Karl-Peter Hopfner

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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	cGAS produces a 2P5Plinked cyclic dinucleotide second messenger that activates STING. *Nature*, **2013**, 498, 380-4	50.4	822
180	Structural biology of Rad50 ATPase: ATP-driven conformational control in DNA double-strand break repair and the ABC-ATPase superfamily. *Cell*, **2000**, 101, 789-800	56.2	820
179	The Rad50 zinc-hook is a structure joining Mre11 complexes in DNA recombination and repair. *Nature*, **2002**, 418, 562-6	50.4	425
178	Structural mechanism of cytosolic DNA sensing by cGAS. *Nature*, **2013**, 498, 332-7	50.4	410
177	The C-terminal regulatory domain is the RNA 5Ptriphosphate sensor of RIG-I. *Molecular Cell*, **2008**, 29, 169-79	17.6	408
176	Structural biochemistry and interaction architecture of the DNA double-strand break repair Mre11 nuclease and Rad50-ATPase. *Cell*, **2001**, 105, 473-85	56.2	397
175	Modulation of protein properties in living cells using nanobodies. *Nature Structural and Molecular Biology*, **2010**, 17, 133-8	17.6	364
174	5Ptriphosphate RNA requires base-paired structures to activate antiviral signaling via RIG-I. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 12067-72	11.5	308
173	Structural biochemistry of a bacterial checkpoint protein reveals diadenylate cyclase activity regulated by DNA recombination intermediates. *Molecular Cell*, **2008**, 30, 167-78	17.6	293
172	Cytosolic viral sensor RIG-I is a 5Ptriphosphate-dependent translocase on double-stranded RNA. *Science*, **2009**, 323, 1070-4	33.3	290
171	Molecular mechanisms and cellular functions of cGAS-STING signalling. *Nature Reviews Molecular Cell Biology*, **2020**, 21, 501-521	48.7	234
170	Structural basis for DNA duplex separation by a superfamily-2 helicase. *Nature Structural and Molecular Biology*, **2007**, 14, 647-52	17.6	233
169	Establishment of sister chromatid cohesion at the S. cerevisiae replication fork. *Molecular Cell*, **2006** , 23, 787-99	17.6	232
168	Crosstalk between the cGAS DNA sensor and Beclin-1 autophagy protein shapes innate antimicrobial immune responses. *Cell Host and Microbe*, **2014**, 15, 228-38	23.4	223
167	cGAS senses long and HMGB/TFAM-bound U-turn DNA by forming protein-DNA ladders. *Nature*, **2017**, 549, 394-398	50.4	212
166	X-ray structures of the Sulfolobus solfataricus SWI2/SNF2 ATPase core and its complex with DNA. *Cell*, **2005**, 121, 363-73	56.2	212
165	Mutations affecting the secretory COPII coat component SEC23B cause congenital dyserythropoietic anemia type II. *Nature Genetics*, **2009**, 41, 936-40	36.3	211

164	Crystal structure of a thermostable type B DNA polymerase from Thermococcus gorgonarius. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 3600-5	11.5	194
163	Epitope interactions of monoclonal antibodies targeting CD20 and their relationship to functional properties. *MAbs*, **2013**, 5, 22-33	6.6	193
162	Syk kinase-coupled C-type lectin receptors engage protein kinase C-□to elicit Card9 adaptor-mediated innate immunity. *Immunity*, **2012**, 36, 32-42	32.3	191
161	Roles of RIG-I N-terminal tandem CARD and splice variant in TRIM25-mediated antiviral signal transduction. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 16743-8	11.5	187
160	Cytosolic RNA:DNA hybrids activate the cGAS-STING axis. *EMBO Journal*, **2014**, 33, 2937-46	13	181
159	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. *Nature*, **2012**, 482, 501-6	50.4	179
158	Bypass of DNA lesions generated during anticancer treatment with cisplatin by DNA polymerase eta. *Science*, **2007**, 318, 967-70	33.3	175
157	OAS proteins and cGAS: unifying concepts in sensing and responding to cytosolic nucleic acids. *Nature Reviews Immunology*, **2014**, 14, 521-8	36.5	174
156	Structure and subunit topology of the INO80 chromatin remodeler and its nucleosome complex. *Cell*, **2013**, 154, 1207-19	56.2	173
155	Epitope characterization and crystal structure of GA101 provide insights into the molecular basis for type I/II distinction of CD20 antibodies. *Blood*, **2011**, 118, 358-67	2.2	168
154	Rad50/SMC proteins and ABC transporters: unifying concepts from high-resolution structures. *Current Opinion in Structural Biology*, **2003**, 13, 249-55	8.1	168
153	The Mre11:Rad50 structure shows an ATP-dependent molecular clamp in DNA double-strand break repair. *Cell*, **2011**, 145, 54-66	56.2	157
152	Sequence-specific activation of the DNA sensor cGAS by Y-form DNA structures as found in primary HIV-1 cDNA. *Nature Immunology*, **2015**, 16, 1025-33	19.1	145
151	Structural framework for the mechanism of archaeal exosomes in RNA processing. *Molecular Cell*, **2005**, 20, 461-71	17.6	135
150	RIG-I detects infection with live Listeria by sensing secreted bacterial nucleic acids. *EMBO Journal*, **2012**, 31, 4153-64	13	132
149	Structural biochemistry of ATP-driven dimerization and DNA-stimulated activation of SMC ATPases. *Current Biology*, **2004**, 14, 1778-82	6.3	130
148	Viral unmasking of cellular 5S rRNA pseudogene transcripts induces RIG-I-mediated immunity. *Nature Immunology*, **2018**, 19, 53-62	19.1	126
147	Species-specific detection of the antiviral small-molecule compound CMA by STING. *EMBO Journal*, **2013**, 32, 1440-50	13	123

146	The ternary microplasmin-staphylokinase-microplasmin complex is a proteinase-cofactor-substrate complex in action. *Nature Structural Biology*, **1998**, 5, 917-23		122
145	Structural basis for ATP-dependent chromatin remodelling by the INO80 complex. *Nature*, **2018**, 556, 386-390	50.4	121
144	GATA2 zinc finger 1 mutations associated with biallelic CEBPA mutations define a unique genetic entity of acute myeloid leukemia. *Blood*, **2012**, 120, 395-403	2.2	120
143	DNA double-strand break repair from head to tail. *Current Opinion in Structural Biology*, **2002**, 12, 115-22	8.1	117
142	Coagulation factor IXa: the relaxed conformation of Tyr99 blocks substrate binding. *Structure*, **1999**, 7, 989-96	5.2	113
141	The regulatory domain of the RIG-I family ATPase LGP2 senses double-stranded RNA. *Nucleic Acids Research*, **2009**, 37, 2014-25	20.1	112
140	Functional and biochemical dissection of the structure-specific nuclease ARTEMIS. *EMBO Journal*, **2004**, 23, 1987-97	13	110
139	Mre11 and Rad50 from Pyrococcus furiosus: cloning and biochemical characterization reveal an evolutionarily conserved multiprotein machine. *Journal of Bacteriology*, **2000**, 182, 6036-41	3.5	106
138	MRE11/RAD50/NBS1: complex activities. *Chromosoma*, **2004**, 113, 157-66	2.8	97
137	Rad50-CARD9 interactions link cytosolic DNA sensing to IL-1▯production. *Nature Immunology*, **2014**, 15, 538-45	19.1	96
136	In vivo ligands of MDA5 and RIG-I in measles virus-infected cells. *PLoS Pathogens*, **2014**, 10, e1004081	7.6	96
135	Point mutations in the juxtamembrane domain of FLT3 define a new class of activating mutations in AML. *Blood*, **2006**, 107, 3700-7	2.2	96
134	Structure of Mre11-Nbs1 complex yields insights into ataxia-telangiectasia-like disease mutations and DNA damage signaling. *Nature Structural and Molecular Biology*, **2012**, 19, 693-700	17.6	91
133	Paramyxovirus V proteins disrupt the fold of the RNA sensor MDA5 to inhibit antiviral signaling. *Science*, **2013**, 339, 690-3	33.3	90
132	Dihydrofolate reductase deficiency due to a homozygous DHFR mutation causes megaloblastic anemia and cerebral folate deficiency leading to severe neurologic disease. *American Journal of Human Genetics*, **2011**, 88, 226-31	11	84
131	RG7116, a therapeutic antibody that binds the inactive HER3 receptor and is optimized for immune effector activation. *Cancer Research*, **2013**, 73, 5183-94	10.1	83
130	ATP driven structural changes of the bacterial Mre11:Rad50 catalytic head complex. *Nucleic Acids Research*, **2012**, 40, 914-27	20.1	82
129	Structural mechanism of ATP-dependent DNA binding and DNA end bridging by eukaryotic Rad50. *EMBO Journal*, **2016**, 35, 759-72	13	79

128	Structure and DNA binding activity of the mouse condensin hinge domain highlight common and diverse features of SMC proteins. *Nucleic Acids Research*, **2010**, 38, 3454-65	20.1	78
127	Snf2 family ATPases and DExx box helicases: differences and unifying concepts from high-resolution crystal structures. *Nucleic Acids Research*, **2006**, 34, 4160-7	20.1	78
126	The RIG-I ATPase domain structure reveals insights into ATP-dependent antiviral signalling. *EMBO Reports*, **2011**, 12, 1127-34	6.5	76
125	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. *Nature Genetics*, **2014**, 46, 901-4	36.3	75
124	The rad50 signature motif: essential to ATP binding and biological function. *Journal of Molecular Biology*, **2004**, 335, 937-51	6.5	75
123	Structural basis for sequestration and autoinhibition of cGAS by chromatin. *Nature*, **2020**, 587, 678-682	50.4	74
122	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. *Genes and Development*, **2011**, 25, 2093-105	12.6	72
121	X-ray structure of the complete ABC enzyme ABCE1 from Pyrococcus abyssi. *Journal of Biological Chemistry*, **2008**, 283, 7962-71	5.4	71
120	Crystal structures of uninhibited factor VIIa link its cofactor and substrate-assisted activation to specific interactions. *Journal of Molecular Biology*, **2002**, 322, 591-603	6.5	71
119	Mec1, INO80, and the PAF1 complex cooperate to limit transcription replication conflicts through RNAPII removal during replication stress. *Genes and Development*, **2016**, 30, 337-54	12.6	68
118	Human TGF-β1 deficiency causes severe inflammatory bowel disease and encephalopathy. *Nature Genetics*, **2018**, 50, 344-348	36.3	67
117	X-ray structure of RLI, an essential twin cassette ABC ATPase involved in ribosome biogenesis and HIV capsid assembly. *Structure*, **2005**, 13, 649-59	5.2	64
116	Search for narrow resonances using the dijet mass spectrum in pp collisions at s=8 TeV. *Physical Review D*, **2013**, 87,	4.9	63
115	Structure and mechanism of the Swi2/Snf2 remodeller Mot1 in complex with its substrate TBP. *Nature*, **2011**, 475, 403-7	50.4	63
114	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. *ELife*, **2015**, 4,	8.9	63
113	Converting blood coagulation factor IXa into factor Xa: dramatic increase in amidolytic activity identifies important active site determinants. *EMBO Journal*, **1997**, 16, 6626-35	13	60
112	Structural biochemistry of nuclear actin-related proteins 4 and 8 reveals their interaction with actin. *EMBO Journal*, **2011**, 30, 2153-66	13	58
111	Structural analysis of phenothiazine derivatives as allosteric inhibitors of the MALT1 paracaspase. *Angewandte Chemie - International Edition*, **2013**, 52, 10384-7	16.4	56

110	Discrimination of cytosolic self and non-self RNA by RIG-I-like receptors. *Journal of Biological Chemistry*, **2017**, 292, 9000-9009	5.4	52
109	Mechanism of DNA End Sensing and Processing by the Mre11-Rad50 Complex. *Molecular Cell*, **2019**, 76, 382-394.e6	17.6	51
108	Bispecific digoxigenin-binding antibodies for targeted payload delivery. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 8194-9	11.5	51
107	Swi2/Snf2 remodelers: hybrid views on hybrid molecular machines. *Current Opinion in Structural Biology*, **2012**, 22, 225-33	8.1	50
106	New enzyme lineages by subdomain shuffling. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 9813-8	11.5	49
105	Structure of the Rad50 DNA double-strand break repair protein in complex with DNA. *EMBO Journal*, **2014**, 33, 2847-59	13	48
104	Differential arrangements of conserved building blocks among homologs of the Rad50/Mre11 DNA repair protein complex. *Journal of Molecular Biology*, **2004**, 339, 937-49	6.5	48
103	Bifunctional PD-1 □□CD3 □□CD33 fusion protein reverses adaptive immune escape in acute myeloid leukemia. *Blood*, **2018**, 132, 2484-2494	2.2	48
102	Invited review: Architectures and mechanisms of ATP binding cassette proteins. *Biopolymers*, **2016**, 105, 492-504	2.2	47
101	Mechanisms of nucleic acid translocases: lessons from structural biology and single-molecule biophysics. *Current Opinion in Structural Biology*, **2007**, 17, 87-95	8.1	46
100	Dramatic enhancement of the catalytic activity of coagulation factor IXa by alcohols. *FEBS Letters*, **1997**, 412, 295-300	3.8	44
99	Structure of Actin-related protein 8 and its contribution to nucleosome binding. *Nucleic Acids Research*, **2012**, 40, 11036-46	20.1	42
98	Activating FLT3 mutants show distinct gain-of-function phenotypes in vitro and a characteristic signaling pathway profile associated with prognosis in acute myeloid leukemia. *PLoS ONE*, **2014**, 9, e89560	3.7	42
97	c-di-AMP recognition by Staphylococcus aureus PstA. *FEBS Letters*, **2015**, 589, 45-51	3.8	41
96	RPA Mediates Recruitment of MRX to Forks and Double-Strand Breaks to Hold Sister Chromatids Together. *Molecular Cell*, **2016**, 64, 951-966	17.6	40
95	Exome sequencing identifies recurring FLT3 N676K mutations in core-binding factor leukemia. *Blood*, **2013**, 122, 1761-9	2.2	40
94	Structural and functional analysis of Mre11-3. *Nucleic Acids Research*, **2004**, 32, 1886-93	20.1	40
93	ZBTB7A mutations in acute myeloid leukaemia with t(8;21) translocation. *Nature Communications*, **2016**, 7, 11733	17.4	39

92	Theory of allosteric effects in serine proteases. *Biophysical Journal*, **1996**, 70, 174-81	2.9	38
91	Conformational changes of a Swi2/Snf2 ATPase during its mechano-chemical cycle. *Nucleic Acids Research*, **2008**, 36, 1881-90	20.1	37
90	The exosome: a macromolecular cage for controlled RNA degradation. *Molecular Microbiology*, **2006**, 61, 1372-9	4.1	37
89	The nuclear actin-containing Arp8 module is a linker DNA sensor driving INO80 chromatin remodeling. *Nature Structural and Molecular Biology*, **2018**, 25, 823-832	17.6	37
88	Mechanism of replication blocking and bypass of Y-family polymerase {eta} by bulky acetylaminofluorene DNA adducts. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 20720-5	11.5	34
87	Correlating calcium binding, Förster resonance energy transfer, and conformational change in the biosensor TN-XXL. *Biophysical Journal*, **2012**, 102, 2401-10	2.9	33
86	Sensing of viral nucleic acids by RIG-I: from translocation to translation. *European Journal of Cell Biology*, **2012**, 91, 78-85	6.1	32
85	MlaA, a hexameric ATPase linked to the Mre11 complex in archaeal genomes. *EMBO Reports*, **2004**, 5, 54-9	6.5	32
84	Physiological fIXa activation involves a cooperative conformational rearrangement of the 99-loop. *Journal of Biological Chemistry*, **2003**, 278, 4121-6	5.4	32
83	Structural basis for dodecameric assembly states and conformational plasticity of the full-length AAA+ ATPases Rvb1 Rvb2. *Structure*, **2015**, 23, 483-495	5.2	31
82	Activity-based probes for detection of active MALT1 paracaspase in immune cells and lymphomas. *Chemistry and Biology*, **2015**, 22, 129-38		30
81	Measuring DNA mechanics on the genome scale. *Nature*, **2021**, 589, 462-467	50.4	29
80	Structural basis for transcription-coupled repair: the N terminus of Mfd resembles UvrB with degenerate ATPase motifs. *Journal of Molecular Biology*, **2006**, 355, 675-83	6.5	28
79	Molecular architecture and regulation of BCL10-MALT1 filaments. *Nature Communications*, **2018**, 9, 4041	17.4	27
78	Crystal structure of an anti-Ang2 CrossFab demonstrates complete structural and functional integrity of the variable domain. *PLoS ONE*, **2013**, 8, e61953	3.7	26
77	Impact of Heterogeneity and Lattice Bond Strength on DNA Triangle Crystal Growth. *ACS Nano*, **2016**, 10, 9156-9164	16.7	26
76	The influence of residue 190 in the S1 site of trypsin-like serine proteases on substrate selectivity is universally conserved. *FEBS Letters*, **2002**, 530, 220-4	3.8	25
75	Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. *Cell Reports*, **2020**, 31, 107522	10.6	24

74	Structure and DNA-binding activity of the Pyrococcus furiosus SMC protein hinge domain. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79, 558-68	4.2	24
73	Structural studies of DNA end detection and resection in homologous recombination. *Cold Spring Harbor Perspectives in Biology*, **2014**, 6, a017962	10.2	20
72	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. *Nucleic Acids Research*, **2010**, 38, 5166-76	20.1	20
71	The cytosolic DNA sensor cGAS recognizes neutrophil extracellular traps. *Science Signaling*, **2021**, 14,	8.8	20
70	Structural and biochemical characterization of the cell fate determining nucleotidyltransferase fold protein MAB21L1. *Scientific Reports*, **2016**, 6, 27498	4.9	19
69	Energetics of thrombin-fibrinogen interaction. *Biochemistry*, **1992**, 31, 11567-71	3.2	19
68	DNA mismatch repair: the hands of a genome guardian. *Structure*, **2000**, 8, R237-41	5.2	18
67	Chemical compensation in macromolecular bridge-binding to thrombin. *Biochemistry*, **1993**, 32, 2947-53	3.2	18
66	Crystal structure of human TWEAK in complex with the Fab fragment of a neutralizing antibody reveals insights into receptor binding. *PLoS ONE*, **2013**, 8, e62697	3.7	17
65	Near-Complete Structure and Model of Tel1ATM from Chaetomium thermophilum Reveals a Robust Autoinhibited ATP State. *Structure*, **2020**, 28, 83-95.e5	5.2	17
64	Structure of the catalytic domain of Mre11 from Chaetomium thermophilum. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 752-7	1.1	16
63	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. *OncoImmunology*, **2018**, 7, e1472195	7.2	16
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	3.3	16
61	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. *ELife*, **2018**, 7,	8.9	16
60	Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. *Nucleic Acids Research*, **2017**, 45, 12025-12038	20.1	15
59	Dual-targeting triplebody 33-3-19 mediates selective lysis of biphenotypic CD19+ CD33+ leukemia cells. *Oncotarget*, **2016**, 7, 22579-89	3.3	15
58	SIRP□-antibody fusion proteins stimulate phagocytosis and promote elimination of acute myeloid leukemia cells. *Oncotarget*, **2017**, 8, 11284-11301	3.3	14
57	Structural analysis of the diadenylate cyclase reaction of DNA-integrity scanning protein A (DisA) and its inhibition by 3PdATP. *Biochemical Journal*, **2015**, 469, 367-74	3.8	14

56	Structural basis for recognition and remodeling of the TBP:DNA:NC2 complex by Mot1. *ELife*, **2015**, 4,	8.9	14
55	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. *BioEssays*, **2014**, 36, 1170-8	4.1	13
54	The bacterial Mre11-Rad50 homolog SbcCD cleaves opposing strands of DNA by two chemically distinct nuclease reactions. *Nucleic Acids Research*, **2018**, 46, 11303-11314	20.1	13
53	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. *Journal of Translational Medicine*, **2013**, 11, 289	8.5	12
52	Lessons from structural and biochemical studies on the archaeal exosome. *Biochemical Society Transactions*, **2009**, 37, 83-7	5.1	12
51	Reversible and controllable nanolocomotion of an RNA-processing machinery. *Nano Letters*, **2010**, 10, 5123-30	11.5	11
50	DNA double-strand breaks come into focus. *Cell*, **2009**, 139, 25-7	56.2	11
49	Molecular architecture of the HerA-NurA DNA double-strand break resection complex. *FEBS Letters* , **2014**, 588, 4637-44	3.8	10
48	Response to: monoclonal antibodies targeting CD20. *MAbs*, **2013**, 5, 337-8	6.6	10
47	Megadalton chromatin remodelers: common principles for versatile functions. *Current Opinion in Structural Biology*, **2020**, 64, 134-144	8.1	10
46	Single-molecule nucleosome remodeling by INO80 and effects of histone tails. *FEBS Letters*, **2018**, 592, 318-331	3.8	9
45	Structural basis for adenylate kinase activity in ABC ATPases. *Journal of Molecular Biology*, **2010**, 401, 265-73	6.5	9
44	Rustless translation. *Biological Chemistry*, **2012**, 393, 1079-88	4.5	9
43	Chromosome biology: the crux of the ring. *Current Biology*, **2006**, 16, R102-5	6.3	8
42	Structure-function analysis of SWI2/SNF2 enzymes. *Methods in Enzymology*, **2006**, 409, 375-88	1.7	8
41	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. *Nature Communications*, **2021**, 12, 3232	17.4	8
40	A Click-Chemistry Linked 2P3PcGAMP Analogue. *Chemistry - A European Journal*, **2019**, 25, 2089-2095	4.8	8
39	Serendipitous crystallization and structure determination of cyanase (CynS) from Serratia proteamaculans. *Acta Crystallographica Section F, Structural Biology Communications*, **2015**, 71, 471-6	1.1	7

38	Chip-based platform for dynamic analysis of NK cell cytolysis mediated by a triplebody. *Analyst, The* , **2016**, 141, 2284-95	5	7
37	Nuclear cGAS: guard or prisoner?. *EMBO Journal*, **2021**, 40, e108293	13	7
36	DuoMab: a novel CrossMab-based IgG-derived antibody format for enhanced antibody-dependent cell-mediated cytotoxicity. *MAbs*, **2019**, 11, 1402-1414	6.6	6
35	RIG-I holds the CARDs in a game of self versus nonself. *Molecular Cell*, **2014**, 55, 505-7	17.6	6
34	Processive RNA decay by the exosome: merits of a quantitative Bayesian sampling approach. *RNA Biology*, **2011**, 8, 55-60	4.8	6
33	Biochemical characterization and crystal structure of a Dim1 family associated protein: Dim2. *Biochemistry*, **2005**, 44, 11997-2008	3.2	6
32	T cell-recruiting triplebody 19-3-19 mediates serial lysis of malignant B-lymphoid cells by a single T cell. *Oncotarget*, **2014**, 5, 6466-83	3.3	6
31	Genome information processing by the INO80 chromatin remodeler positions nucleosomes. *Nature Communications*, **2021**, 12, 3231	17.4	6
30	Nuclear actin-related proteins take shape. *Bioarchitecture*, **2011**, 1, 192-195		5
29	Binding of fibrinogen A alpha 1-50-beta-galactosidase fusion protein to thrombin stabilizes the slow form. *Journal of Biological Chemistry*, **1995**, 270, 24790-3	5.4	5
28	Symmetry conditions for binding processes. *Proceedings of the National Academy of Sciences of the United States of America*, **1992**, 89, 2727-31	11.5	5
27	Crystal and solution structure of the human RIG-I SF2 domain. *Acta Crystallographica Section F, Structural Biology Communications*, **2014**, 70, 1027-31	1.1	4
26	RIG-I-Like Receptors: One STrEP Forward. *Trends in Microbiology*, **2016**, 24, 517-519	12.4	4
25	A modular and controllable T cell therapy platform for acute myeloid leukemia. *Leukemia*, **2021**, 35, 2243-2257	10.7	4
24	OAS1/RNase L executes RIG-I ligand-dependent tumor cell apoptosis. *Science Immunology*, **2021**, 6,	28	4
23	Measuring DNA mechanics on the genome scale		3
22	Envisioning the fourth dimension of the genetic code: the structural biology of macromolecular recognition and conformational switching in DNA repair. *Cold Spring Harbor Symposia on Quantitative Biology*, **2000**, 65, 113-26	3.9	3
21	Structural basis of the (in)activity of the apical DNA damage response kinases ATM, ATR and DNA-PKcs. *Progress in Biophysics and Molecular Biology*, **2021**, 163, 120-129	4.7	3

20	BusR senses bipartite DNA binding motifs by a unique molecular ruler architecture. *Nucleic Acids Research*, **2021**, 49, 10166-10177	20.1	3
19	SIRP□CD123 fusion antibodies targeting CD123 in conjunction with CD47 blockade enhance the clearance of AML-initiating cells. *Journal of Hematology and Oncology*, **2021**, 14, 155	22.4	3
18	Molecular basis of human ATM kinase inhibition. *Nature Structural and Molecular Biology*, **2021**, 28, 789-798	17.6	3
17	Crystal structure of the full Swi2/Snf2 remodeler Mot1 in the resting state. *ELife*, **2018**, 7,	8.9	2
16	Chemical synthesis of the fluorescent, cyclic dinucleotides cthGAMP.. *ChemBioChem*, **2022**,	3.8	2
15	Chromosome cohesion: closing time. *Current Biology*, **2003**, 13, R866-8	6.3	1
14	Exploiting an Anti-CD3/CD33 Bispecific Antibody to Redirect Donor T Cells Against HLA Loss Leukemia Relapses. *Blood*, **2019**, 134, 513-513	2.2	1
13	Evaluation of a Bifunctional Sirp□CD123 Fusion Antibody for the Elimination of Acute Myeloid Leukemia Stem Cells. *Blood*, **2019**, 134, 2544-2544	2.2	1
12	Crystallization of mouse RIG-I ATPase domain: in situ proteolysis. *Methods in Molecular Biology*, **2014**, 1169, 27-35	1.4	1
11	Genome information processing by the INO80 chromatin remodeler positions nucleosomes		1
10	Single-molecule choreography between telomere proteins and G quadruplexes. *Structure*, **2014**, 22, 801-2	3.2	
9	Strukturelle Analyse von Phenothiazin-Derivaten als allosterische Inhibitoren der MALT1-Paracaspase. *Angewandte Chemie*, **2013**, 125, 10575-10579	3.6	
8	Structure and Function of Rad50/SMC Protein Complexes in Chromosome Biology **2005**, 201-218		
7	The exosome, plugged. *EMBO Reports*, **2007**, 8, 456-7	6.5	
6	The chemistry of transcription through damaged DNA and of translesion synthesis at atomic resolution. *Nucleic Acids Symposium Series*, **2007**, 103		
5	Point Mutations Found in the Juxtamembrane Domain of FLT3 Define a New Class of Activating Mutations in AML.. *Blood*, **2005**, 106, 4388-4388	2.2	
4	Aberrant Cathepsin S Induces a Supportive Immune Microenvironment in Follicular Lymphoma. *Blood*, **2019**, 134, 657-657	2.2	
3	Chapter 5:RIG-I-Like RNA Helicases: Multidomain Proteins in Antiviral Innate Immunity and Processing of Small Regulatory RNAs. *RSC Biomolecular Sciences*, **2010**, 121-148		

2	Insights into DNA damage signaling from the structure of an Mre11:Nbs1 complex. *FASEB Journal*, **2010**, 24, lb39	0.9
1	The RNA Exosomes. *Nucleic Acids and Molecular Biology*, **2011**, 223-244	