	Correlating Calcium Binding, F $\hat{\text{A}}$ rster Resonance Energy Transfer, and $\hat{\text{A}}$ Conformational Change in the Biosensor TN-XXL. <i>Biophysical Journal</i> , 2012, 102, 2401-2410.	0.5	42
105	Sensing of viral nucleic acids by RIG-I: From translocation to translation. <i>European Journal of Cell Biology</i> , 2012, 91, 78-85.	3.6	35
106	Swi2/Snf2 remodelers: hybrid views on hybrid molecular machines. <i>Current Opinion in Structural Biology</i> , 2012, 22, 225-233.	5.7	63
107	The Mre11:Rad50 Structure Shows an ATP-Dependent Molecular Clamp in DNA Double-Strand Break Repair. <i>Cell</i> , 2011, 145, 54-66.	28.9	182
108	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

#	ARTICLE	IF	CITATIONS
109	The RIG-I ATPase domain structure reveals insights into ATP-dependent antiviral signalling. <i>EMBO Reports</i> , 2011, 12, 1127-1134.	4.5	81
110	Structural biochemistry of nuclear actin-related proteins 4 and 8 reveals their interaction with actin. <i>EMBO Journal</i> , 2011, 30, 2153-2166.	7.8	63
111	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.	6.2	108
112	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.	2.6	25
113	Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. <i>Nature</i> , 2011, 475, 403-407.	27.8	73
114	Nuclear actin-related proteins take shape. <i>Bioarchitecture</i> , 2011, 1, 192-195.	1.5	7
115	Processive RNA decay by the exosome. <i>RNA Biology</i> , 2011, 8, 55-60.	3.1	6
116	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.	7.1	68
117	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011, 25, 2093-2105.	5.9	87
118	The RNA Exosomes. <i>Nucleic Acids and Molecular Biology</i> , 2011, , 223-244.	0.2	0
119	Modulation of protein properties in living cells using nanobodies. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 133-138.	8.2	494
120	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.	14.5	82
121	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. <i>Nucleic Acids Research</i> , 2010, 38, 5166-5176.	14.5	23
122	Mechanism of replication blocking and bypass of Y-family polymerase $\Psi$ by bulky acetylaminofluorene DNA adducts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20720-20725.	7.1	39
123	232 Unique molecular recognition of CD20 by the type II CD20 antibody GA101. <i>European Journal of Cancer, Supplement</i> , 2010, 8, 75-76.	2.2	0
124	Reversible and Controllable Nanolocomotion of an RNA-Processing Machinery. <i>Nano Letters</i> , 2010, 10, 5123-5130.	9.1	12
125	Structural Basis for Adenylate Kinase Activity in ABC ATPases. <i>Journal of Molecular Biology</i> , 2010, 401, 265-273.	4.2	10
126	Chapter 5. RIG-I-Like RNA Helicases: Multidomain Proteins in Antiviral Innate Immunity and Processing of Small Regulatory RNAs. <i>RSC Biomolecular Sciences</i> , 2010, , 121-148.	0.4	0



#	ARTICLE	IF	CITATIONS
127	Insights into DNA damage signaling from the structure of an Mre11:Nbs1 complex. <i>FASEB Journal</i> , 2010, 24, 1b39.	0.5	0
128	5â€™-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.	7.1	348
129	The regulatory domain of the RIG-I family ATPase LGP2 senses double-stranded RNA. <i>Nucleic Acids Research</i> , 2009, 37, 2014-2025.	14.5	131
130	Cytosolic Viral Sensor RIG-I Is a 5'-Triphosphate-Dependent Translocase on Double-Stranded RNA. <i>Science</i> , 2009, 323, 1070-1074.	12.6	325
131	Mutations affecting the secretory COPII coat component SEC23B cause congenital dyserythropoietic anemia type II. <i>Nature Genetics</i> , 2009, 41, 936-940.	21.4	250
132	DNA Double-Strand Breaks Come into Focus. <i>Cell</i> , 2009, 139, 25-27.	28.9	14
133	Single Molecule Study Of the RNA Degradation and Polyadenylation Activities of the Archaeal Exosome. <i>Biophysical Journal</i> , 2009, 96, 367a.	0.5	0
134	Lessons from structural and biochemical studies on the archaeal exosome. <i>Biochemical Society Transactions</i> , 2009, 37, 83-87.	3.4	16
135	The C-Terminal Regulatory Domain Is the RNA 5â€™-Triphosphate Sensor of RIG-I. <i>Molecular Cell</i> , 2008, 29, 169-179.	9.7	458
136	Structural Biochemistry of a Bacterial Checkpoint Protein Reveals Diadenylate Cyclase Activity Regulated by DNA Recombination Intermediates. <i>Molecular Cell</i> , 2008, 30, 167-178.	9.7	366
137	X-ray Structure of the Complete ABC Enzyme ABCE1 from <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 7962-7971.	3.4	79
138	Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle. <i>Nucleic Acids Research</i> , 2008, 36, 1881-1890.	14.5	40
139	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.	7.1	219
140	Bypass of DNA Lesions Generated During Anticancer Treatment with Cisplatin by DNA Polymerase Î¶. <i>Science</i> , 2007, 318, 967-970.	12.6	193
141	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
142	The exosome, plugged. <i>EMBO Reports</i> , 2007, 8, 456-457.	4.5	1
143	Structural basis for DNA duplex separation by a superfamily-2 helicase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 647-652.	8.2	281
144	Mechanisms of nucleic acid translocases: lessons from structural biology and single-molecule biophysics. <i>Current Opinion in Structural Biology</i> , 2007, 17, 87-95.	5.7	48

#	ARTICLE	IF	CITATIONS
145	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.	4.2	30
146	Establishment of Sister Chromatid Cohesion at the <i>S. cerevisiae</i> Replication Fork. <i>Molecular Cell</i> , 2006, 23, 787-799.	9.7	268
147	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	108
148	The exosome: a macromolecular cage for controlled RNA degradation. <i>Molecular Microbiology</i> , 2006, 61, 1372-1379.	2.5	40
149	Chromosome Biology: The Crux of the Ring. <i>Current Biology</i> , 2006, 16, R102-R105.	3.9	8
150	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.	14.5	93
151	Structure-Function Analysis of SWI2/SNF2 Enzymes. <i>Methods in Enzymology</i> , 2006, 409, 375-388.	1.0	8
152	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.	3.3	69
153	Biochemical Characterization and Crystal Structure of a Dim1 Family Associated Protein: Dim2. <i>Biochemistry</i> , 2005, 44, 11997-12008.	2.5	11
154	Structural Framework for the Mechanism of Archaeal Exosomes in RNA Processing. <i>Molecular Cell</i> , 2005, 20, 461-471.	9.7	145
155	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.	28.9	228
156	Structure and Function of Rad50/SMC Protein Complexes in Chromosome Biology. , 2005, , 201-218.		0
157	The Mre11/Rad50/Nbs1 Complex. , 2005, , .		0
158	Point Mutations Found in the Juxtamembrane Domain of FLT3 Define a New Class of Activating Mutations in AML. <i>Blood</i> , 2005, 106, 4388-4388.	1.4	0
159	Structural and functional analysis of Mre11-3. <i>Nucleic Acids Research</i> , 2004, 32, 1886-1893.	14.5	46
160	Functional and biochemical dissection of the structure-specific nuclease ARTEMIS. <i>EMBO Journal</i> , 2004, 23, 1987-1997.	7.8	122
161	MlaA, a hexameric ATPase linked to the Mre11 complex in archaeal genomes. <i>EMBO Reports</i> , 2004, 5, 54-59.	4.5	39
162	Structural Biochemistry of ATP-Driven Dimerization and DNA-Stimulated Activation of SMC ATPases. <i>Current Biology</i> , 2004, 14, 1778-1782.	3.9	151

#	ARTICLE	IF	CITATIONS
163	MRE11/RAD50/NBS1: complex activities. <i>Chromosoma</i> , 2004, 113, 157-66.	2.2	113
164	The Rad50 Signature Motif: Essential to ATP Binding and Biological Function. <i>Journal of Molecular Biology</i> , 2004, 335, 937-951.	4.2	85
165	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.	4.2	53
166	Rad50/SMC proteins and ABC transporters: unifying concepts from high-resolution structures. <i>Current Opinion in Structural Biology</i> , 2003, 13, 249-255.	5.7	193
167	Chromosome Cohesion: Closing Time. <i>Current Biology</i> , 2003, 13, R866-R868.	3.9	1
168	Physiological fIXa Activation Involves a Cooperative Conformational Rearrangement of the 99-Loop. <i>Journal of Biological Chemistry</i> , 2003, 278, 4121-4126.	3.4	40
169	The influence of residue 190 in the S1 site of trypsin-like serine proteases on substrate selectivity is universally conserved. <i>FEBS Letters</i> , 2002, 530, 220-224.	2.8	32
170	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.	4.2	75
171	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002, 12, 115-122.	5.7	133
172	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. <i>Nature</i> , 2002, 418, 562-566.	27.8	485
173	Structural Biochemistry and Interaction Architecture of the DNA Double-Strand Break Repair Mre11 Nuclease and Rad50-ATPase. <i>Cell</i> , 2001, 105, 473-485.	28.9	448
174	DNA Mismatch Repair. <i>Structure</i> , 2000, 8, R237-R241.	3.3	20
175	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.	2.2	116
176	Structural Biology of Rad50 ATPase. <i>Cell</i> , 2000, 101, 789-800.	28.9	886
177	Envisioning the Fourth Dimension of the Genetic Code: The Structural Biology of Macromolecular Recognition and Conformational Switching in DNA Repair. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2000, 65, 113-126.	1.1	6
178	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.	7.1	205
179	Coagulation factor IXa: the relaxed conformation of Tyr99 blocks substrate binding. <i>Structure</i> , 1999, 7, 989-996.	3.3	123
180	The ternary microplasminâ€“staphylokinaseâ€“microplasmin complex is a proteinaseâ€“cofactorâ€“substrate complex in action. <i>Nature Structural Biology</i> , 1998, 5, 917-923.	9.7	132

#	ARTICLE	IF	CITATIONS
181	New enzyme lineages by subdomain shuffling. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 9813-9818.	7.1	49
182	Dramatic enhancement of the catalytic activity of coagulation factor IXa by alcohols. FEBS Letters, 1997, 412, 295-300.	2.8	45
183	Converting blood coagulation factor IXa into factor Xa: dramatic increase in amidolytic activity identifies important active site determinants. EMBO Journal, 1997, 16, 6626-6635.	7.8	68
184	Theory of allosteric effects in serine proteases. Biophysical Journal, 1996, 70, 174-181.	0.5	42
185	Binding of Fibrinogen A $\beta$ 1-50-Galactosidase Fusion Protein to Thrombin Stabilizes the Slow Form. Journal of Biological Chemistry, 1995, 270, 24790-24793.	3.4	6
186	Chemical compensation in macromolecular bridge-binding to thrombin. Biochemistry, 1993, 32, 2947-2953.	2.5	21
187	Symmetry conditions for binding processes.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 2727-2731.	7.1	5
188	Energetics of the thrombin-fibrinogen interaction. Biochemistry, 1992, 31, 11567-11571.	2.5	21