

Ujjwal Neogi

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

2,801
citations

236612

25
h-index

243296

44
g-index

143
all docs

143
docs citations

143
times ranked

4238
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota diversity predicts immune status in HIV-1 infection. <i>Aids</i> , 2015, 29, 2409-2418.	1.0	238
2	Dysregulation in Akt/mTOR/HIF-1 signaling identified by proteo-transcriptomics of SARS-CoV-2 infected cells. <i>Emerging Microbes and Infections</i> , 2020, 9, 1748-1760.	3.0	221
3	Global epidemiology of drug resistance after failure of WHO recommended first-line regimens for adult HIV-1 infection: a multicentre retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 565-575.	4.6	217
4	Richer gut microbiota with distinct metabolic profile in HIV infected Elite Controllers. <i>Scientific Reports</i> , 2017, 7, 6269.	1.6	79
5	Systemic Inflammation and the Increased Risk of Inflamm-Aging and Age-Associated Diseases in People Living With HIV on Long Term Suppressive Antiretroviral Therapy. <i>Frontiers in Immunology</i> , 2019, 10, 1965.	2.2	77
6	Multiple NF- κ B Sites in HIV-1 Subtype C Long Terminal Repeat Confer Superior Magnitude of Transcription and Thereby the Enhanced Viral Predominance. <i>Journal of Biological Chemistry</i> , 2012, 287, 44714-44735.	1.6	68
7	The Impact of Human Immunodeficiency Virus Infection on Gut Microbiota \pm -Diversity: An Individual-level Meta-analysis. <i>Clinical Infectious Diseases</i> , 2020, 70, 615-627.	2.9	65
8	Metabolic Perturbation Associated With COVID-19 Disease Severity and SARS-CoV-2 Replication. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100159.	2.5	65
9	Molecular Epidemiology of HIV-1 Subtypes in India: Origin and Evolutionary History of the Predominant Subtype C. <i>PLoS ONE</i> , 2012, 7, e39819.	1.1	64
10	Clade C HIV-1 isolates circulating in Southern Africa exhibit a greater frequency of dicysteine motif-containing Tat variants than those in Southeast Asia and cause increased neurovirulence. <i>Retrovirology</i> , 2013, 10, 61.	0.9	63
11	Cell-type-resolved quantitative proteomics map of interferon response against SARS-CoV-2. <i>IScience</i> , 2021, 24, 102420.	1.9	50
12	Temporal Trends in the Swedish HIV-1 Epidemic: Increase in Non-B Subtypes and Recombinant Forms over Three Decades. <i>PLoS ONE</i> , 2014, 9, e99390.	1.1	48
13	Plasma Metabolic Signature and Abnormalities in HIV-Infected Individuals on Long-Term Successful Antiretroviral Therapy. <i>Metabolites</i> , 2019, 9, 210.	1.3	46
14	Virological failure in patients with HIV-1 subtype C receiving antiretroviral therapy: an analysis of a prospective national cohort in Sweden. <i>Lancet HIV</i> , the, 2016, 3, e166-e174.	2.1	43
15	GS-CA Compounds: First-In-Class HIV-1 Capsid Inhibitors Covering Multiple Grounds. <i>Frontiers in Microbiology</i> , 2019, 10, 1227.	1.5	43
16	A high-risk gut microbiota configuration associates with fatal hyperinflammatory immune and metabolic responses to SARS-CoV-2. <i>Gut Microbes</i> , 2022, 14, 2073131.	4.3	40
17	Community prevalence of methicillin and vancomycin resistant <i>Staphylococcus aureus</i> in and around Bangalore, southern India. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2011, 44, 309-312.	0.4	37
18	Subtype-independent near full-length HIV-1 genome sequencing and assembly to be used in large molecular epidemiological studies and clinical management. <i>Journal of the International AIDS Society</i> , 2015, 18, 20035.	1.2	33

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19	Immune Checkpoints as the Immune System Regulators and Potential Biomarkers in HIV-1 Infection. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2000.	1.8	33
20	Utility of Proteomics in Emerging and Re-Emerging Infectious Diseases Caused by RNA Viruses. <i>Journal of Proteome Research</i> , 2020, 19, 4259-4274.	1.8	32
21	Ex-vivo antiretroviral potency of newer integrase strand transfer inhibitors cabotegravir and bicitegravir in HIV type 1 non-B subtypes. <i>Aids</i> , 2018, 32, 469-476.	1.0	31
22	The disproportionate effect of COVID-19 mortality on ethnic minorities: Genetics or health inequalities?. <i>EClinicalMedicine</i> , 2020, 23, 100430.	3.2	29
23	Cost-efficient HIV-1 drug resistance surveillance using multiplexed high-throughput amplicon sequencing: implications for use in low- and middle-income countries. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 3349-3355.	1.3	28
24	Transcriptomics and Targeted Proteomics Analysis to Gain Insights Into the Immune-control Mechanisms of HIV-1 Infected Elite Controllers. <i>EBioMedicine</i> , 2018, 27, 40-50.	2.7	28
25	Pretreatment drug resistance in a large countrywide Ethiopian HIV-1C cohort: a comparison of Sanger and high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 7556.	1.6	28
26	Drug Resistance in Non-B Subtype HIV-1: Impact of HIV-1 Reverse Transcriptase Inhibitors. <i>Viruses</i> , 2014, 6, 3535-3562.	1.5	27
27	The microbial metabolite trimethylamine-N-oxide in association with inflammation and microbial dysregulation in three HIV cohorts at various disease stages. <i>Aids</i> , 2018, 32, 1589-1598.	1.0	26
28	Feasibility of Known RNA Polymerase Inhibitors as Anti-SARS-CoV-2 Drugs. <i>Pathogens</i> , 2020, 9, 320.	1.2	26
29	Human APOBEC3G-mediated hypermutation is associated with antiretroviral therapy failure in HIV-1 subtype C-infected individuals. <i>Journal of the International AIDS Society</i> , 2013, 16, 18472.	1.2	25
30	Sub-attomole detection of HIV-1 using padlock probes and rolling circle amplification combined with microfluidic affinity chromatography. <i>Biosensors and Bioelectronics</i> , 2020, 166, 112442.	5.3	25
31	Nucleoside-Modified mRNA Vaccines Protect IFNAR ^{−/−} Mice against Crimean-Congo Hemorrhagic Fever Virus Infection. <i>Journal of Virology</i> , 2022, 96, JVI0156821.	1.5	24
32	A high rate of HIV-1 acquisition post immigration among migrants in Sweden determined by a CD4 ⁺ cell decline trajectory model. <i>HIV Medicine</i> , 2017, 18, 677-684.	1.0	23
33	Type-I interferon signatures in SARS-CoV-2 infected Huh7 cells. <i>Cell Death Discovery</i> , 2021, 7, 114.	2.0	23
34	Naturally Occurring Polymorphisms and Primary Drug Resistance Profile Among Antiretroviral-Naive Individuals in Bangalore, India. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1097-1101.	0.5	22
35	Long-Term Efficacy of First Line Antiretroviral Therapy in Indian HIV-1 Infected Patients: A Longitudinal Cohort Study. <i>PLoS ONE</i> , 2013, 8, e55421.	1.1	22
36	In silico and in vitro studies reveal complement system drives coagulation cascade in SARS-CoV-2 pathogenesis. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3734-3744.	1.9	22

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37	Analyses of HIV-1 integrase sequences prior to South African national HIV-treatment program and availability of integrase inhibitors in Cape Town, South Africa. <i>Scientific Reports</i> , 2018, 8, 4709.	1.6	21
38	Unique Phenotypic Characteristics of Recently Transmitted HIV-1 Subtype C Envelope Glycoprotein gp120: Use of CXCR6 Coreceptor by Transmitted Founder Viruses. <i>Journal of Virology</i> , 2018, 92, .	1.5	20
39	Characterization of Inducible Transcription and Translation-Competent HIV-1 Using the RNAscope ISH Technology at a Single-Cell Resolution. <i>Frontiers in Microbiology</i> , 2018, 9, 2358.	1.5	20
40	Selection of nonnucleoside reverse transcriptase inhibitor-associated mutations in HIV-1 subtype C: evidence of etravirine cross-resistance. <i>Aids</i> , 2011, 25, 1123-1126.	1.0	19
41	Novel tetra-peptide insertion in Gag-p6 ALIX-binding motif in HIV-1 subtype C associated with protease inhibitor failure in Indian patients. <i>Aids</i> , 2014, 28, 2319-2322.	1.0	19
42	Multiplexed next-generation sequencing and de novo assembly to obtain near full-length HIV-1 genome from plasma virus. <i>Journal of Virological Methods</i> , 2016, 236, 98-104.	1.0	19
43	Structural Implications of Genotypic Variations in HIV-1 Integrase From Diverse Subtypes. <i>Frontiers in Microbiology</i> , 2018, 9, 1754.	1.5	19
44	Altered Gut Microbiome under Antiretroviral Therapy: Impact of Efavirenz and Zidovudine. <i>ACS Infectious Diseases</i> , 2021, 7, 1104-1115.	1.8	19
45	Virological efficacy with first-line antiretroviral treatment in India: predictors of viral failure and evidence of viral resuppression. <i>Tropical Medicine and International Health</i> , 2015, 20, 1462-1472.	1.0	18
46	Phylogenetic Analysis of Ethiopian HIV-1 Subtype C Near Full-Length Genomes Reveals High Intrasubtype Diversity and a Strong Geographical Cluster. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 471-474.	0.5	18
47	High viremia and low level of transmitted drug resistance in anti-retroviral therapy-naïve perinatally-infected children and adolescents with HIV-1 subtype C infection. <i>BMC Infectious Diseases</i> , 2012, 12, 317.	1.3	17
48	Effectiveness of First-line Antiretroviral Therapy and Acquired Drug Resistance Among HIV-1-infected Children in India. <i>Pediatric Infectious Disease Journal</i> , 2013, 32, e227-e229.	1.1	17
49	Plasma soluble factor following two decades prolonged suppressive antiretroviral therapy in HIV-1-positive males. <i>Medicine (United States)</i> , 2018, 97, e9759.	0.4	17
50	Impact of Long COVID on health and quality of life. <i>HRB Open Research</i> , 0, 5, 31.	0.3	17
51	Higher Prevalence of Predicted X4-Tropic Strains in Perinatally Infected Older Children With HIV-1 Subtype C in India. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2012, 59, 347-353.	0.9	15
52	Mutational Heterogeneity in p6 Gag Late Assembly (L) Domains in HIV-1 Subtype C Viruses from South Africa. <i>AIDS Research and Human Retroviruses</i> , 2016, 32, 80-84.	0.5	15
53	Whole-Genome Metagenomic Analysis of the Gut Microbiome in HIV-1-Infected Individuals on Antiretroviral Therapy. <i>Frontiers in Microbiology</i> , 2021, 12, 667718.	1.5	15
54	Azadirachta indica A. Juss bark extract and its Nimbin isomers restrict β -coronaviral infection and replication. <i>Virology</i> , 2022, 569, 13-28.	1.1	15

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55	Novel HIV-1 long terminal repeat (LTR) sequences of subtype B and mosaic intersubtype B/C recombinants in North India. <i>Archives of Virology</i> , 2008, 153, 1961-1966.	0.9	14
56	Genetic and functional characterization of human immunodeficiency virus type 1 VprC variants from north India: presence of unique recombinants with mosaic genomes from B, C and D subtypes within the open reading frame of Vpr. <i>Journal of General Virology</i> , 2009, 90, 2768-2776.	1.3	14
57	Drug Resistance Mutations Against Protease, Reverse Transcriptase and Integrase Inhibitors in People Living With HIV-1 Receiving Boosted Protease Inhibitors in South Africa. <i>Frontiers in Microbiology</i> , 2020, 11, 438.	1.5	14
58	Distinct lipid profile, low-level inflammation, and increased antioxidant defense signature in HIV-1 elite control status. <i>IScience</i> , 2021, 24, 102111.	1.9	14
59	The Association between Out-of-Pocket Expenditure and COVID-19 Mortality Globally. <i>Journal of Epidemiology and Global Health</i> , 2020, 10, 192.	1.1	14
60	The central role of the glutamate metabolism in long-term antiretroviral treated HIV-infected individuals with metabolic syndrome. <i>Aging</i> , 2021, 13, 22732-22751.	1.4	14
61	Genetic analysis of HIV-1 Circulating Recombinant Form O2_AG, B and C subtype-specific envelope sequences from Northern India and their predicted co-receptor usage. <i>AIDS Research and Therapy</i> , 2009, 6, 28.	0.7	13
62	Co-receptor tropism prediction among 1045 Indian HIV-1 subtype C sequences: Therapeutic implications for India. <i>AIDS Research and Therapy</i> , 2010, 7, 24.	0.7	13
63	Genetic Characterization of HIV Type 1 Tat Exon 1 from a Southern Indian Clinical Cohort: Identification of Unique Epidemiological Signature Residues. <i>AIDS Research and Human Retroviruses</i> , 2012, 28, 1152-1156.	0.5	13
64	Recent increased identification and transmission of HIV-1 unique recombinant forms in Sweden. <i>Scientific Reports</i> , 2017, 7, 6371.	1.6	13
65	Trans cohort metabolic reprogramming towards glutaminolysis in long-term successfully treated HIV-infection. <i>Communications Biology</i> , 2022, 5, 27.	2.0	13
66	Global HIV-1 molecular epidemiology with special reference to genetic analysis of HIV-1 subtypes circulating in North India: functional and pathogenic implications of genetic variation. <i>Indian Journal of Experimental Biology</i> , 2009, 47, 424-31.	0.5	13
67	High concordance of genotypic coreceptor prediction in plasma-viral RNA and proviral DNA of HIV-1 subtype C: implications for use of whole blood DNA in resource-limited settings. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2003-2006.	1.3	12
68	The gp120 Protein Is a Second Determinant of Decreased Neurovirulence of Indian HIV-1C Isolates Compared to Southern African HIV-1C Isolates. <i>PLoS ONE</i> , 2014, 9, e107074.	1.1	12
69	Increased replication capacity following evolution of PYX insertion in Gag-Pol is associated with enhanced virulence in HIV-1 subtype C from East Africa. <i>Journal of Medical Virology</i> , 2017, 89, 106-111.	2.5	12
70	Quantitative humoral profiling of the HIV-1 proteome in elite controllers and patients with very long-term efficient antiretroviral therapy. <i>Scientific Reports</i> , 2017, 7, 666.	1.6	12
71	Antiretroviral potency of 4'-ethynyl-2'-fluoro-2'-deoxyadenosine, tenofovir alafenamide and second-generation NNRTIs across diverse HIV-1 subtypes. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2721-2728.	1.3	12
72	Multi-omics insights into host-viral response and pathogenesis in Crimean-Congo hemorrhagic fever viruses for novel therapeutic target. <i>ELife</i> , 2022, 11, .	2.8	12

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73	Microfluidic centrifugation assisted precipitation based DNA quantification. Lab on A Chip, 2019, 19, 1657-1664.	3.1	11
74	HIV-1 Subtype C with PYxE Insertion Has Enhanced Binding of Gag-p6 to Host Cell Protein ALIX and Increased Replication Fitness. Journal of Virology, 2019, 93, .	1.5	11
75	Drug resistance testing through remote genotyping and predicted treatment options in human immunodeficiency virus type 1 infected Tanzanian subjects failing first or second line antiretroviral therapy. PLoS ONE, 2017, 12, e0178942.	1.1	11
76	Genetic architecture of HIV-1 genes circulating in north India & their functional implications. Indian Journal of Medical Research, 2011, 134, 769.	0.4	11
77	Integrative Lipidomics and Metabolomics for System-Level Understanding of the Metabolic Syndrome in Long-Term Treated HIV-Infected Individuals. Frontiers in Immunology, 2021, 12, 742736.	2.2	11
78	Metabolic rewiring and serotonin depletion in patients with postacute sequelae of COVID-19. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 1623-1625.	2.7	11
79	Phenotypic co-receptor tropism and Maraviroc sensitivity in HIV-1 subtype C from East Africa. Scientific Reports, 2018, 8, 2363.	1.6	10
80	Antiviral drug research for Japanese encephalitis: an updated review. Pharmacological Reports, 2022, 74, 273-296.	1.5	10
81	Genetic factors associated with slow progression of HIV among perinatally-infected Indian children. Indian Pediatrics, 2014, 51, 801-803.	0.2	8
82	HIV-1 Coreceptor Tropism in India. Journal of Acquired Immune Deficiency Syndromes (1999), 2014, 65, 397-404.	0.9	8
83	Performance of Genotypic Tools for Prediction of Tropism in HIV-1 Subtype C V3 Loop Sequences. Intervirology, 2015, 58, 1-5.	1.2	7
84	Elevated Numbers of HIV-Specific Poly-Functional CD8+ T Cells With Stem Cell-Like and Follicular Homing Phenotypes in HIV-Exposed Seronegative Individuals. Frontiers in Immunology, 2021, 12, 638144.	2.2	7
85	Fecal Metabolome Signature in the HIV-1 Elite Control Phenotype: Enrichment of Dipeptides Acts as an HIV-1 Antagonist but a <i>Prevotella</i> Agonist. Journal of Virology, 2021, 95, e0047921.	1.5	7
86	Deciphering the Role of Mucosal Immune Responses and the Cervicovaginal Microbiome in Resistance to HIV Infection in HIV-Exposed Seronegative (HESN) Women. Microbiology Spectrum, 2021, 9, e0047021.	1.2	7
87	Integrative proteo-transcriptomic and immunophenotyping signatures of HIV-1 elite control phenotype: A cross-talk between glycolysis and HIF signaling. IScience, 2022, 25, 103607.	1.9	7
88	Genome-scale metabolic models for natural and long-term drug-induced viral control in HIV infection. Life Science Alliance, 2022, 5, e202201405.	1.3	7
89	Limited Evolution but Increasing Trends of Primary Non-Nucleoside Reverse Transcriptase Inhibitor Resistance Mutations in Therapy-Naive HIV-1-Infected Individuals in India. Antiviral Therapy, 2014, 19, 813-818.	0.6	6
90	Factors influencing the efficacy of rilpivirine in HIV-1 subtype C in low- and middle-income countries. Journal of Antimicrobial Chemotherapy, 2016, 71, 367-371.	1.3	6

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91	A viral genome wide association study and genotypic resistance testing in patients failing first line antiretroviral therapy in the first large countrywide Ethiopian HIV cohort. <i>BMC Infectious Diseases</i> , 2019, 19, 569.	1.3	6
92	Strain-specific effect on biphasic DNA binding by HIV-1 integrase. <i>Aids</i> , 2019, 33, 588-592.	1.0	6
93	Following the path: Increasing trends of HIV-1 drug resistance in China. <i>EClinicalMedicine</i> , 2020, 18, 100251.	3.2	6
94	Distinct Metabolic Profile Associated with a Fatal Outcome in COVID-19 Patients during the Early Epidemic in Italy. <i>Microbiology Spectrum</i> , 2021, 9, e0054921.	1.2	6
95	Genetic and functional analysis of HIV-1 Rev Responsive Element (RRE) sequences from North-India. <i>AIDS Research and Therapy</i> , 2010, 7, 28.	0.7	5
96	Diversity of HIV Type 1 Long Terminal Repeat (LTR) Sequences Following Mother-to-Child Transmission in North India. <i>AIDS Research and Human Retroviruses</i> , 2010, 26, 1299-1305.	0.5	5
97	Characterization of HIV Type 1 Subtype C protease Gene: Selection of L63P Mutation in Protease Inhibitor-Naive Indian Patients. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 1249-1253.	0.5	5
98	HIV elite control is associated with reduced TRAILshort expression. <i>Aids</i> , 2019, 33, 1757-1763.	1.0	5
99	Increased acquired protease inhibitor drug resistance mutations in minor HIV-1 quasispecies from infected patients suspected of failing on national second-line therapy in South Africa. <i>BMC Infectious Diseases</i> , 2021, 21, 214.	1.3	5
100	Coordinated pyruvate kinase activity is crucial for metabolic adaptation and cell survival during mitochondrial dysfunction. <i>Human Molecular Genetics</i> , 2021, 30, 2012-2026.	1.4	5
101	In vitro replicative fitness of early Transmitted founder HIV-1 variants and sensitivity to Interferon alpha. <i>Scientific Reports</i> , 2020, 10, 2747.	1.6	4
102	Phylogenetic Characterization of Six Full-Length HIV-1 Subtype C Molecular Clones from Three Patients: Identification of Rare Subtype C Strains Containing Two NF- κ B Motifs in the Long Terminal Repeat. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 586-591.	0.5	3
103	Minor viral population with drug-resistant mutation and risk of persistent low-level viremia or "blips"™ in HIV-1 subtype C. <i>Aids</i> , 2014, 28, 2635-2636.	1.0	3
104	Can HIV reverse transcriptase activity assay be a low-cost alternative for viral load monitoring in resource-limited settings?. <i>BMJ Open</i> , 2016, 6, e008795.	0.8	3
105	Effect of therapy switch on time to second-line antiretroviral treatment failure in HIV-infected patients. <i>PLoS ONE</i> , 2017, 12, e0180140.	1.1	3
106	MiDRMpól: A High-Throughput Multiplexed Amplicon Sequencing Workflow to Quantify HIV-1 Drug Resistance Mutations against Protease, Reverse Transcriptase, and Integrase Inhibitors. <i>Viruses</i> , 2019, 11, 806.	1.5	3
107	Mutations in Long Terminal Repeats κ B Transcription Factor Binding Sites in Plasma Virus Among South African People Living with HIV-1. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 572-576.	0.5	3
108	High-throughput sequencing reveals a high prevalence of pretreatment HIV-1 drug resistance in Sweden. <i>Aids</i> , 2021, 35, 227-234.	1.0	3

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109	Multomics Personalized Network Analyses Highlight Progressive Immune Disruption of Central Metabolism Associated with COVID-19 Severity. SSRN Electronic Journal, 0, , .	0.4	3
110	High Viremia in HIV-1 Subtype C Infection and Spread of the Epidemic. Journal of Infectious Diseases, 2013, 208, 866-867.	1.9	2
111	Cytotoxic Lymphocytes Target HIV-1 Gag Through Granzyme M-Mediated Cleavage. Frontiers in Immunology, 2021, 12, 669347.	2.2	2
112	Peripheral blood CD4+CCR6+ compartment differentiates HIV-1 infected or seropositive elite controllers from long-term successfully treated individuals. Communications Biology, 2022, 5, 357.	2.0	2
113	Emergence of unique recombinant forms (URFs) in Indian HIV-1 epidemic: data from nationwide clinical cohort between 2007 and 2011. Retrovirology, 2012, 9, .	0.9	1
114	Genetic Architecture of HIV Type 1 Nef and Tat from HLA-B57-Typed Long-Term Survivors in an Indian Cohort of Perinatally HIV-Infected Children. AIDS Research and Human Retroviruses, 2013, 29, 1613-1616.	0.5	1
115	Distinct Lipid Profile, Low-Level Inflammation and Increased Antioxidant Defense as a Signature in HIV-1 Elite Control Status. SSRN Electronic Journal, 0, , .	0.4	1
116	P20-05. Emergence of HIV-1 circulatory recombinant forms (CRFs) and unique recombinant forms (URFs) in North India: functional and pathogenic implications. Retrovirology, 2009, 6, .	0.9	0
117	A5â€fNear full-length HIV-1 genome sequencing in newly diagnosed individuals in Sweden. Virus Evolution, 2019, 5, .	2.2	0
118	Deep Profiling Identifies Selection of Nonsynonymous Amino Acid Substitutions in HIV-1 Envelope During Early Infection. AIDS Research and Human Retroviruses, 2020, 36, 1024-1032.	0.5	0
119	Integrative Proteo-Transcriptomic and Immunophenotyping Signatures of HIV-1 Elite Control Phenotype: A Cross-Talk Between Glycolysis and HIF Signaling. SSRN Electronic Journal, 0, , .	0.4	0
120	The expanding HIV-1 epidemic aggravates therapeutics and vaccine development programs in India. Bioinformation, 2009, 4, 90-91.	0.2	0