

# Aneel K Aggarwal

## List of Publications by Year in descending order

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133  
papers

13,272  
citations

29994

54  
h-index

22764

112  
g-index

139  
all docs

139  
docs citations

139  
times ranked

15049  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cryo-EM structure of translesion DNA synthesis polymerase $\epsilon$ with a base pair mismatch. <i>Nature Communications</i> , 2022, 13, 1050.	5.8	7
2	Discovery of a dual WDR5 and Ikaros PROTAC degrader as an anti-cancer therapeutic. <i>Oncogene</i> , 2022, 41, 3328-3340.	2.6	18
3	Shape of promoter antisense RNAs regulates ligand-induced transcription activation. <i>Nature</i> , 2021, 595, 444-449.	13.7	23
4	SOX11 Inhibitors Are Cytotoxic in Mantle Cell Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 4652-4663.	3.2	6
5	Structural basis of DNA synthesis opposite 8-oxoguanine by human PrimPol primase-polymerase. <i>Nature Communications</i> , 2021, 12, 4020.	5.8	18
6	FANCI functions as a repair/apoptosis switch in response to DNA crosslinks. <i>Developmental Cell</i> , 2021, 56, 2207-2222.e7.	3.1	9
7	Simultaneous CK2/TNIK/DYRK1 inhibition by 108600 suppresses triple negative breast cancer stem cells and chemotherapy-resistant disease. <i>Nature Communications</i> , 2021, 12, 4671.	5.8	28
8	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. <i>Science Translational Medicine</i> , 2021, 13, eabj1578.	5.8	67
9	Epigenomic characterization of <i>Clostridioides difficile</i> finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. <i>Nature Microbiology</i> , 2020, 5, 166-180.	5.9	75
10	Structure and mechanism of B-family DNA polymerase $\epsilon$ specialized for translesion DNA synthesis. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 913-924.	3.6	42
11	A Contaminant Impurity, Not Rigosertib, Is a Tubulin Binding Agent. <i>Molecular Cell</i> , 2020, 79, 180-190.e4.	4.5	14
12	Structural insights into mutagenicity of anticancer nucleoside analog cytarabine during replication by DNA polymerase $\beta$ . <i>Scientific Reports</i> , 2019, 9, 16400.	1.6	5
13	Cryo-EM structure and dynamics of eukaryotic DNA polymerase $\delta$ holoenzyme. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 955-962.	3.6	40
14	Phase separation of ligand-activated enhancers licenses cooperative chromosomal enhancer assembly. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 193-203.	3.6	242
15	Structural basis for polymerase $\beta$ -promoted resistance to the anticancer nucleoside analog cytarabine. <i>Scientific Reports</i> , 2018, 8, 12702.	1.6	11
16	Eukaryotic DNA polymerases. <i>Current Opinion in Structural Biology</i> , 2018, 53, 77-87.	2.6	84
17	Dismissal of RNA Polymerase II Underlies a Large Ligand-Induced Enhancer Decommissioning Program. <i>Molecular Cell</i> , 2018, 71, 526-539.e8.	4.5	17
18	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. <i>Oncotarget</i> , 2018, 9, 37753-37765.	0.8	8

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19	Development of a S-adenosylmethionine analog that intrudes the RNA-cap binding site of Zika methyltransferase. <i>Scientific Reports</i> , 2017, 7, 1632.	1.6	25
20	Physiological functions of programmed DNA breaks in signal-induced transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 471-476.	16.1	49
21	Mechanism of error-free DNA synthesis across N1-methyl-deoxyadenosine by human DNA polymerase- $\delta$ . <i>Scientific Reports</i> , 2017, 7, 43904.	1.6	11
22	Structure and Dynamics of an Intrinsically Disordered Protein Region That Partially Folds upon Binding by Chemical-Exchange NMR. <i>Journal of the American Chemical Society</i> , 2017, 139, 12219-12227.	6.6	35
23	Mechanism of error-free replication across benzo[a]pyrene stereoisomers by Rev1 DNA polymerase. <i>Nature Communications</i> , 2017, 8, 965.	5.8	20
24	The focal facial dermal dysplasias: phenotypic spectrum and molecular genetic heterogeneity. <i>Journal of Medical Genetics</i> , 2017, 54, 585-590.	1.5	10
25	Structure of the NS3 helicase from Zika virus. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 752-754.	3.6	86
26	Human DNA polymerase $\delta$ in binary complex with a DNA:DNA template-primer. <i>Scientific Reports</i> , 2016, 6, 23784.	1.6	36
27	A Small Molecule RAS-Mimetic Disrupts RAS Association with Effector Proteins to Block Signaling. <i>Cell</i> , 2016, 165, 643-655.	13.5	228
28	Structures of NS5 Methyltransferase from Zika Virus. <i>Cell Reports</i> , 2016, 16, 3097-3102.	2.9	78
29	Structure and mechanism of human PrimPol, a DNA polymerase with primase activity. <i>Science Advances</i> , 2016, 2, e1601317.	4.7	65
30	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). <i>Bioorganic and Medicinal Chemistry</i> , 2016, 24, 521-544.	1.4	21
31	Inhibiting SOX11-DNA Interaction in Mantle Cell Lymphoma. <i>Blood</i> , 2016, 128, 1840-1840.	0.6	2
32	Structure of Type III Restriction-Modification Enzyme MmeI in Complex with DNA Has Implications for Engineering New Specificities. <i>PLoS Biology</i> , 2016, 14, e1002442.	2.6	23
33	An Inhibitor of PIDDosome Formation. <i>Molecular Cell</i> , 2015, 58, 767-779.	4.5	26
34	Ligand-Dependent Enhancer Activation Regulated by Topoisomerase-I Activity. <i>Cell</i> , 2015, 160, 367-380.	13.5	122
35	Phosphatidylinositol 4,5-Bisphosphate Clusters the Cell Adhesion Molecule CD44 and Assembles a Specific CD44-Ezrin Heterocomplex, as Revealed by Small Angle Neutron Scattering. <i>Journal of Biological Chemistry</i> , 2015, 290, 6639-6652.	1.6	29
36	Structural basis of asymmetric DNA methylation and ATP-triggered long-range diffusion by EcoP15I. <i>Nature Communications</i> , 2015, 6, 7363.	5.8	51

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37	Setleis syndrome: clinical, molecular and structural studies of the first <sc>TWIST2</sc> missense mutation. <i>Clinical Genetics</i> , 2015, 88, 489-493.	1.0	12
38	Crystal Structure of Yeast DNA Polymerase $\hat{\mu}$ Catalytic Domain. <i>PLoS ONE</i> , 2014, 9, e94835.	1.1	42
39	Repurposing of bisphosphonates for the prevention and therapy of nonsmall cell lung and breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17995-18000.	3.3	52
40	Bisphosphonates inactivate human EGFRs to exert antitumor actions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17989-17994.	3.3	57
41	An Iron-Sulfur Cluster in the Polymerase Domain of Yeast DNA Polymerase $\hat{\mu}$ . <i>Journal of Molecular Biology</i> , 2014, 426, 301-308.	2.0	41
42	Rigosertib Blocks RAS Signaling By Acting As a Small Molecule RAS Mimetic That Binds to the RAS-Binding Domains of RAS Effector Proteins. <i>Blood</i> , 2014, 124, 5616-5616.	0.6	3
43	Brd4 and JMJD6-Associated Anti-Pause Enhancers in Regulation of Transcriptional Pause Release. <i>Cell</i> , 2013, 155, 1581-1595.	13.5	330
44	The Architecture of Yeast DNA Polymerase $\hat{\eta}$ . <i>Cell Reports</i> , 2013, 5, 79-86.	2.9	31
45	The Ins and Outs of Bcr-Abl Inhibition. <i>Genes and Cancer</i> , 2012, 3, 447-454.	0.6	93
46	Artemis C-terminal region facilitates V(D)J recombination through its interactions with DNA Ligase IV and DNA-PKcs. <i>Journal of Experimental Medicine</i> , 2012, 209, 955-963.	4.2	51
47	Characterization of Type II and III Restriction-Modification Systems from <i>Bacillus cereus</i> Strains ATCC 10987 and ATCC 14579. <i>Journal of Bacteriology</i> , 2012, 194, 49-60.	1.0	27
48	Human DNA Polymerase $\hat{\delta}$ Is Pre-Aligned for dNTP Binding and Catalysis. <i>Journal of Molecular Biology</i> , 2012, 415, 627-634.	2.0	37
49	Structural Insights into the Assembly and Shape of Type III Restriction-Modification (R-M) EcoP151 Complex by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2012, 420, 261-268.	2.0	10
50	Structure and Dynamics of the Second CARD of Human RIG-I Provide Mechanistic Insights into Regulation of RIG-I Activation. <i>Structure</i> , 2012, 20, 2048-2061.	1.6	41
51	Structural basis for cisplatin DNA damage tolerance by human polymerase $\hat{\delta}$ during cancer chemotherapy. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 628-632.	3.6	72
52	DNA Synthesis across an Abasic Lesion by Yeast Rev1 DNA Polymerase. <i>Journal of Molecular Biology</i> , 2011, 406, 18-28.	2.0	35
53	Role of Human DNA Polymerase $\hat{\epsilon}$ in Extension Opposite from a cis-syn Thymine Dimer. <i>Journal of Molecular Biology</i> , 2011, 408, 252-261.	2.0	22
54	Crystallization and preliminary crystallographic analysis of the type III restriction enzyme <i>MmeI</i> in complex with DNA. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1262-1265.	0.7	6

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55	Asymmetric DNA recognition by the OkrAI endonuclease, an isoschizomer of BamHI. <i>Nucleic Acids Research</i> , 2011, 39, 712-719.	6.5	132
56	Structures of apo IRF-3 and IRF-7 DNA binding domains: effect of loop L1 on DNA binding. <i>Nucleic Acids Research</i> , 2011, 39, 7300-7307.	6.5	17
57	Structural Basis for Error-free Replication of Oxidatively Damaged DNA by Yeast DNA Polymerase $\hat{\epsilon}$ . <i>Structure</i> , 2010, 18, 1463-1470.	1.6	29
58	Structural basis for the suppression of skin cancers by DNA polymerase $\hat{\epsilon}$ . <i>Nature</i> , 2010, 465, 1039-1043.	13.7	136
59	PHF8 mediates histone H4 lysine 20 demethylation events involved in cell cycle progression. <i>Nature</i> , 2010, 466, 508-512.	13.7	367
60	Negative Role of RIG-I Serine 8 Phosphorylation in the Regulation of Interferon- $\hat{\epsilon}^2$ Production. <i>Journal of Biological Chemistry</i> , 2010, 285, 20252-20261.	1.6	96
61	Co-occupancy of two Pumilio molecules on a single hunchback NRE. <i>Rna</i> , 2009, 15, 1029-1035.	1.6	24
62	DNA Synthesis across an Abasic Lesion by Human DNA Polymerase $\hat{\epsilon}^1$ . <i>Structure</i> , 2009, 17, 530-537.	1.6	32
63	Replication across Template T/U by Human DNA Polymerase- $\hat{\epsilon}^1$ . <i>Structure</i> , 2009, 17, 974-980.	1.6	20
64	Structural basis of high-fidelity DNA synthesis by yeast DNA polymerase $\hat{\epsilon}$ . <i>Nature Structural and Molecular Biology</i> , 2009, 16, 979-986.	3.6	236
65	Structure of the Human Rev1- $\hat{\epsilon}$ -DNA-dNTP Ternary Complex. <i>Journal of Molecular Biology</i> , 2009, 390, 699-709.	2.0	67
66	Structural Insights into Yeast DNA Polymerase $\hat{\epsilon}$ by Small Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2009, 394, 377-382.	2.0	38
67	Structure of Human DNA Polymerase $\hat{\epsilon}$ Inserting dATP Opposite an 8-OxoG DNA Lesion. <i>PLoS ONE</i> , 2009, 4, e5766.	1.1	53
68	Protein-Template-Directed Synthesis across an Acrolein-Derived DNA Adduct by Yeast Rev1 DNA Polymerase. <i>Structure</i> , 2008, 16, 239-245.	1.6	59
69	Structures of Human Pumilio with Noncognate RNAs Reveal Molecular Mechanisms for Binding Promiscuity. <i>Structure</i> , 2008, 16, 549-557.	1.6	64
70	Topology of Type II REases revisited; structural classes and the common conserved core. <i>Nucleic Acids Research</i> , 2007, 35, 2227-2237.	6.5	37
71	Functional Specificity of a Hox Protein Mediated by the Recognition of Minor Groove Structure. <i>Cell</i> , 2007, 131, 530-543.	13.5	303
72	An EM View of the FokI Synaptic Complex by Single Particle Analysis. <i>Journal of Molecular Biology</i> , 2007, 370, 207-212.	2.0	7

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73	Human DNA Polymerase $\beta$ Encircles DNA: Implications for Mismatch Extension and Lesion Bypass. <i>Molecular Cell</i> , 2007, 25, 601-614.	4.5	214
74	Structure of IRF-3 Bound to the PRDIII-H Regulatory Element of the Human Interferon- $\beta$ Enhancer. <i>Molecular Cell</i> , 2007, 26, 703-716.	4.5	88
75	BstYI Bound to Noncognate DNA Reveals a $\alpha$ -Hemispecific Complex: Implications for DNA Scanning. <i>Structure</i> , 2007, 15, 449-459.	1.6	29
76	Solution Structure of the Vts1 SAM Domain in the Presence of RNA. <i>Journal of Molecular Biology</i> , 2006, 356, 1065-1072.	2.0	15
77	Hoogsteen base pair formation promotes synthesis opposite the 1,N <sup>6</sup> -ethenodeoxyadenosine lesion by human DNA polymerase $\beta$ . <i>Nature Structural and Molecular Biology</i> , 2006, 13, 619-625.	3.6	105
78	An Incoming Nucleotide Imposes an anti to syn Conformational Change on the Templating Purine in the Human DNA Polymerase $\beta$ Active Site. <i>Structure</i> , 2006, 14, 749-755.	1.6	60
79	mRNA Regulation by Puf Domain Proteins. <i>Science's STKE: Signal Transduction Knowledge Environment</i> , 2006, 2006, pe37-pe37.	4.1	47
80	A view of consecutive binding events from structures of tetrameric endonuclease SfiI bound to DNA. <i>EMBO Journal</i> , 2005, 24, 4198-4208.	3.5	52
81	Hoogsteen base-pairing in DNA replication? (reply). <i>Nature</i> , 2005, 437, E7-E7.	13.7	4
82	Implications for Switching Restriction Enzyme Specificities from the Structure of BstYI Bound to a BglII DNA Sequence. <i>Structure</i> , 2005, 13, 791-801.	1.6	15
83	Human DNA Polymerase $\beta$ Incorporates dCTP Opposite Template G via a G.C+ Hoogsteen Base Pair. <i>Structure</i> , 2005, 13, 1569-1577.	1.6	120
84	Protein-nucleic acid interactions: unlocking mysteries old and new. <i>Current Opinion in Structural Biology</i> , 2005, 15, 65-67.	2.6	1
85	Proximity-induced activation of human Cdc34 through heterologous dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15053-15058.	3.3	33
86	Rev1 Employs a Novel Mechanism of DNA Synthesis Using a Protein Template. <i>Science</i> , 2005, 309, 2219-2222.	6.0	224
87	Structure of adeno-associated virus type 2 Rep40-ADP complex: Insight into nucleotide recognition and catalysis by superfamily 3 helicases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12455-12460.	3.3	39
88	Residues within the $\beta$ Motif Are Critical for DNA Binding by the Superfamily 3 Helicase Rep40 of Adeno-associated Virus Type 2. <i>Journal of Biological Chemistry</i> , 2004, 279, 50472-50481.	1.6	42
89	Dpo4 is hindered in extending a G $\cdot$ T mismatch by a reverse wobble. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 457-462.	3.6	68
90	Replication by human DNA polymerase $\beta$ occurs by Hoogsteen base-pairing. <i>Nature</i> , 2004, 430, 377-380.	13.7	300

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91	Crystal Structure of the Catalytic Core of Human DNA Polymerase Kappa. <i>Structure</i> , 2004, 12, 1395-1404.	1.6	107
92	Crystal Structure of BstYI at 1.85Å... Resolution: A Thermophilic Restriction Endonuclease with Overlapping Specificities to BamHI and BglII. <i>Journal of Molecular Biology</i> , 2004, 338, 725-733.	2.0	15
93	A Corepressor/Coactivator Exchange Complex Required for Transcriptional Activation by Nuclear Receptors and Other Regulated Transcription Factors. <i>Cell</i> , 2004, 116, 511-526.	13.5	493
94	Protein-nucleic acid interactions. <i>Current Opinion in Structural Biology</i> , 2003, 13, 3-5.	2.6	7
95	Crystal Structure of the SF3 Helicase from Adeno-Associated Virus Type 2. <i>Structure</i> , 2003, 11, 1025-1035.	1.6	96
96	Crystallization of restriction endonuclease SfiI in complex with DNA. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1493-1495.	2.5	2
97	Eya protein phosphatase activity regulates Six1's Dach's Eya transcriptional effects in mammalian organogenesis. <i>Nature</i> , 2003, 426, 247-254.	13.7	571
98	Glucocorticoid Receptor-like Zn(Cys) <sub>4</sub> Motifs in BslI Restriction Endonuclease. <i>Journal of Molecular Biology</i> , 2003, 334, 595-603.	2.0	8
99	Energetic and Structural Considerations for the Mechanism of Protein Sliding along DNA in the Nonspecific BamHI-DNA Complex. <i>Biophysical Journal</i> , 2003, 84, 3317-3325.	0.2	28
100	RNA Recognition via the SAM Domain of Smaug. <i>Molecular Cell</i> , 2003, 11, 1537-1548.	4.5	103
101	Deoxynucleotide Triphosphate Binding Mode Conserved in Y Family DNA Polymerases. <i>Molecular and Cellular Biology</i> , 2003, 23, 3008-3012.	1.1	24
102	Model of the Brain Tumor-Pumilio translation repressor complex. <i>Genes and Development</i> , 2003, 17, 2508-2513.	2.7	97
103	New Class of Inhibitors of Amyloid- $\beta^2$ Fibril Formation. <i>Journal of Biological Chemistry</i> , 2002, 277, 42881-42890.	1.6	133
104	Crystallization and characterization of Smaug: a novel RNA-binding motif. <i>Biochemical and Biophysical Research Communications</i> , 2002, 297, 1085-1088.	1.0	8
105	Transcription Corepressor CtBP Is an NAD <sup>+</sup> -Regulated Dehydrogenase. <i>Molecular Cell</i> , 2002, 10, 857-869.	4.5	252
106	Crystal Structure of PU.1/IRF-4/DNA Ternary Complex. <i>Molecular Cell</i> , 2002, 10, 1097-1105.	4.5	151
107	Translational repressors in <i>Drosophila</i> . <i>Trends in Genetics</i> , 2002, 18, 572-576.	2.9	19
108	Structure of NF- $\kappa$ B p50/p65 Heterodimer Bound to the PRDII DNA Element from the Interferon- $\beta^2$ Promoter. <i>Structure</i> , 2002, 10, 383-391.	1.6	69

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109	FokI requires two specific DNA sites for cleavage. <i>Journal of Molecular Biology</i> , 2001, 309, 69-78.	2.0	160
110	Structure of the Catalytic Core of <i>S. cerevisiae</i> DNA Polymerase $\delta$ . <i>Molecular Cell</i> , 2001, 8, 417-426.	4.5	347
111	Structure of Pumilio Reveals Similarity between RNA and Peptide Binding Motifs. <i>Cell</i> , 2001, 105, 281-289.	13.5	237
112	Structure of free BglII reveals an unprecedented scissor-like motion for opening an endonuclease. <i>Nature Structural Biology</i> , 2001, 8, 126-130.	9.7	16
113	Amino-Terminal Domain Exchange Redirects Origin-Specific Interactions of Adeno-Associated Virus Rep78 In Vitro. <i>Journal of Virology</i> , 2001, 75, 3230-3239.	1.5	24
114	Understanding the immutability of restriction enzymes: crystal structure of BglII and its DNA substrate at 1.5 Å resolution. <i>Nature Structural Biology</i> , 2000, 7, 134-140.	9.7	104
115	Crystallization of Restriction Endonuclease BamHI with Nonspecific DNA. <i>Journal of Structural Biology</i> , 2000, 130, 81-85.	1.3	12
116	Gene Repression by Coactivator Repulsion. <i>Molecular Cell</i> , 2000, 6, 931-937.	4.5	69
117	Structure of BamHI Bound to Nonspecific DNA. <i>Molecular Cell</i> , 2000, 5, 889-895.	4.5	168
118	Allosteric Effects of Pit-1 DNA Sites on Long-Term Repression in Cell Type Specification. <i>Science</i> , 2000, 290, 1127-1131.	6.0	227
119	Structure of a DNA-bound Ultrabithorax "Extradenticle homeodomain complex. <i>Nature</i> , 1999, 397, 714-719.	13.7	296
120	Structure and ligand of a histone acetyltransferase bromodomain. <i>Nature</i> , 1999, 399, 491-496.	13.7	1,501
121	<sup>1</sup> H, <sup>15</sup> N and <sup>13</sup> C resonance assignments for the bromodomain of the histone acetyltransferase P/CAF. <i>Journal of Biomolecular NMR</i> , 1999, 14, 291-292.	1.6	4
122	Reciprocal Interactions of Pit1 and GATA2 Mediate Signaling Gradient "Induced Determination of Pituitary Cell Types. <i>Cell</i> , 1999, 97, 587-598.	13.5	292
123	Structure of IRF-1 with bound DNA reveals determinants of interferon regulation. <i>Nature</i> , 1998, 391, 103-106.	13.7	366
124	The role of metals in catalysis by the restriction endonuclease BamHI. <i>Nature Structural Biology</i> , 1998, 5, 910-916.	9.7	144
125	Signal-specific co-activator domain requirements for Pit-1 activation. <i>Nature</i> , 1998, 395, 301-306.	13.7	273
126	Crystallization and preliminary X-ray analysis of restriction endonuclease Fok I bound to DNA. <i>FEBS Letters</i> , 1997, 403, 136-138.	1.3	7



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127	Homing in on intron-encoded endonucleases. <i>Nature Structural Biology</i> , 1997, 4, 423-424.	9.7	3
128	Structure of the multimodular endonuclease FokI bound to DNA. <i>Nature</i> , 1997, 388, 97-100.	13.7	256
129	Crystallization and preliminary X-ray analysis of Pit-1 POU domain complexed to a 28 base pair DNA element. , 1996, 24, 263-265.		12
130	Purification, crystallization, and preliminary X-ray diffraction analysis of even-skipped homeodomain complexed to DNA. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 268-271.	1.5	4
131	Structure and function of restriction endonucleases. <i>Current Opinion in Structural Biology</i> , 1995, 5, 11-19.	2.6	184
132	Overexpression, purification and crystallization of BamHI endonuclease. <i>Nucleic Acids Research</i> , 1991, 19, 1825-1829.	6.5	29
133	DNA Recognition by Proteins with the Helix-Turn-Helix Motif. <i>Annual Review of Biochemistry</i> , 1990, 59, 933-969.	5.0	586