

Hideki Aihara

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.

87
papers

3,767
citations

22
h-index

61
g-index

95
ext. papers

4,991
ext. citations

9.3
avg, IF

6.01
L-index

#	Paper	IF	Citations
87	A Structure-based Design Approach for Generating High Affinity BRD4 D1-Selective Chemical Probes.. <i>Journal of Medicinal Chemistry</i> , 2022 ,	8.3	1
86	Structure and dynamics of SARS-CoV-2 proofreading exoribonuclease ExoN.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	9
85	Structural Basis for Human Receptor Recognition by SARS-CoV Omicron Variant BA.1.. <i>Journal of Virology</i> , 2022 , e0024922	6.6	3
84	DNA ligase and PCNA: Double-ring down to seal a break in DNA.. <i>Structure</i> , 2022 , 30, 324-326	5.2	
83	Mechanisms of SARS-CoV-2 neutralization by shark variable new antigen receptors elucidated through X-ray crystallography.. <i>Nature Communications</i> , 2021 , 12, 7325	17.4	4
82	Structural basis for recognition of distinct deaminated DNA lesions by endonuclease Q. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
81	Cryo-EM structure of the Rous sarcoma virus octameric cleaved synaptic complex intasome. <i>Communications Biology</i> , 2021 , 4, 330	6.7	4
80	Bi-allelic MCM10 variants associated with immune dysfunction and cardiomyopathy cause telomere shortening. <i>Nature Communications</i> , 2021 , 12, 1626	17.4	3
79	Soluble Methane Monooxygenase Component Interactions Monitored by F NMR. <i>Biochemistry</i> , 2021 , 60, 1995-2010	3.2	1
78	4-Benzylideneisoquinoline-1,3(-)-diones as tyrosyl DNA phosphodiesterase 2 (TDP2) inhibitors. <i>Medicinal Chemistry Research</i> , 2021 , 30, 371-386	2.2	2
77	Selective N-Terminal BET Bromodomain Inhibitors by Targeting Non-Conserved Residues and Structured Water Displacement*. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 1220-1226	16.4	13
76	Molecular underpinnings of ssDNA specificity by Rep HUH-endonucleases and implications for HUH-tag multiplexing and engineering. <i>Nucleic Acids Research</i> , 2021 , 49, 1046-1064	20.1	6
75	4-Methyl-1,2,3-Triazoles as -Acetyl-Lysine Mimics Afford Potent BET Bromodomain Inhibitors with Improved Selectivity. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 10497-10511	8.3	3
74	The development of - as anti-SARS-CoV-2 nanobody drug candidates. <i>ELife</i> , 2021 , 10,	8.9	10
73	Identification and Characterization of Two Structurally Related Dipeptides that Enhance Catalytic Efficiency of Neurolysin. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2021 , 379, 191-202	4.7	3
72	New Design Rules for Developing Potent Cell-Active Inhibitors of the Nucleosome Remodeling Factor (NURF) via BPTF Bromodomain Inhibition. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 13902-13917	8.3	0
71	Metal binding 6-arylthio-3-hydroxypyrimidine-2,4-diones inhibited human cytomegalovirus by targeting the pUL89 endonuclease of the terminase complex. <i>European Journal of Medicinal Chemistry</i> , 2021 , 222, 113640	6.8	0

70	Structural basis of receptor recognition by SARS-CoV-2. <i>Nature</i> , 2020 , 581, 221-224	50.4	2085
69	Structural basis for receptor recognition by the novel coronavirus from Wuhan 2020 ,		14
68	DNA aptamers against the DUX4 protein reveal novel therapeutic implications for FSHD. <i>FASEB Journal</i> , 2020 , 34, 4573-4590	0.9	10
67	Active site plasticity and possible modes of chemical inhibition of the human DNA deaminase APOBEC3B. <i>FASEB BioAdvances</i> , 2020 , 2, 49-58	2.8	5
66	Structural insights into the promiscuous DNA binding and broad substrate selectivity of fowlpox virus resolvase. <i>Scientific Reports</i> , 2020 , 10, 393	4.9	1
65	The Development of a Novel Nanobody Therapeutic for SARS-CoV-2 2020 ,		10
64	Structural basis of host protein hijacking in human T-cell leukemia virus integration. <i>Nature Communications</i> , 2020 , 11, 3121	17.4	16
63	Structural basis of superinfection exclusion by bacteriophage T4 Spackle. <i>Communications Biology</i> , 2020 , 3, 691	6.7	8
62	HK022 bacteriophage Integrase mediated RMCE as a potential tool for human gene therapy. <i>Nucleic Acids Research</i> , 2020 , 48, 12804-12816	20.1	0
61	Structural Studies of the OB3b Soluble Methane Monooxygenase Hydroxylase and Regulatory Component Complex Reveal a Transient Substrate Tunnel. <i>Biochemistry</i> , 2020 , 59, 2946-2961	3.2	13
60	Crystal structure of bacteriophage T4 Spackle as determined by native SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 899-904	5.5	2
59	Enhancing subtilisin thermostability through a modified normalized B-factor analysis and loop-grafting strategy. <i>Journal of Biological Chemistry</i> , 2019 , 294, 18398-18407	5.4	8
58	The anti-parasitic agent suramin and several of its analogues are inhibitors of the DNA binding protein Mcm10. <i>Open Biology</i> , 2019 , 9, 190117	7	10
57	Selectivity, ligand deconstruction, and cellular activity analysis of a BPTF bromodomain inhibitor. <i>Organic and Biomolecular Chemistry</i> , 2019 , 17, 2020-2027	3.9	15
56	Novel Deazaflavin Analogues Potently Inhibited Tyrosyl DNA Phosphodiesterase 2 (TDP2) and Strongly Sensitized Cancer Cells toward Treatment with Topoisomerase II (TOP2) Poison Etoposide. <i>Journal of Medicinal Chemistry</i> , 2019 , 62, 4669-4682	8.3	8
55	Insight into subtilisin E-S7 cleavage pattern based on crystal structure and hydrolysates peptide analysis. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 512, 623-628	3.4	1
54	Hybridization of TEDOR and NCX MAS solid-state NMR experiments for simultaneous acquisition of heteronuclear correlation spectra and distance measurements. <i>Journal of Biomolecular NMR</i> , 2019 , 73, 141-153	3	9
53	Determinants of Oligonucleotide Selectivity of APOBEC3B. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 2264-2273	6.1	7

52	Crystal structures of <i>Moorella thermoacetica</i> cyanuric acid hydrolase reveal conformational flexibility and asymmetry important for catalysis. <i>PLoS ONE</i> , 2019 , 14, e0216979	3.7	1
51	The Role of RNA in HIV-1 Vif-Mediated Degradation of APOBEC3H. <i>Journal of Molecular Biology</i> , 2019 , 431, 5019-5031	6.5	2
50	Crystal structure of the Wheat dwarf virus Rep domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 744-749	1.1	3
49	Inhibiting APOBEC3 Activity with Single-Stranded DNA Containing 2SDeoxyzebularine Analogues. <i>Biochemistry</i> , 2019 , 58, 391-400	3.2	11
48	Triazolopyrimidine and triazolopyridine scaffolds as TDP2 inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2019 , 29, 257-261	2.9	12
47	Importance of homo-dimerization of Fanconi-associated nuclease 1 in DNA flap cleavage. <i>DNA Repair</i> , 2018 , 64, 53-58	4.3	4
46	Crystal structure of lipid A disaccharide synthase LpxB from <i>Escherichia coli</i> . <i>Nature Communications</i> , 2018 , 9, 377	17.4	14
45	The Antiviral and Cancer Genomic DNA Deaminase APOBEC3H Is Regulated by an RNA-Mediated Dimerization Mechanism. <i>Molecular Cell</i> , 2018 , 69, 75-86.e9	17.6	47
44	The substrate-binding cap of the UDP-diacylglucosamine pyrophosphatase LpxH is highly flexible, enabling facile substrate binding and product release. <i>Journal of Biological Chemistry</i> , 2018 , 293, 7969-7981	5.4	10
43	New fluorescence-based high-throughput screening assay for small molecule inhibitors of tyrosyl-DNA phosphodiesterase 2 (TDP2). <i>European Journal of Pharmaceutical Sciences</i> , 2018 , 118, 67-79	5.1	11
42	Comment on structural basis of DUX4/IGH-driven transactivation. <i>Leukemia</i> , 2018 , 32, 2090-2092	10.7	1
41	Oligomerization of Retrovirus Integrases. <i>Sub-Cellular Biochemistry</i> , 2018 , 88, 211-243	5.5	1
40	Differential assembly of Rous sarcoma virus tetrameric and octameric intasomes is regulated by the C-terminal domain and tail region of integrase. <i>Journal of Biological Chemistry</i> , 2018 , 293, 16440-16452	5.4	3
39	T4 DNA ligase structure reveals a prototypical ATP-dependent ligase with a unique mode of sliding clamp interaction. <i>Nucleic Acids Research</i> , 2018 , 46, 10474-10488	20.1	24
38	Current Progress in the Structural and Biochemical Characterization of Proteins Involved in the Assembly of Lipopolysaccharide. <i>International Journal of Microbiology</i> , 2018 , 2018, 5319146	3.6	10
37	Crystal Structure of the Double Homeodomain of DUX4 in Complex with DNA. <i>Cell Reports</i> , 2018 , 25, 2955-2962.e3	10.6	14
36	Crystal Structure of Cdc45 Suggests a Conformational Switch that May Regulate DNA Replication. <i>IScience</i> , 2018 , 3, 102-109	6.1	1
35	A C-terminal "Tail" Region in the Rous Sarcoma Virus Integrase Provides High Plasticity of Functional Integrase Oligomerization during Intasome Assembly. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5018-5030	5.4	4

34	Five Fatty Aldehyde Dehydrogenase Enzymes from <i>Marinobacter</i> and <i>Acinetobacter</i> spp. and Structural Insights into the Aldehyde Binding Pocket. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	3
33	Structural basis for targeted DNA cytosine deamination and mutagenesis by APOBEC3A and APOBEC3B. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 131-139	17.6	141
32	Conformational Switch Regulates the DNA Cytosine Deaminase Activity of Human APOBEC3B. <i>Scientific Reports</i> , 2017 , 7, 17415	4.9	21
31	Crystal structure of the Rous sarcoma virus intasome. <i>Nature</i> , 2016 , 530, 362-6	50.4	65
30	Isoquinoline-1,3-diones as Selective Inhibitors of Tyrosyl DNA Phosphodiesterase II (TDP2). <i>Journal of Medicinal Chemistry</i> , 2016 , 59, 2734-46	8.3	37
29	DNA-binding sequence specificity of DUX4. <i>Skeletal Muscle</i> , 2016 , 6, 8	5.1	27
28	Structures of Rpn1 T1:Rad23 and hRpn13:hPLIC2 Reveal Distinct Binding Mechanisms between Substrate Receptors and Shuttle Factors of the Proteasome. <i>Structure</i> , 2016 , 24, 1257-1270	5.2	46
27	1.92 Angstrom Zinc-Free APOBEC3F Catalytic Domain Crystal Structure. <i>Journal of Molecular Biology</i> , 2016 , 428, 2307-2316	6.5	30
26	Deazaflavin Inhibitors of Tyrosyl-DNA Phosphodiesterase 2 (TDP2) Specific for the Human Enzyme and Active against Cellular TDP2. <i>ACS Chemical Biology</i> , 2016 , 11, 1925-33	4.9	23
25	Novel TDP2-ubiquitin interactions and their importance for the repair of topoisomerase II-mediated DNA damage. <i>Nucleic Acids Research</i> , 2016 , 44, 10201-10215	20.1	15
24	Crystal Structure of the DNA Deaminase APOBEC3B Catalytic Domain. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28120-28130	5.4	71
23	An ancient protein-DNA interaction underlying metazoan sex determination. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 442-51	17.6	70
22	Multifunctional facets of retrovirus integrase. <i>World Journal of Biological Chemistry</i> , 2015 , 6, 83-94	3.8	8
21	Rous sarcoma virus synaptic complex capable of concerted integration is kinetically trapped by human immunodeficiency virus integrase strand transfer inhibitors. <i>Journal of Biological Chemistry</i> , 2014 , 289, 19648-58	5.4	6
20	Cyanuric acid hydrolase from <i>Azorhizobium caulinodans</i> ORS 571: crystal structure and insights into a new class of Ser-Lys dyad proteins. <i>PLoS ONE</i> , 2014 , 9, e99349	3.7	8
19	Structural asymmetry in the <i>Thermus thermophilus</i> RuvC dimer suggests a basis for sequential strand cleavages during Holliday junction resolution. <i>Nucleic Acids Research</i> , 2013 , 41, 648-56	20.1	26
18	Crystallization and preliminary X-ray diffraction studies of cyanuric acid hydrolase from <i>Azorhizobium caulinodans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 880-3		3
17	An enzyme-catalyzed multistep DNA refolding mechanism in hairpin telomere formation. <i>PLoS Biology</i> , 2013 , 11, e1001472	9.7	12

16	A possible role for the asymmetric C-terminal domain dimer of Rous sarcoma virus integrase in viral DNA binding. <i>PLoS ONE</i> , 2013 , 8, e56892	3.7	10
15	Structural basis for recognition of 5Sphosphotyrosine adducts by Tdp2. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1372-7	17.6	48
14	Linear chromosome-generating system of <i>Agrobacterium tumefaciens</i> C58: protelomerase generates and protects hairpin ends. <i>Journal of Biological Chemistry</i> , 2012 , 287, 25551-63	5.4	16
13	An interlocked dimer of the protelomerase TelK distorts DNA structure for the formation of hairpin telomeres. <i>Molecular Cell</i> , 2007 , 27, 901-13	17.6	34
12	Non-equivalent interactions between amino-terminal domains of neighboring lambda integrase protomers direct Holliday junction resolution. <i>Journal of Molecular Biology</i> , 2005 , 345, 475-85	6.5	12
11	A structural basis for allosteric control of DNA recombination by lambda integrase. <i>Nature</i> , 2005 , 435, 1059-66	50.4	140
10	Two structural features of lambda integrase that are critical for DNA cleavage by multimers but not by monomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2770-5	11.5	15
9	A conformational switch controls the DNA cleavage activity of lambda integrase. <i>Molecular Cell</i> , 2003 , 12, 187-98	17.6	43
8	An NMR study on the interaction of <i>Escherichia coli</i> DinI with RecA-ssDNA complexes. <i>Nucleic Acids Research</i> , 2003 , 31, 1735-43	20.1	22
7	Differential affinity and cooperativity functions of the amino-terminal 70 residues of lambda integrase. <i>Journal of Molecular Biology</i> , 2002 , 324, 775-89	6.5	29
6	Specific defects in double-stranded DNA unwinding and homologous pairing of a mutant RecA protein. <i>FEBS Letters</i> , 2000 , 477, 129-34	3.8	8
5	The N-terminal domain of the human Rad51 protein binds DNA: structure and a DNA binding surface as revealed by NMR. <i>Journal of Molecular Biology</i> , 1999 , 290, 495-504	6.5	120
4	Human Rad51 amino acid residues required for Rad52 binding. <i>Journal of Molecular Biology</i> , 1999 , 291, 537-48	6.5	63
3	An interaction between a specified surface of the C-terminal domain of RecA protein and double-stranded DNA for homologous pairing. <i>Journal of Molecular Biology</i> , 1997 , 274, 213-21	6.5	68
2	A possible role of the C-terminal domain of the RecA protein. A gateway model for double-stranded DNA binding. <i>Journal of Biological Chemistry</i> , 1996 , 271, 33515-24	5.4	66
1	Bi-allelic MCM10 mutations cause telomere shortening with immune dysfunction and cardiomyopathy		1