

# Publications for Vitali Sintchenko

## 2021

Tong, A., Sorrell, T., Black, A., Caillaud, C., Chrzanowski, W., Li, E., Martinez-Martin, D., McEwan, A., Wang, R., Motion, A., Casas Bedoya, A., Huang, J., Azizi, L., Eggleton, B., Andersen, T., Baillie, A., Barratt, A., Boehm, C., Britton, P., Chadban, S., Chow, C., Fleming, S., Fox, G., Gordon, L., Ho-Baillie, A., Howell, M., Hickie, I., Hunt, N., Iredell, J., Jin, C., Kairaitis, K., Kavehei, O., Kritharides, L., Leon-Saval, S., Lindley, R., Maguire, S., McCluskey, M., McKay, N., Mifsud, G., Palomba, S., Pettigrew, A., Postnova, S., Prinable, J., Rabeau, J., Rees, M., Richmond, K., Scholes Robertson, N., Seppelt, I., Shaw, T., Sintchenko, V., Snelling, T., Teixeira-Pinto, A., Tovey, E., Tuniz, A., Varamini, P., Wang, A., Wang, K., Wise, S., Zoellner, H., et al (2021). Research priorities for COVID-19 sensor technology. *Nature Biotechnology*, Published online: 18 January 2021. <a href="http://dx.doi.org/10.1038/s41587-021-00816-8">[More Information]</a>

## 2020

Eden, J., Rockett, R., Carter, I., Rahman, H., de Ligt, J., Hadfield, J., Storey, M., Ren, X., Tulloch, R., Basile, K., Sintchenko, V., Chen, S., Maddocks, S., Sorrell, T., Holmes, E., Dwyer, D., et al (2020). An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. *Virus Evolution*, 6(1), veaa027. <a href="http://dx.doi.org/10.1093/ve/veaa027">[More Information]</a>

He, W., Kirk, M., Sintchenko, V., Hall, J., Liu, B. (2020). Antibiotic Use Associated with Confirmed Influenza, Pertussis, and Nontyphoidal Salmonella Infections. *Microbial Drug Resistance: Mechanisms Epidemiology And Disease*, 26(12), 1482-1490. <a href="http://dx.doi.org/10.1089/mdr.2020.0017">[More Information]</a>

Degeling, C., Carter, S., Van Oijen, A., McAnulty, J., Sintchenko, V., Braunack-Mayer, A., Yarwood, T., Johnson, J., Gilbert, G. (2020). Community perspectives on the benefits and risks of technologically enhanced communicable disease surveillance systems: A report on four community juries. *BMC Medical Ethics*, 21(1), 31. <a href="http://dx.doi.org/10.1186/s12910-020-00474-6">[More Information]</a>

Baines, S., da Silva, A., Carter, G., Jennison, A., Rathnayake, I., Graham, R., Sintchenko, V., Wang, Q., Rockett, R., Timms, V., et al (2020). Complete microbial genomes for public health in Australia and the southwest Pacific. *Microbial Genomics*, 6(12), 1-12. <a href="http://dx.doi.org/10.1099/mgen.0.000471">[More Information]</a>

Rukambile, E., Muscatello, G., Sintchenko, V., Thomson, P., Maulaga, W., Mmassy, R., Bruyn, J., Kock, R., Darnton-Hill, I., Alders, R. (2020). Determinants of diarrhoeal diseases and height-for-age Z-scores in children under five years of age in rural central Tanzania. *Journal of Preventive Medicine and Hygiene*, 61(3), E409-E423. <a href="http://dx.doi.org/10.15167/2421-4248/jpmh2020.61.3.1486">[More Information]</a>

Struelens, M., Sintchenko, V. (2020). Editorial: Pathogen Genomics: Empowering Infectious Disease Surveillance and Outbreak Investigations. *Frontiers in Public Health*, 8, 179. <a href="http://dx.doi.org/10.3389/fpubh.2020.00179">[More Information]</a>

<a href="http://dx.doi.org/10.3389/fpubh.2020.00179">[More Information]</a>

Outhred, A., Gurjav, U., Jelfs, P., McCallum, N., Wang, Q., Hill-Cawthorne, G., Marais, B., Sintchenko, V. (2020). Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern Mycobacterium tuberculosis Lineages. *Frontiers in Public Health*, 8, 455. <a href="http://dx.doi.org/10.3389/fpubh.2020.00455">[More Information]</a>

Biswas, C., Wang, Q., Van Hal, S., Eyre, D., Hudson, B., Halliday, C., Mazsewska, K., Gordon, A., Lee, A., Irinyi, L., Meyer, W., Sintchenko, V., Chen, S., et al (2020). Genetic Heterogeneity of Australian Candida auris Isolates: Insights From a Nonoutbreak Setting Using Whole-Genome Sequencing. *Open forum infectious diseases*, 7(5), 1-5. <a href="http://dx.doi.org/10.1093/ofid/ofaa158">[More Information]</a>

Rockett, R., Arnott, A., Wang, Q., Howard, P., Sintchenko, V. (2020). Genomic surveillance enables suitability assessment of salmonella gene targets used for culture-independent diagnostic testing. *Journal of Clinical Microbiology*, 58(9), e00038-20. <a href="http://dx.doi.org/10.1128/JCM.00038-20">[More Information]</a>

Zhang, X., Payne, M., Wang, Q., Sintchenko, V., Lan, R. (2020). Highly Sensitive and Specific Detection and Serotyping of Five Prevalent Salmonella Serovars by Multiple Cross-Displacement Amplification. *The Journal of Molecular Diagnostics*, 22(5), 708-719. <a href="http://dx.doi.org/10.1016/j.jmoldx.2020.02.006">[More Information]</a>

McKew, G., Ramsperger, M., Cheong, E., Gottlieb, T., Sintchenko, V., O'Sullivan, M. (2020). Hospital MRSA outbreaks: Multiplex PCR-reverse line blot binary typing as a screening method for WGS, and the role of the environment in transmission. *Infection, Disease and Health*, 25(4), 268-276. <a href="http://dx.doi.org/10.1016/j.idh.2020.05.007">[More Information]</a>

Cliff, O., Mclean, N., Sintchenko, V., Fair, K., Sorrell, T., Kauffman, S., Prokopenko, M. (2020). Inferring evolutionary pathways and directed genotype networks of foodborne pathogens. *PLoS Computational Biology*, 16(10), 1-22. <a href="http://dx.doi.org/10.1371/journal.pcbi.1008401">[More Information]</a>

Rahman, H., Carter, I., Basile, K., Donovan, L., Kumar, S., Tran, T., Ko, D., Alderson, S., Sivaruban, T., Eden, J., O'Sullivan, M., Sintchenko, V., Chen, S., Dwyer, D., et al (2020). Interpret with caution: An evaluation of the commercial AusDiagnostics versus in-house developed assays for the detection of SARS-CoV-2 virus. *Journal Of Clinical Virology*, 127, 104374. <a href="http://dx.doi.org/10.1016/j.jcv.2020.104374">[More Information]</a>

Bachmann, N., Salamzade, R., Manson, A., Whittington, R., Sintchenko, V., Earl, A., Marais, B. (2020). Key Transitions in the Evolution of Rapid and Slow Growing Mycobacteria Identified by Comparative Genomics. *Frontiers in Microbiology*, 10, 1-12. <a href="http://dx.doi.org/10.3389/fmicb.2019.03019">[More Information]</a>

Information]

Meder, K., Jayasinghe, S., Beard, F., Dey, A., Kirk, M., Cook, H., Sintchenko, V., Smith, H., Giele, C., Howden, B., et al (2020). Long-term Impact of Pneumococcal Conjugate Vaccines on Invasive Disease and Pneumonia Hospitalizations in Indigenous and Non-Indigenous Australians. *Clinical Infectious Diseases*, 70(12), 2607-2615. <a href="http://dx.doi.org/10.1093/cid/ciz731">[More Information]

Payne, M., Kaur, S., Wang, Q., Hennessy, D., Luo, L., Octavia, S., Tanaka, M., Sintchenko, V., Lan, R. (2020). Multilevel genome typing: Genomics-guided scalable resolution typing of microbial pathogens. *Eurosurveillance*, 25(20). <a href="http://dx.doi.org/10.2807/1560-7917.ES.2020.25.20.1900519">[More Information]

Fong, W., Rockett, R., Timms, V., Sintchenko, V. (2020). Optimization of sample preparation for culture-independent sequencing of Bordetella pertussis. *Microbial Genomics*, 6(3), 332. <a href="http://dx.doi.org/10.1099/mgen.0.000332">[More Information]

Basile, K., Habibur Rahman, H., Carter, I., Donovan, L., Kumar, S., Tran, T., Ko, D., Alderson, S., Sivaruban, T., Eden, J., Rockett, R., O'Sullivan, M., Sintchenko, V., Chen, S., Maddocks, S., Dwyer, D., Kok, J. (2020). Response. *Journal Of Clinical Virology*, 130. <a href="http://dx.doi.org/10.1016/j.jcv.2020.104484">[More Information]

Rockett, R., Arnott, A., Lam, C., Sadsad, R., Timms, V., Gray, K., Eden, J., Chang, S., Gall, M., Draper, J., O'Sullivan, M., Chen, S., Sorrell, T., Dwyer, D., Holmes, E., Kok, J., Prokopenko, M., Sintchenko, V., et al (2020). Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. *Nature Medicine*, 26(9), 1398-1404. <a href="http://dx.doi.org/10.1038/s41591-020-1000-7">[More Information]

Luu, L., Octavia, S., Aitken, C., Zhong, L., Raftery, M., Sintchenko, V., Lan, R. (2020). Surfaceome analysis of Australian epidemic Bordetella pertussis reveals potential vaccine antigens. *Vaccine*, 38(3), 539-548. <a href="http://dx.doi.org/10.1016/j.vaccine.2019.10.062">[More Information]

Hueston, L., Kok, J., Guibone, A., McDonald, D., Hone, G., Goodwin, J., Carter, I., Basile, K., Sandaradura, I., Maddocks, S., Sintchenko, V., Chen, S., Dwyer, D., O'Sullivan, M., et al (2020). The antibody response to SARS-CoV-2 infection. *Open forum infectious diseases*, 7(9), ofaa387. <a href="http://dx.doi.org/10.1093/ofid/ofaa387">[More Information]

Yeong, C., Byrne, A., Cho, J., Sintchenko, V., Crighton, T., Marais, B. (2020). Use of GeneXpert MTB/RIF on a single pooled sputum specimen to exclude pulmonary tuberculosis among hospital inpatients placed in respiratory isolation. *International Journal of Infectious Diseases*, 92, 175-180. <a href="http://dx.doi.org/10.1016/j.ijid.2019.12.024">[More Information]

## 2019

Collins, J., Simpson, K., Bell, G., Durrheim, D., Hill-Cawthorne, G., Hope, K., Howard, P., Kohlenberg, T., Lawrence, K., Lilly, K., Sintchenko, V., Ward, M., Wiethoelter, A., Mor, S., et al (2019). A One Health investigation of Salmonella enterica serovar Wangata in north-eastern New South Wales, Australia, 2016-2017. *Epidemiology and Infection*, 147, 1-11. <a href="http://dx.doi.org/10.1017/S0950268819000475">[More

Information]

Alffenaar, J., Sintchenko, V., Marais, B. (2019). Acquired Drug Resistance: Recognizing the Potential of Repurposed Drugs. *Clinical Infectious Diseases*, 69(11), 2038-2039. <a href="http://dx.doi.org/10.1093/cid/ciz334">[More Information]

Hunt, M., Bradley, P., Lapierre, S., Heys, S., Thomsit, M., Hall, M., Malone, K., Wintringer, P., Walker, T., Cirillo, D., Sintchenko, V., et al (2019). Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. *Wellcome Open Research*, 4, 1-32. <a href="http://dx.doi.org/10.12688/wellcomeopenres.15603.1">[More Information]

Quan, D., Nagalingam, G., Luck, I., Proschogo, N., Pillalamarri, V., Addlagatta, A., Martinez, E., Sintchenko, V., Rutledge, P., Triccas, J. (2019). Bengamides display potent activity against drug-resistant Mycobacterium tuberculosis. *Scientific Reports*, 9(1), 14396. <a href="http://dx.doi.org/10.1038/s41598-019-50748-2">[More Information]

Marks, G., Nguyen, N., Nguyen, P., Nguyen, T., Nguyen, H., Tran, K., Nguyen, S., Luu, K., Tran, D., Vo, Q., Do, Q., Mason, P., Sintchenko, V., Britton, W., Fox, G., et al (2019). Community-wide Screening for Tuberculosis in a High-Prevalence Setting. *New England Journal of Medicine*, 381(14), 1347-1357. <a href="http://dx.doi.org/10.1056/NEJMoa1902129">[More Information]

Bainomugisa, A., Pandey, S., Donnan, E., Simpson, G., Foster, J., Lavu, E., Hiasihri, S., McBryde, E., Moke, R., Vincent, S., Sintchenko, V., Marais, B., et al (2019). Cross-border movement of highly drug-resistant Mycobacterium tuberculosis from Papua New Guinea to Australia through Torres Strait protected zone, 2010-2015. *Emerging Infectious Diseases*, 25(3), 406-415. <a href="http://dx.doi.org/10.3201/eid2503.181003">[More Information]

Phuong, N., Anh, N., Son, N., Sintchenko, V., Ho, J., Fox, G., Nhung, N., Marks, G. (2019). Effect of two alternative methods of pooling sputum prior to testing for tuberculosis with GeneXpert MTB/RIF. *BMC Infectious Diseases*, 19(1), 1-4. <a href="http://dx.doi.org/10.1186/s12879-019-3778-9">[More Information]

Timms, V., Fong, W., Jeffreys, N., Sintchenko, V. (2019). Evaluation of the BioGX BD-Max PCR assay for detection of pathogenic Bordetella. *Pathology*, 51(3), 323-324. <a href="http://dx.doi.org/10.1016/j.pathol.2018.10.018">[More Information]

Dhakar, R., Wang, Q., Howard, P., Sintchenko, V. (2019). Genome Sequences of Enteroinvasive Escherichia coli Sequence Type 6, 99, and 311 Strains Acquired in Asia Pacific. *Microbiology Resource Announcements*, 8(36), 1-2. <a href="http://dx.doi.org/10.1128/MRA.00944-19">[More Information]

Rukambile, E., Sintchenko, V., Muscatello, G., Kock, R., Alders, R. (2019). Infection, colonization and shedding of Campylobacter and Salmonella in animals and their contribution to human disease: A review. *Zoonoses and Public Health*, 66(6), 562-578. <a href="http://dx.doi.org/10.1111/zph.12611">[More Information]

Cliff, O., Sintchenko, V., Sorrell, T., Vadlamudi, K., Mclean, N., Prokopenko, M. (2019). Network properties of salmonella epidemics. *Scientific Reports*, 9(1), 1-6. <a href="http://dx.doi.org/10.1038/s41598-019-42582-3">[More

Information]

Kim, H., Sintchenko, V., Alffenaar, J. (2019). Nontuberculosis mycobacteria infections: would there be pharmacodynamics without pharmacokinetics? *European Respiratory Journal*, 54(5), 1901508. <a href="http://dx.doi.org/10.1183/13993003.01508-2019">[More Information]

Xu, Z., Octavia, S., Luu, L., Payne, M., Timms, V., Tay, C., Keil, A., Sintchenko, V., Guiso, N., Lan, R. (2019). Pertactin-Negative and Filamentous Hemagglutinin-Negative Bordetella pertussis, Australia, 2013-2017. *Emerging Infectious Diseases*, 25(6), 1196-1199. <a href="http://dx.doi.org/10.3201/eid2506.180240">[More Information]

Schon, T., Matuschek, E., Mohamed, S., Utukuri, M., Heysell, S., Alffenaar, J., Shin, S., Martinez, E., Sintchenko, V., Keller, P., et al (2019). Standards for MIC testing that apply to the majority of bacterial pathogens should also be enforced for Mycobacterium tuberculosis complex. *Clinical Microbiology and Infection*, 25(4), 403-405. <a href="http://dx.doi.org/10.1016/j.cmi.2019.01.019">[More Information]

Williamson, D., Kirk, M., Sintchenko, V., Howden, B. (2019). The importance of public health genomics for ensuring health security for Australia. *Medical Journal of Australia*, 210(7), 295-297.e1. <a href="http://dx.doi.org/10.5694/mja2.50063">[More Information]

Surian, D., Kim, V., Menon, R., Dunn, A., Sintchenko, V., Coiera, E. (2019). Tracking a moving user in indoor environments using Bluetooth low energy beacons. *Journal of Biomedical Informatics*, 98, 1-9. <a href="http://dx.doi.org/10.1016/j.jbi.2019.103288">[More Information]

Mai, T., Martinez, E., Menon, R., Van Anh, N., Hien, N., Lan, N., Giang, D., Hang, P., Thuong, P., Huan, H., Marais, B., Sintchenko, V., et al (2019). Tuberculosis risk factors and Mycobacterium tuberculosis transmission among HIV-infected patients in Vietnam. *Tuberculosis*, 115, 67-75. <a href="http://dx.doi.org/10.1016/j.tube.2019.02.001">[More Information]

## 2018

Bachmann, N., Rockett, R., Timms, V., Sintchenko, V. (2018). Advances in clinical sample preparation for identification and characterization of bacterial pathogens using metagenomics. *Frontiers in Public Health*, 6, 1-8. <a href="http://dx.doi.org/10.3389/fpubh.2018.00363">[More Information]

Leong, L., Lagana, D., Carter, G., Wang, Q., Smith, K., Stinear, T., Shaw, D., Sintchenko, V., Wesselingh, S., Bastian, I., et al (2018). Burkholderia lata infections from intrinsically contaminated chlorhexidine Mouthwash, Australia, 2016. *Emerging Infectious Diseases*, 24(11), 2109-2111. <a href="http://dx.doi.org/10.3201/eid2411.171929">[More Information]

Overton, K., Mennon, V., Mothobi, N., Neild, B., Martinez, E., Masters, J., Grant, P., Akhunji, Z., Su, W., Torda, A., Sintchenko, V., et al (2018). Cluster of invasive Mycobacteria chimaera infections following cardiac surgery demonstrating novel clinical features and risks of aortic valve replacement. *Internal Medicine Journal*, 48(12), 1514-1520. <a href="http://dx.doi.org/10.1111/imj.14093">[More Information]

Luu, L., Octavia, S., Zhong, L., Raftery, M., Sintchenko, V.,

Lan, R. (2018). Comparison of the Whole Cell Proteome and Secretome of Epidemic Bordetella pertussis Strains From the 2008-2012 Australian Epidemic Under Sulfate-Modulating Conditions. *Frontiers in Microbiology*, 9, 1-13. <a href="http://dx.doi.org/10.3389/fmicb.2018.02851">[More Information]

Fong, W., Timms, V., Holmes (nee McCallum), N., Sintchenko, V. (2018). Detection and incidence of Bordetella holmesii in respiratory specimens from patients with pertussis-like symptoms in New South Wales, Australia. *Pathology*, 50(3), 322-326. <a href="http://dx.doi.org/10.1016/j.pathol.2017.10.014">[More Information]

Timms, V., Rockett, R., Bachmann, N., Martinez, E., Wang, Q., Chen, S., Jeoffreys, N., Howard, P., Smith, A., Adamson, S., Sintchenko, V., et al (2018). Genome sequencing links persistent outbreak of legionellosis in Sydney (New South Wales, Australia) to an emerging clone of Legionella pneumophila sequence type 211. *Applied and Environmental Microbiology*, 84(5), 1-10. <a href="http://dx.doi.org/10.1128/AEM.02020-17">[More Information]

Rockett, R., Oftadeh, S., Bachmann, N., Timms, V., Kong, F., Gilbert, G., Sintchenko, V. (2018). Genome-wide analysis of Streptococcus pneumoniae serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. *Scientific Reports*, 8(1), 1-9. <a href="http://dx.doi.org/10.1038/s41598-018-35270-1">[More Information]

Timms, V., Nguyen, T., Crighton, T., Yuen, M., Sintchenko, V. (2018). Genome-wide comparison of Corynebacterium diphtheriae isolates from Australia identifies differences in the Pan-genomes between respiratory and cutaneous strains. *BMC Genomics*, 19(1), 1-10. <a href="http://dx.doi.org/10.1186/s12864-018-5147-2">[More Information]

Ford, L., Carter, G., Wang, Q., Seemann, T., Sintchenko, V., Glass, K., Williamson, D., Howard, P., Valcanis, M., Sotomayor Castillo, C., Sait, M., et al (2018). Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of Salmonella Typhimurium in Australia. *Foodborne Pathogens and Disease*, 15(3), 161-167. <a href="http://dx.doi.org/10.1089/fpd.2017.2352">[More Information]

Arnott, A., Wang, Q., Bachmann, N., Sadsad, R., Biswas, C., Sotomayor Castillo, C., Howard, P., Rockett, R., Wiklendt, A., Iredell, J., Sintchenko, V. (2018). Multidrug-resistant Salmonella enterica 4,[5],12: I- sequence type 34, New South Wales, Australia, 2016-2017. *Emerging Infectious Diseases*, 24(4), 751-753. <a href="http://dx.doi.org/10.3201/eid2404.171619">[More Information]

Martinez, E., Hennessy, D., Jelfs, P., Crighton, T., Chen, S., Sintchenko, V. (2018). Mutations associated with in vitro resistance to bedaquiline in Mycobacterium tuberculosis isolates in Australia. *Tuberculosis*, 111, 31-34. <a href="http://dx.doi.org/10.1016/j.tube.2018.04.007">[More Information]

Mai, T., Martinez, E., Menon, R., Van Anh, N., Hien, N., Marais, B., Sintchenko, V. (2018). Mycobacterium tuberculosis drug resistance and transmission among human immunodeficiency virus<sub>i</sub>½infected patients in Ho Chi Minh City, Vietnam. *American Journal of Tropical Medicine and Hygiene*, 99(6), 1397-1406. <a href="http://dx.doi.org/10.4269/ajtmh.18-0185">[More

Information]</a>

Dhakal, R., Wang, Q., Lan, R., Howard, P., Sintchenko, V. (2018). Novel multiplex PCR assay for identification and subtyping of enteroinvasive escherichia coli and differentiation from shigella based on target genes selected by comparative genomics. *Journal of Medical Microbiology*, 67(9), 1257-1264. <a href="http://dx.doi.org/10.1099/jmm.0.000784">[More Information]</a>

Sotomayor Castillo, C., Wang, Q., Arnott, A., Howard, P., Hope, K., Lan, R., Sintchenko, V. (2018). Novel salmonella enterica serovar typhimurium genotype levels as herald of seasonal salmonellosis epidemics. *Emerging Infectious Diseases*, 24(6), 1079-1082. <a href="http://dx.doi.org/10.3201/eid2406.171096">[More Information]</a>

Luu, L., Octavia, S., Zhong, L., Raftery, M., Sintchenko, V., Lan, R. (2018). Proteomic Adaptation of Australian Epidemic Bordetella pertussis. *Proteomics*, 18(8), 1-12. <a href="http://dx.doi.org/10.1002/pmic.201700237">[More Information]</a>

Parvaresh, L., Crighton, T., Martinez, E., Bustamante, A., Chen, S., Sintchenko, V. (2018). Recurrence of tuberculosis in a low-incidence setting: a retrospective cross-sectional study augmented by whole genome sequencing. *BMC Infectious Diseases*, 18(1), 265. <a href="http://dx.doi.org/10.1186/s12879-018-3164-z">[More Information]</a>

Van Hal, S., Beukers, A., Timms, V., Ellem, J., Taylor, P., Maley, M., Newton, P., Ferguson, J., Lee Andie, S., Chen, S., Sintchenko, V. (2018). Relentless spread and adaptation of non-typeable vanA vancomycin-resistant Enterococcus faecium: a genome-wide investigation. *Journal of Antimicrobial Chemotherapy*, 73(6), 1487-1491. <a href="http://dx.doi.org/10.1093/jac/dky074">[More Information]</a>

Ford, L., Wang, Q., Stafford, R., Ressler, K., Norton, S., Shadbolt, C., Hope, K., Franklin, N., Krsteski, R., Carswell, A., Sotomayor Castillo, C., Sintchenko, V., et al (2018). Seven Salmonella Typhimurium Outbreaks in Australia Linked by Trace-Back and Whole Genome Sequencing. *Foodborne Pathogens and Disease*, 15(5), 285-292. <a href="http://dx.doi.org/10.1089/fpd.2017.2353">[More Information]</a>

Biswas, C., Marcelino, V., Van Hal, S., Halliday, C., Martinez, E., Wang, Q., Kidd, S., Kennedy, K., Marriott, D., Morrissey, C., Sorrell, T., Sintchenko, V., Meyer, W., Chen, S., et al (2018). Whole Genome Sequencing of Australian Candida glabrata Isolates Reveals Genetic Diversity and Novel Sequence Types. *Frontiers in Microbiology*, 9, 1-12. <a href="http://dx.doi.org/10.3389/fmicb.2018.02946">[More Information]</a>

Chawla, K., Martinez, E., Kumar, A., Shenoy, V., Sintchenko, V. (2018). Whole genome sequencing reveals genetic signature of bedaquiline resistance in a clinical isolate of Mycobacterium tuberculosis. *Journal of Global Antimicrobial Resistance*, 15, 103-104. <a href="http://dx.doi.org/10.1016/j.jgar.2018.09.006">[More Information]</a>

## 2017

Marais, B., Walker, T., Cirillo, D., Raviglione, M., Abubakar, I., Van Der Werf, M., Boehme, C., Niemann, S., Castro, K., Zumla, A., Sintchenko, V., et al (2017). Aiming for zero tuberculosis transmission in low-burden countries. *The Lancet Respiratory Medicine*, 5(11), 846-848. <a href="http://dx.doi.org/10.1016/S2213-2600(17)30382-"

X">[More Information]</a>

Luu, L., Octavia, S., Zhong, L., Raftery, M., Sintchenko, V., Lan, R. (2017). Characterisation of the Bordetella pertussis secretome under different media. *Journal of Proteomics*, 158, 43-51. <a href="http://dx.doi.org/10.1016/j.jprot.2017.02.010">[More Information]</a>

Fu, S., Hiley, L., Octavia, S., Tanaka, M., Sintchenko, V., Lan, R. (2017). Comparative genomics of Australian and international isolates of Salmonella Typhimurium: Correlation of core genome evolution with CRISPR and prophage profiles. *Scientific Reports*, 7(9733), 1-12. <a href="http://dx.doi.org/10.1038/s41598-017-06079-1">[More Information]</a>

Mai, T., Van Anh, N., Hien, N., Lan, N., Giang, D., Hang, P., Lan, N., Marais, B., Sintchenko, V. (2017). Drug resistance and Mycobacterium tuberculosis strain diversity in TB/HIV co-infected patients in Ho Chi Minh city, Vietnam. *Journal of Global Antimicrobial Resistance*, 10, 154-160. <a href="http://dx.doi.org/10.1016/j.jgar.2017.07.003">[More Information]</a>

Marais, B., Sintchenko, V. (2017). Epidemic spread of multidrug-resistant tuberculosis in China. *The Lancet Infectious Diseases*, 17(3), 238-239. <a href="http://dx.doi.org/10.1016/S1473-3099(16)30526-6">[More Information]</a>

Thompson, C., Wang, Q., Bag, S., Franklin, N., Shadbolt, C., Howard, P., Fearnley, E., Quinn, H., Sintchenko, V., Hope, K. (2017). Epidemiology and whole genome sequencing of an ongoing point-source Salmonella Agona outbreak associated with sushi consumption in western Sydney, Australia 2015. *Epidemiology and Infection*, 145(10), 2062-2071. <a href="http://dx.doi.org/10.1017/S0950268817000693">[More Information]</a>

Eden, J., Rose, K., Ng, J., Shi, M., Wang, Q., Sintchenko, V., Holmes, E. (2017). Francisella tularensis subsp. holarctica in Ringtail Possums, Australia. *Emerging Infectious Diseases*, 23(7), 1198-1201. <a href="http://dx.doi.org/10.3201/eid2307.161863">[More Information]</a>

Octavia, S., Wang, Q., Tanaka, M., Sintchenko, V., Lan, R. (2017). Genomic heterogeneity of Salmonella enterica serovar Typhimurium bacteriuria from chronic infection. *Infection, Genetics and Evolution*, 51, 17-20. <a href="http://dx.doi.org/10.1016/j.meegid.2017.03.004">[More Information]</a>

Biswas, C., Chen, S., Halliday, C., Kennedy, K., Playford, E., Marriott, D., Slavin, M., Sorrell, T., Sintchenko, V. (2017). Identification of genetic markers of resistance to echinocandins, azoles and 5-fluorocytosine in Candida glabrata by next-generation sequencing: a feasibility study. *Clinical Microbiology and Infection*, 23(9), 676.e7-676.e10. <a href="http://dx.doi.org/10.1016/j.cmi.2017.03.014">[More Information]</a>

Ho, P., Jelfs, P., Nguyen, P., Sintchenko, V., Fox, G., Marks, G. (2017). Pooling sputum samples to improve the feasibility of Xpert(i<sub>2</sub>) MTB/RIF in systematic screening for tuberculosis. *International Journal of Tuberculosis and Lung Disease*, 21(5), 503-508. <a href="http://dx.doi.org/10.5588/ijtld.16.0846">[More Information]</a>

Biswas, C., Chen, S., Halliday, C., Martinez, E., Rockett, R., Wang, Q., Timms, V., Dhakal, R., Sadsad, R., Kennedy, K., Sorrell, T., Sintchenko, V., et al (2017). Whole Genome Sequencing of Candida glabrata for Detection of Markers of

Antifungal Drug Resistance. *Journal of Visualized Experiments*, December(130), 1-13. <a href="http://dx.doi.org/10.3791/56714">[More Information]</a>

## 2016

Subedi, S., Kong, F., Jelfs, P., Gray, T., Xiao, M., Sintchenko, V., Chen, S. (2016). 16S-23S internal transcribed spacer region PCR and sequencer-based capillary gel electrophoresis has potential as an alternative to high performance liquid chromatography for identification of slowly growing nontuberculous mycobacteria. *PLoS One*, 11(10), 1-15. <a href="http://dx.doi.org/10.1371/journal.pone.0164138">[More Information]</a>

Safarchi, A., Octavia, S., Luu, L., Tay, C., Sintchenko, V., Wood, N., Marshall, H., McIntyre, P., Lan, R. (2016). Better colonisation of newly emerged *Bordetella pertussis* in the co-infection mouse model study. *Vaccine*, 34(34), 3967-3971. <a href="http://dx.doi.org/10.1016/j.vaccine.2016.06.052">[More Information]</a>

Dickeson, D., Chen, S., Sintchenko, V. (2016). Concordance of four commercial enzyme immunoassay and three immunoblot formats for the detection of Lyme borreliosis antibodies in human serum: The two-tier approach remains. *Pathology*, 48(3), 251-256. <a href="http://dx.doi.org/10.1016/j.pathol.2016.02.004">[More Information]</a>

Moradigaravand, D., Grandjean, L., Martinez, E., Li, H., Zheng, J., Coronel, J., Moore, D., Torok, M., Sintchenko, V., Huang, H., et al (2016). DfrA-thyA double deletion in para-aminosalicylic acid resistant *Mycobacterium tuberculosis* Beijing strains. *Antimicrobial Agents and Chemotherapy*, 60(6), 3864-3867. <a href="http://dx.doi.org/10.1128/AAC.00253-16">[More Information]</a>

Fu, S., Octavia, S., Wang, Q., Tanaka, M., Tay, C., Sintchenko, V., Lan, R. (2016). Evolution of variable number tandem repeats and its relationship with genomic diversity in *Salmonella typhimurium*. *Frontiers in Microbiology*, 7, 1-12. <a href="http://dx.doi.org/10.3389/fmicb.2016.02002">[More Information]</a>

Safarchi, A., Octavia, S., Wu, S., Kaur, S., Sintchenko, V., Gilbert, G., Wood, N., McIntyre, P., Marshall, H., Keil, A., et al (2016). Genomic dissection of Australian *Bordetella pertussis* isolates from the 2008-2012 epidemic. *Journal of Infection*, 72(4), 468-477. <a href="http://dx.doi.org/10.1016/j.jinf.2016.01.005">[More Information]</a>

Gurjav, U., Jelfs, P., Hill-Cawthorne, G., Marais, B., Sintchenko, V. (2016). Genotype heterogeneity of *Mycobacterium tuberculosis* within geospatial hotspots suggests foci of imported infection in Sydney, Australia. *Infection, Genetics and Evolution*, 40, 346-351. <a href="http://dx.doi.org/10.1016/j.meegid.2015.07.014">[More Information]</a>

Outhred, A., Holmes, N., Sadsad, R., Martinez, E., Jelfs, P., Hill-Cawthorne, G., Gilbert, G., Marais, B., Sintchenko, V. (2016). Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. *PLoS One*, 11(3), 1-15. <a href="http://dx.doi.org/10.1371/journal.pone.0150550">[More Information]</a>

Yu, M., Nagalingam, G., Ellis, S., Martinez, E., Sintchenko, V., Spain, M., Rutledge, P., Todd, M., Triccas, J. (2016). Nontoxic metal-cyclam complexes, a new class of compounds with potency against drug-resistant *Mycobacterium tuberculosis*. *Journal of Medicinal Chemistry*, 59(12), 5917-5921. <a href="http://dx.doi.org/10.1021/acs.jmedchem.6b00432">[More Information]</a>

Chan, C., Octavia, S., Sintchenko, V., Lan, R. (2016). SnpFilt: A pipeline for reference-free assembly-based identification of SNPs in bacterial genomes. *Computational Biology and Chemistry*, 65, 178-184. <a href="http://dx.doi.org/10.1016/j.compbiolchem.2016.09.004">[More Information]</a>

Clarke, M., McIntyre, P., Blyth, C., Wood, N., Octavia, S., Sintchenko, V., Giles, L., Quinn, H., Hill, V., Hanly, G., et al (2016). The relationship between *Bordetella pertussis* genotype and clinical severity in Australian children with pertussis. *Journal of Infection*, 72(2), 171-178. <a href="http://dx.doi.org/10.1016/j.jinf.2015.11.004">[More Information]</a>

Gurjav, U., Erkhembayar, B., Burneebaatar, B., Narmandakh, E., Tumenbayar, O., Hill-Cawthorne, G., Marais, B., Sintchenko, V. (2016). Transmission of multi-drug resistant tuberculosis in Mongolia is driven by Beijing strains of *Mycobacterium tuberculosis* resistant to all first-line drugs. *Tuberculosis*, 101, 49-53. <a href="http://dx.doi.org/10.1016/j.tube.2016.07.010">[More Information]</a>

Trinh, Q., Nguyen, H., Do, T., Nguyen, V., Nguyen, B., Nguyen, T., Sintchenko, V., Marais, B. (2016). Tuberculosis and HIV co-infection in Vietnam. *International Journal of Infectious Diseases*, 46, 56-60. <a href="http://dx.doi.org/10.1016/j.ijid.2016.03.021">[More Information]</a>

Gurjav, U., Outhred, A., Jelfs, P., Holmes (nee McCallum), N., Wang, Q., Hill-Cawthorne, G., Marais, B., Sintchenko, V. (2016). Whole genome sequencing demonstrates limited transmission within identified *Mycobacterium tuberculosis* clusters in New South Wales, Australia. *PLoS One*, 11(10), 1-12. <a href="http://dx.doi.org/10.1371/journal.pone.0163612">[More Information]</a>

Phillips, A., Sotomayor Castillo, C., Wang, Q., Holmes (nee McCallum), N., Furlong, C., Ward, K., Howard, P., Octavia, S., Lan, R., Sintchenko, V. (2016). Whole genome sequencing of *Salmonella Typhimurium* illuminates distinct outbreaks caused by an endemic multi-locus variable number tandem repeat analysis type in Australia, 2014. *BMC Microbiology*, 16(1), 1-9. <a href="http://dx.doi.org/10.1186/s12866-016-0831-3">[More Information]</a>

Martinez, E., Bustamante, A., Menon, R., Wang, Q., Jelfs, J., Marais, B., Chen, S., Sintchenko, V. (2016). Whole-genome sequencing of *Mycobacterium tuberculosis* for rapid diagnostics: Feasibility of a decentralised model. *The Lancet Respiratory Medicine*, 4(4), 13-14. <a href="http://dx.doi.org/10.1016/S2213-2600(16)00092-8">[More Information]</a>

Outhred, A., Jelfs, P., Suliman, B., Hill-Cawthorne, G., Crawford, A., Marais, B., Sintchenko, V. (2015). Added value of whole-genome sequencing for management of highly drug-resistant TB. *Journal of Antimicrobial Chemotherapy*, 70(4), 1198-1202. <a href="http://dx.doi.org/10.1093/jac/dku508">[More Information]</a>

## 2015

Chua, K., Bustamante, A., Jelfs, P., Chen, S., Sintchenko, V. (2015). Antibiotic susceptibility of diverse *Mycobacterium abscessus* complex strains in New South Wales, Australia. *Pathology*, 47(7), 678-682. <a href="http://dx.doi.org/10.1097/PAT.0000000000000327">[More Information]</a>

re Information]

Sintchenko, V., Coiera, E., Kohane, Z. (2015). Bioinformatics. In Enrico Coiera (Eds.), *Guide to Health Informatics*, (pp. 515-535). Boca Raton: CRC Press. <a href="http://dx.doi.org/10.1201/b13617-37">[More Information]

Sintchenko, V., Coiera, E. (2015). Clinical bioinformatics and personalized medicine. In Enrico Coiera (Eds.), *Guide to Health Informatics*, (pp. 537-554). Boca Raton: CRC Press. <a href="http://dx.doi.org/10.1201/b13617-38">[More Information]

Fu, S., Octavia, S., Tanaka, M., Sintchenko, V., Lan, R. (2015). Defining the Core Genome of Salmonella enterica Serovar Typhimurium for Genomic Surveillance and Epidemiological Typing. *Journal of Clinical Microbiology*, 53(8), 2530-2538. <a href="http://dx.doi.org/10.1128/JCM.03407-14">[More Information]

Octavia, S., Wang, Q., Tanaka, M., Kaur, S., Sintchenko, V., Lan, R. (2015). Delineating Community Outbreaks of Salmonella enterica Serovar Typhimurium by Use of Whole-Genome Sequencing: Insights into Genomic Variability within an Outbreak. *Journal of Clinical Microbiology*, 53(4), 1063-1071. <a href="http://dx.doi.org/10.1128/JCM.03235-14">[More Information]

Kok, J., Sintchenko, V., Dwyer, D., Chen, S. (2015). Editorial: Laboratory preparedness for Ebola virus disease. *Pathology*, 47(5), 397-399. <a href="http://dx.doi.org/10.1097/PAT.000000000000290">[More Information]

Khandkar, C., Harrington, Z., Jelfs, P., Sintchenko, V., Dobler, C. (2015). Epidemiology of Peripheral Lymph Node Tuberculosis and Genotyping of M tuberculosis Strains: A Case-Control Study. *PLoS One*, 10(7), 1-10. <a href="http://dx.doi.org/10.1371/journal.pone.0132400">[More Information]

Martinez, E., Holmes (nee McCallum), N., Jelfs, P., Sintchenko, V. (2015). Genome sequencing reveals novel deletions associated with secondary resistance to pyrazinamide in MDR Mycobacterium tuberculosis. *Journal of Antimicrobial Chemotherapy*, 70(9), 2511-2514. <a href="http://dx.doi.org/10.1093/jac/dkv128">[More Information]

McCallum, N., Gray, T., Wang, Q., Ng, J., Hicks, L., Nguyen, T., Yuen, M., Hill-Cawthorne, G., Sintchenko, V. (2015). Genomic Epidemiology of Clostridium botulinum Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. *Journal of Clinical Microbiology*, 53(9), 2846-2853. <a href="http://dx.doi.org/10.1128/JCM.00143-15">[More Information]

Octavia, S., Wang, Q., Tanaka, M., Sintchenko, V., Lang, R. (2015). Genomic Variability of Serial Human Isolates of Salmonella enterica Serovar Typhimurium Associated with Prolonged Carriage. *Journal of Clinical Microbiology*, 53(11), 3507-3514. <a href="http://dx.doi.org/10.1128/JCM.01733-15">[More Information]

Baker, K., Dallman, T., Ashton, P., Day, M., Hughes, G., Crook, P., Gilbert, V., Zittermann, S., Allen, V., Howden, B., Sintchenko, V., et al (2015). Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. *The Lancet Infectious Diseases*, 15(8), 913-921. <a href="http://dx.doi.org/10.1016/S1473-3099(15)00002-X">[More Information]

Wang, Q., Holmes (nee McCallum), N., Martinez, E., Howard, P., Hill-Cawthorne, G., Sintchenko, V. (2015). It is not all about Single Nucleotide Polymorphisms: Comparison of mobile

genetic elements and deletions in Listeria monocytogenes genomes links cases of hospital-acquired listeriosis to the environmental source. *Journal of Clinical Microbiology*, 53(11), 3492-3500. <a href="http://dx.doi.org/10.1128/JCM.00202-15">[More Information]

Gupta, L., Sintchenko, V. (2015). Listeriosis cluster in Sydney linked to hospital food. *Medical Journal of Australia*, 202(8), 448-449. <a href="http://dx.doi.org/10.5694/mja14.00913">[More Information]

Zhou, F., O'Sullivan, M., Iredell, J., Sintchenko, V., Gilbert, G., Dwyer, D. (2015). Molecular analysis of Enterovirus C species using the 5' untranslated region and VP1 region. *Journal of Human Virology & Retrovirology*, 2(2), 1-12. <a href="http://dx.doi.org/10.15406/jhvr.2015.02.00038">[More Information]

Roberts-Witteveen, A., Reinten, T., Christensen, A., Sintchenko, V., Seale, P., Lowbridge, C. (2015). Multidrug-resistant tuberculosis in New South Wales, Australia, 1999-2010: a case series report. *International Journal of Tuberculosis and Lung Disease*, 19(7), 850-856. <a href="http://dx.doi.org/10.5588/ijtld.14.0575">[More Information]

Safarchi, A., Octavia, S., Luu, L., Tay, C., Sintchenko, V., Wood, N., Marshall, H., McIntyre, P., Lan, R. (2015). Pertactin negative Bordetella pertussis demonstrates higher fitness under vaccine selection pressure in a mixed infection model. *Vaccine*, 33(46), 6277-6281. <a href="http://dx.doi.org/10.1016/j.vaccine.2015.09.064">[More Information]

Sintchenko, V., Coiera, E. (2015). Population surveillance and public health informatics. In Enrico Coiera (Eds.), *Guide to Health Informatics*, (pp. 497-513). Boca Raton: CRC Press. <a href="http://dx.doi.org/10.1201/b13617-36">[More Information]

Moran-Gilad, J., Sintchenko, V., Pedersen, S., Wolfgang, W., Pettengill, J., Strain, E., Hendriksen, R. (2015). Proficiency testing for bacterial whole genome sequencing: An end-user survey of current capabilities, requirements and priorities. *BMC Infectious Diseases*, 15(1), 1-10. <a href="http://dx.doi.org/10.1186/s12879-015-0902-3">[More Information]

Gurjav, U., Burneebaatar, B., Narmandakh, E., Tumenbayar, O., Ochirbat, B., Hill-Cawthorne, G., Marais, B., Sintchenko, V. (2015). Spatiotemporal evidence for cross-border spread of MDR-TB along the Trans-Siberian Railway line. *International Journal of Tuberculosis and Lung Disease*, 19(11), 1376-1382. <a href="http://dx.doi.org/10.5588/ijtld.15.0361">[More Information]

Sintchenko, V., Holmes, E. (2015). The role of pathogen genomics in assessing disease transmission. *BMJ*, 350, 1-13. <a href="http://dx.doi.org/10.1136/bmj.h1314">[More Information]

Trinh, Q., Nguyen, H., Nguyen, V., Nguyen, T., Sintchenko, V., Marais, B. (2015). Tuberculosis and HIV co-infection-focus on the Asia-Pacific region. *International Journal of Infectious Diseases*, 32, 170-178. <a href="http://dx.doi.org/10.1016/j.ijid.2014.11.023">[More Information]

Kwong, J., Holmes (nee McCallum), N., Sintchenko, V., Howden, B. (2015). Whole genome sequencing in clinical and public health microbiology. *Pathology*, 47(3), 199-210. <a href="http://dx.doi.org/10.1097/PAT.000000000000235">[More Information]

## 2014

Rhoads, D., Sintchenko, V., Rauch, C., Pantanowitz, L. (2014). Clinical Microbiology Informatics. *Clinical Microbiology Reviews*, 27(4), 1025-1047. <a href="http://dx.doi.org/10.1128/CMR.00049-14">[More Information]</a>

Ho, J., Jelfs, P., Sintchenko, V. (2014). Fluoroquinolone resistance in non-multidrug-resistant tuberculosis- a surveillance study in New South Wales, Australia, and a review of global resistance rates. *International Journal of Infectious Diseases*, 26, 149-153. <a href="http://dx.doi.org/10.1016/j.ijid.2014.03.1388">[More Information]</a>

Bart, M., Harris, S., Advani, A., Arakawa, Y., Bottero, D., Bouchez, V., Cassiday, P., Chiang, C., Dalby, T., Fry, N., Sintchenko, V., et al (2014). Global population structure and evolution of *Bordetella pertussis* and their relationship with vaccination. *mBio*, 5(2), 1-13. <a href="http://dx.doi.org/10.1128/mBio.01074-14">[More Information]</a>

Gray, T., Kong, F., Jelfs, P., Sintchenko, V., Chen, S. (2014). Improved Identification of Rapidly Growing Mycobacteria by a 16S-23S Internal Transcribed Spacer Region PCR and Capillary Gel Electrophoresis. *PloS One*, 9(7), 1-8. <a href="http://dx.doi.org/10.1371/journal.pone.0102290">[More Information]</a>

Muscattello, D., Amin, J., MacIntyre, C., Newall, A., Rawlinson, W., Sintchenko, V., Gilmour, R., Thackway, S. (2014). Inaccurate Ascertainment of Morbidity and Mortality due to Influenza in Administrative Databases: A Population-Based Record Linkage Study. *PloS One*, 9(5), 1-12. <a href="http://dx.doi.org/10.1371/journal.pone.0098446">[More Information]</a>

Lam, C., Octavia, S., Sintchenko, V., Gilbert, G., Lan, R. (2014). Investigating genome reduction of *Bordetella pertussis* using a multiplex PCR-based reverse line blot assay (mPCR/RLB). *BMC Research Notes*, 7(1), 1-8. <a href="http://dx.doi.org/10.1186/1756-0500-7-727">[More Information]</a>

Sintchenko, V., Roper, M. (2014). Pathogen Genome Bioinformatics. In Ronald Trent (Eds.), *Clinical Bioinformatics*, (pp. 173-193). New York, United States: Humana Press. <a href="http://dx.doi.org/10.1007/978-1-4939-0847-9\_10">[More Information]</a>

Ellis, S., Kalinowski, D., Leotta, L., Huang, M., Jelfs, P., Sintchenko, V., Richardson, D., Triccas, J. (2014). Potent Anti-Mycobacterial Activity of the Pyridoxal Isonicotinoyl Hydrazone Analogue, 2-Pyridylcarboxaldehyde Isonicotinoyl Hydrazone: A Lipophilic Transport Vehicle for Isonicotinic Acid Hydrazone. *Molecular Pharmacology*, 85(2), 269-278. <a href="http://dx.doi.org/10.1124/mol.113.090357">[More Information]</a>

Lam, C., Octavia, S., Ricafort, L., Sintchenko, V., Gilbert, G., Wood, N., McIntyre, P., Marshall, H., Guiso, N., Keil, A., et al (2014). Rapid Increase in Pertactin-deficient *Bordetella pertussis* Isolates, Australia. *Emerging Infectious Diseases*, 20(4), 626-633. <a href="http://dx.doi.org/10.3201/eid2004.131478">[More Information]</a>

Gurjav, U., Jelfs, P., Holmes (nee McCallum), N., Marais, B., Sintchenko, V. (2014). Temporal dynamics of Mycobacterium tuberculosis genotypes in New South Wales, Australia. *BMC Infectious Diseases*, 14(455), 1-8. <a href="http://dx.doi.org/10.1186/1471-2334-14-455">[More Information]</a>

Zhou, F., Wang, Q., Sintchenko, V., Gilbert, G., O'Sullivan, M., Iredell, J., Dwyer, D. (2014). Use of the 5' Untranslated Region and VP1 Region to Examine the Molecular Diversity in Enterovirus B Species. *Journal of Medical Microbiology*, 63(PT10), 1339-1355. <a href="http://dx.doi.org/10.1099/jmm.0.074682-0">[More Information]</a>

## 2013

Sadsad, R., Sintchenko, V., McDonnell, G., Gilbert, G. (2013). Effectiveness of Hospital-Wide Methicillin-Resistant *Staphylococcus aureus* (MRSA) Infection Control Policies Differs by Ward Specialty. *PloS One*, 8(12), 1-8. <a href="http://dx.doi.org/10.1371/journal.pone.0083099">[More Information]</a>

Ho, J., Jelfs, P., Sintchenko, V. (2013). Phenotypically occult multidrug-resistant Mycobacterium tuberculosis: Dilemmas in diagnosis and treatment. *Journal of Antimicrobial Chemotherapy*, 68(12), 2915-2920. <a href="http://dx.doi.org/10.1093/jac/dkt284">[More Information]</a>

O'Sullivan, M., Sintchenko, V., Gilbert, G. (2013). Quantitative Estimation of the Stability of Methicillin-Resistant *Staphylococcus aureus* Strain-Typing Systems by Use of Kaplan-Meier Survival Analysis. *Journal of Clinical Microbiology*, 51(1), 112-116. <a href="http://dx.doi.org/10.1128/JCM.01406-12">[More Information]</a>

O'Sullivan, M., Sintchenko, V., Gilbert, G. (2013). Software for selecting the most informative sets of genomic loci for multi-target microbial typing. *BMC Bioinformatics*, 14(148), 1-8. <a href="http://dx.doi.org/10.1186/1471-2105-14-148">[More Information]</a>

McIntyre, P., Sintchenko, V. (2013). The "How" of Polymerase Chain Reaction Testing for *Bordetella pertussis* Depends on the "Why". *Clinical Infectious Diseases*, 56(3), 332-334. <a href="http://dx.doi.org/10.1093/cid/cis897">[More Information]</a>

Le Hello, S., Bekhit, A., Granier, S., Barua, H., Beutlich, J., Zajac, M., Munch, S., Sintchenko, V., Bouchrif, B., Fashae, K., et al (2013). The global establishment of a highly-fluoroquinolone resistant *Salmonella enterica* serotype Kentucky ST198 strain. *Frontiers in Microbiology*, 4, 1-10. <a href="http://dx.doi.org/10.3389/fmicb.2013.00395">[More Information]</a>

Gilbert, G., Sintchenko, V. (2013). The use of mycobacterial interspersed repetitive unit typing and whole genome sequencing to inform tuberculosis prevention and control activities. *NSW Public Health Bulletin*, 24(1), 10-14. <a href="http://dx.doi.org/10.1071/NB12106">[More Information]</a>

Stephens, N., Vogelnest, L., Lowbridge, C., Christensen, A., Marks, G., Sintchenko, V., McAnulty, J. (2013). Transmission of Mycobacterium tuberculosis from an Asian elephant (*Elephas maximus*) to a chimpanzee (*Pan troglodytes*) and humans in an Australian zoo. *Epidemiology and Infection*, 141(7), 1488-1497. <a href="http://dx.doi.org/10.1017/S095026881300068X">[More Information]</a>

Marks, G., Christensen, A., Sintchenko, V., Lowbridge, C. (2013). Tuberculosis: an old world disease providing new world challenges in NSW. *NSW Public Health Bulletin*, 24(1), 22-23. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=23849023">[More Information]</a>

## 2012

Gilbert, G., Sintchenko, V. (2012). Assignment of recA reference sequence types for enhanced identification of the Burkholderia cepacia complex. *Pathology*, 44(4), 373-375. <a href="http://dx.doi.org/10.1097/PAT.0b013e328353e8b9">[More Information]</a>

Jackson, J., McGregor, A., Cooley, L., Ng, J., Brown, M., Ong, C., Darcy, C., Sintchenko, V. (2012). Francisella tularensis subspecies holarctica, Tasmania, Australia, 2011. *Emerging Infectious Diseases*, 18(9), 1484-1486. <a href="http://dx.doi.org/10.3201/eid1809.111856">[More Information]</a>

Pang, S., Octavia, S., Reeves, P., Wang, Q., Gilbert, G., Sintchenko, V., Lan, R. (2012). Genetic Relationships of Phage Types and Single Nucleotide Polymorphism Typing of Salmonella enterica Serovar Typhimurium. *Journal of Clinical Microbiology*, 50(3), 727-734. <a href="http://dx.doi.org/10.1128/JCM.01284-11">[More Information]</a>

Lau, A., Sintchenko, V., Crimmins, J., Magrabi, F., Gallego, B., Coiera, E. (2012). Impact of a web-based personally controlled health management system on influenza vaccination and health services utilization rates: a randomized controlled trial. *Journal of the American Medical Informatics Association*, 19(5), 719-727. <a href="http://dx.doi.org/10.1136/amiajnl-2011-000433">[More Information]</a>

Sintchenko, V., Wang, Q., Howard, P., Ha, C., Kardamanidis, K., Musto, J., Gilbert, G. (2012). Improving resolution of public health surveillance for human Salmonella enterica serovar Typhimurium infection: 3 years of prospective multiple-locus variable-number tandem-repeat analysis (MLVA). *BMC Infectious Diseases*, 12(31 March 2012), 1-10. <a href="http://dx.doi.org/10.1186/1471-2334-12-78">[More Information]</a>

Helal, M., Kong, F., Chen, S., Zhou, F., Dwyer, D., Potter, J., Sintchenko, V. (2012). Linear normalised hash function for clustering gene sequences and identifying reference sequences from multiple sequence alignments. *Microbial Informatics and Experimentation*, 2(1), 1-11. <a href="http://dx.doi.org/10.1186/2042-5783-2-2">[More Information]</a>

Octavia, S., Sintchenko, V., Gilbert, G., Lawrence, A., Keil, A., Hogg, G., Lan, R. (2012). Newly emerging clones of Bordetella pertussis carrying prn2 and ptxP3 alleles implicated in Australian pertussis epidemic in 2008-2010. *The Journal of Infectious Diseases*, 205(8), 1220-1224. <a href="http://dx.doi.org/10.1093/infdis/jis178">[More Information]</a>

O'Sullivan, M., Zhou, F., Sintchenko, V., Gilbert, G. (2012). Prospective Genotyping of Hospital-Acquired Methicillin-Resistant Staphylococcus aureus by Use of a Novel, Highly Discriminatory Binary Typing System. *Journal of Clinical Microbiology*, 50(11), 3513-3519. <a href="http://dx.doi.org/10.1128/JCM.01625-12">[More Information]</a>

Lau, A., Sintchenko, V., Crimmins, J., Magrabi, F., Gallego, B., Coiera, E. (2012). Protocol for a randomised controlled trial examining the impact of a web-based personally controlled health management system on the uptake of influenza vaccination rates. *BMC Health Services Research*, 12(1), 1-10. <a href="http://dx.doi.org/10.1186/1472-6963-12-86">[More Information]</a>

Lam, C., Octavia, S., Bahrame, Z., Sintchenko, V., Gilbert, G., Lan, R. (2012). Selection and emergence of pertussis toxin

promoter ptxP3 allele in the evolution of Bordetella pertussis. *Infection, Genetics and Evolution*, 12(2), 492-495. <a href="http://dx.doi.org/10.1016/j.meegid.2012.01.001">[More Information]</a>

## 2011

Lin, F., Lan, R., Sintchenko, V., Gilbert, G., Kong, F., Coiera, E. (2011). Computational Bacterial Genome-Wide Analysis of Phylogenetic Profiles Reveals Potential Virulence Genes of Streptococcus agalactiae. *PloS One*, 6(4), e17964-1-e17964-10. <a href="http://dx.doi.org/10.1371/journal.pone.0017964">[More Information]</a>

Helal, M., Kong, F., Chen, S., Bain, M., Christen, R., Sintchenko, V. (2011). Defining Reference Sequences for Nocardia Species by Similarity and Clustering Analyses of 16S rRNA Gene Sequence Data. *PloS One*, 6(6), e19517-1-e19517-11. <a href="http://dx.doi.org/10.1371/journal.pone.0019517">[More Information]</a>

Watts, M., Taylor, P., Sintchenko, V., Whelan, C., Farnsworth, R., Jones, P., Jelfs, P., Carr, D., Goldberg, H. (2011). Implications of isoniazid resistance in Mycobacterium bovis Bacillus Calmette-Guérin used for immunotherapy in bladder cancer. *Clinical Infectious Diseases*, 52(1), 86-88. <a href="http://dx.doi.org/10.1093/cid/ciq002">[More Information]</a>

Wang, T., Kong, F., Chen, S., Xiao, M., Sorrell, T., Wang, X., Wang, S., Sintchenko, V. (2011). Improved identification of Gordonia, Rhodococcus and Tsukamurella species by 5'-end 16S rRNA gene sequencing. *Pathology*, 43(1), 58-63. <a href="http://dx.doi.org/10.1097/PAT.0b013e328340e431">[More Information]</a>

Octavia, S., Maharjan, R., Sintchenko, V., Stevenson, G., Reeves, P., Gilbert, G., Lan, R. (2011). Insight into evolution of Bordetella pertussis from comparative genomic analysis: evidence of vaccine-driven selection. *Molecular Biology and Evolution*, 28(1), 707-715. <a href="http://dx.doi.org/10.1093/molbev/msq245">[More Information]</a>

O'Sullivan, M., Zhou, F., Sintchenko, V., Kong, F., Gilbert, G. (2011). Multiplex PCR and Reverse Line Blot Hybridization Assay (mPCR/RLB). *Journal of Visualized Experiments*, 6(54), e2781-1-e2781-5. <a href="http://dx.doi.org/10.3791/2781">[More Information]</a>

Sintchenko, V., Coiera, E. (2011). Translational web robots for pathogen genome analysis. *Microbial Informatics and Experimentation*, 1(1), 1-4. <a href="http://dx.doi.org/10.1186/2042-5783-1-10">[More Information]</a>

## 2010

Sintchenko, V., Anthony, S., Phan, X., Lin, F., Coiera, E. (2010). A PubMed-wide associational study of infectious diseases. *PloS One*, 5(3), e9535-1-e9535-12. <a href="http://dx.doi.org/10.1371/journal.pone.0009535">[More Information]</a>

Kurniawan, J., Maharjan, R., Chan, W., Reeves, P., Sintchenko, V., Gilbert, G., Mooi, F., Lan, R. (2010). Bordetella pertussis clones identified by multilocus variable-number tandem-repeat analysis. *Emerging Infectious Diseases*, 16(2), 297-300. <a href="http://dx.doi.org/10.3201/eid1602.081707">[More Information]</a>

Xiao, M., Kong, F., Sorrell, T., Cao, Y., Lee, O., Liu, Y., Sintchenko, V., Chen, S. (2010). Identification of Pathogenic



Nocardia Species by Reverse Line Blot Hybridization Targeting the 16S rRNA and 16S-23S rRNA Gene Spacer Regions.

*Journal of Clinical Microbiology*, 48(2), 503-511. <a href="http://dx.doi.org/10.1128/JCM.01761-09">[More Information]</a>

Sintchenko, V. (2010). *Infectious Disease Informatics*. New York: Springer. <a href="http://dx.doi.org/10.1007/978-1-4419-1327-2">[More Information]</a>

Sintchenko, V. (2010). Informatics for Infectious Disease Research and Control. In Vitali Sintchenko (Eds.), *Infectious Disease Informatics*, (pp. 1-26). New York: Springer. <a href="http://dx.doi.org/10.1007/978-1-4419-1327-2">[More Information]</a>

O'Sullivan, M., Kong, F., Sintchenko, V., Gilbert, G. (2010). Rapid Identification of MRSA Transmission in Hospitals using Phage-Derived ORF Typing enhanced by Multiplex PCR and Reverse Line Blot Assay. *Journal of Clinical Microbiology*, 48(8), 2741-2748. <a href="http://dx.doi.org/10.1128/JCM.02201-09">[More Information]</a>

Wang, X., Xiao, M., Kong, F., Sintchenko, V., Wang, H., Wang, B., Lian, S., Sorrell, T., Chen, S. (2010). Reverse line blot hybridization and DNA sequencing studies of the 16S-23S rRNA gene intergenic spacer regions of five emerging pathogenic Nocardia species. *Journal of Medical Microbiology*, 59(Pt 5), 548-555. <a href="http://dx.doi.org/10.1099/jmm.0.017921-0">[More Information]</a>

Wang, X., Xiao, M., Kong, F., Sintchenko, V., Wang, H., Wang, B., Lian, S., Sorrell, T., Chen, S. (2010). Reverse line blot hybridization and DNA sequencing studies of the 16S-23S rRNA gene intergenic spacer regions of five emerging pathogenic Nocardia species. *Journal of Medical Microbiology*, 59(Pt 5), 548-555. <a href="http://dx.doi.org/10.1099/jmm.0.017921-0">[More Information]</a>

Kong, F., Wang, H., Zhang, E., Sintchenko, V., Xiao, M., Sorrell, T., Chen, X., Chen, S. (2010). SecA1 Gene Sequence Polymorphisms for Species Identification of Nocardia and Recognition of Intraspecies Genetic Diversity. *Journal of Clinical Microbiology*, 48(11), 3928-3934. <a href="http://dx.doi.org/10.1128/JCM.01113-10">[More Information]</a>

Anthony, S., Sintchenko, V., Coiera, E. (2010). Text Mining for Discovery of Host-Pathogen Interactions. In Vitali Sintchenko (Eds.), *Infectious Disease Informatics*, (pp. 149-165). New York: Springer. <a href="http://dx.doi.org/10.1007/978-1-4419-1327-2\_7">[More Information]</a>

Gallego, B., Sintchenko, V., Jelfs, P., Coiera, E., Gilbert, G. (2010). Three-year longitudinal study of genotypes of Mycobacterium tuberculosis in a low prevalence population. *Pathology*, 42(3), 267-272. <a href="http://dx.doi.org/10.3109/00313021003631346">[More Information]</a>

Liu, Y., Kong, F., Xiao, M., Wang, Q., O'Sullivan, M., Sintchenko, V., Lin, M., Gilbert, G. (2010). Unexpected Diversity of Staphylococcal Cassette Chromosome mec Type IV in Methicillin-Resistant Staphylococcus aureus Strains. *Journal of Clinical Microbiology*, 48(10), 3628-3634. <a href="http://dx.doi.org/10.1128/JCM.00351-10">[More Information]</a>

Couldwell, D., Gidding, H., Freedman, E., Mckechnie, M., Biggs, K., Sintchenko, V., Gilbert, G. (2010). Ureaplasma urealyticum is significantly associated with non-gonococcal urethritis in heterosexual Sydney men. *International Journal of STD and AIDS*, 21(5), 337-341. <a href="http://dx.doi.org/10.1258/ijsa.2009.009499">[More Information]</a>

## 2009

Cai, L., Kong, F., Wang, Q., Wang, H., Xiao, M., Sintchenko, V., Gilbert, G. (2009). A new multiplex PCR-based reverse line-blot hybridization (mPCR/RLB) assay for rapid staphylococcal

cassette chromosome mec (SCCmec) typing. *Journal of Medical Microbiology*, 58(8), 1045-1057. <a href="http://dx.doi.org/10.1099/jmm.0.007955-0">[More Information]</a>

Kong, F., Chen, S., Chen, X., Sintchenko, V., Halliday, C., Cai, L., Tong, Z., Lee, O., Sorrell, T. (2009). Assignment of Reference 5'-end 16S rDNA Sequences and Species-Specific Sequence Polymorphisms Improves Species Identification of Nocardia. *The Open Microbiology Journal*, 3, 97-105. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=19639036">[More Information]</a>

Gallego, B., Sintchenko, V., Wang, Q., Hiley, L., Gilbert, G., Coiera, E. (2009). Biosurveillance of emerging biothreats using scalable genotype clustering. *Journal of Biomedical Informatics*, 42(1), 66-73. <a href="http://dx.doi.org/10.1016/j.jbi.2008.07.002">[More Information]</a>

Lin, F., Sintchenko, V., Kong, F., Gilbert, G., Coiera, E. (2009). Commonly used molecular epidemiology markers of Streptococcus agalactiae do not appear to predict virulence. *Pathology*, 41(6), 576-581. <a href="http://dx.doi.org/10.1080/00313020903071447">[More Information]</a>

Helal, M., Sintchenko, V. (2009). Dynamic programming algorithms for discovery of antibiotic resistance in microbial genomes. *17th National Health Informatics Conference (HIC 2009)*, Brunswick East, Victoria: Health Informatics Society of Australia (HISA).

Lee, A., Jelfs, P., Sintchenko, V., Gilbert, G. (2009). Identification of non-tuberculous mycobacteria: Utility of the GenoType Mycobacterium CM/AS assay compared with HPLC and 16S rRNA gene sequencing. *Journal of Medical Microbiology*, 58(7), 900-904. <a href="http://dx.doi.org/10.1099/jmm.0.007484-0">[More Information]</a>

Lin, F., Coiera, E., Lan, R., Sintchenko, V. (2009). In silico prioritisation of candidate genes for prokaryotic gene function discovery: An application of phylogenetic profiles. *BMC Bioinformatics*, 10, 1-12. <a href="http://dx.doi.org/10.1186/1471-2105-10-86">[More Information]</a>

van Hal, S., Foo, H., Blyth, C., McPhie, K., Armstrong, P., Sintchenko, V., Dwyer, D. (2009). Influenza outbreak during Sydney World Youth Day 2008: the utility of laboratory testing and case definitions on mass gathering outbreak containment. *PloS One*, 4(9), e6620 - 1-e6620 - 10. <a href="http://dx.doi.org/10.1371/journal.pone.0006620">[More Information]</a>

Sintchenko, V., Gallego, B. (2009). Laboratory-guided detection of disease outbreaks: three generations of surveillance systems. *Archives of Pathology & Laboratory Medicine*, 133(6), 916-925. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=19492884">[More Information]</a>

Akhtar, M., Gallego, B., Shiue, A., Sintchenko, V. (2009). Prospective Biosurveillance for Early Detection of Disease Outbreaks. *17th National Health Informatics Conference (HIC 2009)*, Brunswick East, Victoria: Health Informatics Society of Australia (HISA).

Cai, L., Kong, F., Jelfs, P., Gilbert, G., Sintchenko, V. (2009). Rolling circle amplification and multiplex allele-specific PCR for rapid detection of katG and inhA gene mutations in Mycobacterium tuberculosis. *International Journal of Medical*

*Microbiology*, 299(8), 574-581. <a href="http://dx.doi.org/10.1016/j.ijmm.2009.05.006">[More Information]</a>

Coiera, E., Lau, A., Tsafnat, G., Sintchenko, V., Magrabi, F. (2009). The changing nature of clinical decision support systems: a focus on consumers, genomics, public health and decision safety. *Yearbook of medical informatics*, , 84-95. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=19855878">[More Information]</a>

Sintchenko, V., Gallego, B., Chung, G., Coiera, E. (2009). Towards bioinformatics assisted infectious disease control. *BMC Bioinformatics*, 10(Suppl 2), S10-1-S10-9. <a href="http://dx.doi.org/10.1186/1471-2105-10-s2-s10">[More Information]</a>

## 2008

Sintchenko, V., Coiera, E., Gilbert, G. (2008). Decision support systems for antibiotic prescribing. *Current Opinion in Infectious Diseases*, 21(6), 573-579. <a href="http://dx.doi.org/10.1097/QCO.0b013e3283118932">[More Information]</a>

Sintchenko, V., Coiera, E. (2008). Developing Decision Support Systems in Clinical Bioinformatics. In Ronald J.A. Trent (Eds.), *Clinical Bioinformatics: Methods in Molecular Medicine*, (pp. 331-351). New Jersey: Humana Press. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=18453098">[More Information]</a>

Maharjan, R., Gu, C., Reeves, P., Sintchenko, V., Gilbert, G., Lan, R. (2008). Genome-wide analysis of single nucleotide polymorphisms in *Bordetella pertussis* using comparative genomic sequencing. *Research in Microbiology*, 159, 602-608. <a href="http://dx.doi.org/10.1016/j.resmic.2008.08.004">[More Information]</a>

Sintchenko, V. (2008). The re-emergence of pertussis: implications for diagnosis and surveillance. *NSW Public Health Bulletin*, 19(7-8), 143-145. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=19007547">[More Information]</a>

## 2007

Merritt, T., Sintchenko, V., Jelfs, P., Worthing, M., Robinson, B., Durrheim, D., Gilbert, G. (2007). An outbreak of pulmonary tuberculosis in young Australians. *Medical Journal of Australia*, 186(5), 240-242.

Sintchenko, V., Usherwood, T., Coiera, E. (2007). Are clinicians' information needs and decision support affected by different models of care? Experimental study. *Studies in Health Technology and Informatics*, 129(2), 895-899. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=17911845">[More Information]</a>

Sintchenko, V., Usherwood, T., Coiera, E. (2007). Are Clinicians' Information Needs and Decision Support Affected by Different Models of Care? Experimental Study. *MedInfo 2007:12th World Congress on Health (Medical) Informatics*, Netherlands: IOS Press.

Sintchenko, V., Magrabi, F., Tipper, S. (2007). Are we measuring the right end-points? Variables that affect the impact of computerised decision support on patient outcomes: A systematic review. *Medical Informatics and the Internet in Medicine*, 32(3), 225-240. <a href="http://dx.doi.org/10.1080/14639230701447701">[More Information]</a>

Cai, Y., Kong, F., Wang, Q., Tong, Z., Sintchenko, V., Zeng, X., Gilbert, G. (2007). Comparison of Single- and Multilocus Sequence Typing and Toxin Gene Profiling for Characterization of Methicillin-Resistant *Staphylococcus aureus*. *Journal of Clinical Microbiology*, 45(10), 3302-3308. <a href="http://dx.doi.org/10.1128/JCM.01082-07">[More Information]</a>

Sintchenko, V., Brown, M., Gilbert, G. (2007). Is *Bordetella pertussis* susceptibility to erythromycin changing? MIC trends among Australian isolates 1971-2006. *Journal of Antimicrobial Chemotherapy*, 60(5), 1178-1179. <a href="http://dx.doi.org/10.1093/jac/dkm343">[More Information]</a>

Sintchenko, V., Iredell, J., Gilbert, G. (2007). Pathogen profiling for disease management and surveillance. *Nature Reviews Microbiology*, 5(6), 464-470. <a href="http://dx.doi.org/10.1038/nrmicro1656">[More Information]</a>

Dwyer, D., Sintchenko, V. (2007). Point-of-care testing for community-acquired pneumonia: do we have all the answers? *Medical Journal of Australia*, 187(1), 40-42. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=17605702">[More Information]</a>

Coiera, E., Magrabi, F., Sintchenko, V., Zrimec, T., McDonnell, G., Chung, G., Tsafnat, G. (2007). The Centre for Health Informatics at the University of New South Wales â€“ a Clinical Informatics Research Centre. *Methods of Information in Medicine*, 46(Suppl. 1), 141-148. <a href="http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list\_uids=17700917">[More Information]</a>

## 2006

Sintchenko, V., Jelfs, P., Dally, M., Crighton, T., Gilbert, G. (2006). A case of urinary tuberculosis due to *Mycobacterium bovis* subspecies *caprae*. *Pathology*, 38(4), 376-378. <a href="http://dx.doi.org/10.1080/00313020600821391">[More Information]</a>

Sintchenko, V., Persson, L., Lanser, J. (2006). Communicable Disease Informatics â€“ Emerging Concepts in Disease Surveillance. *14th National Health Informatics Conference (HIC 2006 Bridging the Digital Divide: Clinicians, Consumers and Computers)*, New Zealand: Health Informatics Society of Australia (HISA).

Sintchenko, V., Coiera, E. (2006). Decision Complexity Affects the Extent and Type of Decision Support Use. *AMIA 2006: Biomedical and Health Informatics*, USA: American Medical Informatics Association.

Jelfs, P., Sintchenko, V., Gilbert, G. (2006). Genotyping of *Mycobacterium tuberculosis* in New South Wales: Results from 18 months of a statewide trial. *NSW Public Health Bulletin*, 17, 81-85. <a href="http://dx.doi.org/10.1071/nb06020">[More Information]</a>

Sintchenko, V. (2006). Information Processing in Clinical Decision-Making. In Athina A. Lazakidou (Eds.), *Handbook of Research on Informatics in Healthcare And Biomedicine*, (pp. 147-153). United States: Idea Group Publishing.

Iredell, J., Sintchenko, V. (2006). Screening for antibiotic resistant Gram-negative bacteria. *The Lancet Infectious Diseases*, 6, 316-317. <a href="http://dx.doi.org/10.1016/S1473-3099(06)70470-4">[More Information]</a>

Sintchenko, V., Gilbert, G. (2006). Utility of genotyping of *Mycobacterium tuberculosis* in the contact investigation: A decision analysis. *Tuberculosis*, 87(3), 176-184. <a href="http://dx.doi.org/10.1016/j.tube.2006.10.003">[More Information]</a>

## 2005

Sintchenko, V., Iredell, J., Gilbert, G., Coiera, E. (2005). Handheld computer-based decision support reduces patient length of stay and antibiotic prescribing in critical care. *Journal of the American Medical Informatics Association*, 12(4), 398-402. <a href="http://dx.doi.org/10.1197/jamia.M1798">[More Information]</a>

## 2004

Sintchenko, V., Coiera, E., Iredell, J., Gilbert, G. (2004). Comparative Impact Of Guidelines, Clinical Data, And Decision Support On Prescribing Decisions: An Interactive Web Experiment With Simulated Cases. *Journal of the American Medical Informatics Association*, 11(1), 71-77. <a href="http://dx.doi.org/10.1197/jamia.M1166">[More Information]</a>

## 2003

Sintchenko, V., Coiera, E. (2003). Which clinical decisions benefit from automation? A task complexity approach. *International Journal of Medical Informatics*, 70(2-3), 309-316. <a href="http://dx.doi.org/10.1016/S1386-5056(03)00040-6">[More Information]</a>

## 2002

Sintchenko, V., Westbrook, J., Tipper, S., Mathieu, M., Coiera, E. (2002). Electronic decision support activities in different healthcare settings in Australia. In Dr. David Brand (Eds.), *Electronic decision support for Australia's health sector: Report to Health Ministers by the National Electronic Decision Support Taskforce*, (pp. Appendix A - 1-Appendix A - 167). Canberra: Commonwealth of Australia.