## Global landscape of HIV–human protein complexes

Nature 481, 365-370 DOI: 10.1038/nature10719

Citation Report

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Inhibition of a NEDD8 Cascade Restores Restriction of HIV by APOBEC3G. PLoS Pathogens, 2012, 8, e1003085.   | 2.1  | 55        |
| 2  | Running Loose or Getting Lost: How HIV-1 Counters and Capitalizes on APOBEC3-Induced Mutagenesis through Its Vif Protein. Viruses, 2012, 4, 3132-3161.                    | 1.5  | 20        |
| 3  | Tagged for destruction. Nature Reviews Microbiology, 2012, 10, 81-81.   | 13.6 | 0         |
| 4  | Identification of Cellular Proteins Required for Replication of Human Immunodeficiency Virus Type 1.<br>AIDS Research and Human Retroviruses, 2012, 28, 1329-1339.        | 0.5  | 25        |
| 5  | The BioGRID interaction database: 2013 update. Nucleic Acids Research, 2012, 41, D816-D823.   | 6.5  | 643       |
| 6  | A catalogue of putative HIV-1 protease host cell substrates. Biological Chemistry, 2012, 393, 915-931.  | 1.2  | 32        |
| 7  | Cellular Cofactors of Lentiviral Integrase: From Target Validation to Drug Discovery. Molecular<br>Biology International, 2012, 2012, 1-16.                               | 1.7  | 26        |
| 8  | HIV-1 Gag co-opts a cellular complex containing DDX6, a helicase that facilitates capsid assembly.<br>Journal of Cell Biology, 2012, 198, 439-456.                        | 2.3  | 76        |
| 9  | COMPUTATIONAL BIOLOGY IN THE CLOUD: METHODS AND NEW INSIGHTS FROM COMPUTING AT SCALE. , 2012, , .   |      | 5         |
| 10 | An overview of intracellular interactions between immunodeficiency viruses and their hosts. Aids, 2012, 26, 1243-1254.  | 1.0  | 18        |
| 11 | Exploring the human diseasome: the human disease network. Briefings in Functional Genomics, 2012, 11, 533-542.  | 1.3  | 118       |
| 12 | New horizons for antiviral drug discovery from virus–host protein interaction networks. Current<br>Opinion in Virology, 2012, 2, 606-613.                                 | 2.6  | 53        |
| 13 | Differential network biology. Molecular Systems Biology, 2012, 8, 565.  | 3.2  | 689       |
| 14 | Rules of Engagement: Molecular Insights from Host-Virus Arms Races. Annual Review of Genetics, 2012, 46, 677-700.   | 3.2  | 462       |
| 15 | Reacquisition of Nef-Mediated Tetherin Antagonism in a Single InÂVivo Passage of HIV-1 through Its<br>Original Chimpanzee Host. Cell Host and Microbe, 2012, 12, 373-380. | 5.1  | 35        |
| 16 | The role of Vif oligomerization and RNA chaperone activity in HIV-1 replication. Virus Research, 2012, 169, 361-376.  | 1.1  | 13        |
| 17 | Multiple roles of the capsid protein in the early steps of HIV-1 infection. Virus Research, 2012, 170, 15-24.   | 1.1  | 87        |
| 18 | Vif hijacks CBF-β to degrade APOBEC3G and promote HIV-1 infection. Nature, 2012, 481, 371-375.  | 13.7 | 312       |

|    |   | CITATION REPORT       |     |           |
|----|---|-----------------------|-----|-----------|
| #  | ARTICLE<br>Comprehensive Analysis of Host Cellular Interactions with Human Papillomavirus E6 Prot   | eins                  | IF  | CITATIONS |
| 19 | Identifies New E6 Binding Partners and Reflects Viral Diversity. Journal of Virology, 2012, 13174-13186.  | 86,                   | 1.5 | 178       |
| 20 | Beyond hairballs: The use of quantitative mass spectrometry data to understand proteina interactions. FEBS Letters, 2012, 586, 2723-2731.   | )€"protein            | 1.3 | 31        |
| 21 | From base pair to bedside: molecular simulation and the translation of genomics to perso<br>medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 585-5                                     |                       | 6.6 | 11        |
| 22 | Host restriction factors in retroviral infection: promises in virus-host interaction. Retroviro 2012, 9, 112.   | blogy,                | 0.9 | 88        |
| 23 | Proteomic analysis of HIV-1 Nef cellular binding partners reveals a role for exocyst comple<br>in mediating enhancement of intercellular nanotube formation. Retrovirology, 2012, 9, 3                                  | ex proteins<br>3.     | 0.9 | 75        |
| 24 | Virus-producing cells determine the host protein profiles of HIV-1 virion cores. Retrovirolo 65.  | ngy, 2012, 9,         | 0.9 | 62        |
| 25 | From promoting to inhibiting: diverse roles of helicases in HIV-1 Replication. Retrovirolog   | y, 2012, 9, 79.       | 0.9 | 32        |
| 26 | Human Immunodeficiency Virus Infection : from Biological Observations to Mechanistic M<br>Modelling. Mathematical Modelling of Natural Phenomena, 2012, 7, 78-104.  | Nathematical          | 0.9 | 43        |
| 27 | Translation of Purâ€Î± is targeted by cellular miRNAs to modulate the differentiationâ€de<br>susceptibility of monocytes to HIVâ€1 infection. FASEB Journal, 2012, 26, 4755-4764.                                       | pendent               | 0.2 | 52        |
| 28 | Functional genomic and high-content screening for target discovery and deconvolution.<br>Opinion on Drug Discovery, 2012, 7, 955-968.   | Expert                | 2.5 | 21        |
| 29 | Prediction of Mutational Tolerance in HIV-1 Protease and Reverse Transcriptase Using Fle<br>Backbone Protein Design. PLoS Computational Biology, 2012, 8, e1002639.   | xible                 | 1.5 | 21        |
| 30 | Characterization of the Interaction of Full-Length HIV-1 Vif Protein with its Key Regulator CRL5 E3 Ubiquitin Ligase Components. PLoS ONE, 2012, 7, e33495.   | CBFÎ <sup>2</sup> and | 1.1 | 47        |
| 32 | Role of the HIV-1 Matrix Protein in Gag Intracellular Trafficking and Targeting to the Plasm for Virus Assembly. Frontiers in Microbiology, 2012, 3, 55.  | na Membrane           | 1.5 | 45        |
| 33 | Proteomic analysis of HIV–T cell interaction: an update. Frontiers in Microbiology, 2012  | 2, 3, 240.            | 1.5 | 11        |
| 34 | Characterization of Staufen1 Ribonucleoproteins by Mass Spectrometry and Biochemical<br>Reveal the Presence of Diverse Host Proteins Associated with Human Immunodeficiency<br>Frontiers in Microbiology, 2012, 3, 367. |                       | 1.5 | 56        |
| 35 | Toward a three-dimensional view of protein networks between species. Frontiers in Micro 2012, 3, 428.   | biology,              | 1.5 | 26        |
| 36 | Rendezvous with Tat: Transactivator of Transcription during Human Immunodeficiency V<br>Pathogenesis. American Journal of Infectious Diseases, 2012, 8, 79-91.  | irus                  | 0.1 | 0         |
| 37 | Dynamic Post-Transcriptional Regulation of HIV-1 Gene Expression. Biology, 2012, 1, 116   | -133.                 | 1.3 | 9         |

| #  | Article   | IF   | CITATIONS |
|----|---|------|-----------|
| 38 | Viral immune modulators perturb the human molecular network by common and unique strategies.<br>Nature, 2012, 487, 486-490.   | 13.7 | 249       |
| 39 | The interaction map. Nature, 2012, 484, 271-275.  | 13.7 | 29        |
| 40 | Proteome-wide prediction of protein-protein interactions from high-throughput data. Protein and Cell, 2012, 3, 508-520.   | 4.8  | 36        |
| 41 | <i>Inâ€fvitro</i> studies reveal that different modes of initiation on HIVâ€1 mRNA have different levels of requirement for eukaryotic initiation factorâ€f4F. FEBS Journal, 2012, 279, 3098-3111.  | 2.2  | 30        |
| 42 | Quantitative proteomic analysis of HIV-1 infected CD4+ T cells reveals an early host response in<br>important biological pathways: Protein synthesis, cell proliferation, and T-cell activation. Virology,<br>2012, 429, 37-46.                       | 1.1  | 43        |
| 43 | HIV-1 transcription and latency: an update. Retrovirology, 2013, 10, 67.  | 0.9  | 271       |
| 44 | DNA damage enhances integration of HIV-1 into macrophages by overcoming integrase inhibition.<br>Retrovirology, 2013, 10, 21.   | 0.9  | 26        |
| 45 | Proteomic changes in HEK-293 cells induced by hepatitis delta virus replication. Journal of Proteomics, 2013, 89, 24-38.  | 1.2  | 20        |
| 46 | Ligand-based receptor identification on living cells and tissues using TRICEPS. Nature Protocols, 2013, 8, 1321-1336.   | 5.5  | 55        |
| 47 | Genome-wide search for the genes accountable for the induced resistance to HIV-1 infection in activated CD4+ T cells: apparent transcriptional signatures, co-expression networks and possible cellular processes. BMC Medical Genomics, 2013, 6, 15. | 0.7  | 26        |
| 48 | Selective recognition of viral promoters by host cell transcription complexes: challenges and opportunities to control latency. Current Opinion in Virology, 2013, 3, 380-386.  | 2.6  | 4         |
| 49 | Integrative avenues for exploring the dynamics and evolution of protein interaction networks.<br>Current Opinion in Biotechnology, 2013, 24, 775-783.   | 3.3  | 14        |
| 50 | The Lectin ERGIC-53 Goes Viral. Cell Host and Microbe, 2013, 14, 485-487.   | 5.1  | 2         |
| 52 | Protein production from the structural genomics perspective: achievements and future needs.<br>Current Opinion in Structural Biology, 2013, 23, 335-344.  | 2.6  | 37        |
| 53 | High-resolution network biology: connecting sequence with function. Nature Reviews Genetics, 2013, 14, 865-879.   | 7.7  | 92        |
| 54 | The Intracellular Cargo Receptor ERGIC-53 Is Required for the Production of Infectious Arenavirus,<br>Coronavirus, and Filovirus Particles. Cell Host and Microbe, 2013, 14, 522-534.   | 5.1  | 62        |
| 55 | Edgotype: a fundamental link between genotype and phenotype. Current Opinion in Genetics and Development, 2013, 23, 649-657.  | 1.5  | 129       |
| 56 | Translation initiation is driven by different mechanisms on the HIV-1 and HIV-2 genomic RNAs. Virus<br>Research, 2013, 171, 366-381.  | 1.1  | 29        |

| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 57 | Interactions between HIV-1 Vif and human ElonginB-ElonginC are important for CBF-Î <sup>2</sup> binding to Vif.<br>Retrovirology, 2013, 10, 94.  | 0.9 | 24        |
| 58 | Structure homology and interaction redundancy for discovering virus–host protein interactions.<br>EMBO Reports, 2013, 14, 938-944.   | 2.0 | 39        |
| 59 | High throughput strategies for probing the different organizational levels of protein interaction networks. Molecular BioSystems, 2013, 9, 2201.   | 2.9 | 13        |
| 60 | Proteomic approaches to the study of papillomavirus–host interactions. Virology, 2013, 435, 57-69.   | 1.1 | 60        |
| 61 | Systems biology of pathogenâ€host interaction: Networks of proteinâ€protein interaction within<br>pathogens and pathogenâ€human interactions in the postâ€genomic era. Biotechnology Journal, 2013, 8,<br>85-96. | 1.8 | 39        |
| 62 | Next-generation proteomics: towards an integrative view of proteome dynamics. Nature Reviews<br>Genetics, 2013, 14, 35-48.   | 7.7 | 656       |
| 63 | Proteomics-Based Methods for Discovery, Quantification, and Validation of Protein–Protein<br>Interactions. Analytical Chemistry, 2013, 85, 749-768.  | 3.2 | 85        |
| 64 | Nucleotide embargo by SAMHD1: A strategy to block retroviral infection. Antiviral Research, 2013, 97, 180-182.   | 1.9 | 17        |
| 65 | Quantifying proteomes and their post-translational modifications by stable isotope label-based mass spectrometry. Current Opinion in Chemical Biology, 2013, 17, 779-786.  | 2.8 | 20        |
| 66 | Rational design of LEDGINs as first allosteric integrase inhibitors for the treatment of HIV infection.<br>Drug Discovery Today: Technologies, 2013, 10, e517-e522.  | 4.0 | 7         |
| 67 | Curing a viral infection by targeting the host: The example of cyclophilin inhibitors. Antiviral Research, 2013, 99, 68-77.  | 1.9 | 101       |
| 68 | Cellular RNA helicases and HIV-1: Insights from genome-wide, proteomic, and molecular studies. Virus<br>Research, 2013, 171, 357-365.  | 1.1 | 20        |
| 69 | Genotype to phenotype via network analysis. Current Opinion in Genetics and Development, 2013, 23, 611-621.  | 1.5 | 126       |
| 71 | Microfluidic large scale integration of viral–host interaction analysis. Lab on A Chip, 2013, 13, 2202.  | 3.1 | 21        |
| 72 | From Systems to Structure: Bridging Networks and Mechanism. Molecular Cell, 2013, 49, 222-231.   | 4.5 | 46        |
| 73 | Using Guanidine-Hydrochloride for Fast and Efficient Protein Digestion and Single-step<br>Affinity-purification Mass Spectrometry. Journal of Proteome Research, 2013, 12, 1020-1030.                            | 1.8 | 41        |
| 74 | Structural and Functional Role of INI1 and LEDGF in the HIV-1 Preintegration Complex. PLoS ONE, 2013, 8, e60734.   | 1.1 | 24        |
| 75 | Protein-protein interaction networks: probing disease mechanisms using model systems. Genome<br>Medicine, 2013, 5, 37.   | 3.6 | 124       |

| #  | ARTICLE<br>Network Biology editorial 2013. Molecular BioSystems, 2013, 9, 1557.  | IF<br>2.9 | CITATIONS |
|----|--|-----------|-----------|
| 77 | A "Candidate-Interactome―Aggregate Analysis of Genome-Wide Association Data in Multiple Sclerosis.<br>PLoS ONE, 2013, 8, e63300.   | 1.1       | 66        |
| 78 | The APOBEC3 Family of Retroelement Restriction Factors. Current Topics in Microbiology and Immunology, 2013, 371, 1-27.  | 0.7       | 177       |
| 79 | CBFβ Stabilizes HIV Vif to Counteract APOBEC3 at the Expense of RUNX1 Target Gene Expression.<br>Molecular Cell, 2013, 49, 632-644.  | 4.5       | 108       |
| 80 | Protein interaction networks in innate immunity. Trends in Immunology, 2013, 34, 610-619.  | 2.9       | 26        |
| 81 | Identification of RNA partners of viral proteins in infected cells. RNA Biology, 2013, 10, 943-956.  | 1.5       | 13        |
| 82 | Fluorescence, Circular Dichroism and Mass Spectrometry as Tools to Study Virus Structure.<br>Sub-Cellular Biochemistry, 2013, 68, 177-202.   | 1.0       | 7         |
| 83 | Host Genetics of HIV Acquisition and Viral Control. Annual Review of Medicine, 2013, 64, 203-217.  | 5.0       | 29        |
| 84 | Proteomic Analysis of Early HIV-1 Nucleoprotein Complexes. Journal of Proteome Research, 2013, 12, 559-572.  | 1.8       | 33        |
| 85 | Novel Role of HSP40/DNAJ in the Regulation of HIV-1 Replication. Journal of Acquired Immune<br>Deficiency Syndromes (1999), 2013, 64, 154-162.   | 0.9       | 21        |
| 86 | 24 Hours in the Life of HIV-1 in a T Cell Line. PLoS Pathogens, 2013, 9, e1003161.   | 2.1       | 134       |
| 87 | Histone Deacetylases in Herpesvirus Replication and Virus-Stimulated Host Defense. Viruses, 2013, 5, 1607-1632.  | 1.5       | 30        |
| 88 | Depletion of hnRNP A2/B1 overrides the nuclear retention of the HIV-1 genomic RNA. RNA Biology, 2013, 10, 1714-1725.   | 1.5       | 26        |
| 89 | Proteomics as a novel HIV immune monitoring tool. Current Opinion in HIV and AIDS, 2013, 8, 140-146.   | 1.5       | 5         |
| 90 | A genome-wide association study of resistance to HIV infection in highly exposed uninfected individuals with hemophilia A. Human Molecular Genetics, 2013, 22, 1903-1910.  | 1.4       | 38        |
| 91 | An Intronic G Run within HIV-1 Intron 2 Is Critical for Splicing Regulation of <i>vif</i> mRNA. Journal of Virology, 2013, 87, 2707-2720.  | 1.5       | 33        |
| 92 | Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity<br>Purification and Mass Spectrometry (AP-MS) Experiments. Molecular and Cellular Proteomics, 2013, 12,<br>1-13. | 2.5       | 46        |
| 93 | Cell type specificity and structural determinants of IRES activity from the 5′ leaders of different HIV-1 transcripts. Nucleic Acids Research, 2013, 41, 6698-6714.  | 6.5       | 47        |

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 94  | Cellular Cofactors of HIV as Drug Targets. , 2013, , 1-7.  |     | 0         |
| 95  | Human Immunodeficiency Virus Reverse Transcriptase. , 2013, , .  |     | 0         |
| 96  | HIV Life Cycle: Overview. , 2013, , 1-9.   |     | 14        |
| 97  | A sampling framework for incorporating quantitative mass spectrometry data in protein interaction analysis. BMC Bioinformatics, 2013, 14, 299.   | 1.2 | 4         |
| 98  | Bringing it all together. Aids, 2013, 27, 835-838.   | 1.0 | 14        |
| 99  | HIV-1 Vpr Modulates Macrophage Metabolic Pathways: A SILAC-Based Quantitative Analysis. PLoS ONE, 2013, 8, e68376.   | 1.1 | 75        |
| 100 | A Viral-Human Interactome Based on Structural Motif-Domain Interactions Captures the Human<br>Infectome. PLoS ONE, 2013, 8, e71526.  | 1.1 | 27        |
| 101 | HIV-1 Vpr Induces the Degradation of ZIP and sZIP, Adaptors of the NuRD Chromatin Remodeling<br>Complex, by Hijacking DCAF1/VprBP. PLoS ONE, 2013, 8, e77320.                                | 1.1 | 23        |
| 102 | Footprints of Directional Selection in Wild Atlantic Salmon Populations: Evidence for Parasite-Driven Evolution?. PLoS ONE, 2014, 9, e91672.   | 1.1 | 37        |
| 103 | Proteomic Analysis of Saliva in HIV-Positive Heroin Addicts Reveals Proteins Correlated with Cognition. PLoS ONE, 2014, 9, e89366.   | 1.1 | 23        |
| 104 | An Integrated Map of HIV-Human Protein Complexes that Facilitate Viral Infection. PLoS ONE, 2014, 9, e96687.   | 1.1 | 13        |
| 105 | The HIVToolbox 2 Web System Integrates Sequence, Structure, Function and Mutation Analysis. PLoS ONE, 2014, 9, e98810.   | 1.1 | 6         |
| 106 | RNA-directed remodeling of the HIV-1 protein Rev orchestrates assembly of the Rev–Rev response element complex. ELife, 2014, 3, e04120.  | 2.8 | 61        |
| 107 | Simian Immunodeficiency Virus and Human Immunodeficiency Virus Type 1 Matrix Proteins Specify<br>Different Capabilities To Modulate B Cell Growth. Journal of Virology, 2014, 88, 5706-5717. | 1.5 | 23        |
| 108 | Kaposi's Sarcoma-Associated Herpesvirus ORF45 Mediates Transcriptional Activation of the HIV-1 Long<br>Terminal Repeat via RSK2. Journal of Virology, 2014, 88, 7024-7035.                   | 1.5 | 19        |
| 109 | Mass spectrometry-based proteomic approaches for discovery of HIV–host interactions. Future Virology, 2014, 9, 979-992.  | 0.9 | 14        |
| 110 | A Mass Spectrometry View of Stable and Transient Protein Interactions. Advances in Experimental<br>Medicine and Biology, 2014, 806, 263-282.   | 0.8 | 31        |
| 111 | HIV-1 and HIV-2 Vif Interact with Human APOBEC3 Proteins Using Completely Different Determinants.<br>Journal of Virology, 2014, 88, 9893-9908.   | 1.5 | 31        |

| #   | Article   | IF   | CITATIONS |
|-----|---|------|-----------|
| 112 | Determinants of Efficient Degradation of APOBEC3 Restriction Factors by HIV-1 Vif. Journal of Virology, 2014, 88, 14380-14395.  | 1.5  | 32        |
| 113 | Translation initiation of the HIV-1 mRNA. Translation, 2014, 2, e960242.  | 2.9  | 16        |
| 114 | Suppression of APOBEC3-mediated restriction of HIV-1 by Vif. Frontiers in Microbiology, 2014, 5, 450.   | 1.5  | 100       |
| 115 | The activity of Nef on HIV-1 infectivity. Frontiers in Microbiology, 2014, 5, 232.  | 1.5  | 67        |
| 116 | Dynamics of HIV Latency and Reactivation in a Primary CD4+ T Cell Model. PLoS Pathogens, 2014, 10, e1004156.  | 2.1  | 70        |
| 117 | Recruitment of RED-SMU1 Complex by Influenza A Virus RNA Polymerase to Control Viral mRNA<br>Splicing. PLoS Pathogens, 2014, 10, e1004164.  | 2.1  | 43        |
| 118 | Cullin E3 Ligases and Their Rewiring by Viral Factors. Biomolecules, 2014, 4, 897-930.  | 1.8  | 78        |
| 119 | In Vivo Functions of CPSF6 for HIV-1 as Revealed by HIV-1 Capsid Evolution in HLA-B27-Positive Subjects.<br>PLoS Pathogens, 2014, 10, e1003868.   | 2.1  | 41        |
| 120 | Lentivirus-mediated knockdown of eukaryotic translation initiation factor 3 subunit D inhibits proliferation of HCT116 colon cancer cells. Bioscience Reports, 2014, 34, e00161.                | 1.1  | 34        |
| 121 | Vimentin—a potential biomarker for therapeutic efficiency of HAART. Acta Biochimica Et<br>Biophysica Sinica, 2014, 46, 1001-1006.   | 0.9  | 5         |
| 122 | Comprehensive Identification of Host Modulators of HIV-1 Replication using Multiple Orthologous RNAi Reagents. Cell Reports, 2014, 9, 752-766.  | 2.9  | 48        |
| 123 | A Cell-penetrating Antibody Fragment against HIV-1 Rev Has High Antiviral Activity. Journal of<br>Biological Chemistry, 2014, 289, 20222-20233.   | 1.6  | 20        |
| 124 | The Impact of Mass Spectrometry–Based Proteomics on Fundamental Discoveries in Virology. Annual<br>Review of Virology, 2014, 1, 581-604.  | 3.0  | 55        |
| 125 | The Structural Basis of Substrate Recognition by the Eukaryotic Chaperonin TRiC/CCT. Cell, 2014, 159, 1042-1055.  | 13.5 | 131       |
| 126 | Singleâ€molecule pullâ€down (SiMPull) for newâ€age biochemistry. BioEssays, 2014, 36, 1109-1119.  | 1.2  | 25        |
| 127 | Spotlite: Web Application and Augmented Algorithms for Predicting Co-Complexed Proteins from Affinity Purification – Mass Spectrometry Data. Journal of Proteome Research, 2014, 13, 5944-5955. | 1.8  | 18        |
| 128 | Mapping orphan proteases by proteomics: Meprin metalloproteases deciphered as potential therapeutic targets. Proteomics - Clinical Applications, 2014, 8, 382-388.                              | 0.8  | 6         |
| 129 | Targeting Cellular Cofactors in HIV Therapy. Topics in Medicinal Chemistry, 2014, , 183-222.  | 0.4  | 8         |

| #   | Article   | IF   | CITATIONS |
|-----|---|------|-----------|
| 130 | Human protein Staufen-2 promotes HIV-1 proliferation by positively regulating RNA export activity of viral protein Rev. Retrovirology, 2014, 11, 18.  | 0.9  | 20        |
| 131 | HIV-1 protease-induced apoptosis. Retrovirology, 2014, 11, 37.  | 0.9  | 35        |
| 132 | Detection of HIV-1 Matrix Protein p17 Quasispecies Variants in Plasma of Chronic HIV-1–Infected<br>Patients by Ultra-Deep Pyrosequencing. Journal of Acquired Immune Deficiency Syndromes (1999), 2014,<br>66, 332-339. | 0.9  | 8         |
| 133 | Functional and Biochemical Characterization of Human Eukaryotic Translation Initiation Factor 3 in<br>Living Cells. Molecular and Cellular Biology, 2014, 34, 3041-3052.  | 1.1  | 69        |
| 134 | Autophagy plays an important role in the containment of HIV-1 in nonprogressor-infected patients.<br>Autophagy, 2014, 10, 1167-1178.  | 4.3  | 70        |
| 135 | Identification of molecular sub-networks associated with cell survival in a chronically<br>SIVmac-infected human CD4+ T cell line. Virology Journal, 2014, 11, 152.   | 1.4  | 5         |
| 136 | A functional conserved intronic G run in HIV-1 intron 3 is critical to counteract APOBEC3G-mediated host restriction. Retrovirology, 2014, 11, 72.  | 0.9  | 23        |
| 137 | Positive selection of primate genes that promote HIV-1 replication. Virology, 2014, 454-455, 291-298.   | 1.1  | 43        |
| 138 | Mutational and fitness landscapes of an RNA virus revealed through population sequencing. Nature, 2014, 505, 686-690.   | 13.7 | 343       |
| 139 | Next generation approaches to study virus entry and infection. Current Opinion in Virology, 2014, 4, 8-14.  | 2.6  | 17        |
| 140 | A primary CD4+ T cell model of HIV-1 latency established after activation through the T cell receptor and subsequent return to quiescence. Nature Protocols, 2014, 9, 2755-2770.  | 5.5  | 46        |
| 141 | eEF2 and Ras-GAP SH3 domain-binding protein (G3BP1) modulate stress granule assembly during HIV-1 infection. Nature Communications, 2014, 5, 4819.  | 5.8  | 76        |
| 142 | Exploring intercellular signaling by proteomic approaches. Proteomics, 2014, 14, 498-512.   | 1.3  | 14        |
| 143 | A computational analysis of the structural determinants of APOBEC3's catalytic activity and vulnerability to HIV-1 Vif. Virology, 2014, 471-473, 105-116.   | 1.1  | 23        |
| 144 | Affinity purification–mass spectrometry and network analysis to understand protein-protein<br>interactions. Nature Protocols, 2014, 9, 2539-2554.   | 5.5  | 169       |
| 145 | Validation of host factors of HIV integration as novel drug targets for anti-HIV therapy.<br>MedChemComm, 2014, 5, 314-320.   | 3.5  | 4         |
| 146 | abFASP-MS: Affinity-Based Filter-Aided Sample Preparation Mass Spectrometry for Quantitative Analysis of Chemically Labeled Protein Complexes. Journal of Proteome Research, 2014, 13, 1147-1155.                       | 1.8  | 16        |
| 147 | Quantitative Proteomic Analysis of Host-virus Interactions Reveals a Role for Golgi Brefeldin A<br>Resistance Factor 1 (GBF1) in Dengue Infection. Molecular and Cellular Proteomics, 2014, 13, 2836-2854.              | 2.5  | 49        |

|     |   | CITATION R         | EPORT |           |
|-----|---|--------------------|-------|-----------|
| #   | Article   |                    | IF    | CITATIONS |
| 148 | Alterations in the nuclear proteome of HIV-1 infected T-cells. Virology, 2014, 468-470,   | 409-420.           | 1.1   | 15        |
| 149 | Exploring mitochondrial system properties of neurodegenerative diseases through inte mapping. Journal of Proteomics, 2014, 100, 8-24.   | ractome            | 1.2   | 13        |
| 150 | The dual role of tetraspanin CD63 in HIV-1 replication. Virology Journal, 2014, 11, 23.   |                    | 1.4   | 37        |
| 151 | The PI3K pathway acting on alternative HIV-1 pre-mRNA splicing. Journal of General Viro 1809-1815.  | ology, 2014, 95,   | 1.3   | 4         |
| 152 | Viral proteins that bridge unconnected proteins and components in the human PPI net<br>Molecular BioSystems, 2014, 10, 2448-2458.   | work.              | 2.9   | 11        |
| 153 | Manipulation of host pathways by human cytomegalovirus: insights from genome-wide<br>Seminars in Immunopathology, 2014, 36, 651-658.  | e studies.         | 2.8   | 13        |
| 154 | A combination HIV reporter virus system for measuring post-entry event efficiency and in primary CD4+ T cell subsets. Journal of Virological Methods, 2014, 195, 164-169.               | viral outcome      | 1.0   | 14        |
| 155 | Proteome analysis of the HIV-1 Gag interactome. Virology, 2014, 460-461, 194-206.   |                    | 1.1   | 46        |
| 156 | Protein–protein interactions and genetic diseases: The interactome. Biochimica Et Bi<br>Molecular Basis of Disease, 2014, 1842, 1971-1980.  | iophysica Acta -   | 1.8   | 105       |
| 157 | Host Factors in Retroviral Integration and the Selection of Integration Target Sites. Mic Spectrum, 2014, 2, .  | crobiology         | 1.2   | 40        |
| 159 | Interactions of HIV-1 proteins as targets for developing anti-HIV-1 peptides. Future Me<br>2015, 7, 1055-1077.  | dicinal Chemistry, | 1.1   | 2         |
| 160 | Clobal multiple protein-protein interaction network alignment by combining pairwise n<br>alignments. BMC Bioinformatics, 2015, 16, S11.   | etwork             | 1.2   | 10        |
| 161 | HIV-1 Recruits UPF1 but Excludes UPF2 to Promote Nucleocytoplasmic Export of the G<br>Biomolecules, 2015, 5, 2808-2839.   | enomic RNA.        | 1.8   | 52        |
| 162 | HIV Tat controls RNA Polymerase II and the epigenetic landscape to transcriptionally re<br>immune cells. ELife, 2015, 4, .  | program target     | 2.8   | 47        |
| 163 | From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass<br>Spectrometry-Based Proteomics. Journal of the American Society for Mass Spectromet<br>1820-1826. | ry, 2015, 26,      | 1.2   | 17        |
| 164 | Therapy of Viral Infections. Topics in Medicinal Chemistry, 2015, , .   |                    | 0.4   | 6         |
| 165 | HIV-1 IN/Pol recruits LEDGF/p75 into viral particles. Retrovirology, 2015, 12, 16.  |                    | 0.9   | 19        |
| 166 | The Mechanism and Function of Group II Chaperonins. Journal of Molecular Biology, 20 2919-2930.   | )15, 427,          | 2.0   | 158       |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 167 | The Cancer Cell Map Initiative: Defining the Hallmark Networks of Cancer. Molecular Cell, 2015, 58, 690-698.   | 4.5  | 117       |
| 168 | Scoring Largeâ€Scale Affinity Purification Mass Spectrometry Datasets with MiST. Current Protocols in Bioinformatics, 2015, 49, 8.19.1-8.19.16.                              | 25.8 | 58        |
| 169 | Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. Retrovirology, 2015, 12, 41.                      | 0.9  | 78        |
| 170 | Histone Deacetylase Inhibitor Romidepsin Inhibits <i>De Novo</i> HIV-1 Infections. Antimicrobial Agents<br>and Chemotherapy, 2015, 59, 3984-3994.                            | 1.4  | 26        |
| 171 | A review on computational systems biology of pathogenââ,¬â€œhost interactions. Frontiers in<br>Microbiology, 2015, 6, 235.   | 1.5  | 93        |
| 172 | Non-POU Domain-Containing Octamer-Binding Protein Negatively Regulates HIV-1 Infection in CD4 <sup>+</sup> T Cells. AIDS Research and Human Retroviruses, 2015, 31, 806-816. | 0.5  | 21        |
| 173 | Retroviral Integrase: Then and Now. Annual Review of Virology, 2015, 2, 241-264.   | 3.0  | 24        |
| 174 | Meta- and Orthogonal Integration of Influenza "OMICs―Data Defines a Role for UBR4 in Virus<br>Budding. Cell Host and Microbe, 2015, 18, 723-735.                             | 5.1  | 868       |
| 175 | Association with PAK2 Enables Functional Interactions of Lentiviral Nef Proteins with the Exocyst Complex. MBio, 2015, 6, e01309-15.   | 1.8  | 23        |
| 176 | Global Mapping of Herpesvirus-Host Protein Complexes Reveals a Transcription Strategy for Late<br>Genes. Molecular Cell, 2015, 57, 349-360.                                  | 4.5  | 165       |
| 177 | Proteomics in the investigation of HIVâ $\in$ interactions with host proteins. Proteomics - Clinical Applications, 2015, 9, 221-234.   | 0.8  | 12        |
| 178 | A Combined Proteomics/Genomics Approach Links Hepatitis C Virus Infection with Nonsense-Mediated mRNA Decay. Molecular Cell, 2015, 57, 329-340.                              | 4.5  | 124       |
| 179 | Proteomic alteration of equine monocyteâ€derived macrophages infected with equine infectious anemia virus. Proteomics, 2015, 15, 1843-1858.                                  | 1.3  | 15        |
| 180 | PPI network inference from AP-MS data. , 2015, , 51-59.  |      | 1         |
| 181 | Identification of an HIV-1 replication inhibitor which rescues host restriction factor APOBEC3G in Vif–APOBEC3G complex. Antiviral Research, 2015, 122, 20-27.               | 1.9  | 23        |
| 182 | Recent strategies and progress in identifying host factors involved in virus replication. Current<br>Opinion in Microbiology, 2015, 26, 79-88.                               | 2.3  | 22        |
| 183 | HIV-1 Replication and the Cellular Eukaryotic Translation Apparatus. Viruses, 2015, 7, 199-218.  | 1.5  | 45        |
| 184 | Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection.<br>Cell Host and Microbe, 2015, 18, 109-121.                                | 5.1  | 174       |

ARTICLE IF CITATIONS # Molecular dynamics simulations of large macromolecular complexes. Current Opinion in Structural 185 2.6 347 Biology, 2015, 31, 64-74. Bioinformatics and HIV Latency. Current HIV/AIDS Reports, 2015, 12, 97-106. 1.1 An integrated map of HIV genome-wide variation from a population perspective. Retrovirology, 2015, 12, 187 0.9 90 18. Extracting high confidence protein interactions from affinity purification data: At the crossroads. 1.2 Journal of Proteomics, 2015, 118, 63-80. The impact of host genetic variation on infection with HIV-1. Nature Immunology, 2015, 16, 577-583. 189 7.0 119 Balanced splicing at the Tat-specific HIV-1 3â€<sup>2</sup>ss A3 is critical for HIV-1 replication. Retrovirology, 2015, 12, 29 The Road Less Traveled: HIV's Use of Alternative Routes through Cellular Pathways. Journal of 191 1.5 9 Virology, 2015, 89, 5204-5212. Proteomics methods for discovering viral–host interactions. Methods, 2015, 90, 21-27. 1.9 193 Rapid, optimized interactomic screening. Nature Methods, 2015, 12, 553-560. 9.0 68 194 Proteomic approaches to analyzing hepatitis C virus biology. Proteomics, 2015, 15, 2051-2065. 1.3 Multidimensional proteomics for cell biology. Nature Reviews Molecular Cell Biology, 2015, 16, 195 16.1 375 269-280. Analysis of HIV-1 Gag Protein Interactions via Biotin Ligase Tagging. Journal of Virology, 2015, 89, 1.5 3988-4001. Host-Microbe Protein Interactions during Bacterial Infection. Chemistry and Biology, 2015, 22, 197 6.2 103 1521-1530. HIV-1 Nef hijacks clathrin coats by stabilizing AP-1:Arf1 polygons. Science, 2015, 350, aac5137. 198 6.0 39 Coevolutionary analyses require phylogenetically deep alignments and better null models to 199 1.2 12 accurately detect inter-protein contacts within and between species. BMC Bioinformatics, 2015, 16, 268. Lineage-Specific Viral Hijacking of Non-canonical E3ÂUbiquitin Ligase Cofactors in the Evolution of Vif Anti-ĂPOBEC3 Activity. Cell Reports, 2015, 11, 1236-1250. Comparative mapping of hostâ€"pathogen proteinâ€"protein interactions. Current Opinion in 201 2.337 Microbiology, 2015, 27, 62-68. HIV-1 protease cleaves the serine-threonine kinases RIPK1 and RIPK2. Retrovirology, 2015, 12, 74.

| #   | Article   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 203 | No-Go'ing Back: Co-opting RVB-2 to Control HIV-1 Gene Expression and Immune Response. Trends in<br>Microbiology, 2015, 23, 593-595.   | 3.5 | 1         |
| 204 | RNA helicase MOV10 functions as a co-factor of HIV-1 Rev to facilitate Rev/RRE-dependent nuclear export of viral mRNAs. Virology, 2015, 486, 15-26.   | 1.1 | 21        |
| 205 | CDK11 in TREX/THOC Regulates HIV mRNA 3′ End Processing. Cell Host and Microbe, 2015, 18, 560-570.  | 5.1 | 53        |
| 206 | How pathogens use linear motifs to perturb host cell networks. Trends in Biochemical Sciences, 2015, 40, 36-48.   | 3.7 | 85        |
| 207 | Molecular principles of human virus protein–protein interactions. Bioinformatics, 2015, 31, 1025-1033.  | 1.8 | 41        |
| 208 | Network inference from AP-MS data: computational challenges and solutions. Briefings in Bioinformatics, 2015, 16, 658-674.  | 3.2 | 21        |
| 209 | Analysis of Host Gene Expression Profile in HIV-1 and HIV-2 Infected T-Cells. PLoS ONE, 2016, 11, e0147421.   | 1.1 | 23        |
| 210 | The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. PLoS<br>Pathogens, 2016, 12, e1005841.  | 2.1 | 176       |
| 211 | The Virus–Host Interactome. , 2016, , 157-167.  |     | 4         |
| 212 | Computational modeling of Repeat1 region of INI1/hSNF5: An evolutionary link with ubiquitin. Protein<br>Science, 2016, 25, 1593-1604.   | 3.1 | 1         |
| 213 | Effect of internal cleavage site mutations in human immunodeficiency virus type 1 capsid protein on its structure and function. FEBS Open Bio, 2016, 6, 847-859.                                      | 1.0 | 2         |
| 214 | A structurally plastic ribonucleoprotein complex mediates postâ€transcriptional gene regulation in<br><scp>HIV</scp> â€1. Wiley Interdisciplinary Reviews RNA, 2016, 7, 470-486.                      | 3.2 | 25        |
| 215 | A scaffold protein connects type IV pili with the Chp chemosensory system to mediate activation of virulence signaling in <i>Pseudomonas aeruginosa</i> . Molecular Microbiology, 2016, 101, 590-605. | 1.2 | 69        |
| 216 | HIV Genome-Wide Protein Associations: a Review of 30 Years of Research. Microbiology and Molecular<br>Biology Reviews, 2016, 80, 679-731.   | 2.9 | 61        |
| 217 | Advances in Zika Virus Research: Stem Cell Models, Challenges, and Opportunities. Cell Stem Cell, 2016, 19, 690-702.  | 5.2 | 103       |
| 218 | Eukaryotic translation initiation factor 3 subunit D overexpression is associated with the occurrence and development of ovarian cancer. FEBS Open Bio, 2016, 6, 1201-1210.                           | 1.0 | 9         |
| 220 | An interâ€species protein–protein interaction network across vast evolutionary distance. Molecular<br>Systems Biology, 2016, 12, 865.   | 3.2 | 42        |
| 221 | Identification of Novel Host Interactors of Effectors Secreted by <i>Salmonella</i> and <i>Citrobacter</i> . MSystems, 2016, 1, .   | 1.7 | 22        |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 222 | A time-resolved molecular map of the macrophage response to VSV infection. Npj Systems Biology and Applications, 2016, 2, 16027.   | 1.4  | 42        |
| 223 | Pathogen receptor discovery with a microfluidic human membrane protein array. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4344-4349.   | 3.3  | 19        |
| 224 | Assembly of eIF3 Mediated by Mutually Dependent Subunit Insertion. Structure, 2016, 24, 886-896.   | 1.6  | 39        |
| 225 | Predicting Protein–Protein Interactions from the Molecular to the Proteome Level. Chemical Reviews, 2016, 116, 4884-4909.  | 23.0 | 289       |
| 226 | Controllability analysis of the directed human protein interaction network identifies disease genes<br>and drug targets. Proceedings of the National Academy of Sciences of the United States of America,<br>2016, 113, 4976-4981. | 3.3  | 249       |
| 227 | Using biological networks to integrate, visualize and analyze genomics data. Genetics Selection Evolution, 2016, 48, 27.   | 1.2  | 86        |
| 228 | Improving Viral Protease Inhibitors to Counter Drug Resistance. Trends in Microbiology, 2016, 24, 547-557.   | 3.5  | 81        |
| 229 | Patterns of amino acid conservation in human and animal immunodeficiency viruses. Bioinformatics, 2016, 32, i685-i692.   | 1.8  | 8         |
| 230 | Oligomeric viral proteins: small in size, large in presence. Critical Reviews in Biochemistry and<br>Molecular Biology, 2016, 51, 379-394.   | 2.3  | 23        |
| 231 | Development and validation of a cell-based assay system to assess human immunodeficiency virus type 1 integrase multimerization. Journal of Virological Methods, 2016, 236, 196-206.   | 1.0  | 2         |
| 232 | Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function.<br>Molecular Cell, 2016, 63, 621-632.   | 4.5  | 241       |
| 233 | Proteomics, biomarkers, and HIVâ€1: A current perspective. Proteomics - Clinical Applications, 2016, 10, 110-125.  | 0.8  | 15        |
| 234 | Global profiling of protein complexes: current approaches and their perspective in biomedical research. Expert Review of Proteomics, 2016, 13, 951-964.  | 1.3  | 15        |
| 235 | Deep interactome profiling of membrane proteins by co-interacting protein identification technology.<br>Nature Protocols, 2016, 11, 2515-2528.   | 5.5  | 54        |
| 236 | Herb-target interaction network analysis helps to disclose molecular mechanism of traditional<br>Chinese medicine. Scientific Reports, 2016, 6, 36767.   | 1.6  | 26        |
| 237 | A Cas9 Ribonucleoprotein Platform for Functional Genetic Studies of HIV-Host Interactions in Primary<br>Human T Cells. Cell Reports, 2016, 17, 1438-1452.  | 2.9  | 167       |
| 238 | HIV–host interactome revealed directly from infected cells. Nature Microbiology, 2016, 1, 16068.   | 5.9  | 49        |
| 239 | HIV-1 Vpr N-terminal tagging affects alternative splicing of the viral genome. Scientific Reports, 2016, 6, 34573.   | 1.6  | 9         |

| #   | Article   | IF  | Citations |
|-----|---|-----|-----------|
| 241 | Casp8p41: The Protean Mediator of Death in CD4 T-cells that Replicate HIV. Journal of Cell Death, 2016, 9, JCD.S39872.  | 0.8 | 2         |
| 242 | Heat Shock Factor 1 Mediates Latent HIV Reactivation. Scientific Reports, 2016, 6, 26294.   | 1.6 | 29        |
| 243 | Characterization of the interaction between the HIV-1 Gag structural polyprotein and the cellular ribosomal protein L7 and its implication in viral nucleic acid remodeling. Retrovirology, 2016, 13, 54. | 0.9 | 17        |
| 244 | Investigation of the HIVâ€1 matrix interactome during virus replication. Proteomics - Clinical Applications, 2016, 10, 156-163.   | 0.8 | 21        |
| 245 | <scp>HIV</scp> ″ Nef: Taking Control of Protein Trafficking. Traffic, 2016, 17, 976-996.  | 1.3 | 101       |
| 246 | Complex Interplay between HIV-1 Capsid and MX2-Independent Alpha Interferon-Induced Antiviral<br>Factors. Journal of Virology, 2016, 90, 7469-7480.   | 1.5 | 40        |
| 247 | Targeting Viral Proteostasis Limits Influenza Virus, HIV, and Dengue Virus Infection. Immunity, 2016, 44,<br>46-58.   | 6.6 | 110       |
| 248 | Making the right connections: Network biology and plant immune system dynamics. Current Plant<br>Biology, 2016, 5, 2-12.  | 2.3 | 34        |
| 249 | HSP70 binding protein 1 (HspBP1) suppresses HIV-1 replication by inhibiting NF-κB mediated activation of viral gene expression. Nucleic Acids Research, 2016, 44, 1613-1629.                              | 6.5 | 37        |
| 250 | The Dynamic Landscape of the Full-Length HIV-1 Transactivator of Transcription. Biochemistry, 2016, 55, 1314-1325.  | 1.2 | 7         |
| 251 | Proteomic approaches to uncovering virus–host protein interactions during the progression of viral infection. Expert Review of Proteomics, 2016, 13, 325-340.   | 1.3 | 76        |
| 252 | PP2A as a master regulator of the cell cycle. Critical Reviews in Biochemistry and Molecular Biology, 2016, 51, 162-184.  | 2.3 | 263       |
| 253 | Polyomavirus and Naturally Occuring Neuroglial Tumors in Raccoons (Procyon Lotor). ILAR Journal, 2016, 56, 297-305.   | 1.8 | 6         |
| 254 | Decoding protein networks during virus entry by quantitative proteomics. Virus Research, 2016, 218, 25-39.  | 1.1 | 24        |
| 255 | Identifying novel protein interactions: Proteomic methods, optimisation approaches and data analysis pipelines. Methods, 2016, 95, 46-54.   | 1.9 | 25        |
| 256 | Inter-helical conformational preferences of HIV-1 TAR-RNA from maximum occurrence analysis of NMR data and molecular dynamics simulations. Physical Chemistry Chemical Physics, 2016, 18, 5743-5752.      | 1.3 | 15        |
| 257 | Genome-Wide Analyses Reveal Gene Influence on HIV Disease Progression and HIV-1C Acquisition in Southern Africa. AIDS Research and Human Retroviruses, 2017, 33, 597-609.                                 | 0.5 | 14        |
| 258 | Role of autophagy in <scp>HIV</scp> infection and pathogenesis. Journal of Internal Medicine, 2017, 281, 422-432.   | 2.7 | 54        |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 259 | Deciphering the HIV–host interactome: overcoming the bottleneck of previous approaches. Future Virology, 2017, 12, 5-7.  | 0.9  | 0         |
| 260 | Interaction between FMDV Lpro and transcription factor ADNP is required for optimal viral replication. Virology, 2017, 505, 12-22.   | 1.1  | 19        |
| 261 | Cullin-RING E3 Ubiquitin Ligases: Bridges to Destruction. Sub-Cellular Biochemistry, 2017, 83, 323-347.  | 1.0  | 45        |
| 262 | Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. Nature Microbiology, 2017, 2, 17022.                   | 5.9  | 25        |
| 263 | Dynamics of IRES-mediated translation. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160177.  | 1.8  | 80        |
| 264 | Discovering Proteinâ€Protein Interactions Using Nucleic Acid Programmable Protein Arrays. Current<br>Protocols in Cell Biology, 2017, 74, 15.21.1-15.21.14.                | 2.3  | 11        |
| 265 | Macromolecular Protein Complexes. Sub-Cellular Biochemistry, 2017, , .   | 1.0  | 5         |
| 266 | Regulation of human immunodeficiency virus type 1 (HIV-1) mRNA translation. Biochemical Society<br>Transactions, 2017, 45, 353-364.  | 1.6  | 14        |
| 267 | Similarity in viral and host promoters couples viral reactivation with host cell migration. Nature Communications, 2017, 8, 15006.   | 5.8  | 16        |
| 268 | The RNA Exosome Syncs IAV-RNAPII Transcription to Promote Viral Ribogenesis and Infectivity. Cell, 2017, 169, 679-692.e14.   | 13.5 | 48        |
| 269 | Recent 5-year Findings and Technological Advances in the Proteomic Study of HIV-associated Disorders. Genomics, Proteomics and Bioinformatics, 2017, 15, 110-120.          | 3.0  | 9         |
| 270 | Proteomics Tracing the Footsteps of Infectious Disease. Molecular and Cellular Proteomics, 2017, 16, S5-S14.   | 2.5  | 32        |
| 271 | Proteomics and integrative omic approaches for understanding host–pathogen interactions and infectious diseases. Molecular Systems Biology, 2017, 13, 922.                 | 3.2  | 164       |
| 272 | An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. Cell, 2017, 169, 350-360.e12.  | 13.5 | 322       |
| 273 | Virus-host interactome: Putting the accent on how it changes. Journal of Proteomics, 2017, 156, 1-4.   | 1.2  | 12        |
| 274 | A genome-wide CRISPR screen identifies a restricted set of HIV host dependency factors. Nature<br>Genetics, 2017, 49, 193-203.   | 9.4  | 290       |
| 275 | Comparative interactomics for virus–human protein–protein interactions: <scp>DNA</scp> viruses<br>versus <scp>RNA</scp> viruses. FEBS Open Bio, 2017, 7, 96-107.           | 1.0  | 42        |
| 276 | Systematic Identification of Mycobacterium tuberculosis Effectors Reveals that BfrB Suppresses<br>Innate Immunity. Molecular and Cellular Proteomics, 2017, 16, 2243-2253. | 2.5  | 18        |

| #   | Article   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 277 | A systematic analysis of the RNA-targeting potential of secreted bacterial effector proteins. Scientific Reports, 2017, 7, 9328.  | 1.6 | 25        |
| 278 | Quantitative Assessment of the Effects of Trypsin Digestion Methods on Affinity Purification–Mass<br>Spectrometry-based Protein–Protein Interaction Analysis. Journal of Proteome Research, 2017, 16,<br>3068-3082. | 1.8 | 39        |
| 279 | Tandem Affinity Purification of Protein Complexes from Eukaryotic Cells. Journal of Visualized Experiments, 2017, , .   | 0.2 | 6         |
| 280 | Contribution of the clathrin adaptor AP-1 subunit µ1 to acidic cluster protein sorting. Journal of Cell<br>Biology, 2017, 216, 2927-2943.   | 2.3 | 35        |
| 281 | PJA2 ubiquitinates the HIV-1 Tat protein with atypical chain linkages to activate viral transcription.<br>Scientific Reports, 2017, 7, 45394.   | 1.6 | 30        |
| 282 | Elucidation of host–pathogen protein–protein interactions to uncover mechanisms of host cell rewiring. Current Opinion in Microbiology, 2017, 39, 7-15.   | 2.3 | 61        |
| 283 | Elucidating the in vivo interactome of HIV-1 RNA by hybridization capture and mass spectrometry.<br>Scientific Reports, 2017, 7, 16965.   | 1.6 | 36        |
| 284 | Identification of a tripartite interaction between the N-terminus of HIV-1 Vif and CBFÎ <sup>2</sup> that is critical for Vif function. Retrovirology, 2017, 14, 19.  | 0.9 | 10        |
| 285 | compleXView: a server for the interpretation of protein abundance and connectivity information to identify protein complexes. Nucleic Acids Research, 2017, 45, W276-W284.  | 6.5 | 6         |
| 286 | CD4-gp120 interaction interface - a gateway for HIV-1 infection in human: molecular network, modeling and docking studies. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2631-2644.                     | 2.0 | 5         |
| 287 | A Global Interactome Map of the Dengue Virus NS1 Identifies Virus Restriction and Dependency Host<br>Factors. Cell Reports, 2017, 21, 3900-3913.  | 2.9 | 90        |
| 288 | Mutations in the X-linked <i>ATP6AP2</i> cause a glycosylation disorder with autophagic defects.<br>Journal of Experimental Medicine, 2017, 214, 3707-3729.   | 4.2 | 62        |
| 289 | Knockdown of TBRG4 affects tumorigenesis in human H1299 lung cancer cells by regulating DDIT3, CAV1 and RRM2. Oncology Letters, 2017, 15, 121-128.  | 0.8 | 14        |
| 290 | Embraced by eIF3: structural and functional insights into the roles of eIF3 across the translation cycle. Nucleic Acids Research, 2017, 45, 10948-10968.  | 6.5 | 102       |
| 291 | Identification of HIV-1 Tat-Associated Proteins Contributing to HIV-1 Transcription and Latency.<br>Viruses, 2017, 9, 67.   | 1.5 | 18        |
| 292 | Inference of a Geminivirusâ^'Host Proteinâ^'Protein Interaction Network through Affinity Purification and Mass Spectrometry Analysis. Viruses, 2017, 9, 275.  | 1.5 | 35        |
| 293 | Influenza A Virus–Host Protein Interactions Control Viral Pathogenesis. International Journal of<br>Molecular Sciences, 2017, 18, 1673.   | 1.8 | 45        |
| 294 | Beyond Paralogs: The Multiple Layers of Redundancy in Bacterial Pathogenesis. Frontiers in Cellular and Infection Microbiology, 2017, 7, 467.   | 1.8 | 84        |

| #   | Article   | IF  | CITATIONS |
|-----|---|-----|-----------|
| 295 | Dynamics and regulation of nuclear import and nuclear movements of HIV-1 complexes. PLoS<br>Pathogens, 2017, 13, e1006570.  | 2.1 | 93        |
| 296 | Characterization of host proteins interacting with the lymphocytic choriomeningitis virus L protein.<br>PLoS Pathogens, 2017, 13, e1006758.   | 2.1 | 19        |
| 297 | A two-step framework for inferring direct protein-protein interaction network from AP-MS data. BMC<br>Systems Biology, 2017, 11, 82.  | 3.0 | 8         |
| 298 | Perturbed human sub-networks by Fusobacterium nucleatum candidate virulence proteins.<br>Microbiome, 2017, 5, 89.   | 4.9 | 27        |
| 299 | Large-Scale Arrayed Analysis of Protein Degradation Reveals Cellular Targets for HIV-1 Vpu. Cell<br>Reports, 2018, 22, 2493-2503.   | 2.9 | 21        |
| 300 | Behind the scenes of HIV-1 replication: Alternative splicing as the dependency factor on the quiet.<br>Virology, 2018, 516, 176-188.  | 1.1 | 44        |
| 301 | Proteomic profiling of HIV-infected T-cells by SWATH mass spectrometry. Virology, 2018, 516, 246-257.   | 1.1 | 6         |
| 302 | A path to the powerhouse: systemsâ€toâ€structure approaches for studying mitochondrial proteins.<br>Protein Science, 2018, 27, 1518-1525.   | 3.1 | 0         |
| 303 | Vaccine Efforts Against AIDS. , 2018, , 2139-2149.  |     | 0         |
| 304 | DDX49 is an RNA helicase that affects translation by regulating mRNA export and the levels of pre-ribosomal RNA. Nucleic Acids Research, 2018, 46, 6304-6317.   | 6.5 | 29        |
| 305 | Cellular and molecular mechanisms of HIV-1 integration targeting. Cellular and Molecular Life Sciences, 2018, 75, 2491-2507.  | 2.4 | 53        |
| 306 | Nef Secretion into Extracellular Vesicles or Exosomes Is Conserved across Human and Simian<br>Immunodeficiency Viruses. MBio, 2018, 9, .  | 1.8 | 84        |
| 307 | Multiple Inhibitory Factors Act in the Late Phase of HIV-1 Replication: a Systematic Review of the<br>Literature. Microbiology and Molecular Biology Reviews, 2018, 82, .                                   | 2.9 | 10        |
| 308 | <scp>DNA</scp> â€damage inducible protein 1 is a conserved metacaspase substrate that is cleaved and further destabilized in yeast under specific metabolic conditions. FEBS Journal, 2018, 285, 1097-1110. | 2.2 | 10        |
| 309 | Systems Biology Modeling to Study Pathogen–Host Interactions. Methods in Molecular Biology, 2018,<br>1734, 97-112.  | 0.4 | 13        |
| 310 | A decade of RNA virus metagenomics is (not) enough. Virus Research, 2018, 244, 218-229.   | 1.1 | 129       |
| 311 | Viral internal ribosomal entry sites: four classes for one goal. Wiley Interdisciplinary Reviews RNA, 2018, 9, e1458.   | 3.2 | 83        |
| 312 | The role of exosomal transport of viral agents in persistent HIV pathogenesis. Retrovirology, 2018, 15, 79.   | 0.9 | 33        |

|     |  | CITATION R        | EPORT |           |
|-----|--|-------------------|-------|-----------|
| #   | Article  |                   | IF    | CITATIONS |
| 313 | Mosquito Transmission of HIV: Rare or Not Possible?. Parasitology Research Monograph   | s, 2018, , 9-21.  | 0.4   | 0         |
| 314 | Protein Interaction Mapping Identifies RBBP6 as a Negative Regulator of Ebola Virus Rep<br>2018, 175, 1917-1930.e13.   | blication. Cell,  | 13.5  | 108       |
| 315 | Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengu<br>Pathogenesis. Cell, 2018, 175, 1931-1945.e18.   | ie and Zika Virus | 13.5  | 252       |
| 316 | Integrating Multifaceted Information to Predict <i>Mycobacterium tuberculosis</i> Hur<br>Protein-Protein Interactions. Journal of Proteome Research, 2018, 17, 3810-3823.                      | nan               | 1.8   | 8         |
| 317 | Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus–Host Pro<br>Cancer Discovery, 2018, 8, 1474-1489.  | otein Network.    | 7.7   | 67        |
| 318 | Virus–Host Interactions in Retrovirus Integration. , 2018, , 163-198.  |                   |       | 8         |
| 319 | Cellular RNA Helicases Support Early and Late Events in Retroviral Replication. , 2018, , 2  | 253-271.          |       | 1         |
| 320 | Strategies to Discover Novel Cellular Factors Involved in Retrovirus Replication. , 2018, ,  | .527-568.         |       | 0         |
| 321 | Systematic detection of positive selection in the human-pathogen interactome and last infectious disease susceptibility. PLoS ONE, 2018, 13, e0196676.   | ing effects on    | 1.1   | 7         |
| 322 | CRL4 <sup>AMBRA1</sup> targets Elongin C for ubiquitination and degradation to mo signaling. EMBO Journal, 2018, 37, .   | dulate CRL5       | 3.5   | 13        |
| 323 | Understanding mucosal and microbial functionality of the female reproductive tract by metaproteomics: Implications for HIV transmission. American Journal of Reproductive In 2018, 80, e12977. | nmunology,        | 1.2   | 12        |
| 324 | Smc5/6 Antagonism by HBx Is an Evolutionarily Conserved Function of Hepatitis B Virus<br>Mammals. Journal of Virology, 2018, 92, .   | Infection in      | 1.5   | 34        |
| 325 | Gp41 dynamically interacts with the TCR in the immune synapse and promotes early T c Scientific Reports, 2018, 8, 9747.  | ell activation.   | 1.6   | 8         |
| 326 | Viral journeys on the intracellular highways. Cellular and Molecular Life Sciences, 2018,  | 75, 3693-3714.    | 2.4   | 70        |
| 327 | The Psychiatric Cell Map Initiative: A Convergent Systems Biological Approach to Illumin<br>Molecular Pathways in Neuropsychiatric Disorders. Cell, 2018, 174, 505-520.                        | lating Key        | 13.5  | 108       |
| 328 | Host Interaction Analysis of PA-N155 and PA-N182 in Chicken Cells Reveals an Essential for Replication of H5N1 Avian Influenza Virus. Frontiers in Microbiology, 2018, 9, 936.                 | Role of UBA52     | 1.5   | 13        |
| 329 | Structural Hole Spanner in HumanNet Identifies Disease Gene and Drug targets. IEEE Ac 35392-35401.   | cess, 2018, 6,    | 2.6   | 3         |
| 330 | Y-box-binding protein 1 supports the early and late steps of HIV replication. PLoS ONE, 2 e0200080.  | 2018, 13,         | 1.1   | 11        |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 331 | An Mtb-Human Protein-Protein Interaction Map Identifies a Switch between Host Antiviral and<br>Antibacterial Responses. Molecular Cell, 2018, 71, 637-648.e5.  | 4.5  | 100       |
| 332 | Unconventional RNAâ€binding proteins step into the virus–host battlefront. Wiley Interdisciplinary<br>Reviews RNA, 2018, 9, e1498.   | 3.2  | 65        |
| 333 | Defining Pharmacological Targets by Analysis of Virus–Host Protein Interactions. Advances in Protein<br>Chemistry and Structural Biology, 2018, 111, 223-242.  | 1.0  | 3         |
| 334 | Design of Tat-Activated Cdk9 Inhibitor. International Journal of Peptide Research and Therapeutics, 2019, 25, 807-817.   | 0.9  | 7         |
| 335 | Genome Analysis – Identification of Genes Involved in Host-Pathogen Protein-Protein Interaction<br>Networks. , 2019, , 410-424.  |      | 0         |
| 336 | Network-Based Analysis of Host-Pathogen Interactions. , 2019, , 932-937.   |      | 2         |
| 337 | Ring finger protein 121 is a potent regulator of adeno-associated viral genome transcription. PLoS<br>Pathogens, 2019, 15, e1007988.   | 2.1  | 22        |
| 338 | Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation<br>Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPKα2 Interactome. Journal of<br>Proteome Research, 2019, 18, 3703-3714. | 1.8  | 6         |
| 339 | ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. Cell Host and Microbe, 2019, 26, 86-99.e7.  | 5.1  | 42        |
| 340 | Host factor heat-shock protein 90 contributes to baculovirus budded virus morphogenesis via facilitating nuclear actin polymerization. Virology, 2019, 535, 200-209.   | 1.1  | 7         |
| 341 | Analysis of networks of host proteins in the early time points following HIV transduction. BMC Bioinformatics, 2019, 20, 398.  | 1.2  | 10        |
| 342 | TOX transcriptionally and epigenetically programs CD8+ T cell exhaustion. Nature, 2019, 571, 211-218.  | 13.7 | 934       |
| 343 | The autophagy protein ATG9A promotes HIV-1 infectivity. Retrovirology, 2019, 16, 18.   | 0.9  | 10        |
| 344 | Common Nodes of Virus–Host Interaction Revealed Through an Integrated Network Analysis.<br>Frontiers in Immunology, 2019, 10, 2186.  | 2.2  | 67        |
| 345 | How HIV Nef Proteins Hijack Membrane Traffic To Promote Infection. Journal of Virology, 2019, 93, .  | 1.5  | 41        |
| 346 | Synthetic Essentiality of Metabolic Regulator PDHK1 in PTEN-Deficient Cells and Cancers. Cell Reports, 2019, 28, 2317-2330.e8.   | 2.9  | 12        |
| 347 | Multifaceted HIV integrase functionalities and therapeutic strategies for their inhibition. Journal of<br>Biological Chemistry, 2019, 294, 15137-15157.  | 1.6  | 57        |
| 348 | A Structure-Informed Atlas of Human-Virus Interactions. Cell, 2019, 178, 1526-1541.e16.  | 13.5 | 108       |

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 349 | Mapping Interactome Networks of DNAJC11, a Novel Mitochondrial Protein Causing Neuromuscular Pathology in Mice. Journal of Proteome Research, 2019, 18, 3896-3912.   | 1.8 | 6         |
| 350 | Role of host tRNAs and aminoacyl-tRNA synthetases in retroviral replication. Journal of Biological<br>Chemistry, 2019, 294, 5352-5364.   | 1.6 | 34        |
| 351 | CRISPR-Based Tools in Immunity. Annual Review of Immunology, 2019, 37, 571-597.  | 9.5 | 38        |
| 352 | HIV-1 Nef and host proteome analysis: Current perspective. Life Sciences, 2019, 219, 322-328.  | 2.0 | 6         |
| 353 | Virus-Like Particles as an Instrument of Vaccine Production. Molecular Biology, 2019, 53, 323-334.   | 0.4 | 62        |
| 354 | Two Accessory Proteins Govern MmpL3 Mycolic Acid Transport in Mycobacteria. MBio, 2019, 10, .  | 1.8 | 32        |
| 355 | A CRISPR/Cas9 screen identifies the histone demethylase MINA53 as a novel HIV-1 latency-promoting gene (LPG). Nucleic Acids Research, 2019, 47, 7333-7347.   | 6.5 | 35        |
| 356 | Tat inhibition by didehydro-Cortistatin A promotes heterochromatin formation at the HIV-1 long terminal repeat. Epigenetics and Chromatin, 2019, 12, 23.   | 1.8 | 46        |
| 357 | Reduced eIF3d accelerates HIV disease progression by attenuating CD8+ T cell function. Journal of Translational Medicine, 2019, 17, 167.   | 1.8 | 7         |
| 358 | Destabilization of the human RED–SMU1 splicing complex as a basis for host-directed antiinfluenza<br>strategy. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116,<br>10968-10977. | 3.3 | 7         |
| 359 | Understanding Human-Virus Protein-Protein Interactions Using a Human Protein Complex-Based<br>Analysis Framework. MSystems, 2019, 4, .   | 1.7 | 42        |
| 360 | How host genetics dictates successful viral zoonosis. PLoS Biology, 2019, 17, e3000217.  | 2.6 | 59        |
| 361 | Considerations for Identifying Endogenous Protein Complexes from Tissue via Immunoaffinity<br>Purification and Quantitative Mass Spectrometry. Methods in Molecular Biology, 2019, 1977, 115-143.                          | 0.4 | 5         |
| 362 | Experimental Analysis of Viral–Host Interactions. Frontiers in Physiology, 2019, 10, 425.  | 1.3 | 22        |
| 363 | Promiscuous Targeting of Cellular Proteins by Vpr Drives Systems-Level Proteomic Remodeling in HIV-1<br>Infection. Cell Reports, 2019, 27, 1579-1596.e7.   | 2.9 | 75        |
| 364 | Anti-virus reagents targeting the capsid protein assembly. Journal of Materials Chemistry B, 2019, 7, 3331-3340.   | 2.9 | 2         |
| 365 | Identification of antiviral roles for the exon–junction complex and nonsense-mediated decay in flaviviral infection. Nature Microbiology, 2019, 4, 985-995.  | 5.9 | 52        |
| 366 | A Two-Way Proteome Microarray Strategy to Identify Novel Mycobacterium tuberculosis-Human<br>Interactors. Frontiers in Cellular and Infection Microbiology, 2019, 9, 65.   | 1.8 | 4         |

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 367 | G protein-coupled and ATP-sensitive inwardly rectifying potassium ion channels are essential for HIV entry. Scientific Reports, 2019, 9, 4113.                                       | 1.6 | 13        |
| 368 | Conformational Dynamics of the HIV-Vif Protein Complex. Biophysical Journal, 2019, 116, 1432-1445.   | 0.2 | 8         |
| 369 | Highly Mutable Linker Regions Regulate HIV-1 Rev Function and Stability. Scientific Reports, 2019, 9, 5139.  | 1.6 | 14        |
| 370 | Inferring pathogen-host interactions between Leptospira interrogans and Homo sapiens using network theory. Scientific Reports, 2019, 9, 1434.  | 1.6 | 20        |
| 371 | Enterovirus pathogenesis requires the host methyltransferase SETD3. Nature Microbiology, 2019, 4, 2523-2537.   | 5.9 | 51        |
| 372 | Virus and host interactions critical for filoviral RNA synthesis as therapeutic targets. Antiviral Research, 2019, 162, 90-100.  | 1.9 | 12        |
| 373 | Focus on Translation Initiation of the HIV-1 mRNAs. International Journal of Molecular Sciences, 2019, 20, 101.  | 1.8 | 28        |
| 374 | Interface-Based Structural Prediction of Novel Host-Pathogen Interactions. Methods in Molecular<br>Biology, 2019, 1851, 317-335.   | 0.4 | 21        |
| 375 | Reinforce: An Ensemble Approach for Inferring PPI Network from AP-MS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 365-376.                     | 1.9 | 2         |
| 376 | Cellular roles of the human Obg-like ATPase 1 (hOLA1) and its YchF homologs. Biochemistry and Cell<br>Biology, 2020, 98, 1-11.   | 0.9 | 7         |
| 377 | Protein-protein interactions of human viruses. Seminars in Cell and Developmental Biology, 2020, 99, 31-39.  | 2.3 | 34        |
| 378 | The functional landscape of the human phosphoproteome. Nature Biotechnology, 2020, 38, 365-373.  | 9.4 | 273       |
| 379 | Fluorescence "Turn-on―Lectin Sensors Fabricated by Ligand-Assisted Labeling Probes for Detecting<br>Protein–Glycoprotein Interactions. Biomacromolecules, 2020, 21, 815-824.         | 2.6 | 3         |
| 380 | Novel association of genetic variants in non-coding regulatory regions with HIV-1 infection.<br>Infection, Genetics and Evolution, 2020, 85, 104514.                                 | 1.0 | 1         |
| 381 | System-Based Approaches to Delineate the Antiviral Innate Immune Landscape. Viruses, 2020, 12, 1196.   | 1.5 | 5         |
| 382 | Zinc and Copper Ions Differentially Regulate Prion-Like Phase Separation Dynamics of Pan-Virus<br>Nucleocapsid Biomolecular Condensates. Viruses, 2020, 12, 1179.                    | 1.5 | 34        |
| 383 | A computational study of Tat–CDK9–Cyclin binding dynamics and its implication in<br>transcription-dependent HIV latency. Physical Chemistry Chemical Physics, 2020, 22, 25474-25482. | 1.3 | 8         |
| 384 | Comparative host-coronavirus protein interaction networks reveal pan-viral disease mechanisms.<br>Science, 2020, 370, .  | 6.0 | 508       |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 385 | Vpu modulates DNA repair to suppress innate sensing and hyper-integration of HIV-1. Nature Microbiology, 2020, 5, 1247-1261.   | 5.9  | 22        |
| 386 | Ubiquitin E3 Ligase c-Cbl Is a Host Negative Regulator of Nef Protein of HIV-1. Frontiers in<br>Microbiology, 2020, 11, 597972.  | 1.5  | 3         |
| 387 | Modelling of pathogen-host systems using deeper ORF annotations and transcriptomics to inform proteomics analyses. Computational and Structural Biotechnology Journal, 2020, 18, 2836-2850.                            | 1.9  | 7         |
| 388 | A phosphorylation-regulated elF3d translation switch mediates cellular adaptation to metabolic stress. Science, 2020, 370, 853-856.  | 6.0  | 68        |
| 389 | The E3 Ubiquitin-Protein Ligase Cullin 3 Regulates HIV-1 Transcription. Cells, 2020, 9, 2010.  | 1.8  | 5         |
| 390 | Multiplexed Proximity Biotinylation Coupled to Mass Spectrometry for Defining Integrin Adhesion<br>Complexes. Current Protocols in Cell Biology, 2020, 88, e113.   | 2.3  | 4         |
| 391 | Structure, function, and inhibitor targeting of HIV-1 Nef-effector kinase complexes. Journal of<br>Biological Chemistry, 2020, 295, 15158-15171.   | 1.6  | 34        |
| 392 | How HIV-1 Gag Manipulates Its Host Cell Proteins: A Focus on Interactors of the Nucleocapsid Domain.<br>Viruses, 2020, 12, 888.  | 1.5  | 7         |
| 393 | Retroviral Restriction Factors and Their Viral Targets: Restriction Strategies and Evolutionary<br>Adaptations. Microorganisms, 2020, 8, 1965.   | 1.6  | 21        |
| 394 | HIV-1 Proviral Transcription and Latency in the New Era. Viruses, 2020, 12, 555.   | 1.5  | 29        |
| 395 | Endoplasmic Reticulum Calcium Pumps and Tumor Cell Differentiation. International Journal of<br>Molecular Sciences, 2020, 21, 3351.  | 1.8  | 13        |
| 396 | HSF1 Activation Can Restrict HIV Replication. ACS Infectious Diseases, 2020, 6, 1659-1666.   | 1.8  | 6         |
| 398 | Very-long-chain fatty acid metabolic capacity of 17-beta-hydroxysteroid dehydrogenase type 12<br>(HSD17B12) promotes replication of hepatitis C virus and related flaviviruses. Scientific Reports, 2020,<br>10, 4040. | 1.6  | 20        |
| 399 | A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. Nature, 2020, 583, 459-468.   | 13.7 | 3,542     |
| 400 | Human Virus Transcriptional Regulators. Cell, 2020, 182, 24-37.  | 13.5 | 52        |
| 401 | Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteria–human protein interactions. Medical Microbiology and Immunology, 2020, 209, 265-275.                                    | 2.6  | 13        |
| 402 | A Quantitative Genetic Interaction Map of HIV Infection. Molecular Cell, 2020, 78, 197-209.e7.   | 4.5  | 17        |
| 403 | HIV protease cleaves the antiviral m6A reader protein YTHDF3 in the viral particle. PLoS Pathogens, 2020, 16, e1008305.  | 2.1  | 40        |

|     | CITATION R   | EPORT |           |
|-----|--|-------|-----------|
| #   | Article  | IF    | CITATIONS |
| 404 | A systems approach to infectious disease. Nature Reviews Genetics, 2020, 21, 339-354.  | 7.7   | 72        |
| 405 | The Multifarious Role of 14-3-3 Family of Proteins in Viral Replication. Viruses, 2020, 12, 436.   | 1.5   | 24        |
| 406 | Deciphering cell–cell interactions and communication from gene expression. Nature Reviews<br>Genetics, 2021, 22, 71-88.  | 7.7   | 575       |
| 407 | HIV p17 enhances T cell proliferation by suppressing autophagy through the p17â€OLA1â€CSK3β axis under nutrient starvation. Journal of Medical Virology, 2021, 93, 3607-3620.  | 2.5   | 2         |
| 408 | Affinity and chemical enrichment strategies for mapping lowâ€abundance protein modifications and proteinâ€interaction networks. Journal of Separation Science, 2021, 44, 310-322.  | 1.3   | 6         |
| 409 | Identifying and Validating MYC:Protein Interactors in Pursuit of Novel Anti-MYC Therapies. Methods in<br>Molecular Biology, 2021, 2318, 45-67.   | 0.4   | 0         |
| 410 | Proteomic Approaches to Study SARS-CoV-2 Biology and COVID-19 Pathology. Journal of Proteome Research, 2021, 20, 1133-1152.  | 1.8   | 27        |
| 411 | Mass spectrometryâ€based protein–protein interaction networks for the study of human diseases.<br>Molecular Systems Biology, 2021, 17, e8792.  | 3.2   | 96        |
| 413 | Mass spectrometry-based protein-protein interaction techniques and their applications in studies of DNA damage repair. Journal of Zhejiang University: Science B, 2021, 22, 1-20.  | 1.3   | 3         |
| 414 | Proteomics approaches for the identification of protease substrates during virus infection. Advances in Virus Research, 2021, 109, 135-161.  | 0.9   | 5         |
| 415 | Characterization of an A3G-VifHIV-1-CRL5-CBFβ Structure Using a Cross-linking Mass Spectrometry<br>Pipeline for Integrative Modeling of Host–Pathogen Complexes. Molecular and Cellular Proteomics,<br>2021, 20, 100132.   | 2.5   | 4         |
| 416 | Virus systems biology: Proteomics profiling of dynamic protein networks during infection. Advances in Virus Research, 2021, 109, 1-29.   | 0.9   | 5         |
| 419 | Mapping the SARS-CoV-2–Host Protein–Protein Interactome by Affinity Purification Mass Spectrometry<br>and Proximity-Dependent Biotin Labeling: A Rational and Straightforward Route to Discover<br>Host-Directed Anti-SARS-CoV-2 Therapeutics. International Journal of Molecular Sciences, 2021, 22, 532. | 1.8   | 38        |
| 420 | An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. Genomics, Proteomics and Bioinformatics, 2021, 19, 108-122.   | 3.0   | 7         |
| 421 | Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. Journal of Proteome<br>Research, 2021, 20, 1464-1475.   | 1.8   | 11        |
| 422 | Human Paraoxonase-2 (PON2): Protein Functions and Modulation. Antioxidants, 2021, 10, 256.   | 2.2   | 37        |
| 424 | Identification of Ku70 Domain-Specific Interactors Using BioID2. Cells, 2021, 10, 646.   | 1.8   | 2         |
| 425 | Interactions of HIV-1 Capsid with Host Factors and Their Implications for Developing Novel Therapeutics. Viruses, 2021, 13, 417.   | 1.5   | 22        |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 427 | Current status and future perspectives of computational studies on human–virus protein–protein<br>interactions. Briefings in Bioinformatics, 2021, 22, .   | 3.2  | 17        |
| 428 | InÂvivo structural characterization of the SARS-CoV-2 RNA genome identifies host proteins vulnerable to repurposed drugs. Cell, 2021, 184, 1865-1883.e20.  | 13.5 | 153       |
| 429 | Viral–Host Interactome Analysis Reveals Chicken STAU2 Interacts With Non-structural Protein 1 and Promotes the Replication of H5N1 Avian Influenza Virus. Frontiers in Immunology, 2021, 12, 590679. | 2.2  | 5         |
| 430 | Discrimination between Functional and Non-functional Cellular Gag Complexes involved in HIV-1<br>Assembly. Journal of Molecular Biology, 2021, 433, 166842.  | 2.0  | 8         |
| 432 | Viral Interactions with Adaptor-Protein Complexes: A Ubiquitous Trait among Viral Species.<br>International Journal of Molecular Sciences, 2021, 22, 5274.   | 1.8  | 6         |
| 434 | Identification of recombinant Fabs for structural and functional characterization of HIV-host factor complexes. PLoS ONE, 2021, 16, e0250318.  | 1.1  | 0         |
| 435 | The peripheral and core regions of virus-host network of COVID-19. Briefings in Bioinformatics, 2021, 22, .  | 3.2  | 3         |
| 438 | The RNA-Binding Proteins SRP14 and HMGB3 Control HIV-1 Tat mRNA Processing and Translation During HIV-1 Latency. Frontiers in Genetics, 2021, 12, 680725.  | 1.1  | 7         |
| 439 | Discovery of candidate HIV-1 latency biomarkers using an OMICs approach. Virology, 2021, 558, 86-95.   | 1.1  | 2         |
| 440 | Molecular signatures of silencing suppression degeneracy from a complex RNA virus. PLoS<br>Computational Biology, 2021, 17, e1009166.  | 1.5  | 3         |
| 442 | Flavonoids as Promising Antiviral Agents against SARS-CoV-2 Infection: A Mechanistic Review.<br>Molecules, 2021, 26, 3900.   | 1.7  | 43        |
| 443 | Synergistic Chromatin-Modifying Treatments Reactivate Latent HIV and Decrease Migration of Multiple<br>Host-Cell Types. Viruses, 2021, 13, 1097.   | 1.5  | 3         |
| 444 | Human Immunodeficiency Virus Type 1 Vpr Mediates Degradation of APC1, a Scaffolding Component of the Anaphase-Promoting Complex/Cyclosome. Journal of Virology, 2021, 95, e0097120.                  | 1.5  | 2         |
| 445 | An atlas of protein-protein interactions across mouse tissues. Cell, 2021, 184, 4073-4089.e17.   | 13.5 | 59        |
| 446 | Global mapping of Salmonella enterica-host protein-protein interactions during infection. Cell Host and Microbe, 2021, 29, 1316-1332.e12.  | 5.1  | 39        |
| 447 | Interactome Analysis of the Nucleocapsid Protein of SARS-CoV-2 Virus. Pathogens, 2021, 10, 1155.   | 1.2  | 25        |
| 448 | Candidate host epigenetic marks predictive for HIV reservoir size, responsiveness to latency reversal, and viral rebound. Aids, 2021, 35, 2269-2279.   | 1.0  | 6         |
| 449 | Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy.<br>Nature Microbiology, 2021, 6, 1319-1333.  | 5.9  | 23        |

| #   | Article   | IF   | CITATIONS |
|-----|---|------|-----------|
| 450 | Interactome Networks of FOSL1 and FOSL2 in Human Th17 Cells. ACS Omega, 2021, 6, 24834-24847.   | 1.6  | 6         |
| 451 | Quantitative Temporal Viromics. Annual Review of Virology, 2021, 8, 159-181.  | 3.0  | 5         |
| 452 | Target Discovery for Host-Directed Antiviral Therapies: Application of Proteomics Approaches.<br>MSystems, 2021, 6, e0038821.   | 1.7  | 10        |
| 453 | Integration of Mass Spectrometry Data for Structural Biology. Chemical Reviews, 2022, 122, 7952-7986.   | 23.0 | 36        |
| 454 | STUB1/CHIP promotes ubiquitination and degradation of HIV-1 Vif to restore the cellular level of APOBEC3G protein. Biochemical and Biophysical Research Communications, 2021, 574, 27-32.   | 1.0  | 3         |
| 455 | A protein network map of head and neck cancer reveals PIK3CA mutant drug sensitivity. Science, 2021, 374, eabf2911.   | 6.0  | 37        |
| 457 | Tandem Affinity Purification and Mass Spectrometry (TAPâ€MS) for the Analysis of Protein Complexes.<br>Current Protocols in Protein Science, 2019, 96, e84.   | 2.8  | 17        |
| 458 | Human Acute and Chronic Viruses: Host-Pathogen Interactions and Therapeutics. , 2020, , 1-120.  |      | 3         |
| 459 | The TRiC/CCT Chaperonin and Its Role in Uncontrolled Proliferation. Advances in Experimental Medicine and Biology, 2020, 1243, 21-40.   | 0.8  | 21        |
| 460 | Drug Resistance to HIV-1 Protease Inhibitors: Molecular Mechanisms and Substrate Coevolution. , 2017, , 535-544.  |      | 5         |
| 461 | Proteomics Defines Protein Interaction Network of Signaling Pathways. Translational Bioinformatics, 2013, , 17-38.  | 0.0  | 1         |
| 462 | Diverse Mechanisms of Translation Regulation and Their Role in Cancer. , 2014, , 39-71.   |      | 2         |
| 463 | KAP1 Is a Chromatin Reader that Couples Steps of RNA Polymerase II Transcription to Sustain<br>Oncogenic Programs. Molecular Cell, 2020, 78, 1133-1151.e14.   | 4.5  | 26        |
| 464 | Evolution toward beta common chain receptor usage links the matrix proteins of HIV-1 and its ancestors to human erythropoietin. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2021366118.                    | 3.3  | 4         |
| 465 | Nef homodimers down-regulate SERINC5 by AP-2–mediated endocytosis to promote HIV-1 infectivity.<br>Journal of Biological Chemistry, 2020, 295, 15540-15552.   | 1.6  | 15        |
| 466 | HIV Rev-isited. Open Biology, 2020, 10, 200320.   | 1.5  | 20        |
| 467 | Pre-infection transcript levels of FAM26F in peripheral blood mononuclear cells inform about<br>overall plasma viral load in acute and post-acute phase after simian immunodeficiency virus infection.<br>Journal of General Virology, 2016, 97, 3400-3412. | 1.3  | 5         |
| 468 | Deployment of the human immunodeficiency virus type 1 protein arsenal: combating the host to enhance viral transcription and providing targets for therapeutic development. Journal of General Virology, 2012, 93, 1151-1172.                               | 1.3  | 8         |

|     |   | CITATION REPORT  |     |           |
|-----|---|------------------|-----|-----------|
| #   | Article   |                  | IF  | CITATIONS |
| 478 | Host Factors in Retroviral Integration and the Selection of Integration Target Sites. , 0, ,  | 1035-1050.       |     | 2         |
| 479 | Efficient SIVcpz replication in human lymphoid tissue requires viral matrix protein adapt of Clinical Investigation, 2012, 122, 1644-1652.                            | ation. Journal   | 3.9 | 44        |
| 480 | Stem-loop binding protein is a multifaceted cellular regulator of HIV-1 replication. Journa<br>Investigation, 2016, 126, 3117-3129.                                   | al of Clinical   | 3.9 | 5         |
| 481 | enhancedGraphics: a Cytoscape app for enhanced node graphics. F1000Research, 2014   | , 3, 147.        | 0.8 | 45        |
| 482 | Systems Biology-Based Investigation of Cellular Antiviral Drug Targets Identified by Gene<br>Insertional Mutagenesis. PLoS Computational Biology, 2016, 12, e1005074. | e-Trap           | 1.5 | 52        |
| 483 | Structural host-microbiota interaction networks. PLoS Computational Biology, 2017, 13   | s, e1005579.     | 1.5 | 51        |
| 484 | Brain Transcriptome-Wide Screen for HIV-1 Nef Protein Interaction Partners Reveals Vari<br>Membrane-Associated Proteins. PLoS ONE, 2012, 7, e51578.                   | ous              | 1.1 | 19        |
| 485 | Investigating the Cellular Distribution and Interactions of HIV-1 Nucleocapsid Protein by Fluorescence Microscopy. PLoS ONE, 2015, 10, e0116921.                      | Quantitative     | 1.1 | 20        |
| 486 | Uncovering New Pathogen–Host Protein–Protein Interactions by Pairwise Structure<br>ONE, 2016, 11, e0147612.   | Similarity. PLoS | 1.1 | 13        |
| 487 | HIV-1 Protease in the Fission Yeast Schizosaccharomyces pombe. PLoS ONE, 2016, 11, o  | e0151286.        | 1.1 | 15        |
| 488 | Hepatitis C Virus Protein Interaction Network Analysis Based on Hepatocellular Carcinor 2016, 11, e0153882.   | na. PLoS ONE,    | 1.1 | 9         |
| 489 | Comparative Proteomics Reveals Strain-Specific β-TrCP Degradation via Rotavirus NSP1<br>Cullin-3-Rbx1 Complex. PLoS Pathogens, 2016, 12, e1005929.                    | Hijacking a Host | 2.1 | 59        |
| 490 | Optimization And ZSPORE Analysis Of Affinity Purification Coupled With Tandem Mass Mammalian Cells. Journal of Proteomics and Genomics Research, 2012, 1, 9-20.       | Spectrometry In  | 0.7 | 2         |
| 491 | An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Jour   | rnal, O, , .     | 0.4 | 8         |
| 492 | Targeting Virus-host Interactions of HIV Replication. Current Topics in Medicinal Chemis 1167-1190.   | try, 2015, 16,   | 1.0 | 14        |
| 493 | Manipulation of the host protein acetylation network by human immunodeficiency virus<br>Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 314-25.     | s type 1.        | 2.3 | 16        |
| 494 | The AFF4 scaffold binds human P-TEFb adjacent to HIV Tat. ELife, 2013, 2, e00327.   |                  | 2.8 | 65        |
| 495 | How HIV-1 Nef hijacks the AP-2 clathrin adaptor to downregulate CD4. ELife, 2014, 3, e  | 01754.           | 2.8 | 102       |

| #   | Article   | IF   | CITATIONS |
|-----|---|------|-----------|
| 496 | AFF4 binding to Tat-P-TEFb indirectly stimulates TAR recognition of super elongation complexes at the HIV promoter. ELife, 2014, 3, e02375.           | 2.8  | 45        |
| 497 | Viruses are a dominant driver of protein adaptation in mammals. ELife, 2016, 5, .   | 2.8  | 267       |
| 498 | Suppression of C9orf72 RNA repeat-induced neurotoxicity by the ALS-associated RNA-binding protein Zfp106. ELife, 2017, 6, .                           | 2.8  | 44        |
| 499 | Chlamydia interfere with an interaction between the mannose-6-phosphate receptor and sorting nexins to counteract host restriction. ELife, 2017, 6, . | 2.8  | 61        |
| 500 | The HIV-1 Tat protein recruits a ubiquitin ligase to reorganize the 7SK snRNP for transcriptional activation. ELife, 2018, 7, .                       | 2.8  | 29        |
| 501 | Cellular Proteo-Transcriptomic Changes in the Immediate Early-Phase of Lentiviral Transduction.<br>Microorganisms, 2021, 9, 2207.                     | 1.6  | 4         |
| 502 | Systems-level effects of allosteric perturbations to a model molecular switch. Nature, 2021, 599, 152-157.  | 13.7 | 13        |
| 504 | tRNA Primer Sequestration as an Antiviral Strategy. , 2013, , 205-221.  |      | 0         |
| 505 | Systems Biology. , 2013, , 1-9.   |      | 0         |
| 506 | Cellular Trafficking Mechanisms in the Assembly and Release of HIV. , 2013, , 23-53.  |      | 2         |
| 507 | DDX3, Cofactors, and RNA Export. , 2013, , 1-4.   |      | 0         |
| 508 | Identification and Validation of HIV Cofactors. , 2013, , 1-6.  |      | 0         |
| 510 | Sphingoproteomics: Proteomic Strategies to Examine Sphingolipid Biology. , 2015, , 359-384.   |      | 0         |
| 511 | Viral Fitness in Hosts. , 2015, , 1-11.   |      | 0         |
| 514 | Proteomic Studies of HIV-1., 2016,, 39-58.  |      | 0         |
| 517 | HIV Life Cycle: Overview. , 2018, , 722-730.  |      | 0         |
| 518 | Systems Biology. , 2018, , 1949-1956.   |      | 0         |
| 519 | Viral Fitness in Hosts. , 2018, , 2150-2158.  |      | 0         |

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 520 | Identification and Validation of HIV Cofactors. , 2018, , 1043-1047.   |     | 0         |
| 521 | Cellular Cofactors of HIV as Drug Targets. , 2018, , 253-259.  |     | 0         |
| 522 | DDX3, Cofactors, and RNA Export. , 2018, , 437-439.  |     | 0         |
| 527 | A Structure Informed Atlas of Pan-Viral Interactions Reveals Features of Human Infection. SSRN<br>Electronic Journal, 0, , .   | 0.4 | 0         |
| 532 | Human Gene Functional Network-Informed Prediction of HIV-1 Host Dependency Factors. MSystems, 2020, 5, .   | 1.7 | 4         |
| 533 | Protein–Protein Interaction Networks in Human Disease. RSC Drug Discovery Series, 2020, , 25-48.   | 0.2 | 0         |
| 536 | From Molecular Recognition to the "Vehicles―of Evolutionary Complexity: An Informational<br>Approach. International Journal of Molecular Sciences, 2021, 22, 11965.      | 1.8 | 8         |
| 537 | Comparison of viral RNA–host protein interactomes across pathogenic RNA viruses informs rapid<br>antiviral drug discovery for SARS-CoV-2. Cell Research, 2022, 32, 9-23. | 5.7 | 55        |
| 539 | Eukaryotic translation initiation factor 3 subunit G promotes human colorectal cancer. American<br>Journal of Translational Research (discontinued), 2019, 11, 612-623.  | 0.0 | 6         |
| 540 | Huntingtin-Interacting Protein 1 Promotes Vpr-Induced G2 Arrest and HIV-1 Infection in Macrophages.<br>Viruses, 2021, 13, 2308.  | 1.5 | 3         |
| 541 | A combined EM and proteomic analysis places HIV-1 Vpu at the crossroads of retromer and ESCRT complexes: PTPN23 is a Vpu-cofactor. PLoS Pathogens, 2021, 17, e1009409.   | 2.1 | 0         |
| 542 | A 3D structural SARS-CoV-2–human interactome to explore genetic and drug perturbations. Nature<br>Methods, 2021, 18, 1477-1488.  | 9.0 | 17        |
| 544 | Comparative Analysis of T-Cell Spatial Proteomics and the Influence of HIV Expression. Molecular and Cellular Proteomics, 2022, 21, 100194.                              | 2.5 | 2         |
| 545 | From systems to structure — using genetic data to model protein structures. Nature Reviews<br>Genetics, 2022, 23, 342-354.   | 7.7 | 14        |
| 546 | The biological information flow: From cell theory to a new evolutionary synthesis. BioSystems, 2022, 213, 104631.  | 0.9 | 5         |
| 547 | Next-Generation Sequencing for Confronting Virus Pandemics. Viruses, 2022, 14, 600.  | 1.5 | 24        |
| 548 | A point mutation in HIV-1 integrase redirects proviral integration into centromeric repeats. Nature<br>Communications, 2022, 13, 1474.                                   | 5.8 | 6         |
| 549 | Circular RNA Profiles in Viremia and ART Suppression Predict Competing circRNA–miRNA–mRNA<br>Networks Exclusive to HIV-1 Viremic Patients. Viruses, 2022, 14, 683.       | 1.5 | 3         |

| #   | Article  | IF   | CITATIONS |
|-----|--|------|-----------|
| 551 | The E3 ligase TRIM1 ubiquitinates LRRK2 and controls its localization, degradation, and toxicity.<br>Journal of Cell Biology, 2022, 221, .   | 2.3  | 8         |
| 552 | A functional map of HIV-host interactions in primary human T cells. Nature Communications, 2022, 13, 1752.   | 5.8  | 27        |
| 553 | Epigenetic landscape in the kick-and-kill therapeutic vaccine BCN02 clinical trial is associated with antiretroviral treatment interruption (ATI) outcome. EBioMedicine, 2022, 78, 103956.                                 | 2.7  | 5         |
| 554 | Similarities and Differences between COVID-19-Associated Nephropathy and HIV-Associated Nephropathy. Kidney Diseases (Basel, Switzerland), 2022, 8, 1-12.  | 1.2  | 6         |
| 555 | Spotted Fever Group <i>Rickettsia</i> Trigger Species-Specific Alterations in Macrophage Proteome<br>Signatures with Different Impacts in Host Innate Inflammatory Responses. Microbiology Spectrum,<br>2021, 9, e0081421. | 1.2  | 4         |
| 556 | Interactome of SARS-CoV-2 Modulated Host Proteins With Computationally Predicted PPIs: Insights<br>From Translational Systems Biology Studies. Frontiers in Systems Biology, 2022, 2, .                                    | 0.5  | 6         |
| 557 | Aggresome assembly at the centrosome is driven by CP110–CEP97–CEP290 and centriolar satellites.<br>Nature Cell Biology, 2022, 24, 483-496.   | 4.6  | 18        |
| 558 | The Intricacy of the Viral-Human Protein Interaction Networks: Resources, Data, and Analyses.<br>Frontiers in Microbiology, 2022, 13, 849781.  | 1.5  | 2         |
| 567 | Tag Thy Neighbour: Nanometre-Scale Insights Into Kinetoplastid Parasites With Proximity Dependent<br>Biotinylation. Frontiers in Cellular and Infection Microbiology, 2022, 12, .  | 1.8  | 1         |
| 568 | Systems Biology of Virus-Host Protein Interactions: From Hypothesis Generation to Mechanisms of Replication and Pathogenesis. Annual Review of Virology, 2022, 9, .  | 3.0  | 5         |
| 569 | Viral hijacking mechanism in humans through protein–protein interactions. Advances in Protein<br>Chemistry and Structural Biology, 2022, , .   | 1.0  | 1         |
| 570 | HIV-1 exploits the Fanconi anemia pathway for viral DNA integration. Cell Reports, 2022, 39, 110840.   | 2.9  | 10        |
| 571 | Catchet-MS identifies IKZF1-targeting thalidomide analogues as novel HIV-1 latency reversal agents.<br>Nucleic Acids Research, 2022, 50, 5577-5598.  | 6.5  | 5         |
| 572 | Beyond Inhibition: A Novel Strategy of Targeting HIV-1 Protease to Eliminate Viral Reservoirs. Viruses, 2022, 14, 1179.  | 1.5  | 8         |
| 573 | Methodology-Centered Review of Molecular Modeling, Simulation, and Prediction of SARS-CoV-2.<br>Chemical Reviews, 2022, 122, 11287-11368.  | 23.0 | 38        |
| 574 | DLX1 and the NuRD complex cooperate in enhancer decommissioning and transcriptional repression.<br>Development (Cambridge), 2022, 149, .   | 1.2  | 6         |
| 575 | DEAD-ly Affairs: The Roles of DEAD-Box Proteins on HIV-1 Viral RNA Metabolism. Frontiers in Cell and<br>Developmental Biology, 0, 10, .  | 1.8  | 2         |
| 576 | A glycine-rich PE_PGRS protein governs mycobacterial actin-based motility. Nature Communications, 2022, 13, .  | 5.8  | 4         |

ARTICLE IF CITATIONS # PHILM2Web: A high-throughput database of macromolecular host–pathogen interactions on the Web. 579 1.4 1 Database: the Journal of Biological Databases and Curation, 2022, 2022, . A protein–protein interaction map reveals that the Coxiella burnetii effector CirB inhibits host 2.1 proteasome activity. PLoS Pathogens, 2022, 18, e1010660. Origination of LTR retroelement-derived <i>NYNRIN</i> coincides with therian placental emergence. 581 3.5 2 Molecular Biology and Evolution, 0, , . Upstream of N-Ras (Unr/CSDE1) Interacts with NCp7 and Gag, Modulating HIV-1 IRES-Mediated Translation Initiation. Viruses, 2022, 14, 1798. Binding stoichiometry and structural model of the HIV-1 Rev/importin Î<sup>2</sup> complex. Life Science Alliance, 583 1.3 3 2022, 5, e202201431. Rapidly evolving viral motifs mostly target biophysically constrained binding pockets of host 584 proteins. Cell Reports, 2022, 40, 111212. 586 Forging a Functional Cure for HIV: Transcription Regulators and Inhibitors. Viruses, 2022, 14, 1980. 1.5 9 Structure-function analysis of enterovirus protease 2A in complex with its essential host factor 5.8 SETD3. Nature Communications, 2022, 13, . Predicted cellular interactors of the endogenous retrovirus-K protease enzyme. Frontiers in 588 0 0.7 Virology, 0, 2, . Mechanistic insights into protein folding by the eukaryotic chaperonin complex CCT. Biochemical 589 1.6 Society Transactions, 2022, 50, 1403-1414. Open Modification Searching of SARS-CoV-2â€"Human Protein Interaction Data Reveals Novel Viral 591 2.5 5 Modification Sites. Molecular and Cellular Proteomics, 2022, 21, 100425. A network view of human immune system and virus-human interaction. Frontiers in Immunology, 0, 13, . 2.2 KCNQ1OT1 promotes genome-wide transposon repression by guiding RNA–DNA triplexes and HP1 593 4.6 20 binding. Nature Cell Biology, 2022, 24, 1617-1629. Structural Insights into the Mechanism of HIV-1 Tat Secretion from the Plasma Membrane. Journal of Molecular Biology, 2023, 435, 167880. DExD/H-box helicases in HIV-1 replication and their inhibition. Trends in Microbiology, 2023, 31, 393-404. 597 3.53 Inhibition of coronavirus HCoV-OC43 by targeting the eIF4F complex. Frontiers in Pharmacology, 0, 13, . Trans-Proteomic Pipeline: Robust Mass Spectrometry-Based Proteomics Data Analysis Suite. Journal of 601 1.8 21 Proteome Research, 2023, 22, 615-624. A binary interaction map between turnip mosaic virus and Arabidopsis thaliana proteomes. Communications Biology, 2023, 6, .

| #   | Article  | IF  | CITATIONS |
|-----|--|-----|-----------|
| 604 | Interactome of Paraoxonase PON2 Reveals New Pathways for Tumor Growth Regulation. Doklady<br>Biochemistry and Biophysics, 2023, 508, 31-36.  | 0.3 | 1         |
| 605 | Analysis of affinity purification-related proteomic data for studying protein–protein interaction networks in cells. Briefings in Bioinformatics, 2023, 24, .  | 3.2 | 1         |
| 606 | Cellular Targets of HIV-1 Protease: Just the Tip of the Iceberg?. Viruses, 2023, 15, 712.  | 1.5 | 0         |
| 607 | A Virus-Packageable CRISPR System Identifies Host Dependency Factors Co-Opted by Multiple HIV-1<br>Strains. MBio, 2023, 14, .  | 1.8 | 4         |
| 609 | HIV-1 Gag Binds the Multi-Aminoacyl-tRNA Synthetase Complex via the EPRS Subunit. Viruses, 2023, 15, 474.  | 1.5 | 3         |
| 611 | The lysine methyltransferase SMYD5 amplifies HIV-1 transcription and is post-transcriptionally upregulated by Tat and USP11. Cell Reports, 2023, 42, 112234.   | 2.9 | 5         |
| 612 | The CARD8 inflammasome in HIV infection. Advances in Immunology, 2023, , 59-100.   | 1.1 | 1         |
| 613 | elF3d: A driver of noncanonical cap–dependent translation of specific mRNAs and a trigger of<br>biological/pathological processes. Journal of Biological Chemistry, 2023, 299, 104658.                         | 1.6 | 4         |
| 614 | Computer-aided de novo design and optimization of novel potential inhibitors of HIV-1 Nef protein.<br>Computational Biology and Chemistry, 2023, 104, 107871.  | 1.1 | 1         |
| 621 | Affinity-Purification Combined with Crosslinking Mass Spectrometry for Identification and<br>Structural Modeling of Host–Pathogen Protein–Protein Complexes. Methods in Molecular Biology,<br>2023, , 181-200. | 0.4 | 0         |