Aneel K Aggarwal

List of Publications by Year
in descending order

133	13,272	29994	22764
papers	citations	54 h-index	112 g-index

139	139	139	15049
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structure and ligand of a histone acetyltransferase bromodomain. Nature, 1999, 399, 491-496.	13.7	1,501
2	DNA Recognition by Proteins with the Helix-Turn-Helix Motif. Annual Review of Biochemistry, 1990, 59, 933-969.	5.0	586
3	Eya protein phosphatase activity regulates Six1â€“Dachâ€“Eya transcriptional effects in mammalian organogenesis. Nature, 2003, 426, 247-254.	13.7	571
4	A Corepressor/Coactivator Exchange Complex Required for Transcriptional Activation by Nuclear Receptors and Other Regulated Transcription Factors. Cell, 2004, 116, 511-526.	13.5	493
5	PHF8 mediates histone H4 lysine 20 demethylation events involved in cell cycle progression. Nature, 2010, 466, 508-512.	13.7	367
6	Structure of IRF-1 with bound DNA reveals determinants of interferon regulation. Nature, 1998, 391, 103-106.	13.7	366
7	Structure of the Catalytic Core of S. cerevisiae DNA Polymerase Î·. Molecular Cell, 2001, 8, 417-426.	4.5	347
8	Brd4 and JMJD6-Associated Anti-Pause Enhancers in Regulation of Transcriptional Pause Release. Cell, 2013, 155, 1581-1595.	13.5	330
9	Functional Specificity of a Hox Protein Mediated by the Recognition of Minor Groove Structure. Cell, 2007, 131, 530-543.	13.5	303
10	Replication by human DNA polymerase-Î¹ occurs by Hoogsteen base-pairing. Nature, 2004, 430, 377-380.	13.7	300
11	Structure of a DNA-bound Ultrabithoraxâ€“Extradenticle homeodomain complex. Nature, 1999, 397, 714-719.	13.7	296
12	Reciprocal Interactions of Pit1 and GATA2 Mediate Signaling Gradientâ€“Induced Determination of Pituitary Cell Types. Cell, 1999, 97, 587-598.	13.5	292
13	Signal-specific co-activator domain requirements for Pit-1 activation. Nature, 1998, 395, 301-306.	13.7	273
14	Structure of the multimodular endonuclease FokI bound to DNA. Nature, 1997, 388, 97-100.	13.7	256
15	Transcription Corepressor CtBP Is an NAD+-Regulated Dehydrogenase. Molecular Cell, 2002, 10, 857-869.	4.5	252
16	Phase separation of ligand-activated enhancers licenses cooperative chromosomal enhancer assembly. Nature Structural and Molecular Biology, 2019, 26, 193-203.	3.6	242
17	Structure of Pumilio Reveals Similarity between RNA and Peptide Binding Motifs. Cell, 2001, 105, 281-289.	13.5	237
18	Structural basis of high-fidelity DNA synthesis by yeast DNA polymerase Î´. Nature Structural and Molecular Biology, 2009, 16, 979-986.	3.6	236

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19	A Small Molecule RAS-Mimetic Disrupts RAS Association with Effector Proteins to Block Signaling. Cell, 2016, 165, 643-655.	13.5	228
20	Allosteric Effects of Pit-1 DNA Sites on Long-Term Repression in Cell Type Specification. Science, 2000, 290, 1127-1131.	6.0	227
21	Rev1 Employs a Novel Mechanism of DNA Synthesis Using a Protein Template. Science, 2005, 309, 2219-2222.	6.0	224
22	Human DNA Polymerase Î¹ Encircles DNA: Implications for Mismatch Extension and Lesion Bypass. Molecular Cell, 2007, 25, 601-614.	4.5	214
23	Structure and function of restriction endonucleases. Current Opinion in Structural Biology, 1995, 5, 11-19.	2.6	184
24	Structure of BamHI Bound to Nonspecific DNA. Molecular Cell, 2000, 5, 889-895.	4.5	168
25	FokI requires two specific DNA sites for cleavage. Journal of Molecular Biology, 2001, 309, 69-78.	2.0	160
26	Crystal Structure of PU.1/IRF-4/DNA Ternary Complex. Molecular Cell, 2002, 10, 1097-1105.	4.5	151
27	The role of metals in catalysis by the restriction endonuclease BamHI. Nature Structural Biology, 1998, 5, 910-916.	9.7	144
28	Structural basis for the suppression of skin cancers by DNA polymerase Î·. Nature, 2010, 465, 1039-1043.	13.7	136
29	New Class of Inhibitors of Amyloid-Î² Fibril Formation. Journal of Biological Chemistry, 2002, 277, 42881-42890.	1.6	133
30	Asymmetric DNA recognition by the OkrAI endonuclease, an isoschizomer of BamHI. Nucleic Acids Research, 2011, 39, 712-719.	6.5	132
31	Ligand-Dependent Enhancer Activation Regulated by Topoisomerase-I Activity. Cell, 2015, 160, 367-380.	13.5	122
32	Human DNA Polymerase Î¹ Incorporates dCTP Opposite Template G via a G.C+ Hoogsteen Base Pair. Structure, 2005, 13, 1569-1577.	1.6	120
33	Crystal Structure of the Catalytic Core of Human DNA Polymerase Kappa. Structure, 2004, 12, 1395-1404.	1.6	107
34	Hoogsteen base pair formation promotes synthesis opposite the 1,N6-ethenodeoxyadenosine lesion by human DNA polymerase Î¹. Nature Structural and Molecular Biology, 2006, 13, 619-625.	3.6	105
35	Understanding the immutability of restriction enzymes: crystal structure of BglII and its DNA substrate at 1.5 A resolution. Nature Structural Biology, 2000, 7, 134-140.	9.7	104
36	RNA Recognition via the SAM Domain of Smaug. Molecular Cell, 2003, 11, 1537-1548.	4.5	103

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37	Model of the Brain Tumor-Pumilio translation repressor complex. Genes and Development, 2003, 17, 2508-2513.	2.7	97
38	Crystal Structure of the SF3 Helicase from Adeno-Associated Virus Type 2. Structure, 2003, 11, 1025-1035.	1.6	96
39	Negative Role of RIG-I Serine 8 Phosphorylation in the Regulation of Interferon-Î² Production. Journal of Biological Chemistry, 2010, 285, 20252-20261.	1.6	96
40	The Ins and Outs of Bcr-Abl Inhibition. Genes and Cancer, 2012, 3, 447-454.	0.6	93
41	Structure of IRF-3 Bound to the PRDIII-I Regulatory Element of the Human Interferon-Î² Enhancer. Molecular Cell, 2007, 26, 703-716.	4.5	88
42	Structure of the NS3 helicase from Zika virus. Nature Structural and Molecular Biology, 2016, 23, 752-754.	3.6	86
43	Eukaryotic DNA polymerases. Current Opinion in Structural Biology, 2018, 53, 77-87.	2.6	84
44	Structures of NS5 Methyltransferase from Zika Virus. Cell Reports, 2016, 16, 3097-3102.	2.9	78
45	Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature Microbiology, 2020, 5, 166-180.	5.9	75
46	Structural basis for cisplatin DNA damage tolerance by human polymerase Î· during cancer chemotherapy. Nature Structural and Molecular Biology, 2012, 19, 628-632.	3.6	72
47	Gene Repression by Coactivator Repulsion. Molecular Cell, 2000, 6, 931-937.	4.5	69
48	Structure of NF-ÎºB p50/p65 Heterodimer Bound to the PRDII DNA Element from the Interferon-Î² Promoter. Structure, 2002, 10, 383-391.	1.6	69
49	Dpo4 is hindered in extending a GÂ·T mismatch by a reverse wobble. Nature Structural and Molecular Biology, 2004, 11, 457-462.	3.6	68
50	Structure of the Human Rev1â€“DNAâ€“dNTP Ternary Complex. Journal of Molecular Biology, 2009, 390, 699-709.	2.0	67
51	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. Science Translational Medicine, 2021, 13, eabj1578.	5.8	67
52	Structure and mechanism of human PrimPol, a DNA polymerase with primase activity. Science Advances, 2016, 2, e1601317.	4.7	65
53	Structures of Human Pumilio with Noncognate RNAs Reveal Molecular Mechanisms for Binding Promiscuity. Structure, 2008, 16, 549-557.	1.6	64
54	An Incoming Nucleotide Imposes an anti to syn Conformational Change on the Templating Purine in the Human DNA Polymerase-Î¹ Active Site. Structure, 2006, 14, 749-755.	1.6	60

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55	Protein-Template-Directed Synthesis across an Acrolein-Derived DNA Adduct by Yeast Rev1 DNA Polymerase. Structure, 2008, 16, 239-245.	1.6	59
56	Bisphosphonates inactivate human EGFRs to exert antitumor actions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17989-17994.	3.3	57
57	Structure of Human DNA Polymerase Îº Inserting dATP Opposite an 8-OxoG DNA Lesion. PLoS ONE, 2009, 4, e5766.	1.1	53
58	A view of consecutive binding events from structures of tetrameric endonucleaseSfiI bound to DNA. EMBO Journal, 2005, 24, 4198-4208.	3.5	52
59	Repurposing of bisphosphonates for the prevention and therapy of nonsmall cell lung and breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17995-18000.	3.3	52
60	Artemis C-terminal region facilitates V(D)J recombination through its interactions with DNA Ligase IV and DNA-PKcs. Journal of Experimental Medicine, 2012, 209, 955-963.	4.2	51
61	Structural basis of asymmetric DNA methylation and ATP-triggered long-range diffusion by EcoP15I. Nature Communications, 2015, 6, 7363.	5.8	51
62	Physiological functions of programmed DNA breaks in signal-induced transcription. Nature Reviews Molecular Cell Biology, 2017, 18, 471-476.	16.1	49
63	mRNA Regulation by Puf Domain Proteins. Science's STKE: Signal Transduction Knowledge Environment, 2006, 2006, pe37-pe37.	4.1	47
64	Residues within the Bâ€² Motif Are Critical for DNA Binding by the Superfamily 3 Helicase Rep40 of Adeno-associated Virus Type 2. Journal of Biological Chemistry, 2004, 279, 50472-50481.	1.6	42
65	Crystal Structure of Yeast DNA Polymerase Îµ Catalytic Domain. PLoS ONE, 2014, 9, e94835.	1.1	42
66	Structure and mechanism of B-family DNA polymerase Î¶ specialized for translesion DNA synthesis. Nature Structural and Molecular Biology, 2020, 27, 913-924.	3.6	42
67	Structure and Dynamics of the Second CARD of Human RIG-I Provide Mechanistic Insights into Regulation of RIG-I Activation. Structure, 2012, 20, 2048-2061.	1.6	41
68	An Ironâ€“Sulfur Cluster in the Polymerase Domain of Yeast DNA Polymerase Îµ. Journal of Molecular Biology, 2014, 426, 301-308.	2.0	41
69	Cryo-EM structure and dynamics of eukaryotic DNA polymerase Î´ holoenzyme. Nature Structural and Molecular Biology, 2019, 26, 955-962.	3.6	40
70	Structure of adeno-associated virus type 2 Rep40-ADP complex: Insight into nucleotide recognition and catalysis by superfamily 3 helicases. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12455-12460.	3.3	39
71	Structural Insights into Yeast DNA Polymerase Î´ by Small Angle X-ray Scattering. Journal of Molecular Biology, 2009, 394, 377-382.	2.0	38
72	Topology of Type II REases revisited; structural classes and the common conserved core. Nucleic Acids Research, 2007, 35, 2227-2237.	6.5	37

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73	Human DNA Polymerase Î· Is Pre-Aligned for dNTP Binding and Catalysis. Journal of Molecular Biology, 2012, 415, 627-634.	2.0	37
74	Human DNA polymerase Î± in binary complex with a DNA:DNA template-primer. Scientific Reports, 2016, 6, 23784.	1.6	36
75	DNA Synthesis across an Abasic Lesion by Yeast Rev1 DNA Polymerase. Journal of Molecular Biology, 2011, 406, 18-28.	2.0	35
76	Structure and Dynamics of an Intrinsically Disordered Protein Region That Partially Folds upon Binding by Chemical-Exchange NMR. Journal of the American Chemical Society, 2017, 139, 12219-12227.	6.6	35
77	Proximity-induced activation of human Cdc34 through heterologous dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15053-15058.	3.3	33
78	DNA Synthesis across an Abasic Lesion by Human DNA Polymerase Î¹. Structure, 2009, 17, 530-537.	1.6	32
79	The Architecture of Yeast DNA Polymerase Î¶. Cell Reports, 2013, 5, 79-86.	2.9	31
80	Overexpression, purification and crystallization ofBamHI endonuclease. Nucleic Acids Research, 1991, 19, 1825-1829.	6.5	29
81	BstYI Bound to Noncognate DNA Reveals a â€œHemispecificâ€•Complex: Implications for DNA Scanning. Structure, 2007, 15, 449-459.	1.6	29
82	Structural Basis for Error-free Replication of Oxidatively Damaged DNA by Yeast DNA Polymerase Î·. Structure, 2010, 18, 1463-1470.	1.6	29
83	Phosphatidylinositol 4,5-Bisphosphate Clusters the Cell Adhesion Molecule CD44 and Assembles a Specific CD44-Ezrin Heterocomplex, as Revealed by Small Angle Neutron Scattering. Journal of Biological Chemistry, 2015, 290, 6639-6652.	1.6	29
84	Energetic and Structural Considerations for the Mechanism of Protein Sliding along DNA in the Nonspecific BamHI-DNA Complex. Biophysical Journal, 2003, 84, 3317-3325.	0.2	28
85	Simultaneous CK2/TNIK/DYRK1 inhibition by 108600 suppresses triple negative breast cancer stem cells and chemotherapy-resistant disease. Nature Communications, 2021, 12, 4671.	5.8	28
86	Characterization of Type II and III Restriction-Modification Systems from Bacillus cereus Strains ATCC 10987 and ATCC 14579. Journal of Bacteriology, 2012, 194, 49-60.	1.0	27
87	An Inhibitor of PIDDosome Formation. Molecular Cell, 2015, 58, 767-779.	4.5	26
88	Development of a S-adenosylmethionine analog that intrudes the RNA-cap binding site of Zika methyltransferase. Scientific Reports, 2017, 7, 1632.	1.6	25
89	Amino-Terminal Domain Exchange Redirects Origin-Specific Interactions of Adeno-Associated Virus Rep78 In Vitro. Journal of Virology, 2001, 75, 3230-3239.	1.5	24
90	Deoxynucleotide Triphosphate Binding Mode Conserved in Y Family DNA Polymerases. Molecular and Cellular Biology, 2003, 23, 3008-3012.	1.1	24

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91	Co-occupancy of two Pumilio molecules on a single hunchback NRE. Rna, 2009, 15, 1029-1035.	1.6	24
92	Shape of promoter antisense RNAs regulates ligand-induced transcription activation. Nature, 2021, 595, 444-449.	13.7	23
93	Structure of Type IIL Restriction-Modification Enzyme MmeI in Complex with DNA Has Implications for Engineering New Specificities. PLoS Biology, 2016, 14, e1002442.	2.6	23
94	Role of Human DNA Polymerase Î¹ in Extension Opposite from a cisâ€“syn Thymine Dimer. Journal of Molecular Biology, 2011, 408, 252-261.	2.0	22
95	Discovery of 2-(1H-indol-5-ylamino)-6-(2,4-difluorophenylsulfonyl)-8-methylpyrido[2,3-d]pyrimidin-7(8H)-one (7ao) as a potent selective inhibitor of Polo like kinase 2 (PLK2). Bioorganic and Medicinal Chemistry, 2016, 24, 521-544.	1.4	21
96	Replication across Template T/U by Human DNA Polymerase-Î¹. Structure, 2009, 17, 974-980.	1.6	20
97	Mechanism of error-free replication across benzo[a]pyrene stereoisomers by Rev1 DNA polymerase. Nature Communications, 2017, 8, 965.	5.8	20
98	Translational repressors in Drosophila. Trends in Genetics, 2002, 18, 572-576.	2.9	19
99	Structural basis of DNA synthesis opposite 8-oxoguanine by human PrimPol primase-polymerase. Nature Communications, 2021, 12, 4020.	5.8	18
100	Discovery of a dual WDR5 and Ikaros PROTAC degrader as an anti-cancer therapeutic. Oncogene, 2022, 41, 3328-3340.	2.6	18
101	Structures of apo IRF-3 and IRF-7 DNA binding domains: effect of loop L1 on DNA binding. Nucleic Acids Research, 2011, 39, 7300-7307.	6.5	17
102	Dismissal of RNA Polymerase II Underlies a Large Ligand-Induced Enhancer Decommissioning Program. Molecular Cell, 2018, 71, 526-539.e8.	4.5	17
103	Structure of free BglII reveals an unprecedented scissor-like motion for opening an endonuclease. Nature Structural Biology, 2001, 8, 126-130.	9.7	16
104	Crystal Structure of BstYI at 1.85Ã... Resolution: A Thermophilic Restriction Endonuclease with Overlapping Specificities to BamHI and BglII. Journal of Molecular Biology, 2004, 338, 725-733.	2.0	15
105	Implications for Switching Restriction Enzyme Specificities from the Structure of BstYI Bound to a BglII DNA Sequence. Structure, 2005, 13, 791-801.	1.6	15
106	Solution Structure of the Vts1 SAM Domain in the Presence of RNA. Journal of Molecular Biology, 2006, 356, 1065-1072.	2.0	15
107	A Contaminant Impurity, Not Rigosertib, Is a Tubulin Binding Agent. Molecular Cell, 2020, 79, 180-190.e4.	4.5	14
108	Crystallization and preliminary X-ray analysis of Pit-1 POU domain complexed to a 28 base pair DNA element. , 1996, 24, 263-265.		12

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109	Crystallization of Restriction Endonuclease BamHI with Nonspecific DNA. Journal of Structural Biology, 2000, 130, 81-85.	1.3	12
110	Setleis syndrome: clinical, molecular and structural studies of the first <scp>TWIST2</scp> missense mutation. Clinical Genetics, 2015, 88, 489-493.	1.0	12
111	Mechanism of error-free DNA synthesis across N1-methyl-deoxyadenosine by human DNA polymerase-Î¹. Scientific Reports, 2017, 7, 43904.	1.6	11
112	Structural basis for polymerase Î·â€“promoted resistance to the anticancer nucleoside analog cytarabine. Scientific Reports, 2018, 8, 12702.	1.6	11
113	Structural Insights into the Assembly and Shape of Type III Restrictionâ€“Modification (Râ€“M) EcoP15I Complex by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2012, 420, 261-268.	2.0	10
114	The focal facial dermal dysplasias: phenotypic spectrum and molecular genetic heterogeneity. Journal of Medical Genetics, 2017, 54, 585-590.	1.5	10
115	FANCI functions as a repair/apoptosis switch in response to DNA crosslinks. Developmental Cell, 2021, 56, 2207-2222.e7.	3.1	9
116	Crystallization and characterization of Smaug: a novel RNA-binding motif. Biochemical and Biophysical Research Communications, 2002, 297, 1085-1088.	1.0	8
117	Glucocorticoid Receptor-like Zn(Cys)4 Motifs in BslI Restriction Endonuclease. Journal of Molecular Biology, 2003, 334, 595-603.	2.0	8
118	Targeting protein kinase CK2 and CDK4/6 pathways with a multi-kinase inhibitor ON108110 suppresses pro-survival signaling and growth in mantle cell lymphoma and T-acute lymphoblastic leukemia. Oncotarget, 2018, 9, 37753-37765.	0.8	8
119	Crystallization and preliminary X-ray analysis of restriction endonuclease Fok I bound to DNA. FEBS Letters, 1997, 403, 136-138.	1.3	7
120	Proteinâ€“nucleic acid interactions. Current Opinion in Structural Biology, 2003, 13, 3-5.	2.6	7
121	An EM View of the FokI Synaptic Complex by Single Particle Analysis. Journal of Molecular Biology, 2007, 370, 207-212.	2.0	7
122	Cryo-EM structure of translesion DNA synthesis polymerase Î¶ with a base pair mismatch. Nature Communications, 2022, 13, 1050.	5.8	7
123	Crystallization and preliminary crystallographic analysis of the type IIL restriction enzymeMmeI in complex with DNA. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 1262-1265.	0.7	6
124	SOX11 Inhibitors Are Cytotoxic in Mantle Cell Lymphoma. Clinical Cancer Research, 2021, 27, 4652-4663.	3.2	6
125	Structural insights into mutagenicity of anticancer nucleoside analog cytarabine during replication by DNA polymerase Î·. Scientific Reports, 2019, 9, 16400.	1.6	5
126	Purification, crystallization, and preliminary X-ray diffraction analysis of even-skipped homeodomain complexed to DNA. Proteins: Structure, Function and Bioinformatics, 1995, 21, 268-271.	1.5	4

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127	1H, 15N and 13C resonance assignments for the bromodomain of the histone acetyltransferase P/CAF. Journal of Biomolecular NMR, 1999, 14, 291-292.	1.6	4
128	Hoogsteen base-pairing in DNA replication? (reply). Nature, 2005, 437, E7-E7.	13.7	4
129	Homing in on intron-encoded endonucleases. Nature Structural Biology, 1997, 4, 423-424.	9.7	3
130	Rigosertib Blocks RAS Signaling By Acting As a Small Molecule RAS Mimetic That Binds to the RAS-Binding Domains of RAS Effector Proteins. Blood, 2014, 124, 5616-5616.	0.6	3
131	Crystallization of restriction endonucleaseSfiI in complex with DNA. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1493-1495.	2.5	2
132	Inhibiting SOX11-DNA Interaction in Mantle Cell Lymphoma. Blood, 2016, 128, 1840-1840.	0.6	2
133	Proteinâ€“nucleic acid interactions: unlocking mysteries old and new. Current Opinion in Structural Biology, 2005, 15, 65-67.	2.6	1