Kalyan Das

List of Publications by Year in descending order

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138	10,784	36691	36203
papers	citations	53 h-index	101 g-index

146	146	146	8722
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A systematic approach to identify host targets and rapidly deliver broad-spectrum antivirals. Molecular Therapy, 2022, 30, 1797-1800.	3.7	5
2	Insights into HIV-1 Reverse Transcriptase (RT) Inhibition and Drug Resistance from Thirty Years of Structural Studies. Viruses, 2022, 14, 1027.	1.5	8
3	Cryo-EM Structures Reveal Transcription Initiation Steps by Yeast Mitochondrial RNA Polymerase. Molecular Cell, 2021, 81, 268-280.e5.	4.5	15
4	Assembly and Cryo-EM structure determination of yeast mitochondrial RNA polymerase initiation complex intermediates. STAR Protocols, 2021, 2, 100431.	0.5	3
5	Crystal Structure of a Retroviral Polyprotein: Prototype Foamy Virus Protease-Reverse Transcriptase (PR-RT). Viruses, 2021, 13, 1495.	1.5	4
6	Exploring the dNTP -binding site of HIV-1 reverse transcriptase for inhibitor design. European Journal of Medicinal Chemistry, 2021, 225, 113785.	2.6	3
7	Tenofovir-Amino Acid Conjugates Act as Polymerase Substratesâ€”Implications for Avoiding Cellular Phosphorylation in the Discovery of Nucleotide Analogues. Journal of Medicinal Chemistry, 2021, 64, 782-796.	2.9	2
8	HIV-1 gp120 Antagonists Also Inhibit HIV-1 Reverse Transcriptase by Bridging the NNRTI and NRTI Sites. Journal of Medicinal Chemistry, 2021, 64, 16530-16540.	2.9	4
9	Sliding of HIV-1 reverse transcriptase over DNA creates a transient P pocket â€“ targeting P-pocket by fragment screening. Nature Communications, 2021, 12, 7127.	5.8	6
10	Integrative structural biology studies of HIV-1 reverse transcriptase binding to a high-affinity DNA aptamer. Current Research in Structural Biology, 2020, 2, 116-129.	1.1	8
11	Development of a Novel SPR Assay to Study CXCR4â€“Ligand Interactions. Biosensors, 2020, 10, 150.	2.3	8
12	The dynamic landscape of transcription initiation in yeast mitochondria. Nature Communications, 2020, 11, 4281.	5.8	18
13	Structure, mechanism, and regulation of mitochondrial DNA transcription initiation. Journal of Biological Chemistry, 2020, 295, 18406-18425.	1.6	43
14	Structural Basis of HIV-1 Inhibition by Nucleotide-Competing Reverse Transcriptase Inhibitor INDOPY-1. Journal of Medicinal Chemistry, 2019, 62, 9996-10002.	2.9	20
15	Structure of HIV-1 RT/dsRNA initiation complex prior to nucleotide incorporation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7308-7313.	3.3	26
16	Structural basis of ECF-Ïƒ-factor-dependent transcription initiation. Nature Communications, 2019, 10, 710.	5.8	37
17	Alpha-carboxynucleoside phosphonates: direct-acting inhibitors of viral DNA polymerases. Future Medicinal Chemistry, 2019, 11, 137-154.	1.1	6
18	Structure of HIVâ€1 reverse transcriptase/d4TTP complex: Novel DNA crossâ€linking site and pHâ€dependent conformational changes. Protein Science, 2019, 28, 587-597.	3.1	11

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19	Developing and Evaluating Inhibitors against the RNase H Active Site of HIV-1 Reverse Transcriptase. Journal of Virology, 2018, 92, .	1.5	30
20	Structural Basis of Transcription Inhibition by Fidaxomicin (Lipiarmycin A3). Molecular Cell, 2018, 70, 60-71.e15.	4.5	81
21	Guanine Î±-carboxy nucleoside phosphonate (G-Î±-CNP) shows a different inhibitory kinetic profile against the DNA polymerases of human immunodeficiency virus (HIV) and herpes viruses. Biochemical Pharmacology, 2017, 136, 51-61.	2.0	9
22	Structural Insights into HIV Reverse Transcriptase Mutations Q151M and Q151M Complex That Confer Multinucleoside Drug Resistance. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	16
23	Structural Basis of Mycobacterium tuberculosis Transcription and Transcription Inhibition. Molecular Cell, 2017, 66, 169-179.e8.	4.5	130
24	Conformational States of HIV-1 Reverse Transcriptase for Nucleotide Incorporation vs Pyrophosphorolysisâ€"Binding of Foscarnet. ACS Chemical Biology, 2016, 11, 2158-2164.	1.6	38
25	Structure of <scp>HIV</scp>â€1 reverse transcriptase bound to a novel 38â€mer hairpin templateâ€primer <scp>DNA</scp> aptamer. Protein Science, 2016, 25, 46-55.	3.1	33
26	Exploring the role of the Î±-carboxyphosphonate moiety in the HIV-RT activity of Î±-carboxy nucleoside phosphonates. Organic and Biomolecular Chemistry, 2016, 14, 2454-2465.	1.5	17
27	Alpha-carboxy nucleoside phosphonates as universal nucleoside triphosphate mimics. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3475-3480.	3.3	29
28	Negative-Strand RNA Virus L Proteins: One Machine, Many Activities. Cell, 2015, 162, 239-241.	13.5	17
29	Pronounced Inhibition Shift from HIV Reverse Transcriptase to Herpetic DNA Polymerases by Increasing the Flexibility of Î±-Carboxy Nucleoside Phosphonates. Journal of Medicinal Chemistry, 2015, 58, 8110-8127.	2.9	9
30	Analysis of the Zidovudine Resistance Mutations T215Y, M41L, and L210W in HIV-1 Reverse Transcriptase. Antimicrobial Agents and Chemotherapy, 2015, 59, 7184-7196.	1.4	8
31	Considerations for Structure-Based Drug Design Targeting HIV-1 Reverse Transcriptase. NATO Science for Peace and Security Series A: Chemistry and Biology, 2015, , 69-81.	0.5	1
32	Drug Resistance in Non-B Subtype HIV-1: Impact of HIV-1 Reverse Transcriptase Inhibitors. Viruses, 2014, 6, 3535-3562.	1.5	27
33	Structures of HIV-1 RT-RNA/DNA ternary complexes with dATP and nevirapine reveal conformational flexibility of RNA/DNA: insights into requirements for RNase H cleavage. Nucleic Acids Research, 2014, 42, 8125-8137.	6.5	60
34	Molecular dynamics study of HIVâ€1 RTâ€DNAâ€nevirapine complexes explains NNRTI inhibition and resistance by connection mutations. Proteins: Structure, Function and Bioinformatics, 2014, 82, 815-829.	1.5	15
35	Phenyl Substituted 4-Hydroxypyridazin-3(2H)-ones and 5-Hydroxypyrimidin-4(3H)-ones: Inhibitors of Influenza A Endonuclease. Journal of Medicinal Chemistry, 2014, 57, 8086-8098.	2.9	50
36	Mutations in HIV-1 Reverse Transcriptase Affect the Errors Made in a Single Cycle of Viral Replication. Journal of Virology, 2014, 88, 7589-7601.	1.5	46

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37	Extension into the entrance channel of HIV-1 reverse transcriptaseâ€"Crystallography and enhanced solubility. Bioorganic and Medicinal Chemistry Letters, 2013, 23, 5209-5212.	1.0	33
38	Crystallographic Fragment Screening and Structure-Based Optimization Yields a New Class of Influenza Endonuclease Inhibitors. ACS Chemical Biology, 2013, 8, 2501-2508.	1.6	76
39	Phenyl substituted 3-hydroxypyridin-2(1H)-ones: Inhibitors of influenza A endonuclease. Bioorganic and Medicinal Chemistry, 2013, 21, 6435-6446.	1.4	30
40	Snapshot of the equilibrium dynamics of a drug bound to HIV-1 reverse transcriptase. Nature Chemistry, 2013, 5, 174-181.	6.6	88
41	Detecting Allosteric Sites of HIV-1 Reverse Transcriptase by X-ray Crystallographic Fragment Screening. Journal of Medicinal Chemistry, 2013, 56, 2738-2746.	2.9	78
42	HIV-1 reverse transcriptase and antiviral drug resistance. Part 1. Current Opinion in Virology, 2013, 3, 111-118.	2.6	126
43	HIV-1 reverse transcriptase and antiviral drug resistance. Part 2. Current Opinion in Virology, 2013, 3, 119-128.	2.6	83
44	3-Hydroxyquinolin-2(1H)-ones As Inhibitors of Influenza A Endonuclease. ACS Medicinal Chemistry Letters, 2013, 4, 547-550.	1.3	44
45	Structural requirements for RNA degradation by HIV-1 reverse transcriptase. Nature Structural and Molecular Biology, 2013, 20, 1341-1342.	3.6	5
46	Nonnucleoside Reverse Transcriptase Inhibitors (NNRTIs). , 2013, , 123-139.		1
47	HIV-1 reverse transcriptase complex with DNA and nevirapine reveals non-nucleoside inhibition mechanism. Nature Structural and Molecular Biology, 2012, 19, 253-259.	3.6	176
48	A comparison of the ability of rilpivirine (TMC278) and selected analogues to inhibit clinically relevant HIV-1 reverse transcriptase mutants. Retrovirology, 2012, 9, 99.	0.9	29
49	Antivirals Targeting Influenza A Virus. Journal of Medicinal Chemistry, 2012, 55, 6263-6277.	2.9	97
50	Crystal Structure oftert-Butyldimethylsilyl-spiroaminooxathioledioxide-thymine (TSAO-T) in Complex with HIV-1 Reverse Transcriptase (RT) Redefines the Elastic Limits of the Non-nucleoside Inhibitor-Binding Pocket. Journal of Medicinal Chemistry, 2011, 54, 2727-2737.	2.9	66
51	Structure of the guanylyltransferase domain of human mRNA capping enzyme. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10104-10108.	3.3	40
52	Structures of influenza A proteins and insights into antiviral drug targets. Nature Structural and Molecular Biology, 2010, 17, 530-538.	3.6	292
53	Structural basis of HIV-1 resistance to AZT by excision. Nature Structural and Molecular Biology, 2010, 17, 1202-1209.	3.6	115
54	Mutations in the Thumb Allow Human Immunodeficiency Virus Type 1 Reverse Transcriptase To Be Cleaved by Protease in Virions. Journal of Virology, 2009, 83, 12336-12344.	1.5	20

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55	Crystal Structure and Autoactivation Pathway of the Precursor Form of Human Tripeptidyl-peptidase 1, the Enzyme Deficient in Late Infantile Ceroid Lipofuscinosis. Journal of Biological Chemistry, 2009, 284, 3985-3997.	1.6	50
56	Structural Basis for the Role of the K65R Mutation in HIV-1 Reverse Transcriptase Polymerization, Excision Antagonism, and Tenofovir Resistance. Journal of Biological Chemistry, 2009, 284, 35092-35100.	1.6	81
57	Structures of RNA polymeraseâ€“antibiotic complexes. Current Opinion in Structural Biology, 2009, 19, 715-723.	2.6	132
58	Structure of HIV-1 Reverse Transcriptase with the Inhibitor Î²-Thujaplicinol Bound at the RNase H Active Site. Structure, 2009, 17, 1625-1635.	1.6	135
59	Structure and Function of HIV-1 Reverse Transcriptase: Molecular Mechanisms of Polymerization and Inhibition. Journal of Molecular Biology, 2009, 385, 693-713.	2.0	426
60	Crystallographic Study of a Novel Subnanomolar Inhibitor Provides Insight on the Binding Interactions of Alkenyldiarylmethanes with Human Immunodeficiency Virus-1 Reverse Transcriptase. Journal of Medicinal Chemistry, 2009, 52, 6467-6473.	2.9	11
61	Molecular Dynamics Study of Non-nucleoside Reverse Transcriptase Inhibitor 4-[[4-[[4-[(E)-2-Cyanoethenyl]-2,6-dimethylphenyl]amino]-2-pyrimidinyl]amino]benzonitrile (TMC278/Rilpivirine) Aggregates: Correlation between Amphiphilic Properties of the Drug and Oral Bioavailability. Journal of Medicinal Chemistry, 2009, 52, 5896-5905.	2.9	17
62	Conformational Landscape of the Human Immunodeficiency Virus Type 1 Reverse Transcriptase Non-Nucleoside Inhibitor Binding Pocket: Lessons for Inhibitor Design from a Cluster Analysis of Many Crystal Structures. Journal of Medicinal Chemistry, 2009, 52, 6413-6420.	2.9	33
63	3D Jigsaw Puzzle in Rotavirus Assembly. Structure, 2008, 16, 1601-1602.	1.6	1
64	High-resolution structures of HIV-1 reverse transcriptase/TMC278 complexes: Strategic flexibility explains potency against resistance mutations. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1466-1471.	3.3	310
65	The RNA Polymerase â€œSwitch Regionâ€•Is a Target for Inhibitors. Cell, 2008, 135, 295-307.	13.5	234
66	Crystal engineering of HIV-1 reverse transcriptase for structure-based drug design. Nucleic Acids Research, 2008, 36, 5083-5092.	6.5	91
67	Structural basis for suppression of a host antiviral response by influenza A virus. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13093-13098.	3.3	193
68	Two-dimensional infrared spectra reveal relaxation of the nonnucleoside inhibitor TMC278 complexed with HIV-1 reverse transcriptase. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1472-1477.	3.3	131
69	Crystal Structures of Clinically Relevant Lys103Asn/Tyr181Cys Double Mutant HIV-1 Reverse Transcriptase in Complexes with ATP and Non-nucleoside Inhibitor HBY 097. Journal of Molecular Biology, 2007, 365, 77-89.	2.0	83
70	A Conserved Structural Module Regulates Transcriptional Responses to Diverse Stress Signals in Bacteria. Molecular Cell, 2007, 27, 793-805.	4.5	136
71	Synthesis, Biological Activity, and Crystal Structure of Potent Nonnucleoside Inhibitors of HIV-1 Reverse Transcriptase That Retain Activity against Mutant Forms of the Enzyme. Journal of Medicinal Chemistry, 2007, 50, 4003-4015.	2.9	87
72	Linear Interaction Energy (LIE) Models for Ligand Binding in Implicit Solvent:â€‰ Theory and Application to the Binding of NNRTIs to HIV-1 Reverse Transcriptase. Journal of Chemical Theory and Computation, 2007, 3, 256-277.	2.3	45

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73	Structures of Wildâ€Type and AZTâ€Resistant HIVâ€1 Reverse Transcriptase Complexed with AZTppppA Yield Insights into the Nucleotide Excision Mechanism. FASEB Journal, 2007, 21, A640.	0.2	0
74	Spectroscopic Studies of Rilpivirine (TMC278/R278474) in Complex with HIVâ€1 Reverse Transcriptase. FASEB Journal, 2007, 21, A630.	0.2	0
75	Crystallography and the design of anti-AIDS drugs: conformational flexibility and positional adaptability are important in the design of non-nucleoside HIV-1 reverse transcriptase inhibitors. Progress in Biophysics and Molecular Biology, 2005, 88, 209-231.	1.4	210
76	The 2.35â€…Ã… structure of the TenA homolog fromPyrococcus furiosussupports an enzymatic function in thiamine metabolism. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 589-598.	2.5	12
77	Synthesis of Novel Diarylpyrimidine Analogues and Their Antiviral Activity against Human Immunodeficiency Virus Type 1. Journal of Medicinal Chemistry, 2005, 48, 2072-2079.	2.9	118
78	Crystal Structures for HIV-1 Reverse Transcriptase in Complexes with Three Pyridinone Derivatives:Â A New Class of Non-Nucleoside Inhibitors Effective against a Broad Range of Drug-Resistant Strains. Journal of Medicinal Chemistry, 2005, 48, 7582-7591.	2.9	132
79	Concentration and pH Dependent Aggregation of Hydrophobic Drug Molecules and Relevance to Oral Bioavailability. Journal of Medicinal Chemistry, 2005, 48, 1974-1983.	2.9	119
80	Design, Synthesis, and SAR of a Novel Pyrazinone Series with Non-Nucleoside HIV-1 Reverse Transcriptase Inhibitory Activity. Journal of Medicinal Chemistry, 2005, 48, 1910-1918.	2.9	49
81	4-Benzyl and 4-Benzoyl-3-dimethylaminopyridin-2(1H)-ones:Â In Vitro Evaluation of New C-3-Amino-Substituted and C-5,6-Alkyl-Substituted Analogues against Clinically Important HIV Mutant Strains. Journal of Medicinal Chemistry, 2005, 48, 1948-1964.	2.9	38
82	In Search of a Novel Anti-HIV Drug:Â Multidisciplinary Coordination in the Discovery of 4-[[4-[[4-[(1E)-2-Cyanoethenyl]-2,6-dimethylphenyl]amino]-2- pyrimidinyl]amino]benzonitrile (R278474,) Tj ETQq0 0 0 rgBT /Overlock 1	2.9	324
83	Crystal structure of RlmAI: Implications for understanding the 23S rRNA G745/G748-methylation at the macrolide antibiotic-binding site. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4041-4046.	3.3	31
84	Crystal Structures of Arginine Deiminase with Covalent Reaction Intermediates. Structure, 2004, 12, 657-667.	1.6	90
85	Taking aim at a moving target: designing drugs to inhibit drug-resistant HIV-1 reverse transcriptases. Current Opinion in Structural Biology, 2004, 14, 716-730.	2.6	130
86	Correlations between Factors Determining the Pharmacokinetics and Antiviral Activity of HIV-1 Non-Nucleoside Reverse Transcriptase Inhibitors of the Diaryltriazine and Diarylpyrimidine Classes of Compounds. Drugs in R and D, 2004, 5, 245-257.	1.1	19
87	HIV-1 Reverse Transcriptase Structure. , 2004, , 388-392.		0
88	Roles of Conformational and Positional Adaptability in Structure-Based Design of TMC125-R165335 (Etravirine) and Related Non-nucleoside Reverse Transcriptase Inhibitors That Are Highly Potent and Effective against Wild-Type and Drug-Resistant HIV-1 Variants. Journal of Medicinal Chemistry, 2004, 47, 2550-2560.	2.9	507
89	382 In vitro characterization and molecular modeling analysis of a novel adefovir resistance mutation RTN236T in the HBV polymerase. Journal of Hepatology, 2004, 40, 114.	1.8	18
90	On the detection of multiple-binding modes of ligands to proteins, from biological, structural, and modeling data. Journal of Computer-Aided Molecular Design, 2003, 17, 129-134.	1.3	42

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91	Trapping HIV-1 Reverse Transcriptase Before and After Translocation on DNA. Journal of Biological Chemistry, 2003, 278, 16280-16288.	1.6	79
92	The Hepatitis B Virus Polymerase Mutation rtV173L Is Selected during Lamivudine Therapy and Enhances Viral Replication In Vitro. Journal of Virology, 2003, 77, 11833-11841.	1.5	531
93	Structural basis of BLyS receptor recognition. Nature Structural Biology, 2002, 9, 288-292.	9.7	76
94	Structures of HIV-1 reverse transcriptase with pre- and post-translocation AZTMP-terminated DNA. EMBO Journal, 2002, 21, 6614-6624.	3.5	185
95	HIV-1 Reverse Transcriptase Mutations Found in a Drug-Experienced Patient Confer Reduced Susceptibility to Multiple Nucleoside Reverse Transcriptase Inhibitors. Antiviral Therapy, 2002, 6, 231-238.	0.6	1
96	The Lys103Asn mutation of HIV-1 RT: a novel mechanism of drug resistance. Journal of Molecular Biology, 2001, 309, 437-445.	2.0	175
97	Evolution of Anti-HIV Drug CandidatesPart 2: Diaryltriazine (DATA) Analogues. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 2229-2234.	1.0	119
98	Evolution of anti-HIV drug candidates. Part 3: diarylpyrimidine (DAPY) analogues. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 2235-2239.	1.0	183
99	X-ray crystal structure of MTH938 fromMethanobacterium thermoautotrophicumat 2.2 Ã... resolution reveals a novel tertiary protein fold. Proteins: Structure, Function and Bioinformatics, 2001, 45, 486-488.	1.5	5
100	Crystal structure of HIV-1 reverse transcriptase in complex with a polypurine tract RNA:DNA. EMBO Journal, 2001, 20, 1449-1461.	3.5	388
101	Molecular Modeling and Biochemical Characterization Reveal the Mechanism of Hepatitis B Virus Polymerase Resistance to Lamivudine (3TC) and Emtricitabine (FTC). Journal of Virology, 2001, 75, 4771-4779.	1.5	263
102	A Mutation in Human Immunodeficiency Virus Type 1 Protease, N88S, That Causes In Vitro Hypersensitivity to Amprenavir. Journal of Virology, 2000, 74, 4414-4419.	1.5	85
103	Lamivudine (3TC) resistance in HIV-1 reverse transcriptase involves steric hindrance with beta -branched amino acids. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 10027-10032.	3.3	288
104	Touching the heart of HIV-1 drug resistance: the fingers close down on the dNTP at the polymerase active site. Chemistry and Biology, 1999, 6, R137-R146.	6.2	107
105	Structure-based design of inhibitors of HIV-1 reverse transcriptase: a potential class of bidentate nonnucleoside inhibitors. Computational and Theoretical Chemistry, 1998, 423, 101-111.	1.5	4
106	Dithiaheterocycle-annelated tetrathiafulvalene Ï€-donors: a structureâ€“property correlation study. Journal of the Chemical Society Perkin Transactions 1, 1998, , 1769-1778.	0.9	10
107	Structures of Tyr188Leu mutant and wild-type HIV-1 reverse transcriptase complexed with the non-nucleoside inhibitor HBY 097: inhibitor flexibility is a useful design feature for reducing drug resistance 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 284, 313-323.	2.0	135
108	Structure and functional implications of the polymerase active site region in a complex of HIV-1 RT with a double-stranded DNA template-primer and an antibody fab fragment at 2.8 Ã... resolution. Journal of Molecular Biology, 1998, 284, 1095-1111.	2.0	317

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109	Synthesis and Reactivity of Chiral Tellurium Azomethines:Â Pseudopolymorphism of [o-((((1S,2R)-2-Hydroxy-2-phenyl-1-methylethyl)amino)methinyl)phenyl]tellurium(IV) Bromide. Organometallics, 1997, 16, 563-571.	1.1	40
110	Synthesis of some functionalised isomeric bis(ethylenedithio)tetrathiafulvalene (BEDT-TTF) and dithiophenetetrathiafulvalene (DTTTF) Ï€-donors. Tetrahedron, 1997, 53, 11627-11644.	1.0	19
111	Conformation, Protein-Carbohydrate Interactions and a Novel Subunit Association in the Refined Structure of Peanut Lectin-Lactose Complex. Journal of Molecular Biology, 1996, 259, 281-296.	2.0	174
112	Crystal Structures of 8-Cl and 9-Cl TIBO Complexed with Wild-type HIV-1 RT and 8-Cl TIBO Complexed with the Tyr181Cys HIV-1 RT Drug-resistant Mutant. Journal of Molecular Biology, 1996, 264, 1085-1100.	2.0	214
113	Structure of unliganded HIV-1 reverse transcriptase at 2.7 Ã¥ resolution: implications of conformational changes for polymerization and inhibition mechanisms. Structure, 1996, 4, 853-860.	1.6	286
114	Electron density averaging using multiple crystal forms or diffraction datasets in structure determination of protein at moderate resolution. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C81-C81.	0.3	0
115	Refined structure of HIV-1 reverse transcriptase complexed with a double-stranded DNA and an antibody Fab fragment at 2.8â€…Ã… resolution. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C155-C155.	0.3	0
116	Non-nucleoside RT inhibitors give HIV-1 RT a crooked back. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C234-C235.	0.3	0
117	Structure of HIV-1 reverse transcriptase in a complex with the non-nucleoside inhibitor Î±-APA R 95845 at 2.8 Ã¥ resolution. Structure, 1995, 3, 365-379.	1.6	225
118	Molecular modeling studies of HIVâ€‘1 reverse transcriptase nonnucleoside inhibitors: Total energy of complexation as a predictor of drug placement and activity. Protein Science, 1995, 4, 2203-2222.	3.1	66
119	Structure of HIV-1 RT/TIBO R 86183 complex reveals similarity in the binding of diverse nonnucleoside inhibitors. Nature Structural and Molecular Biology, 1995, 2, 407-415.	3.6	296
120	1-O-(2-Iodophenyl)-Î²-D-galactopyranose. Acta Crystallographica Section C: Crystal Structure Communications, 1994, 50, 1726-1728.	0.4	1
121	Crystal structure of peanut lectin, a protein with an unusual quaternary structure.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 227-231.	3.3	122
122	Acetylenic derivatives of [Fe2(CO)6(Âµ-Se2)]: acetylenic bond reduction on a selenium-stabilised Fe2Pt mixed-metal complex. Journal of the Chemical Society Chemical Communications, 1993, , 46-48.	2.0	27
123	Crystal structure of cis-(carbonato) bis(2,2â€²-bipyridine) cobalt(III) chloride trihydrate, (Co(C10H8N2)2CO3)Cl(H2O)3. Zeitschrift Fur Kristallographie - Crystalline Materials, 1993, 205, 316-318.	0.4	8
124	Structure of bis(butylenedithio)tetrathiafulvalene: an organic Ï€-donor molecule. Acta Crystallographica Section C: Crystal Structure Communications, 1992, 48, 488-490.	0.4	2
125	Structure of an intermediate methylated product in the synthesis of drimanes. Acta Crystallographica Section C: Crystal Structure Communications, 1992, 48, 525-527.	0.4	1
126	Structure of a Te-methylene-Te bridged double-butterfly complex. Acta Crystallographica Section C: Crystal Structure Communications, 1992, 48, 1386-1389.	0.4	1

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127	Bis[naphthalene-1,8-diylbis(methylthio)]tetrathiafulvalene (BNMT-TTF) and bis(tetramethylenedithio)tetrathiafulvalene (BMDT-TTF): new electron donors. Journal of the Chemical Society Chemical Communications, 1991, , 952.	2.0	9
128	Structure of 17-epinimbocinol. Acta Crystallographica Section C: Crystal Structure Communications, 1991, 47, 1426-1429.	0.4	2
129	Structure of hexamethylhexahydropyrnopetrocarpan. Acta Crystallographica Section C: Crystal Structure Communications, 1991, 47, 1863-1866.	0.4	1
130	Structure of a 4-phenylcoumarin derivative. Acta Crystallographica Section C: Crystal Structure Communications, 1991, 47, 1922-1925.	0.4	1
131	Structure of a new benzofuran derivative. Acta Crystallographica Section C: Crystal Structure Communications, 1991, 47, 1925-1927.	0.4	1
132	Synthesis and structural characterisation of a new methylene bridged double butterfly shaped complex [(Î¼-CH3Te)Fe2(CO)6]2[Î¼-Te(CH2)Te-Î¼]. Journal of Organometallic Chemistry, 1991, 409, 255-261.	0.8	22
133	Structure of 7,7-dimethyldihydropyrnopetrocropane. Acta Crystallographica Section C: Crystal Structure Communications, 1990, 46, 1888-1890.	0.4	1
134	Structure of 1,4-bis(3-quinolyl)-1,3-butadiyne. Acta Crystallographica Section C: Crystal Structure Communications, 1990, 46, 2126-2128.	0.4	4
135	Heterocyclic compounds containing antimony 1. Synthesis, physicochemical properties, crystal and molecular structure of 2-(Î²-hydroxyethylthio) 1,3,2-oxathiastibolane. Inorganica Chimica Acta, 1990, 170, 191-197.	1.2	7
136	Synthesis and structure of di-2-benzo[b]thienyl ditelluride. Journal of Organometallic Chemistry, 1990, 397, 161-167.	0.8	15
137	Structure of (ethylenediamine)(cis-Î±-ethylenediamine-N,N'-diacetato)cobalt(III) perchlorate. Acta Crystallographica Section C: Crystal Structure Communications, 1989, 45, 398-400.	0.4	5
138	Structure of a pentacoordinate complex of bis(diphenyldithiophosphinato)cobalt(II) with 3-methylpyridine. Acta Crystallographica Section C: Crystal Structure Communications, 1989, 45, 890-892.	0.4	0