

Karl-Peter Hopfner

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

181
papers

14,063
citations

64
h-index

116
g-index

208
ext. papers

16,375
ext. citations

13.6
avg, IF

6.52
L-index

#	Paper	IF	Citations
181	Chemical synthesis of the fluorescent, cyclic dinucleotides cthGAMP.. <i>ChemBioChem</i> , 2022 ,	3.8	2
180	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. <i>Science Signaling</i> , 2021 , 14,	8.8	20
179	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021 , 12, 3232	17.4	8
178	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. <i>Nature Communications</i> , 2021 , 12, 3231	17.4	6
177	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	4.7	3
176	Measuring DNA mechanics on the genome scale. <i>Nature</i> , 2021 , 589, 462-467	50.4	29
175	A modular and controllable T cell therapy platform for acute myeloid leukemia. <i>Leukemia</i> , 2021 , 35, 2243-2254	13.7	4
174	Nuclear cGAS: guard or prisoner?. <i>EMBO Journal</i> , 2021 , 40, e108293	13	7
173	OAS1/RNase L executes RIG-I ligand-dependent tumor cell apoptosis. <i>Science Immunology</i> , 2021 , 6,	28	4
172	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. <i>Nucleic Acids Research</i> , 2021 , 49, 10166-10177	20.1	3
171	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	22.4	3
170	Molecular basis of human ATM kinase inhibition. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 789-796	19.6	3
169	Structural basis for sequestration and autoinhibition of cGAS by chromatin. <i>Nature</i> , 2020 , 587, 678-682	50.4	74
168	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. <i>Cell Reports</i> , 2020 , 31, 107522	10.6	24
167	Molecular mechanisms and cellular functions of cGAS-STING signalling. <i>Nature Reviews Molecular Cell Biology</i> , 2020 , 21, 501-521	48.7	234
166	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	5.2	17
165	Megadalton chromatin remodelers: common principles for versatile functions. <i>Current Opinion in Structural Biology</i> , 2020 , 64, 134-144	8.1	10

164	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. <i>Molecular Cell</i> , 2019 , 76, 382-394.e6	17.6	51
163	DuoMab: a novel CrossMab-based IgG-derived antibody format for enhanced antibody-dependent cell-mediated cytotoxicity. <i>MAbs</i> , 2019 , 11, 1402-1414	6.6	6
162	Exploiting an Anti-CD3/CD33 Bispecific Antibody to Redirect Donor T Cells Against HLA Loss Leukemia Relapses. <i>Blood</i> , 2019 , 134, 513-513	2.2	1
161	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	2.2	1
160	Aberrant Cathepsin S Induces a Supportive Immune Microenvironment in Follicular Lymphoma. <i>Blood</i> , 2019 , 134, 657-657	2.2	
159	A Click-Chemistry Linked 2 β PcGAMP Analogue. <i>Chemistry - A European Journal</i> , 2019 , 25, 2089-2095	4.8	8
158	Human TGF- β 1 deficiency causes severe inflammatory bowel disease and encephalopathy. <i>Nature Genetics</i> , 2018 , 50, 344-348	36.3	67
157	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. <i>Nature</i> , 2018 , 556, 386-390	50.4	121
156	Single-molecule nucleosome remodeling by INO80 and effects of histone tails. <i>FEBS Letters</i> , 2018 , 592, 318-331	3.8	9
155	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>Onc Immunology</i> , 2018 , 7, e1472195	7.2	16
154	Crystal structure of the full Swi2/Snf2 remodeler Mot1 in the resting state. <i>ELife</i> , 2018 , 7,	8.9	2
153	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. <i>ELife</i> , 2018 , 7,	8.9	16
152	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. <i>Nature Immunology</i> , 2018 , 19, 53-62	19.1	126
151	Bifunctional PD-1 α CD3 α CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. <i>Blood</i> , 2018 , 132, 2484-2494	2.2	48
150	Molecular architecture and regulation of BCL10-MALT1 filaments. <i>Nature Communications</i> , 2018 , 9, 4041	17.4	27
149	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	20.1	13
148	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	17.6	37
147	Discrimination of cytosolic self and non-self RNA by RIG-I-like receptors. <i>Journal of Biological Chemistry</i> , 2017 , 292, 9000-9009	5.4	52

146	SIRP α antibody fusion proteins stimulate phagocytosis and promote elimination of acute myeloid leukemia cells. <i>Oncotarget</i> , 2017 , 8, 11284-11301	3.3	14
145	Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017 , 45, 12025-12038	20.1	15
144	cGAS senses long and HMGB/TFAM-bound U-turn DNA by forming protein-DNA ladders. <i>Nature</i> , 2017 , 549, 394-398	50.4	212
143	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. <i>Molecular Cell</i> , 2016 , 64, 951-966	17.6	40
142	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. <i>Nature Communications</i> , 2016 , 7, 11733	17.4	39
141	Structural and biochemical characterization of the cell fate determining nucleotidyltransferase fold protein MAB21L1. <i>Scientific Reports</i> , 2016 , 6, 27498	4.9	19
140	Invited review: Architectures and mechanisms of ATP binding cassette proteins. <i>Biopolymers</i> , 2016 , 105, 492-504	2.2	47
139	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, 337-54	12.6	68
138	Chip-based platform for dynamic analysis of NK cell cytotoxicity mediated by a triplebody. <i>Analyst, The</i> , 2016 , 141, 2284-95	5	7
137	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	3.3	16
136	Dual-targeting triplebody 33-3-19 mediates selective lysis of biphenotypic CD19+ CD33+ leukemia cells. <i>Oncotarget</i> , 2016 , 7, 22579-89	3.3	15
135	Structural mechanism of ATP-dependent DNA binding and DNA end bridging by eukaryotic Rad50. <i>EMBO Journal</i> , 2016 , 35, 759-72	13	79
134	RIG-I-Like Receptors: One STRIP Forward. <i>Trends in Microbiology</i> , 2016 , 24, 517-519	12.4	4
133	Impact of Heterogeneity and Lattice Bond Strength on DNA Triangle Crystal Growth. <i>ACS Nano</i> , 2016 , 10, 9156-9164	16.7	26
132	Serendipitous crystallization and structure determination of cyanase (CynS) from <i>Serratia proteamaculans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 471-6	1.1	7
131	Structure of the catalytic domain of Mre11 from <i>Chaetomium thermophilum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015 , 71, 752-7	1.1	16
130	Structural basis for dodecameric assembly states and conformational plasticity of the full-length AAA+ ATPases Rvb1 and Rvb2. <i>Structure</i> , 2015 , 23, 483-495	5.2	31
129	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, 1025-33	19.1	145

128	c-di-AMP recognition by <i>Staphylococcus aureus</i> PstA. <i>FEBS Letters</i> , 2015 , 589, 45-51	3.8	41
127	Structural analysis of the diadenylate cyclase reaction of DNA-integrity scanning protein A (DisA) and its inhibition by 3PdATP. <i>Biochemical Journal</i> , 2015 , 469, 367-74	3.8	14
126	Activity-based probes for detection of active MALT1 paracaspase in immune cells and lymphomas. <i>Chemistry and Biology</i> , 2015 , 22, 129-38		30
125	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. <i>ELife</i> , 2015 , 4,	8.9	14
124	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. <i>ELife</i> , 2015 , 4,	8.9	63
123	Crosstalk between the cGAS DNA sensor and Beclin-1 autophagy protein shapes innate antimicrobial immune responses. <i>Cell Host and Microbe</i> , 2014 , 15, 228-38	23.4	223
122	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1 β production. <i>Nature Immunology</i> , 2014 , 15, 538-45	19.1	96
121	Structure of the Rad50 DNA double-strand break repair protein in complex with DNA. <i>EMBO Journal</i> , 2014 , 33, 2847-59	13	48
120	ATP puts the brake on DNA double-strand break repair: a new study shows that ATP switches the Mre11-Rad50-Nbs1 repair factor between signaling and processing of DNA ends. <i>BioEssays</i> , 2014 , 36, 1170-8	4.1	13
119	RIG-I holds the CARDs in a game of self versus nonself. <i>Molecular Cell</i> , 2014 , 55, 505-7	17.6	6
118	Structural studies of DNA end detection and resection in homologous recombination. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014 , 6, a017962	10.2	20
117	OAS proteins and cGAS: unifying concepts in sensing and responding to cytosolic nucleic acids. <i>Nature Reviews Immunology</i> , 2014 , 14, 521-8	36.5	174
116	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. <i>Nature Genetics</i> , 2014 , 46, 901-4	36.3	75
115	Single-molecule choreography between telomere proteins and G quadruplexes. <i>Structure</i> , 2014 , 22, 801-32		32
114	Crystal and solution structure of the human RIG-I SF2 domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1027-31	1.1	4
113	In vivo ligands of MDA5 and RIG-I in measles virus-infected cells. <i>PLoS Pathogens</i> , 2014 , 10, e1004081	7.6	96
112	Cytosolic RNA:DNA hybrids activate the cGAS-STING axis. <i>EMBO Journal</i> , 2014 , 33, 2937-46	13	181
111	Molecular architecture of the HerA-NurA DNA double-strand break resection complex. <i>FEBS Letters</i> , 2014 , 588, 4637-44	3.8	10

110	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	3.7	42
109	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, 6466-83	3.3	6
108	Crystallization of mouse RIG-I ATPase domain: in situ proteolysis. <i>Methods in Molecular Biology</i> , 2014 , 1169, 27-35	1.4	1
107	Structural analysis of phenothiazine derivatives as allosteric inhibitors of the MALT1 paracaspase. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 10384-7	16.4	56
106	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	8.5	12
105	Structure and subunit topology of the INO80 chromatin remodeler and its nucleosome complex. <i>Cell</i> , 2013 , 154, 1207-19	56.2	173
104	Paramyxovirus V proteins disrupt the fold of the RNA sensor MDA5 to inhibit antiviral signaling. <i>Science</i> , 2013 , 339, 690-3	33.3	90
103	RG7116, a therapeutic antibody that binds the inactive HER3 receptor and is optimized for immune effector activation. <i>Cancer Research</i> , 2013 , 73, 5183-94	10.1	83
102	Species-specific detection of the antiviral small-molecule compound CMA by STING. <i>EMBO Journal</i> , 2013 , 32, 1440-50	13	123
101	Crystal structure of an anti-Ang2 CrossFab demonstrates complete structural and functional integrity of the variable domain. <i>PLoS ONE</i> , 2013 , 8, e61953	3.7	26
100	Epitope interactions of monoclonal antibodies targeting CD20 and their relationship to functional properties. <i>MAbs</i> , 2013 , 5, 22-33	6.6	193
99	Structural mechanism of cytosolic DNA sensing by cGAS. <i>Nature</i> , 2013 , 498, 332-7	50.4	410
98	cGAS produces a 2P5Plinked cyclic dinucleotide second messenger that activates STING. <i>Nature</i> , 2013 , 498, 380-4	50.4	822
97	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. <i>Blood</i> , 2013 , 122, 1761-9	2.2	40
96	Search for narrow resonances using the dijet mass spectrum in pp collisions at s=8 TeV. <i>Physical Review D</i> , 2013 , 87,	4.9	63
95	Response to: monoclonal antibodies targeting CD20. <i>MAbs</i> , 2013 , 5, 337-8	6.6	10
94	Strukturelle Analyse von Phenothiazin-Derivaten als allosterische Inhibitoren der MALT1-Paracaspase. <i>Angewandte Chemie</i> , 2013 , 125, 10575-10579	3.6	
93	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	3.7	17

92	Sensing of viral nucleic acids by RIG-I: from translocation to translation. <i>European Journal of Cell Biology</i> , 2012 , 91, 78-85	6.1	32
91	Swi2/Snf2 remodelers: hybrid views on hybrid molecular machines. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 225-33	8.1	50
90	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	2.2	120
89	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012 , 482, 501-6	50.4	179
88	Syk kinase-coupled C-type lectin receptors engage protein kinase C- β to elicit Card9 adaptor-mediated innate immunity. <i>Immunity</i> , 2012 , 36, 32-42	32.3	191
87	RIG-I detects infection with live <i>Listeria</i> by sensing secreted bacterial nucleic acids. <i>EMBO Journal</i> , 2012 , 31, 4153-64	13	132
86	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	17.6	91
85	Correlating calcium binding, Förster resonance energy transfer, and conformational change in the biosensor TN-XXL. <i>Biophysical Journal</i> , 2012 , 102, 2401-10	2.9	33
84	Rustless translation. <i>Biological Chemistry</i> , 2012 , 393, 1079-88	4.5	9
83	ATP driven structural changes of the bacterial Mre11:Rad50 catalytic head complex. <i>Nucleic Acids Research</i> , 2012 , 40, 914-27	20.1	82
82	Structure of Actin-related protein 8 and its contribution to nucleosome binding. <i>Nucleic Acids Research</i> , 2012 , 40, 11036-46	20.1	42
81	The Mre11:Rad50 structure shows an ATP-dependent molecular clamp in DNA double-strand break repair. <i>Cell</i> , 2011 , 145, 54-66	56.2	157
80	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, 358-67	2.2	168
79	The RIG-I ATPase domain structure reveals insights into ATP-dependent antiviral signalling. <i>EMBO Reports</i> , 2011 , 12, 1127-34	6.5	76
78	Structural biochemistry of nuclear actin-related proteins 4 and 8 reveals their interaction with actin. <i>EMBO Journal</i> , 2011 , 30, 2153-66	13	58
77	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, 226-31	11	84
76	Structure and DNA-binding activity of the <i>Pyrococcus furiosus</i> SMC protein hinge domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79, 558-68	4.2	24
75	Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. <i>Nature</i> , 2011 , 475, 403-7	50.4	63

74	Nuclear actin-related proteins take shape. <i>Bioarchitecture</i> , 2011 , 1, 192-195		5
73	Processive RNA decay by the exosome: merits of a quantitative Bayesian sampling approach. <i>RNA Biology</i> , 2011 , 8, 55-60	4.8	6
72	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, 8194-9	11.5	51
71	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011 , 25, 2093-105	12.6	72
70	The RNA Exosomes. <i>Nucleic Acids and Molecular Biology</i> , 2011 , 223-244		
69	Modulation of protein properties in living cells using nanobodies. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 133-8	17.6	364
68	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, 3454-65	20.1	78
67	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. <i>Nucleic Acids Research</i> , 2010 , 38, 5166-76	20.1	20
66	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, 20720-5	11.5	34
65	Reversible and controllable nanolocomotion of an RNA-processing machinery. <i>Nano Letters</i> , 2010 , 10, 5123-30	11.5	11
64	Structural basis for adenylate kinase activity in ABC ATPases. <i>Journal of Molecular Biology</i> , 2010 , 401, 265-73	6.5	9
63	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		
62	Insights into DNA damage signaling from the structure of an Mre11:Nbs1 complex. <i>FASEB Journal</i> , 2010 , 24, lb39	0.9	
61	5Ptriphosphate 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, 12067-72	11.5	308
60	The regulatory domain of the RIG-I family ATPase LGP2 senses double-stranded RNA. <i>Nucleic Acids Research</i> , 2009 , 37, 2014-25	20.1	112
59	Cytosolic viral sensor RIG-I is a 5Ptriphosphate-dependent translocase on double-stranded RNA. <i>Science</i> , 2009 , 323, 1070-4	33.3	290
58	Mutations affecting the secretory COPII coat component SEC23B cause congenital dyserythropoietic anemia type II. <i>Nature Genetics</i> , 2009 , 41, 936-40	36.3	211
57	DNA double-strand breaks come into focus. <i>Cell</i> , 2009 , 139, 25-7	56.2	11

56	Lessons from structural and biochemical studies on the archaeal exosome. <i>Biochemical Society Transactions</i> , 2009 , 37, 83-7	5.1	12
55	The C-terminal regulatory domain is the RNA 5P triphosphate sensor of RIG-I. <i>Molecular Cell</i> , 2008 , 29, 169-79	17.6	408
54	Structural biochemistry of a bacterial checkpoint protein reveals diadenylate cyclase activity regulated by DNA recombination intermediates. <i>Molecular Cell</i> , 2008 , 30, 167-78	17.6	293
53	X-ray structure of the complete ABC enzyme ABCE1 from <i>Pyrococcus abyssi</i> . <i>Journal of Biological Chemistry</i> , 2008 , 283, 7962-71	5.4	71
52	Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle. <i>Nucleic Acids Research</i> , 2008 , 36, 1881-90	20.1	37
51	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, 16743-8	11.5	187
50	The exosome, plugged. <i>EMBO Reports</i> , 2007 , 8, 456-7	6.5	
49	Structural basis for DNA duplex separation by a superfamily-2 helicase. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 647-52	17.6	233
48	Mechanisms of nucleic acid translocases: lessons from structural biology and single-molecule biophysics. <i>Current Opinion in Structural Biology</i> , 2007 , 17, 87-95	8.1	46
47	Bypass of DNA lesions generated during anticancer treatment with cisplatin by DNA polymerase ϵ . <i>Science</i> , 2007 , 318, 967-70	33.3	175
46	The chemistry of transcription through damaged DNA and of translesion synthesis at atomic resolution. <i>Nucleic Acids Symposium Series</i> , 2007 , 103		
45	Chromosome biology: the crux of the ring. <i>Current Biology</i> , 2006 , 16, R102-5	6.3	8
44	Snf2 family ATPases and DExx box helicases: differences and unifying concepts from high-resolution crystal structures. <i>Nucleic Acids Research</i> , 2006 , 34, 4160-7	20.1	78
43	Structure-function analysis of SWI2/SNF2 enzymes. <i>Methods in Enzymology</i> , 2006 , 409, 375-88	1.7	8
42	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, 675-83	6.5	28
41	Establishment of sister chromatid cohesion at the <i>S. cerevisiae</i> replication fork. <i>Molecular Cell</i> , 2006 , 23, 787-99	17.6	232
40	Point mutations in the juxtamembrane domain of FLT3 define a new class of activating mutations in AML. <i>Blood</i> , 2006 , 107, 3700-7	2.2	96
39	The exosome: a macromolecular cage for controlled RNA degradation. <i>Molecular Microbiology</i> , 2006 , 61, 1372-9	4.1	37

38	Structure and Function of Rad50/SMC Protein Complexes in Chromosome Biology 2005 , 201-218		
37	Biochemical characterization and crystal structure of a Dim1 family associated protein: Dim2. <i>Biochemistry</i> , 2005 , 44, 11997-2008	3.2	6
36	Structural framework for the mechanism of archaeal exosomes in RNA processing. <i>Molecular Cell</i> , 2005 , 20, 461-71	17.6	135
35	X-ray structures of the <i>Sulfolobus solfataricus</i> SWI2/SNF2 ATPase core and its complex with DNA. <i>Cell</i> , 2005 , 121, 363-73	56.2	212
34	X-ray structure of RLI, an essential twin cassette ABC ATPase involved in ribosome biogenesis and HIV capsid assembly. <i>Structure</i> , 2005 , 13, 649-59	5.2	64
33	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	2.2	
32	Structural and functional analysis of Mre11-3. <i>Nucleic Acids Research</i> , 2004 , 32, 1886-93	20.1	40
31	Functional and biochemical dissection of the structure-specific nuclease ARTEMIS. <i>EMBO Journal</i> , 2004 , 23, 1987-97	13	110
30	MlaA, a hexameric ATPase linked to the Mre11 complex in archaeal genomes. <i>EMBO Reports</i> , 2004 , 5, 54-9	6.5	32
29	Structural biochemistry of ATP-driven dimerization and DNA-stimulated activation of SMC ATPases. <i>Current Biology</i> , 2004 , 14, 1778-82	6.3	130
28	MRE11/RAD50/NBS1: complex activities. <i>Chromosoma</i> , 2004 , 113, 157-66	2.8	97
27	The rad50 signature motif: essential to ATP binding and biological function. <i>Journal of Molecular Biology</i> , 2004 , 335, 937-51	6.5	75
26	Differential arrangements of conserved building blocks among homologs of the Rad50/Mre11 DNA repair protein complex. <i>Journal of Molecular Biology</i> , 2004 , 339, 937-49	6.5	48
25	Rad50/SMC proteins and ABC transporters: unifying concepts from high-resolution structures. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 249-55	8.1	168
24	Chromosome cohesion: closing time. <i>Current Biology</i> , 2003 , 13, R866-8	6.3	1
23	Physiological fIXa activation involves a cooperative conformational rearrangement of the 99-loop. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4121-6	5.4	32
22	DNA double-strand break repair from head to tail. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 115-228.1		117
21	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. <i>Nature</i> , 2002 , 418, 562-6	50.4	425

20	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, 220-4	3.8	25
19	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	6.5	71
18	Structural biochemistry and interaction architecture of the DNA double-strand break repair Mre11 nuclease and Rad50-ATPase. <i>Cell</i> , 2001 , 105, 473-85	56.2	397
17	DNA mismatch repair: the hands of a genome guardian. <i>Structure</i> , 2000 , 8, R237-41	5.2	18
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2	Measuring DNA mechanics on the genome scale	3
1	Genome information processing by the INO80 chromatin remodeler positions nucleosomes	1