

## REFERENCES

1. Ogun Adebali, Aylin Bircan, Defne Circi, Burak Islek, Zeynep Kilinc, Berkay Selcuk, and Berk Turhan, *Phylogenetic Analysis of SARS-CoV-2 Genomes in Turkey*, bioRxiv (2020), 2020.05.15.095794 (en), S0135.
2. Castillo Ae, Parra B, Tapia P, Acevedo A, Lagos J, Andrade W, Arata L, Leal G, Barra G, Tambley C, Tognarelli J, Bustos P, Ulloa S, Fasce R, and Fernndez J, *Phylogenetic analysis of the first four SARS-CoV-2 cases in Chile.*, Journal of Medical Virology (2020) (English), S0000.
3. Maria Artesi, Sebastien Bontems, Paul Gobbels, Marc Franckh, Raphael Boreux, Cecile Meex, Pierrette Melin, Marie-Pierre Hayette, Vincent Bours, and Keith Durkin, *Failure of the cobas SARS-CoV-2 (Roche) E-gene assay is associated with a C-to-T transition at position 26340 of the SARS-CoV-2 genome*, medRxiv (2020), 2020.04.28.20083337 (en), S0087.
4. Mustak Ibn Ayub, *Reporting Two SARS-CoV-2 Strains Based on A Unique Trinucleotide-Bloc Mutation and Their Potential Pathogenic Difference*, (2020) (en), S0044.
5. Yunmeng Bai, Dawei Jiang, Jerome R. Lon, Xiaoshi Chen, Meiling Hu, Shudai Lin, Zixi Chen, Xiaoning Wang, Yuhuan Meng, and Hongli Du, *Evolution and molecular characteristics of SARS-CoV-2 genome*, bioRxiv (2020), 2020.04.24.058933 (en), S0138.
6. A. Bal, G. Destras, A. Gaynard, M. Bouscambert-Duchamp, M. Valette, V. Escuret, E. Frobert, G. Billaud, S. Trouillet-Assant, V. Cheynet, K. Brengel-Pesce, F. Morfin, B. Lina, and L. Josset, *Molecular characterization of SARS-CoV-2 in the first COVID-19 cluster in France reveals an amino acid deletion in nsp2 (Asp268del)*, Clinical Microbiology and Infection (2020), S0134.
7. Shuvam Banerjee, Sohan Seal, Riju Dey, Kousik Kr Mondal, and Pritha Bhattacharjee, *Mutational spectra of SARS-CoV-2 orf1ab polyprotein and Signature mutations in the United States of America*, bioRxiv (2020), 2020.05.01.071654 (en), S0068.
8. Denis C. Bauer, Aidan P. Tay, Laurence O. W. Wilson, Daniel Reti, Cameron Hosking, Alexander J. McAuley, Elizabeth Pharo, Shawn Todd, Vicky Stevens, Matthew J. Neave, Mary Tachedjian, Trevor W. Drew, and S. S. Vasani, *Supporting pandemic response using genomics and bioinformatics: a case study on the emergent SARS-CoV-2 outbreak*, Transboundary and Emerging Diseases n/a (2020), no. n/a (en), S0045.
9. Daniel Becker, Gregory F. Albery, Anna R. Sjodin, Timothee Poisot, Tad Dallas, Evan A. Eskew, Maxwell J. Farrell, Sarah Guth, Barbara A. Han, Nancy B. Simmons, and Colin J. Carlson, *Predicting wildlife hosts of betacoronaviruses for SARS-CoV-2 sampling prioritization*, bioRxiv (2020), 2020.05.22.111344 (en), S0166.
10. Trevor Bedford, *Twitter thread by @trvr: We now have enough #SARSCoV2 genomic data from different states to make some broad conclusions about how the #COVID19 epidemic has unfolded*, techreport, Fred Hutchinson Cancer Research Center, 2020, S0118.
11. Trevor Bedford, Alexander L. Greninger, Pavitra Roychoudhury, Lea M. Starita, Michael Famulare, Meei-Li Huang, Arun Nalla, Gregory Pepper, Adam Reinhardt, Hong Xie, Lasata Shrestha, Truong N. Nguyen, Amanda Adler, Elisabeth Brandstetter, Shari Cho, Danielle Giroux, Peter D. Han, Kairsten Fay, Chris D. Frazar, Misja Ilcisin, Kirsten Lacombe, Jover Lee, Anahita Kiavand, Matthew Richardson, Thomas R. Sibley, Melissa Truong, Caitlin R. Wolf, Deborah A. Nickerson, Mark J. Rieder, Janet A. Englund, the Seattle Flu Study Investigators, James Hadfield, Emma B. Hodcroft, John Huddleston, Louise H. Moncla, Nicola F. Mller, Richard A. Neher, Xianding Deng, Wei Gu, Scot Federman, Charles Chiu, Jeff Duchin, Romesh Gautam, Geoff Melly, Brian Hiatt, Philip Dykema, Scott Lindquist, Krista Queen, Ying Tao, Anna Uehara, Suxiang Tong, Duncan MacCannell, Gregory L. Armstrong, Geoffrey S. Baird, Helen Y. Chu, and Keith R. Jerome, *Cryptic transmission of SARS-CoV-2 in Washington State*, medRxiv (2020), 2020.04.02.20051417 (en), S0016.
12. Chandrika Bhattacharyya, Chitrapita Das, Arnab Ghosh, Animesh K. Singh, Souvik Mukherjee, Partha P. Majumder, Anabha Basu, and Nidhan K. Biswas, *Global Spread of SARS-CoV-2 Subtype with Spike Protein Mutation D614G is Shaped by Human Genomic Variations that Regulate Expression of TMPRSS2 and MX1 Genes*, bioRxiv (2020), 2020.05.04.075911 (en), S0092.

13. Sourav Biswas, Suparna Saha, Sanghamitra Bandyopadhyay, and Malay Bhattacharyya, *Tracing Back the Temporal Change of SARS-Cov-2 with Genomic Signatures*, bioRxiv (2020), 2020.04.24.057380 (en), S0059.
14. Jeffrey Brainard, *Scientists are drowning in COVID-19 papers. Can new tools keep them afloat?*, Science AAAS **368** (2020), no. 6491 (en), S0112.
15. Anderson Brito, *Update 3 — 2020.04.14 - yale sars-cov-2 genome surveillance initiative*, 2020, S0036.
16. Merle M. Bhmer, Udo Buchholz, Victor M. Corman, Martin Hoch, Katharina Katz, Durdica V. Marosevic, Stefanie Bhm, Tom Woudenberg, Nikolaus Ackermann, Regina Konrad, Ute Eberle, Bianca Treis, Alexandra Dangel, Katja Bengs, Volker Fingerle, Anja Berger, Stefan Hrmansdorfer, Siegfried Ippisch, Bernd Wicklein, Andreas Grahl, Kirsten Prtner, Nadine Muller, Nadine Zeitlmann, T. Sonia Boender, Wei Cai, Andreas Reich, Maria an der Heiden, Ute Rexroth, Osamah Hamouda, Julia Schneider, Talitha Veith, Barbara Mhlemann, Roman Wlfel, Markus Antwerpen, Mathias Walter, Ulrike Protzer, Bernhard Liebl, Walter Haas, Andreas Sing, Christian Drosten, and Andreas Zapf, *Investigation of a COVID-19 outbreak in Germany resulting from a single travel-associated primary case: a case series*, The Lancet Infectious Diseases **0** (2020), no. 0 (English), S0141.
17. Rachele Cagliani, Diego Forni, Mario Clerici, and Manuela Sironi, *Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses*, Infection, Genetics and Evolution **83** (2020), 104353 (en), S0116.
18. Hugh Y. Cai, Kimberly K. Cai, and Julang Li, *Identification of Novel Missense Mutations in a Large Number of Recent SARS-CoV-2 Genome Sequences*, Preprints **2020040482** (2020) (en), S0072.
19. Carmine Ceraolo and Federico M. Giorgi, *Genomic variance of the 2019-nCoV coronavirus*, Journal of Medical Virology **92** (2020), no. 5, 522–528 (en), S0021.
20. Gyanendra Bahadur Chand and Gajendra Kumar Azad, *Identification of novel mutations in RNA-dependent RNA polymerases of SARS-CoV-2 and their implications*, bioRxiv (2020), 2020.05.05.079939 (en), S0104.
21. Nanhua Chen, Xinshuai Li, Shubin Li, Yanzhao Xiao, Mengxue Ye, Xilin Yan, and Xiangdong Li, *How related is SARS-CoV-2 to other coronaviruses?*, Veterinary Record **186** (2020), no. 15, 496–496 (en), S0076.
22. Wei Chen, Pengmian Feng, Kewei Liu, Meng Wu, and Hao Lin, *Computational Identification of Small Interfering RNA Targets in SARS-CoV-2*, Virologica Sinica (2020) (en), S0037.
23. Mary Hongying Cheng, She Zhang, Rebecca A. Porritt, Moshe Arditi, and Ivet Bahar, *An insertion unique to SARS-CoV-2 exhibits superantigenic character strengthened by recent mutations*, bioRxiv (2020), 2020.05.21.109272 (en), S0156.
24. Matteo Chiara, David Stephen Horner, and Graziano Pesole, *Comparative genomics suggests limited variability and similar evolutionary patterns between major clades of SARS-Cov-2*, bioRxiv (2020), 2020.03.30.016790 (en), S0007.
25. Simone Ciccolella, Luca Denti, Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, and Marco Previtali, *MALVIRUS: an integrated web application for viral variant calling*, bioRxiv (2020), 2020.05.05.076992 (en), S0096.
26. Giovanni Colavizza, Rodrigo Costas, Vincent A. Traag, Nees Jan van Eck, Thed van Leeuwen, and Ludo Waltman, *A scientometric overview of CORD-19*, bioRxiv (2020), 2020.04.20.046144 (en), S0113.
27. Francesco Comandatore, Alice Chiodi, Paolo Gabrieli, Gherard Batisti Biffignandi, Matteo Perini, Matteo Ramazzotti, Stefano Ricagno, Sara Giordana Rimoldi, Mariarita Gismondo, Valeria Micheli, Claudio Bandi, and Matteo Brillì, *Identification of variable sites in Sars-CoV-2 and their abundance profiles in time*, bioRxiv (2020), 2020.04.30.071027 (en), S0066.
28. Marti Cortey, Yanli Li, Ivan Diaz, Hepzibar Clilverd, Laila Darwich, and Enric Mateu, *SARS-CoV-2 amino acid substitutions widely spread in the human population are mainly located in highly conserved segments of the structural proteins*, bioRxiv (2020), 2020.05.16.099499 (en), S0145.
29. Alex Crits-Christoph, *Reproducible analyses for rejecting rare genomic inversions in sars-cov-2*, April 2020, S0010.
30. Bethany Dearlove, Eric Lewitus, Hongjun Bai, Yifan Li, Daniel B. Reeves, M. Gordon Joyce, Paul T. Scott, Mihret F. Amare, Sandhya Vasani, Nelson L. Michael, Kayvon Modjarrad,

- and Morgane Rolland, *A SARS-CoV-2 vaccine candidate would likely match all currently circulating strains*, bioRxiv (2020), 2020.04.27.064774 (en), S0075.
31. Simon Dellicour, Keith Durkin, Samuel L. Hong, Bert Vanmechelen, Joan Mart-Carreras, Mandev S. Gill, Ccile Meex, Sbastien Bontems, Emmanuel Andr, Marius Gilbert, Conor Walker, Nicola De Maio, James Hadfield, Marie-Pierre Hayette, Vincent Bours, Tony Wawina-Bokalanga, Maria Artesi, Guy Baele, and Piet Maes, *A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages*, bioRxiv (2020), 2020.05.05.078758 (en), S0108.
  32. Nicola DeMaio, Conor Walker, Rui Borges, Lukas Weilguny, Greg Slodkowitz, and Nick Goldman, *Issues with SARS-CoV-2 sequencing data*, May 2020, S0085.
  33. Xianding Deng, Asmeeta Achari, Scot Federman, Guixia Yu, Sneha Somasekar, Ins Brtolto, Shigeo Yagi, Placide Mbala-Kingebeni, Jimmy Kapetshi, Steve Ahuka-Mundeye, Jean-Jacques Muyembe-Tamfum, Asim A. Ahmed, Vijay Ganesh, Manasi Tamhankar, Jean L. Patterson, Nicaise Ndembi, Dora Mbanya, Lazare Kaptue, Carole McArthur, Jos E. Muoz-Medina, Cesar R. Gonzalez-Bonilla, Susana Lpez, Carlos F. Arias, Shaun Arevalo, Steve Miller, Mars Stone, Michael Busch, Kristina Hsieh, Sharon Messenger, Debra A. Wadford, Mary Rodgers, Gavin Cloherty, Nuno R. Faria, Julien Thz, Oliver G. Pybus, Zoraima Neto, Joana Morais, Nuno Taveira, John R Hackett, and Charles Y. Chiu, *Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance*, Nature Microbiology **5** (2020), no. 3, 443–454 (eng), S0014.
  34. Xianding Deng, Wei Gu, Scot Federman, Louis Du Plessis, Oliver Pybus, Nuno Faria, Candace Wang, Guixia Yu, Chao-Yang Pan, Hugo Guevara, Alicia Sotomayor-Gonzalez, Kelsey Zorn, Allan Gopez, Venice Servellita, Elaine Hsu, Steve Miller, Trevor Bedford, Alexander Greninger, Pavitra Roychoudhury, Michael Famulare, Helen Y. Chu, Jay Shendure, Lea Starita, Catie Anderson, Karthik Gangavarapu, Mark Zeller, Emily Spencer, Kristian Andersen, Duncan MacCannell, Suxiang Tong, Gregory Armstrong, Clinton Paden, Yan Li, Ying Zhang, Scott Morrow, Matthew Willis, Bela Matyas, Sundari Mase, Olivia Kasirye, Maggie Park, Curtis Chan, Alexander Yu, Shua Chai, Elsa Villarino, Brandon Bonin, Debra Wadford, and Charles Y. Chiu, *A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage*, medRxiv (2020), 2020.03.27.20044925 (en), S0004.
  35. Christian A Devaux, Lucille Pinault, Ikram Omar Osman, and Didier Raoult, *Can ACE2 receptor polymorphism predicts species susceptibility to SARS-CoV-2?*, Research Square **rs-25753** (2020) (en), S0073.
  36. Paul Digard, Hui-Min Lee, Colin Sharp, Finn Grey, and Eleanor R. Gaunt, *Intra-genome variability in the dinucleotide composition of SARS-CoV-2*, bioRxiv (2020), 2020.05.08.083816 (en), S0105.
  37. Lucy van Dorp, Damien Richard, Cedric CS Tan, Liam P. Shaw, Mislav Acman, and Francois Balloux, *No evidence for increased transmissibility from recurrent mutations in SARS-CoV-2*, bioRxiv (2020), 2020.05.21.108506 (en), S0157.
  38. Sebastian Duchene, Leo Featherstone, Melina Haritopoulou-Sinapidou, Andrew Rambaut, Philippe Lemey, and Guy Baele, *Temporal signal and the phylodynamic threshold of SARS-CoV-2*, bioRxiv (2020), 2020.05.04.077735 (en), S0081.
  39. Doa Eskier, Gkhan Karaklah, Asl Suner, and Yavuz Oktay, *RdRp mutations are associated with SARS-CoV-2 genome evolution*, bioRxiv (2020), 2020.05.20.104885 (en), S0153.
  40. Muhamad Fahmi, Yukihiko Kubota, and Masahiro Ito, *Nonstructural proteins NS7b and NS8 are likely to be phylogenetically associated with evolution of 2019-nCoV*, Infection, Genetics and Evolution **81** (2020), 104272 (en), S0144.
  41. Bing Fang, Linlin Liu, Xiao Yu, Xiang Li, Guojun Ye, Juan Xu, Ling Zhang, Faxian Zhan, Guiming Liu, Tao Pan, Yilin Shu, and Yongzhong Jiang, *Genome-wide data inferring the evolution and population demography of the novel pneumonia coronavirus (SARS-CoV-2)*, bioRxiv (2020), 2020.03.04.976662 (en), S0111.
  42. Joseph R. Fauver, Mary E. Petrone, Emma B. Hodcroft, Kayoko Shioda, Hanna Y. Ehrlich, Alexander G. Watts, Chantal B. F. Vogels, Anderson F. Brito, Tara Alpert, Anthony Muyombwe, Jafar Razeq, Randy Downing, Nagarjuna R. Cheemarla, Anne L. Wyllie, Chaney C. Kalinich, Isabel Ott, Josh Quick, Nicholas J. Loman, Karla M. Neugebauer, Alexander L. Greninger, Keith R. Jerome, Pavitra Roychoudhury, Hong Xie, Lasata Shrestha, Meei-Li Huang, Virginia E. Pitzer, Akiko Iwasaki, Saad B. Omer, Kamran Khan, Isaac Bogoch,

- Richard A. Martinello, Ellen F. Foxman, Marie-Louise Landry, Richard A. Neher, Albert I. Ko, and Nathan D. Grubaugh, *Coast-to-coast spread of SARS-CoV-2 in the United States revealed by genomic epidemiology*, medRxiv (2020), 2020.03.25.20043828 (en), S0017.
43. Andrew E. Firth, *A putative new SARS-CoV protein, 3a\*, encoded in an ORF overlapping ORF3a*, bioRxiv (2020), 2020.05.12.088088 (en), S0115.
  44. Sergio Forcelloni, Anna Benedetti, Maddalena Dilucca, and Andrea Giansanti, *Identification of conserved epitopes in SARS-CoV-2 spike and nucleocapsid protein.*, bioRxiv (2020), 2020.05.14.095133 (en), S0127.
  45. Peter Forster, Lucy Forster, Colin Renfrew, and Michael Forster, *Phylogenetic network analysis of SARS-CoV-2 genomes*, Proceedings of the National Academy of Sciences of the United States of America (2020) (eng), S0023.
  46. Nicholas M. Fountain-Jones, Raima Carol Appaw, Scott Carver, Xavier Didelot, Erik M. Volz, and Michael Charleston, *Emerging phylogenetic structure of the SARS-CoV-2 pandemic*, bioRxiv (2020), 2020.05.19.103846 (en), S0151.
  47. Francisco Dez Fuertes, Mara Iglesias Caballero, Sara Monzn, Pilar Jimnez, Sarai Varona, Isabel Cuesta, ngel Zaballos, Michael M. Thomson, Mercedes Jimnez, Javier Garca Prez, Francisco Pozo, Mayte Prez Olmeda, Jos Alcam, and Inmaculada Casas, *Phylogenetics of SARS-CoV-2 transmission in Spain*, bioRxiv (2020), 2020.04.20.050039 (en), S0047.
  48. Jacob D. Galson, Sebastian Schaetzle, Rachael J. M. Bashford-Rogers, Matthew I. J. Raybould, Aleksandr Kovaltsuk, Gavin J. Kilpatrick, Ralph Minter, Donna K. Finch, Jorge Dias, Louisa James, Gavin Thomas, Wing-Yiu Jason Lee, Jason Betley, Olivia Cavlan, Alex Leech, Charlotte M. Deane, Joan Seoane, Carlos Caldas, Dan Pennington, Paul Pfeffer, and Jane Osbourn, *Deep sequencing of B cell receptor repertoires from COVID-19 patients reveals strong convergent immune signatures*, bioRxiv (2020), 2020.05.20.106294 (en), S0159.
  49. Fabiana Gambaro, Artem Baidaliuk, Sylvie Behillil, Flora Donati, Melanie Albert, Andreea Alexandru, Maud Vanpeene, Meline Bizard, Angela Brisebarre, Marion Barbet, Fawzi Derar, Sylvie van der Werf, Vincent Enouf, and Etienne Simon-Loriere, *Introductions and early spread of SARS-CoV-2 in France*, bioRxiv (2020), 2020.04.24.059576 (en), S0061.
  50. Salvatore Di Giorgio, Filippo Martignano, Maria Gabriella Torcia, Giorgio Mattiuz, and Silvestro G. Conticello, *Evidence for host-dependent RNA editing in the transcriptome of SARS-CoV-2*, Science Advances (2020), eabb5813 (en), S0150.
  51. Daryl M. Gohl, John Garbe, Patrick Grady, Jerry Daniel, Ray H. B. Watson, Benjamin Auch, Andrew Nelson, Sophia Yohe, and Kenneth B. Beckman, *A Rapid, Cost-Effective Tailed Amplicon Method for Sequencing SARS-CoV-2*, bioRxiv (2020), 2020.05.11.088724 (en), S0117.
  52. Alberto Gomez-Carballa, Xabi Bello, Jacobo Pardo-Seco, Federico Martinon-Torres, and Antonio Salas, *The impact of super-spreaders in COVID-19: mapping genome variation worldwide*, bioRxiv (2020), 2020.05.19.097410 (en), S0152.
  53. Ricardo Lemes Goncalves, Tulio Cesar Rodrigues Leite, Bruna de Paula Dias, Camila Carla da Silva Caetano, Ana Clara Gomes de Souza, Ubiratan da Silva Batista, Camila Cavadas Barbosa, Arturo Reyes-Sandoval, Luiz Felipe Leomil Coelho, and Breno de Mello Silva, *SARS-CoV-2 mutations and where to find them: An in silico perspective of structural changes and antigenicity of the Spike protein*, bioRxiv (2020), 2020.05.21.108563 (en), S0162.
  54. Yu-Nong Gong, Kuo-Chien Tsao, Mei-Jen Hsiao, Chung-Guei Huang, Peng-Nien Huang, Po-Wei Huang, Kuo-Ming Lee, Yi-Chun Liu, Shu-Li Yang, Rei-Lin Kuo, Ming-Tsan Liu, Ji-Rong Yang, Cheng-Hsun Chiu, Cheng-Ta Yang, Shin-Ru Shih, and Guang-Wu Chen, *Sequence variation among SARS-CoV-2 isolates in Taiwan*, bioRxiv (2020), 2020.03.29.014290 (en), S0006.
  55. Ana S. Gonzalez-Reiche, Matthew M. Hernandez, Mitchell Sullivan, Brianne Ciferri, Hala Alshammery, Ajay Obla, Shelcie Fabre, Giulio Kleiner, Jose Polanco, Zenab Khan, Bremy Albuquerque, Adriana van de Guchte, Jayeeta Dutta, Nancy Francoeur, Betsaida Salom Melo, Irina Oussenko, Gintaras Deikus, Juan Soto, Shwetha Hara Sridhar, Ying-Chih Wang, Kathryn Twyman, Andrew Kasarskis, Deena Rose Altman, Melissa Smith, Robert Sebra, Judith Aberg, Florian Krammer, Adolfo Garcia-Sarstre, Marta Luksza, Gopi Patel, Alberto Paniz-Mondolfi, Melissa Gitman, Emilia Mia Sordillo, Viviana Simon, and Harm van Bakel, *Introductions and early spread of SARS-CoV-2 in the New York City area*, medRxiv (2020), 2020.04.08.20056929 (en), S0026.

56. Daniel F. Gudbjartsson, Agnar Helgason, Hakon Jonsson, Olafur T. Magnusson, Pall Melsted, Gudmundur L. Norddahl, Jona Saemundsdottir, Asgeir Sigurdsson, Patrick Sulem, Arna B. Agustsdottir, Berglind Eiriksdoottir, Run Fridriksdoottir, Elisabet E. Gardarsdoottir, Gudmundur Georgsson, Olafia S. Gretarsdoottir, Kjartan R. Gudmundsson, Thora R. Gunnarsdoottir, Arnaldur Gylfason, Hilma Holm, Brynjar O. Jensson, Aslaug Jonasdoottir, Frosti Jonsson, Kamilla S. Josefsdoottir, Thordur Kristjansson, Droplaug N. Magnusdoottir, Louise le Roux, Gudrun Sigmundsdottir, Gardar Sveinbjornsson, Kristin E. Sveinsdoottir, Maney Sveinsdoottir, Emil A. Thorarensen, Bjarni Thorbjornsson, Arthur Lve, Gisli Masson, Ingileif Jonsdoottir, Alma D. Miller, Thorolfur Gudnason, Karl G. Kristinsson, Unnur Thorsteinsdoottir, and Kari Stefansson, *Spread of SARS-CoV-2 in the Icelandic Population*, *New England Journal of Medicine* **0** (2020), no. 0, null, S0028.
57. Ruchir Gupta, Jacob Charron, Cynthia Stenger, Jared Painter, Hunter Steward, Taylor Cook, William Faber, Austin Frisch, Eric Lind, Jacob Bauss, Xiaopeng Li, Olivia Sirpilla, Xavier Soehnen, Adam Underwood, David Hinds, Michele Morris, Neil Lamb, Joseph Carcillo, Caleb Bupp, Bruce Uhal, Surender Rajasekaran, and Jeremy W. Prokop, *SARS-CoV2 (COVID-19) Structural/Evolution Dynamicome: Insights into functional evolution and human genomics.*, *bioRxiv* (2020), 2020.05.15.098616 (en), S0137.
58. Peter Habib, Alsamman M. Alsamman, Maha Saber-Ayad, Sameh E. Hassanein, and Aladdin Hamwieh, *COVIDier: A Deep-learning Tool For Coronaviruses Genome And Virulence Proteins Classification*, *bioRxiv* (2020), 2020.05.03.075549 (en), S0090.
59. J. Hadfield, *RAMPART v1.1.0 released*, April 2020, S0022.
60. Georg Hahn, Sanghun Lee, Scott Weiss, and Christoph Lange, *Unsupervised cluster analysis of SARS-CoV-2 genomes reflects its geographic progression and identifies distinct genetic subgroups of SARS-CoV-2 virus*, *bioRxiv* (2020), 2020.05.05.079061 (en), S0082.
61. Mehrdad Hajibabaei and Gregory AC Singer, *The Red Queen's Crown: an evolutionary arms race between coronaviruses and mammalian species reflected in positive selection of the ACE2 receptor among many species*, *bioRxiv* (2020), 2020.05.14.096131 (en), S0125.
62. Saam Hasan, Salim Khan, Gias U. Ahsan, and Muhammad Maqsood Hossain, *Genome Analysis of SARS-CoV-2 Isolate from Bangladesh*, *bioRxiv* (2020), 2020.05.13.094441 (en), S0131.
63. Sk Sarif Hassan, Atanu Moitrab, Ranjeet K. Rout, Pabitra Pal Choudhury, Prasanta Pramanik, and Siddhartha Sankar Jana, *On spatial molecular arrangements of SARS-CoV2 genomes of Indian patients*, *bioRxiv* (2020), 2020.05.01.071985 (en), S0070.
64. Brian Glenn St Hilaire, Neva C. Durand, Namita Mitra, Saul Godinez Pulido, Ragini Mahajan, Alyssa Blackburn, Zane L. Colaric, Joshua W. M. Theisen, David Weisz, Olga Dudchenko, Andreas Gnirke, Suhas Rao, Parwinder Kaur, Erez Lieberman Aiden, and Aviva P. Aiden, *A rapid, low cost, and highly sensitive SARS-CoV-2 diagnostic based on whole genome sequencing*, *bioRxiv* (2020), 2020.04.25.061499 (en), S0054.
65. LaRinda A. Holland, Emily A. Kaelin, Rabia Maqsood, Bereket Estifanos, Lily I. Wu, Arvind Varsani, Rolf U. Halden, Brenda G. Hogue, Matthew Scotch, and Efreem S. Lim, *An 81 nucleotide deletion in SARS-CoV-2 ORF7a identified from sentinel surveillance in Arizona (Jan-Mar 2020)*, *Journal of Virology* (2020) (en), S0086.
66. X Hu, W Li, and Z He, *Identification sus scrofa and mus musculus as potential hosts of sars-cov-2 via phylogenetic and homologous recombination analysis [version 2; peer review: awaiting peer review]*, *F1000Research* **9** (2020), 190, S0049.
67. Elizabeth Hnaff, Devora Najjar, Miguel Perez, Regina Flores, Christopher Wobken, Christopher E. Mason, and Kevin Slavin, *Holobiont Urbanism: sampling urban beehives reveals cities metagenomes*, *bioRxiv* (2020), 2020.05.07.075093 (en), S0114.
68. Rafiul M Islam, M. N. Hoque, M. S. Rahman, J. A. Puspo, M. Akhter, S. Akter, A. S. M. Rubayet-Ul-Alam, M. Sultana, K. A. Crandall, and M. A. Hossain, *Genome wide analysis of severe acute respiratory syndrome coronavirus-2 implicates world-wide circulatory virus strains heterogeneity*, *Preprints* (2020), S0020.
69. Elio Issa, Georgi Merhi, Balig Panossian, Tamara Salloum, and Sima Tokajian, *SARS-CoV-2 and ORF3a: Nonsynonymous Mutations, Functional Domains, and Viral Pathogenesis*, *mSystems* **5** (2020), no. 3 (en), S0094.
70. Javier A. Jaimes, Nicole M. Andr, Joshua S. Chappie, Jean K. Millet, and Gary R. Whittaker, *Phylogenetic Analysis and Structural Modeling of SARS-CoV-2 Spike Protein Reveals an Evolutionary Distinct and Proteolytically Sensitive Activation Loop*, *Journal of Molecular Biology* (2020) (en), S0050.

71. Terry C Jones, Barbara Mhlemann, Julia Schneider, Jrn Beheim-Schwarzbach, Talitha Veith, Victor M Corman, and Christian Drosten, *German sars-cov-2 sequences*, April 2020, S0032.
72. Aditi Joshi and Sushmita Paul, *Phylogenetic Analysis of the Novel Coronavirus Reveals Important Variants in Indian Strains*, bioRxiv (2020), 2020.04.14.041301 (en), S0031.
73. Ivair Jose Morais Junior, Richard Costa Polveiro, Gabriel Medeiros Souza, Daniel Insera Bortolin, Flavio Tetsuo Sasaki, and Alison Talis Martins Lima, *The global population of SARS-CoV-2 is composed of six major subtypes*, bioRxiv (2020), 2020.04.14.040782 (en), S0034.
74. Abdoulie Kanteh, Jarra Manneh, Sona Jabang, Mariama A. Kujabo, Bakary Sanyang, Mary Aigbiremo Obob, Abdoulie Bojang, Haruna S. Jallow, Davis Nwakama, Ousman Secka, Anna Roca, Alfred Amambua-Ngwa, Martin Antonio, Ignatius Baldeh, Karen Forest, Ahmadou Lamin Samateh, Umberto D'Alessandro, and Abdul Karim Sesay, *Origin of imported SARS-CoV-2 strains in The Gambia identified from Whole Genome Sequences.*, bioRxiv (2020), 2020.04.30.070771 (en), S0064.
75. Paschalia Kapli, Ziheng Yang, and Maximilian J. Telford, *Phylogenetic tree building in the genomic age*, Nature Reviews. Genetics (2020) (eng), S0146.
76. Timokratis Karamitros, Gethsimani Papadopoulou, Maria Bousali, Anastasios Mexias, Sotiris Tsiodras, and Andreas Mentis, *SARS-CoV-2 exhibits intra-host genomic plasticity and low-frequency polymorphic quasispecies*, bioRxiv (2020), 2020.03.27.009480 (en), S0001.
77. Gabor Kemenesi, Safia Zeghib, Balazs Somogyi, Gabor E. Toth, Krisztian Banyai, Norbert Solymosi, Peter M. Szabo, Istvan Szabo, Adam Balint, Peter Urban, Robert Herczeg, Attila Gyenesei, Agnes Nagy, Csaba I. Pereszlenyi, Gergely Babinszky, Gabor Dudas, Gabriella Terhes, Viktor Zoldi, Robert Lovas, Szabolcs Tenczer, Laszlo Kornya, and Ferenc Jakab, *Multiple SARS-CoV-2 introductions shaped the early outbreak in Central Eastern Europe: comparing Hungarian data to a worldwide sequence data-matrix*, bioRxiv (2020), 2020.05.06.080119 (en), S0083.
78. Rozhgar A. Khailany, Muhamad Safdar, and Mehmet Ozaslan, *Genomic characterization of a novel SARS-CoV-2*, Gene Reports **19** (2020), 100682 (en), S0103.
79. Bette Korber, Will Fischer, S. Gnana Gnanakaran, Heyjin Yoon, James Theiler, Werner Abfalterer, Brian Foley, Elena E. Giorgi, Tanmoy Bhattacharya, Matthew D. Parker, David G. Partridge, Cariad M. Evans, Thushan de Silva, Celia C. LaBranche, David C. Montefiori, and Sheffield COVID-19 Genomics Group, *Spike mutation pipeline reveals the emergence of a more transmissible form of SARS-CoV-2*, bioRxiv (2020), 2020.04.29.069054 (en), S0063.
80. Meriem Laamarti, Tarek Alouane, Souad Kartti, M. W. Chemaou-Elfihri, Mohammed Hakmi, Abdelmunim Essabbar, Mohamed Laamart, Haitam Hlali, Loubna Allam, Naima EL Hafidi, Rachid EL Jaoudi, Imane Allali, Nabila Marchoudi, Jamal Fekkek, Houda Benrahma, Chakib Nejari, Saaid Amzazi, Lahcen Belyamani, and Azeddine Ibrahim, *Large scale genomic analysis of 3067 SARS-CoV-2 genomes reveals a clonal geodistribution and a rich genetic variations of hotspots mutations*, bioRxiv (2020), 2020.05.03.074567 (en), S0080.
81. Grubaugh Lab, *Update 5 — 2020.04.28 (yale sars-cov-2 genomic surveillance initiative)*, April 2020, S0056.
82. Sayantan Laha, Joyeeta Chakraborty, Shantanab Das, Sampa Biswas, Soumen Kanti Manna, and Raghunath Chatterjee, *Characterizations of SARS-CoV-2 mutational profile, spike protein stability and viral transmission*, bioRxiv (2020), 2020.05.03.066266 (en), S0093.
83. Robert Lanfear, *What's the best method to get a tree of  $\approx 10k$  sars-cov-2 sequences?*, Github repository, 2020, S0088.
84. Siu-Ying Lau, Pui Wang, Bobo Wing-Yee Mok, Anna Jinxia Zhang, Hin Chu, Andrew Chak-Yiu Lee, Shaofeng Deng, Pin Chen, Kwok-Hung Chan, Wenjun Song, Zhiwei Chen, Kelvin Kai-Wang To, Jasper Fuk-Woo Chan, Kwok-Yung Yuen, and Honglin Chen, *Attenuated SARS-CoV-2 variants with deletions at the S1/S2 junction*, Emerging Microbes & Infections **0** (2020), no. ja, 1–15, S0040.
85. Chenyu Li, David N. DeBruyne, Julia Spencer, Vidushi Kapoor, Lily Y. Liu, Bo Zhou, Utsav Pandey, Moiz Bootwalla, Dejerianne Ostrow, Dennis T. Maglinte, David Ruble, Alex Ryutov, Lishuang Shen, Lucie Lee, Rounak Feigelman, Grayson Burdon, Jeffrey Liu, Alejandra Oliva, Adam Borcharding, Hongdong Tan, Alexander E. Urban, Xiaowu Gai, Jennifer Dien Bard, Guoying Liu, and Zhitong Liu, *Highly sensitive and full-genome interrogation of SARS-CoV-2 using multiplexed PCR enrichment followed by next-generation sequencing*, bioRxiv (2020), 2020.03.12.988246 (en), S0149.

86. Jianguo Li, Zhen Li, Xiaogang Cui, and Changxin Wu, *Bayesian phylodynamic inference on the temporal evolution and global transmission of SARS-CoV-2*, *Journal of Infection* **0** (2020), no. 0 (English), S0052.
87. Xingguang Li, Wei Wang, Xiaofang Zhao, Junjie Zai, Qiang Zhao, Yi Li, and Antoine Chailion, *Transmission dynamics and evolutionary history of 2019-nCoV*, *Journal of Medical Virology* **92** (2020), no. 5, 501–511 (en), S0107.
88. Xingguang Li, Junjie Zai, Qiang Zhao, Qing Nie, Yi Li, Brian T. Foley, and Antoine Chailion, *Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2*, *Journal of Medical Virology* **92** (2020), no. 6, 602–611 (en), S0155.
89. You Li, Ye Wang, Yaping Qiu, Zhen Gong, Lei Deng, Min Pan, Huiping Yang, Jianan Xu, Li Yang, and Jin Li, *SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain is Subject to Negative Selection with Predicted Positive Selection Mutations*, *bioRxiv* (2020), 2020.05.04.077842 (en), S0091.
90. Boxiang Liu, Kaibo Liu, He Zhang, Liang Zhang, and Liang Huang, *CoV-Seq: SARS-CoV-2 Genome Analysis and Visualization*, *bioRxiv* (2020), 2020.05.01.071050 (en), S0077.
91. Zhe Liu, Huanying Zheng, Runyu Yuan, Mingyue Li, Huifang Lin, Jingju Peng, Qianlin Xiong, Jiufeng Sun, Baisheng Li, Jie Wu, Changwen Ke, Ruben J. G. Hulswit, Thomas A. Bowden, Andrew Rambaut, Oliver G. Pybus, Nick Loman, and Jing Lu, *Identification of a common deletion in the spike protein of SARS-CoV-2*, *bioRxiv* (2020), 2020.03.31.015941 (en), S0008.
92. S. Wesley Long, Paul A. Christensen, David W. Bernard, James R. Davis, Maulik Shukla, Marcus Nguyen, Matthew Ojeda Saavedra, Concepcion C. Cantu, Prasanti Yerramilli, Layne Pruitt, Sishir Subedi, Heather Hendrickson, Ghazaleh Eskandari, Muthiah Kumaraswami, Jason S. McLellan, and James M. Musser, *Molecular Architecture of Early Dissemination and Evolution of the SARS-CoV-2 Virus in Metropolitan Houston, Texas*, *bioRxiv* (2020), 2020.05.01.072652 (en), S0062.
93. Jing Lu, Louis du Plessis, Zhe Liu, Verity Hill, Min Kang, Huifang Lin, Jiufeng Sun, Sarah Francois, Moritz U. G. Kraemer, Nuno R. Faria, John T. McCrone, Jinju Peng, Qianling Xiong, Runyu Yuan, Lilian Zeng, Pingping Zhou, Chuming Liang, Lina Yi, Jun Liu, Jianpeng Xiao, Jianxiong Hu, Tao Liu, Wenjun Ma, Wei Li, Juan Su, Huanying Zheng, Bo Peng, Shisong Fang, Wenzhe Su, Kuibiao Li, Ruilin Sun, Ru Bai, Xi Tang, Minfeng Liang, Josh Quick, Tie Song, Andrew Rambaut, Nick Loman, Jayna Raghvani, Oliver Pybus, and Changwen Ke, *Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China*, *medRxiv* (2020), 2020.04.01.20047076 (en), S0011.
94. Junwen Luan, Yue Lu, Xiaolu Jin, and Leiliang Zhang, *Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection*, *Biochemical and Biophysical Research Communications* **526** (2020), no. 1, 165–169 (en), S0074.
95. Meghan May, Bahman Rostama, and Ryan F. Relich, *Selectomic and Evolvability Analyses of the Highly Pathogenic Betacoronaviruses SARS-CoV-2, SARS-CoV, and MERS-CoV*, *bioRxiv* (2020), 2020.05.05.078956 (en), S0089.
96. Luke W. Meredith, William L. Hamilton, Ben Warne, Charlotte J. Houldcroft, Myra Hosmillo, Aminu Jahun, Martin D. Curran, Surendra Parmar, Laura Caller, Sarah L. Caddy, Fahad A. Khokhar, Anna Yakovleva, Grant R. Hall, Theresa Feltwell, Sally N. Forret, Sushmita Sridhar, Michael p Weekes, Stephen Baker, Nicholas Brown, Elinor Moore, Theodore Gouliouris, Ashley Popay, Iain Roddick, Mark Reacher, Sharon Peacock, Gordon Dougan, M. Estee Torok, and Ian Goodfellow, *Rapid implementation of real-time SARS-CoV-2 sequencing to investigate healthcare-associated COVID-19 infections*, *medRxiv* (2020), 2020.05.08.20095687 (en), S0124.
97. Danielle Miller, Michael A. Martin, Noam Harel, Talia Kustin, Omer Tirosh, Moran Meir, Nadav Sorek, Shiraz Gefen-Halevi, Sharon Amit, Olesya Vorontsov, Dana Wolf, Avi Peretz, Yonat Shemer-Avni, Diana Roif-Kaminsky, Na’ama Kopelman, Amit Huppert, Katia Koelle, and Adi Stern, *Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel*, *medRxiv* (2020), 2020.05.21.20104521 (en), S0164.
98. Akhilesh Mishra, Ashutosh Kumar Pandey, Parul Gupta, Prashant Pradhan, Sonam Dhamija, James Gomes, Bishwajit Kundu, Perumal Vivekanandan, and Manoj B. Menon, *Mutation landscape of SARS-CoV-2 reveals three mutually exclusive clusters of leading and trailing single nucleotide substitutions*, *bioRxiv* (2020), 2020.05.07.082768 (en), S0122.

99. Leigh Monahan, *A protocol for massively parallel diagnosis and genome sequencing of SARS-CoV-2*, protocols.io (2020) (en), S0030.
100. Mami Nagashima, Ryota Kumagai, Isao Yoshida, Mamiyo Kawakami, Miyuki Nagano, Hiroyuki Asakura, Emiko Kaku, Yurie Kitamura, Michiya Hasegawa, Yukinao Hayashi, Takashi Chiba, Kenji Sadamasu, and Kazuhisa Yoshimura, *Characteristics of SARS-CoV-2 isolated from asymptomatic carrier in Tokyo*, Japanese Journal of Infectious Diseases **advpub** (2020), S0060.
101. Chase W. Nelson, Zachary Arden, Tony L. Goldberg, Chen Meng, Chen-Hao Kuo, Christina Ludwig, Sergios-Orestis Kolokotronis, and Xinzhu Wei, *A previously uncharacterized gene in SARS-CoV-2 illuminates the functional dynamics and evolutionary origins of the COVID-19 pandemic*, bioRxiv (2020), 2020.05.21.109280 (en), S0161.
102. Shijulal Nelson-Sathi, Umashankar Perunthottathu K, Sreekumar Easwaran, Radhakrishnan R. Nair, Iype Joseph, Sai Ravi Chandra Nori, Jamiema Sara Philip, Roshny Prasad, Kolaparamba V. Kolaparamba, Shikha Ramesh, Heera Pillai, Sanu Gosh, Santhosh Kumar Tr, and M. Radhakrishna Pillai, *Structural and Functional Implications of Non-synonymous Mutations in the Spike protein of 2,954 SARS-CoV-2 Genomes*, bioRxiv (2020), 2020.05.02.071811 (en), S0078.
103. Artem Nemudryi, Anna Nemudraia, Kevin Surya, Tanner Wiegand, Murat Buyukyoruk, Royce Wilkinson, and Blake Wiedenheft, *Temporal detection and phylogenetic assessment of SARS-CoV-2 in municipal wastewater*, medRxiv (2020), 2020.04.15.20066746 (en), S0046.
104. Rasmus Nielsen, Hongru Wang, and Lenore Pipes, *Synonymous mutations and the molecular evolution of SARS-Cov-2 origins*, bioRxiv (2020), 2020.04.20.052019 (en), S0048.
105. Islam Nour, Ibrahim O. Alanazi, Atif Hanif, Alain Kohl, and Saleh A. Eifan, *Insights into molecular evolution recombination of pandemic SARS-CoV-2 using Saudi Arabian sequences*, bioRxiv (2020), 2020.05.13.093971 (en), S0123.
106. Nadia Oreshkova, Robert-Jan Molenaar, Sandra Vreman, Frank Harders, Bas B. Oude Munnink, Renate W. Hakze-vd Honing, Nora Gerhards, Paulien Tolsma, Ruth Bouwstra, Reina Sikkema, Mirriam Tacken, Myrna M. T. de Rooij, Eefke Weesendorp, Marc Engelsma, Christianne Brusckke, Lidwien A. M. Smit, Marion Koopmans, Wim H. M. van der Poel, and J. A. Stegeman, *SARS-CoV2 infection in farmed mink, Netherlands, April 2020*, bioRxiv (2020), 2020.05.18.101493 (en), S0147.
107. Houcemeddine Othman, Zied Bouslama, Jean-Tristan Brandenburg, Jorge da Rocha, Yosr Hamdi, Kais Ghedira, Najet-Srairi Abid, and Scott Hazelhurst, *Interaction of the spike protein RBD from SARS-CoV-2 with ACE2: similarity with SARS-CoV, hot-spot analysis and effect of the receptor polymorphism*, bioRxiv (2020), 2020.03.04.976027 (en), S0097.
108. ine O'Toole and J T McCrone, *hCoV-2019/pangolin*, GitHub, April 2020, S0041.
109. Xumin Ou, Zhishuang Yang, Dekang Zhu, Sai Mao, Mingshu Wang, Renyong Jia, Shun Chen, Mafeng Liu, Qiao Yang, Ying Wu, Xinxin Zhao, Shaqiu Zhang, Juan Huang, Qun Gao, Yunya Liu, Ling Zhang, Maikel Peoplenbosch, Qiuwei Pan, and An-chun Cheng, *Tracing two causative SNPs reveals SARS-CoV-2 transmission in North America population*, bioRxiv (2020), 2020.05.12.092056 (en), S0130.
110. Szymon Pach, Trung Ngoc Nguyen, Jakob Trimpert, Dusan Kunec, Nikolaus Osterrieder, and Gerhard Wolber, *ACE2-Variants Indicate Potential SARS-CoV-2-Susceptibility in Animals: An Extensive Molecular Dynamics Study*, bioRxiv (2020), 2020.05.14.092767 (en), S0129.
111. Clinton R. Paden, Ying Tao, Krista Queen, Jing Zhang, Yan Li, Anna Uehara, and Suxiang Tong, *Rapid, sensitive, full genome sequencing of Severe Acute Respiratory Syndrome Virus Coronavirus 2 (SARS-CoV-2)*, bioRxiv (2020), 2020.04.22.055897 (en), S0053.
112. David J. Pascall, Kyriaki Nomikou, Emmanuel Brard, Stephan Zientara, Ana da Silva Filipe, Bernd Hoffmann, Maude Jacquot, Joshua B. Singer, Kris De Clercq, Anette Btner, Corinne Sailleau, Cyril Viarouge, Carrie Batten, Giantonella Puggioni, Ciriaco Ligios, Giovanni Savini, Piet A. van Rijn, Peter P. C. Mertens, Roman Biek, and Massimo Palmarini, *Frozen evolution of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence*, PLOS Biology **18** (2020), no. 4, e3000673 (en), S0057.
113. Jordan Peccia, Alessandro Zulli, Doug E. Brackney, Nathan D. Grubaugh, Edward H. Kaplan, Arnau Casanovas-Massana, Albert I. Ko, Aryn A. Malik, Dennis Wang, Mike Wang, Daniel M. Weinberger, and Saad B. Omer, *SARS-CoV-2 RNA concentrations in primary municipal sewage sludge as a leading indicator of COVID-19 outbreak dynamics*, medRxiv (2020), 2020.05.19.20105999 (en), S0163.



114. Vikas Peddu, Ryan C. Shean, Hong Xie, Lasata Shrestha, Garrett A. Perchetti, Samuel S. Minot, Pavitra Roychoudhury, Meei-Li Huang, Arun Nalla, Shriya B. Reddy, Quynh Phung, Adam Reinhardt, Keith R. Jerome, and Alexander L. Greninger, *Metagenomic analysis reveals clinical SARS-CoV-2 infection and bacterial or viral superinfection and colonization*, *Clinical Chemistry* (2020) (en), S0098.
115. Tung Phan, *Genetic diversity and evolution of SARS-CoV-2*, *Infection, Genetics and Evolution* **81** (2020), 104260, S0071.
116. Jody Phelan, Wouter Deelder, Daniel Ward, Susana Campino, Martin L. Hibberd, and Taane G. Clark, *Controlling the SARS-CoV-2 outbreak, insights from large scale whole genome sequences generated across the world*, *bioRxiv* (2020), 2020.04.28.066977 (en), S0158.
117. Ilya Plyusnin, Ravi Kant, Anne J. Jskelinen, Tarja Sironen, Liisa Holm, Olli Vapalahti, and Teemu Smura, *Novel NGS Pipeline for Virus Discovery from a Wide Spectrum of Hosts and Sample Types*, *bioRxiv* (2020), 2020.05.07.082107 (en), S0109.
118. Sergei Pond, *Natural selection analysis of SARS-CoV-2/COVID-19*, March 2020, S0019.
119. J Quick, *Artic-ncov2019 primer schemes*, 2020, S0013.
120. Ali Hosseini Rad and Alexander Donald McLellan, *Implications of SARS-CoV-2 mutations for genomic RNA structure and host microRNA targeting*, *bioRxiv* (2020), 2020.05.15.098947 (en), S0140.
121. Daniele Ramazzotti, Fabrizio Angaroni, Davide Maspero, Carlo Gambacorti-Passerini, Marco Antoniotti, Alex Graudenzi, and Rocco Piazza, *Characterization of intra-host SARS-CoV-2 variants improves phylogenomic reconstruction and may reveal functionally convergent mutations*, *bioRxiv* (2020), 2020.04.22.044404 (en), S0055.
122. Andrew Rambaut, Edward C Holmes, and Oliver G Pybus, *A dynamic nomenclature for SARS-CoV-2 to assist genomic epidemiology*, April 2020, S0018.
123. Walter Randazzo, Pilar Truchado, Enric Cuevas-Ferrando, Pedro Simn, Ana Allende, and Gloria Snchez, *SARS-CoV-2 RNA in wastewater anticipated COVID-19 occurrence in a low prevalence area*, *Water Research* (2020), 115942 (en), S0142.
124. Mikhail Rayko and Aleksey Komissarov, *Quality control of low-frequency variants in SARS-CoV-2 genomes*, *bioRxiv* (2020), 2020.04.26.062422 (en), S0084.
125. Paola Cristina Resende, Fernando Couto Motta, Sunando Roy, Luciana Appolinario, Alison Fabri, Joilson Xavier, Kathryn Harris, Aline Rocha Matos, Braulia Costa Caetano, Cristiana Couto Garcia, Milene Dias Miranda, Maria Ogrzewalska, Andre Abreu, Rachel Williams, Judith Breuer, and Marilda M. Siqueira, *SARS-CoV-2 genomes recovered by long amplicon tiling multiplex approach using nanopore sequencing and applicable to other sequencing platforms*, *bioRxiv* (2020), 2020.04.30.069039 (en), S0067.
126. Ranjit Sah, Alfonso J. Rodriguez-Morales, Runa Jha, Daniel K. W. Chu, Haogao Gu, Malik Peiris, Anup Bastola, Bibek Kumar Lal, Hemant Chanda Ojha, Ali A. Rabaan, Lysien I. Zambrano, Anthony Costello, Kouichi Morita, Basu Dev Pandey, and Leo L. M. Poon, *Complete Novel Coronavirus (SARS-CoV-2) Strain Isolated in Nepal*, *Microbiology Resource Announcements* **9** (2020), no. 11 (en), S0106.
127. Priyanka Saha, Arup Kumar Banerjee, Prem Prakash Tripathi, Amit Kumar Srivastava, and Upasana Ray, *A virus that has gone viral: Amino-acid mutation in S protein of Indian-isolate of Coronavirus COVID-19 might impact receptor-binding, thus infectivity*, *Bioscience Reports* (2020) (en), S0100.
128. Rashid Saif, Tania Mahmood, and Aniqaj Ejaz, *Whole Genome Comparison of Pakistani Corona Virus with Chinese and US Strains along with its Predictive Severity of COVID-19*, *bioRxiv* (2020), 2020.05.01.072942 (en), S0069.
129. Cecilia Salazar, Florencia Diaz-Viraque, Marianoel Pereira-Gomez, Ignacio Ferres, Pilar Moreno, Gonzalo Moratorio, and Gregorio Iraola, *Multiple introductions, regional spread and local differentiation during the first week of COVID-19 epidemic in Montevideo, Uruguay*, *bioRxiv* (2020), 2020.05.09.086223 (en), S0110.
130. Palash Sashittal, Yunan Luo, Jian Peng, and Mohammed El-Kebir, *Characterization of SARS-CoV-2 viral diversity within and across hosts*, *bioRxiv* (2020), 2020.05.07.083410 (en), S0121.
131. Torsten Seemann, Courtney Lane, Norelle Sherry, Sebastian Duchene, Anders Goncalves da Silva, Leon Caly, Michelle Sait, Susan A. Ballard, Kristy Horan, Mark B. Schultz, Tuyet Hoang, Marion Easton, Sally Dougall, Tim Stinear, Julian Druce, Mike Catton, Brett Sutton, Annaliese van Diemen, Charles Alpre, Deborah Williamson, and Benjamin P.

- Howden, *Tracking the COVID-19 pandemic in Australia using genomics*, medRxiv (2020), 2020.05.12.20099929 (en), S0139.
132. Tsuyoshi Sekizuka, Kentaro Itokawa, Tsutomu Kageyama, Shinji Saito, Ikuyo Takayama, Hideki Asanuma, Nao Naganori, Rina Tanaka, Masanori Hashino, Takuri Takahashi, Hajime Kamiya, Takuya Yamagishi, Kensaku Kakimoto, Motoi Suzuki, Hideki Hasegawa, Takaji Wakita, and Makoto Kuroda, *Haplotype networks of SARS-CoV-2 infections in the Diamond Princess cruise ship outbreak*, medRxiv (2020), 2020.03.23.20041970 (en), S0002.
  133. Amresh Kumar Sharma and Anup Som, *Deep phylogenetic analysis of Orthocoronavirinae genomes traces the origin, evolution and transmission route of 2019 novel coronavirus*, bioRxiv (2020), 2020.05.12.091199 (en), S0133.
  134. Lishuang Shen, Dennis Maglinte, Dejerianne Ostrow, Utsav Pandey, Moiz Bootwalla, Alex Ryutov, Ananthanarayanan Govindarajan, David Ruble, Jennifer Han, Timothy J. Triche, Jennifer Dien Bard, Jaclyn A. Biegel, Alexander R. Judkins, and Xiaowu Gai, *Children's Hospital Los Angeles COVID-19 Analysis Research Database (CARD) - A Resource for Rapid SARS-CoV-2 Genome Identification Using Interactive Online Phylogenetic Tools*, bioRxiv (2020), 2020.05.11.089763 (en), S0119.
  135. Peter Simmonds, *Rampant *c-zu* hypermutation in the genomes of SARS-CoV-2 and other coronaviruses causes and consequences for their short and long evolutionary trajectories*, bioRxiv (2020), 2020.05.01.072330 (en), S0065.
  136. Fang Song, Xiangyan Zhang, Yan Zha, and Weijia Liu, *COVID-19: Recommended sampling sites at different stage of the disease*, Journal of Medical Virology **n/a** (2020), no. n/a (en), S0039.
  137. Paola Stefanelli, Giovanni Faggioni, Alessandra Lo Presti, Stefano Fiore, Antonella Marchi, Eleonora Benedetti, Concetta Fabiani, Anna Anselmo, Andrea Ciammaruconi, Antonella Fortunato, Riccardo De Santis, Silvia Fillo, Maria Rosaria Capobianchi, Maria Rita Gismondo, Alessandra Ciervo, Giovanni Rezza, Maria Rita Castrucci, Florigio Lista, and on behalf of ISS COVID-19 study Group, *Whole genome and phylogenetic analysis of two SARS-CoV-2 strains isolated in Italy in January and February 2020: additional clues on multiple introductions and further circulation in Europe*, Eurosurveillance **25** (2020), no. 13, 2000305 (en), S0051.
  138. Ahmad Abou Tayoun, Tom Loney, Hamda Khansaheb, Sathishkumar Ramaswamy, Divinlal Harilal, Zulfa Deesi, Rupa Varghese, Hanan Al Suwaidi, Abdulmajeed Alkhajeh, Laila AID-abal, Mohammed Uddin, Abiola Senok, Rifat Hamoudi, Rabih Halwani, Qutayba Hamid, Norbert Nowotny, and Alawi Alsheikh-Ali, *Whole genome sequencing and phylogenetic analysis of SARS-CoV-2 strains from the index and early patients with COVID-19 in Dubai, United Arab Emirates, 29 January to 18 March 2020*, bioRxiv (2020), 2020.05.06.080606 (en), S0128.
  139. Shaolei Teng, Adebisi Sobotian, Raina Rhoades, Dongxiao Liu, and Qiyi Tang, *Systemic Effects of Missense Mutations on SARS-CoV-2 Spike Glycoprotein Stability and Receptor Binding Affinity*, bioRxiv (2020), 2020.05.21.109835 (en), S0160.
  140. Tran Thi Nhu Thao, Fabien Labrousseau, Nadine Ebert, Philip V'kovski, Hanspeter Stalder, Jasmine Portmann, Jenna Kelly, Silvio Steiner, Melle Holwerda, Annika Kratzel, Mitra Gultom, Kimberly Schmied, Laura Laloli, Linda Hsner, Manon Wider, Stephanie Pfaender, Dagny Hirt, Valentina Cipp, Silvia Crespo-Pomar, Simon Schrder, Doreen Muth, Daniela Niemeyer, Victor Corman, Marcel A. Mller, Christian Drosten, Ronald Dijkman, Joerg Jores, and Volker Thiel, *Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform*, Nature (2020) (eng), S0095.
  141. Fernando L. Tort, Matas Castells, and Juan Cristina, *A COMPREHENSIVE ANALYSIS OF GENOME COMPOSITION AND CODON USAGE PATTERNS OF EMERGING CORONAVIRUSES*, Virus Research (2020), 197976 (en), S0038.
  142. Emiliano Trucchi, Paolo Gratton, Fabrizio Mafessoni, Stefano Motta, Francesco Cicconardi, Giorgio Bertorelle, Ilda D'Annessa, and Daniele Di Marino, *Unveiling diffusion pattern and structural impact of the most invasive SARS-CoV-2 spike mutation*, bioRxiv (2020), 2020.05.14.095620 (en), S0126.
  143. Marc T. Valitutto, Ohnmar Aung, Kyaw Yan Naing Tun, Megan E. Vodzak, Dawn Zimmerman, Jennifer H. Yu, Ye Tun Win, Min Thein Maw, Wai Zin Thein, Htay Htay Win, Jasjeet Dhanota, Victoria Ontiveros, Brett Smith, Alexandre Tremereau-Brevard, Tracey Goldstein,

- Christine K. Johnson, Suzan Murray, and Jonna Mazet, *Detection of novel coronaviruses in bats in Myanmar*, PLOS ONE **15** (2020), no. 4, e0230802 (en), S0102.
144. Various, *Expert reaction to new paper making suggestions about stray dogs being a possible origin of SARS-CoV-2, the virus that causes COVID-19*, Science Media Centre, 2020, S0042.
  145. Timothy G. Vaughan, Gabriel E. Leventhal, David A. Rasmussen, Alexei J. Drummond, David Welch, and Tanja Stadler, *Estimating Epidemic Incidence and Prevalence from Genomic Data*, Molecular Biology and Evolution **36** (2019), no. 8, 1804–1816 (en), S0099.
  146. Lauro Velazquez-Salinas, Selene Zarate, Samantha Eberl, Douglas P. Gladue, Isabel Novella, and Manuel V. Borca, *Positive selection of ORF3a and ORF8 genes drives the evolution of SARS-CoV-2 during the 2020 COVID-19 pandemic*, bioRxiv (2020), 2020.04.10.035964 (en), S0027.
  147. C Julin Villabona-Arenas, William P. Hanage, and Damien C. Tully, *Phylogenetic interpretation during outbreaks requires caution*, Nature Microbiology (2020) (en), S0148.
  148. Thomas Villmann, Marika Kaden, Katrin Sophie Bohnsack, Mirko Weber, Mateusz Kudla, Kaja Gutowska, and Jacek Blazewicz, *Analysis of SARS-CoV-2 RNA-Sequences by Interpretable Machine Learning Models*, bioRxiv (2020), 2020.05.15.097741 (en), S0136.
  149. Erik M Volz, Han Fu, Haowei Wang, Xiaoyue Xi, Wei Chen, Dehui Liu, Chen Yingying, Mengmeng Tian, Wei Tan, Junji Zai, Wanying Sun, Jiandong Li, Junhua Li, Xingguang Li, and Qing Nie, *Phylogenetic analysis of a densely sampled COVID19 outbreak in Weifang, China*, March 2020, S0005.
  150. Andreas Walker, Torsten Houwaart, Tobias Wienemann, Malte Kohns Vasconcelos, Daniel Strelow, Tina Senff, Lisanna Hlse, Ortwin Adams, Marcel Andree, Sandra Hauka, Torsten Feldt, Bjrn-Erik Jensen, Verena Keitel, Detlef Kindgen-Milles, Jrg Timm, Klaus Pfeffer, and Alexander T. Dilthey, *Genetic structure of SARS-CoV-2 in Western Germany reflects clonal superspreading and multiple independent introduction events*, medRxiv (2020), 2020.04.25.20079517 (en), S0058.
  151. Jann-Tay Wang, You-Yu Lin, Sui-Yuan Chang, Shiou-Hwei Yeh, Bor-Hsian Hu, Pei-Jer Chen, and Shan-Chwen Chang, *The role of phylogenetic analysis in clarifying the infection source of a COVID-19 patient*, Journal of Infection **0** (2020), no. 0 (English), S0033.
  152. Yanqun Wang, Daxi Wang, Lu Zhang, Wanying Sun, Zhaoyong Zhang, Weijun Chen, Airu Zhu, Yongbo Huang, Fei Xiao, Jinxiu Yao, Mian Gan, Fang Li, Ling Luo, Xiaofang Huang, Yanjun Zhang, Sook-san Wong, Xinyi Cheng, Jingkai Ji, Zhihua Ou, Minfeng Xiao, Min Li, Jiandong Li, Peidi Ren, Ziqing Deng, Huanzi Zhong, Huanming Yang, Jian Wang, Xun Xu, Tie Song, Chris Mok, Malik Peiris, Nanshan Zhong, Jingxian Zhao, Yimin Li, Junhua Li, and Jincun Zhao, *Intra-host Variation and Evolutionary Dynamics of SARS-CoV-2 Population in COVID-19 Patients*, bioRxiv (2020), 2020.05.20.103549 (en), S0154.
  153. Daniel Ward, Matthew Higgins, Jody Phelan, Martin L. Hibberd, Susana Campino, and Taane G. Clark, *An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets*, bioRxiv (2020), 2020.05.11.089409 (en), S0132.
  154. Feng Wen, Hai Yu, Jinyue Guo, Yong Li, Kaijian Luo, and Shujian Huang, *Identification of the hyper-variable genomic hotspot for the novel coronavirus SARS-CoV-2*, Journal of Infection **80** (2020), no. 6, 671–693 (English), S0143.
  155. Shaoqing Wen and Xiao Zhang, *A High-Coverage SARS-CoV-2 Genome Sequence Acquired by Target Capture Sequencing*, medRxiv (2020), 2020.04.11.20061507 (en), S0035.
  156. Michael Worobey, Jonathan Pekar, Brendan B. Larsen, Martha I. Nelson, Verity Hill, Jeffrey B. Joy, Andrew Rambaut, Marc A. Suchard, Joel O. Wertheim, and Philippe Lemey, *The emergence of SARS-CoV-2 in Europe and the US*, bioRxiv (2020), 2020.05.21.109322 (en), S0165.
  157. Xuhua Xia, *Extreme genomic CpG deficiency in SARS-CoV-2 and evasion of host antiviral defense*, Molecular Biology and Evolution (2020) (eng), S0029.
  158. Kangpeng Xiao, Junqiong Zhai, Yaoyu Feng, Niu Zhou, Xu Zhang, Jie-Jian Zou, Na Li, Yaqiong Guo, Xiaobing Li, Xuejuan Shen, Zhipeng Zhang, Fanfan Shu, Wanyi Huang, Yu Li, Ziding Zhang, Rui-Ai Chen, Ya-Jiang Wu, Shi-Ming Peng, Mian Huang, Wei-Jun Xie, Qin-Hui Cai, Fang-Hui Hou, Wu Chen, Lihua Xiao, and Yongyi Shen, *Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins*, Nature (2020) (eng), S0101.

159. Hangping Yao, Xiangyun Lu, Qiong Chen, Kaijin Xu, Yu Chen, Linfang Cheng, Fumin Liu, Zhigang Wu, Haibo Wu, Changzhong Jin, Min Zheng, Nanping Wu, Chao Jiang, and Lanjuan Li, *Patient-derived mutations impact pathogenicity of SARS-CoV-2*, medRxiv (2020), 2020.04.14.20060160 (en), S0043.
160. Wen-Bin Yu, Guang-Da Tang, Li Zhang, and Richard T. Corlett, *Decoding the evolution and transmissions of the novel pneumonia coronavirus (SARS-CoV-2 / HCoV-19) using whole genomic data*, Zoological Research **41** (2020), no. 3, 247–257 (en), S0120.
161. Gianguglielmo Zehender, Alessia Lai, Annalisa Bergna, Luca Meroni, Agostino Riva, Claudia Balotta, Maciej Tarkowski, Arianna Gabrieli, Dario Bernacchia, Stefano Rusconi, Giuliano Rizzardini, Spinello Antinori, and Massimo Galli, *Genomic Characterisation and Phylogenetic Analysis of Sars-Cov-2 in Italy*, Journal of Medical Virology **n/a** (2020), no. n/a (en), S0003.
162. Shing Hei Zhan, Benjamin E. Deverman, and Yulia Alina Chan, *SARS-CoV-2 is well adapted for humans. What does this mean for re-emergence?*, bioRxiv (2020), 2020.05.01.073262 (en), S0079.