

Jinwoo Ahn

List of Publications by Year in descending order

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70
papers

4,407
citations

117625

34
h-index

114465

63
g-index

74
all docs

74
docs citations

74
times ranked

4970
citing authors

#	ARTICLE	IF	CITATIONS
1	Mature HIV-1 capsid structure by cryo-electron microscopy and all-atom molecular dynamics. <i>Nature</i> , 2013, 497, 643-646.	27.8	712
2	Structural Convergence between Cryo-EM and NMR Reveals Intersubunit Interactions Critical for HIV-1 Capsid Function. <i>Cell</i> , 2009, 139, 780-790.	28.9	241
3	The Chk2 protein kinase. <i>DNA Repair</i> , 2004, 3, 1039-1047.	2.8	212
4	HIV/Simian Immunodeficiency Virus (SIV) Accessory Virulence Factor Vpx Loads the Host Cell Restriction Factor SAMHD1 onto the E3 Ubiquitin Ligase Complex CRL4DCAF1. <i>Journal of Biological Chemistry</i> , 2012, 287, 12550-12558.	3.4	157
5	Tetramerization of SAMHD1 Is Required for Biological Activity and Inhibition of HIV Infection. <i>Journal of Biological Chemistry</i> , 2013, 288, 10406-10417.	3.4	142
6	Mechanism of allosteric activation of SAMHD1 by dGTP. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1304-1309.	8.2	135
7	The C terminus of p53 binds the N-terminal domain of MDM2. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 982-989.	8.2	133
8	Cyclophilin A stabilizes the HIV-1 capsid through a novel non-canonical binding site. <i>Nature Communications</i> , 2016, 7, 10714.	12.8	126
9	The Host Proteins Transportin SR2/TNPO3 and Cyclophilin A Exert Opposing Effects on HIV-1 Uncoating. <i>Journal of Virology</i> , 2013, 87, 422-432.	3.4	113
10	Solid-State NMR Studies of HIV-1 Capsid Protein Assemblies. <i>Journal of the American Chemical Society</i> , 2010, 132, 1976-1987.	13.7	112
11	The C-terminus of p53: the more you learn the less you know. , 2001, 8, 730-732.		100
12	HIV-1 Vpr Loads Uracil DNA Glycosylase-2 onto DCAF1, a Substrate Recognition Subunit of a Cullin 4A-RING E3 Ubiquitin Ligase for Proteasome-dependent Degradation. <i>Journal of Biological Chemistry</i> , 2010, 285, 37333-37341.	3.4	91
13	Questioning the Role of Checkpoint Kinase 2 in the p53 DNA Damage Response. <i>Journal of Biological Chemistry</i> , 2003, 278, 20480-20489.	3.4	87
14	¹³ C/ ¹⁵ N Heteronuclear Dipolar Recoupling by R-Symmetry Sequences Under Fast Magic Angle Spinning for Dynamics Analysis of Biological and Organic Solids. <i>Journal of the American Chemical Society</i> , 2011, 133, 18646-18655.	13.7	87
15	Evolutionary Toggling of Vpx/Vpr Specificity Results in Divergent Recognition of the Restriction Factor SAMHD1. <i>PLoS Pathogens</i> , 2013, 9, e1003496.	4.7	86
16	CyclinA2-Cyclin-dependent Kinase Regulates SAMHD1 Protein Phosphohydrolase Domain. <i>Journal of Biological Chemistry</i> , 2015, 290, 13279-13292.	3.4	84
17	Motions on the Millisecond Time Scale and Multiple Conformations of HIV-1 Capsid Protein: Implications for Structural Polymorphism of CA Assemblies. <i>Journal of the American Chemical Society</i> , 2012, 134, 6455-6466.	13.7	83
18	Recoupling of chemical shift anisotropy by R-symmetry sequences in magic angle spinning NMR spectroscopy. <i>Journal of Chemical Physics</i> , 2012, 137, 134201.	3.0	78

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19	DNA damage tolerance pathway involving DNA polymerase δ and the tumor suppressor p53 regulates DNA replication fork progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4311-9.	7.1	78
20	The DDB1-DCAF1-Vpr-UNG2 crystal structure reveals how HIV-1 Vpr steers human UNG2 toward destruction. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 933-940.	8.2	77
21	Rhesus TRIM5 α Disrupts the HIV-1 Capsid at the InterHexamer Interfaces. <i>PLoS Pathogens</i> , 2011, 7, e1002009.	4.7	77
22	Dynamic allostery governs cyclophilin A-HIV capsid interplay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14617-14622.	7.1	76
23	Structural Changes and Proapoptotic Peroxidase Activity of Cardiolipin-Bound Mitochondrial Cytochrome c. <i>Biophysical Journal</i> , 2015, 109, 1873-1884.	0.5	75
24	Checkpoint Kinase 2 (Chk2) Monomers or Dimers Phosphorylate Cdc25C after DNA Damage Regardless of Threonine 68 Phosphorylation. <i>Journal of Biological Chemistry</i> , 2002, 277, 48418-48426.	3.4	68
25	Magic Angle Spinning NMR Reveals Sequence-Dependent Structural Plasticity, Dynamics, and the Spacer Peptide 1 Conformation in HIV-1 Capsid Protein Assemblies. <i>Journal of the American Chemical Society</i> , 2013, 135, 17793-17803.	13.7	60
26	Structural Basis of Allosteric Activation of Sterile α Motif and Histidine-Aspartate Domain-containing Protein 1 (SAMHD1) by Nucleoside Triphosphates. <i>Journal of Biological Chemistry</i> , 2014, 289, 32617-32627.	3.4	59
27	Spin Diffusion Driven by R-Symmetry Sequences: Applications to Homonuclear Correlation Spectroscopy in MAS NMR of Biological and Organic Solids. <i>Journal of the American Chemical Society</i> , 2011, 133, 3943-3953.	13.7	58
28	Structure of the HIV-1 Full-Length Capsid Protein in a Conformationally Trapped Unassembled State Induced by Small-Molecule Binding. <i>Journal of Molecular Biology</i> , 2011, 406, 371-386.	4.2	54
29	Capsid-CPSF6 Interaction Is Dispensable for HIV-1 Replication in Primary Cells but Is Selected during Virus Passage <i>In Vivo</i> . <i>Journal of Virology</i> , 2016, 90, 6918-6935.	3.4	50
30	Dynamic Nuclear Polarization Enhanced MAS NMR Spectroscopy for Structural Analysis of HIV-1 Protein Assemblies. <i>Journal of Physical Chemistry B</i> , 2016, 120, 329-339.	2.6	49
31	Insight into the Structural Basis of Pro- and Antiapoptotic p53 Modulation by ASPP Proteins. <i>Journal of Biological Chemistry</i> , 2009, 284, 13812-13822.	3.4	48
32	HIV-1 Capsid Function Is Regulated by Dynamics: Quantitative Atomic-Resolution Insights by Integrating Magic-Angle-Spinning NMR, QM/MM, and MD. <i>Journal of the American Chemical Society</i> , 2016, 138, 14066-14075.	13.7	48
33	Dynamic regulation of HIV-1 capsid interaction with the restriction factor TRIM5 α identified by magic-angle spinning NMR and molecular dynamics simulations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11519-11524.	7.1	47
34	The N Terminus of p53 Regulates Its Dissociation from DNA. <i>Journal of Biological Chemistry</i> , 2000, 275, 39944-39953.	3.4	45
35	Permeability of the HIV-1 capsid to metabolites modulates viral DNA synthesis. <i>PLoS Biology</i> , 2020, 18, e3001015.	5.6	42
36	Interaction of HIV-1 Reverse Transcriptase Ribonuclease H with an Acylhydrazone Inhibitor. <i>Chemical Biology and Drug Design</i> , 2011, 77, 39-47.	3.2	38

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37	Dissection of the sequence-specific DNA binding and exonuclease activities reveals a superactive yet apoptotically impaired mutant p53 protein. <i>Cell Cycle</i> , 2009, 8, 1603-1615.	2.6	35
38	SLX4-SLX1 Protein-independent Down-regulation of MUS81-EME1 Protein by HIV-1 Viral Protein R (Vpr). <i>Journal of Biological Chemistry</i> , 2016, 291, 16936-16947.	3.4	34
39	Inhibition of TFII-I-Dependent Cell Cycle Regulation by p53. <i>Molecular and Cellular Biology</i> , 2005, 25, 10940-10952.	2.3	33
40	The Cullin-RING E3 Ubiquitin Ligase CRL4 ^{DCAF1} Complex Dimerizes via a Short Helical Region in DCAF1. <i>Biochemistry</i> , 2011, 50, 1359-1367.	2.5	33
41	Structural Basis of the Allosteric Inhibitor Interaction on the HIV-1 Reverse Transcriptase RNase H Domain. <i>Chemical Biology and Drug Design</i> , 2012, 80, 706-716.	3.2	33
42	HIV-2 and SIVmac Accessory Virulence Factor Vpx Down-regulates SAMHD1 Enzyme Catalysis Prior to Proteasome-dependent Degradation. <i>Journal of Biological Chemistry</i> , 2013, 288, 19116-19126.	3.4	31
43	Dynamic Nuclear Polarization Magic-Angle Spinning Nuclear Magnetic Resonance Combined with Molecular Dynamics Simulations Permits Detection of Order and Disorder in Viral Assemblies. <i>Journal of Physical Chemistry B</i> , 2019, 123, 5048-5058.	2.6	31
44	Transmission electron microscopy for the evaluation and optimization of crystal growth. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 603-615.	2.3	29
45	Surface-Binding to Cardiolipin Nanodomains Triggers Cytochrome c Pro-apoptotic Peroxidase Activity via Localized Dynamics. <i>Structure</i> , 2019, 27, 806-815.e4.	3.3	28
46	Cytoplasmic CPSF6 Regulates HIV-1 Capsid Trafficking and Infection in a Cyclophilin A-Dependent Manner. <i>MBio</i> , 2021, 12, .	4.1	28
47	HIV-1 Vpr Reprograms CRL4 ^{DCAF1} E3 Ubiquitin Ligase to Antagonize Exonuclease 1-Mediated Restriction of HIV-1 Infection. <i>MBio</i> , 2018, 9, .	4.1	26
48	Substrate Specificity of SAMHD1 Triphosphohydrolase Activity Is Controlled by Deoxyribonucleoside Triphosphates and Phosphorylation at Thr592. <i>Biochemistry</i> , 2016, 55, 5635-5646.	2.5	25
49	Structure of native HIV-1 cores and their interactions with IP6 and CypA. <i>Science Advances</i> , 2021, 7, eabj5715.	10.3	25
50	Stability of Checkpoint Kinase 2 Is Regulated via Phosphorylation at Serine 456. <i>Journal of Biological Chemistry</i> , 2007, 282, 30311-30321.	3.4	24
51	HIV-1 Vpr protein directly loads helicase-like transcription factor (HLTF) onto the CRL4-DCAF1 E3 ubiquitin ligase. <i>Journal of Biological Chemistry</i> , 2017, 292, 21117-21127.	3.4	18
52	Structure, dynamics, and Hck interaction of full-length HIV-1 Nef. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1609-1622.	2.6	14
53	Structural Basis of Clade-specific Engagement of SAMHD1 (Sterile Î± Motif and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Td (f Virulence Factors. <i>Journal of Biological Chemistry</i> , 2015, 290, 17935-17945.	3.4	14
54	Functional organization of human SAMHD1 and mechanisms of HIV-1 restriction. <i>Biological Chemistry</i> , 2016, 397, 373-379.	2.5	14

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55	Lysines in the tetramerization domain of p53 selectively modulate G1 arrest. <i>Cell Cycle</i> , 2016, 15, 1425-1438.	2.6	13
56	Mechanisms of Allosteric Activation and Inhibition of the Deoxyribonucleoside Triphosphate Triphosphohydrolase from <i>Enterococcus faecalis</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 2815-2824.	3.4	12
57	The crystal structure of dGTPase reveals the molecular basis of dGTP selectivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9333-9339.	7.1	12
58	The RNA binding protein HuR does not interact directly with HIV-1 reverse transcriptase and does not affect reverse transcription in vitro. <i>Retrovirology</i> , 2010, 7, 40.	2.0	9
59	Binding of HIV-1 Vpr Protein to the Human Homolog of the Yeast DNA Repair Protein RAD23 (hHR23A) Requires Its Xeroderma Pigmentosum Complementation Group C Binding (XPCB) Domain as Well as the Ubiquitin-associated 2 (UBA2) Domain. <i>Journal of Biological Chemistry</i> , 2014, 289, 2577-2588.	3.4	9
60	HIV-1 Vpr activates host CRL4-DCAF1 E3 ligase to degrade histone deacetylase SIRT7. <i>Virology Journal</i> , 2021, 18, 48.	3.4	9
61	¹ H, ¹⁵ N and ¹³ C assignments of the dimeric C-terminal domain of HIV-1 capsid protein. <i>Biomolecular NMR Assignments</i> , 2010, 4, 21-23.	0.8	7
62	Structural integrity of the ribonuclease H domain in HIV-1 reverse transcriptase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1526-1538.	2.6	6
63	Characterization of sarcoplasmic reticulum Ca ²⁺ ATPase nucleotide binding domain mutants using NMR spectroscopy. <i>Biochemical and Biophysical Research Communications</i> , 2011, 405, 19-23.	2.1	5
64	<i>SAMHD1</i> Gene Mutations Are Associated with Cerebral Large-Artery Atherosclerosis. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	5
65	Activation of Cytochrome C Peroxidase Function Through Coordinated Foldon Loop Dynamics upon Interaction with Anionic Lipids. <i>Journal of Molecular Biology</i> , 2021, 433, 167057.	4.2	5
66	Structure of HIV-1 Vpr in complex with the human nucleotide excision repair protein hHR23A. <i>Nature Communications</i> , 2021, 12, 6864.	12.8	5
67	The Magic of Linking Rings: Discovery of a Unique Photoinduced Fluorescent Protein Crosslink. <i>Journal of the American Chemical Society</i> , 2022, 144, 10809-10816.	13.7	4
68	Complete ¹ H, ¹³ C, ¹⁵ N resonance assignments and secondary structure of the Vpr binding region of hHR23A (residues 223-363). <i>Biomolecular NMR Assignments</i> , 2020, 14, 13-17.	0.8	3
69	Structural Studies of RNase H Domain to Develop HIV-1 Reverse Transcriptase Inhibitors using Solution NMR. <i>Biophysical Journal</i> , 2011, 100, 605a.	0.5	0
70	Cardiolipin's Double Life as a Substrate and Dynamic Regulator in Pro-Apoptotic Lipid Peroxidation. <i>Biophysical Journal</i> , 2020, 118, 56a-57a.	0.5	0