

Umer Zeeshan Ijaz's Publications*

<http://userweb.eng.gla.ac.uk/umer.ijaz>

Last updated: April, 2019

*In publications where I am involved as a senior author, relevant staff/students that I supported, mentored, or supervised are underlined.

Submitted

- [S1] M. Logan, C. Clark, **U. Z. Ijaz**, L. Gervais, H. Duncan, V. Garrick, L. Curtis, E. Buchanan, T. Cardigan, L. Armstrong, C. Delahunty, D. M. Flynn, A. Barclay, R. Tayler, E. McDonald, S. Milling, R. Hansen, K. Gerasimidis, and R. K. Russell. The reduction of faecal calprotectin during exclusive enteral nutrition is lost rapidly within the early stages of food re-introduction and only partially modified by maintenance enteral nutrition. *Submitted for publication.*
- [S2] A. Ch Stratakos, **U. Z. Ijaz**, P. Ward, M. Linton, C. Kelly, L. Pinkerton, P. Scates, J. McBride, I. Pet, A. Criste, D. Stef, J. M. Couto, W. T. Sloan, N. Dorell, B. W. Wren, L. Stef, O. Gundogdu, and N. Corcionivoschi. Genomic and phenotypic analysis reveals differences in stress resistance and virulence of *Listeria monocytogenes* outbreak-like strains. *Submitted for publication.*
- [S3] T. Lynch, G. Peirano, T. Lloyd, R. Read, J. Carter, A. Chu, J. A. Shaman, J. P. Jarvis, E. Diamond, **U. Z. Ijaz**, and D. Church. An integrated approach to diagnose bacterial vaginosis and alternative vaginal infections: comparing microscopy, qPCR and microbiome methods. *Submitted for publication.*
- [S4] S. De Schepper, J. L. Ray, K. S. Skaar, H. Sadatzki, **U. Z. Ijaz**, R. Stein, and A. Larsen. The potential of sedimentary ancient DNA for sea ice reconstructions. *Submitted for publication.*
- [S5] C. A. Jukes, **U. Z. Ijaz**, A. Buckley, J. Spencer, J. Irvine, D. Candlish, J. Lia, J. R. Marchesi, and G. Douce. Microbiome dependent modifications to bile salt acid metabolism and mucin abundance contribute to *Clostridioides (Clostridium) difficile* disease severity. *Submitted for publication.*
- [S6] A. Frau, J. G. Kenny, L. Lenzi, B. J. Campbell, **U. Z. Ijaz**, C. A. Duckworth, M. D. Burkitt, N. Hall, J. Anson, A. C. Darby, and C. S. J. Probert. DNA extraction and amplicon production strategies deeply influence the outcome of gut mycobiome studies. *Submitted for publication.*
- [S7] J. Plancq, J. M. Couto, **U. Z. Ijaz**, P. R. Leavitt, and J. L. Toney. Identifying lacustrine haptophytes in the canadian prairies: significance for temperature proxy applications. *Submitted for publication.*
- [S8] P. B. Wright, E. McDonald, A. Bravo-Blas, C. C. Bain, A. M. Mowat, S. L. Clay, E. V. Robertson, F. Morton, J. S. Nijjar, **U. Z. Ijaz**, S. W. F. Milling, and D. R. Gaya. Expression of the mannose receptor (CD206) defines distinct populations of human colonic macrophages in health and inflammatory bowel disease. *Submitted for publication.*
- [S9] S. Ciucci, C. Durán, A. Palladini, F. P. Sterbini, L. Masucci, G. Cammarota, G. Ianiro, B. Psteraro, M. Sanguinetti, G. Gasbarrini, A. Gasbarrini, B. N. Parsons, **U. Z. Ijaz**, D. M. Pritchard, and C. V. Cannistraci. Machine learning pattern recognition and differential network analysis of gastric microbiome in presence of PPI treatment or *H. pylori* infection. *Submitted for publication.*

Preprints

- [S10] A. C. Trego, C. Morabito, S. Mills, S. Connelly, I. Bourven, G. Guibaud, C. Quince, **U. Z. Ijaz**[#], and G. Collins[#]. Diversity converges during community assembly in methanogenic granules, suggesting a biofilm life-cycle. *bioRxiv* 484642, 2018.

International Journal Articles

- [P1] K. A. Bain, E. McDonald, F. Moffat, M. Tutino, M. Castellino, A. Barton, J. Cavanagh, **U. Z. Ijaz**, S. Siebert, I. B. McInnes, A. Astrand, S. Homes, and S. W. F. Milling. Alopecia areata is characterised by dysregulation in systemic type 17 and type 2 cytokines, which may contribute to disease-associated psychological morbidity. *British Journal of Dermatology*, accepted for publication (2019).
DOI:[10.1111/bjd.18008](https://doi.org/10.1111/bjd.18008)
[Impact Factor: **6.129**, Journal Ranking: **4/64** (Dermatology); JCR 2017]
- [P2] M. J. Ormsby, M. Logan, S. A. Johnson, A. McIntosh, G. Fallata, R. Papadopoulou, E. Papachristou, R. Hansen, **U. Z. Ijaz**, R. K. Russell, K. Gerasimidis, and D. M. Wall. Inflammation associated ethanalamine facilitates infection by Crohn's disease-linked adherent-invasive *Escherichia coli*. *EBioMedicine*, accepted for publication (2019).
[Impact Factor: **6.183**, Journal Ranking: **13/133** (Medicine, Research & Experimental); JCR 2017]
- [P3] C. Gauchotte-Lindsay, T. J. Aspray, M. Knapp, and **U. Z. Ijaz**. Systems biology approach to elucidation of contaminants biodegradation in complex samples- integration of high-resolution analytical and molecular tools. *Faraday Discussions*, 2019.
DOI:[10.1039/C9FD00020H](https://doi.org/10.1039/C9FD00020H)
- [P4] K. E. Dingle, X. Didelot, T. P. Quan, D. W. Eyre, N. Stoesser, C. A. Marwick, J. Coia, D. Brown, S. Buchanan, **U. Z. Ijaz**, C. Goswami, G. Douce, W. N. Fawley, M. H. Wilcox, T. E. A. Peto, A. S. Walker, and D. W. Crook. A role for tetracycline selection in recent evolution of the agriculture-associated *Clostridium difficile* PCR-ribotype 078. *mBio*, 10(2):e02790-18, 2019.
DOI: [10.1128/mBio.02790-18](https://doi.org/10.1128/mBio.02790-18)
[Impact Factor: **6.689**, Journal Ranking: **13/126** (Microbiology); JCR 2017]
- [P5] V. Svolos, R. Hansen, B. Nichols, C. Quince, **U. Z. Ijaz**, R. T. Papadopoulou, C. A. Edwards, D. Watson, A. Alghamdi, A. Brejnrod, C. Ansalone, H. Duncan, J. Salmond, D. Bolognini, R. Klopffleisch, D. R. Gaya, S. Milling, R. K. Russell, and K. Gerasimidis. Treatment of active Crohn's disease with an ordinary food-based diet that replicates exclusive enteral nutrition. *Gastroenterology*, 2019.
DOI:[10.1053/j.gastro.2018.12.002](https://doi.org/10.1053/j.gastro.2018.12.002)
[Press Release: *Exclusive Enteral Nutrition Unneeded in Crohn's? - Pilot study suggests ordinary whole-foods diet produces same effects in GI tract*, 14 December 2018, <https://www.medpagetoday.com/gastroenterology/inflammatoryboweldisease/76931>]
[Impact Factor: **20.773**, Journal Ranking: **1/80** (Gastroenterology & Hepatology); JCR 2017]
- [P6] F. Cholet, **U. Z. Ijaz**, and C. J. Smith. Differential ratio amplicons (R_{amp}) for the evaluation of RNA integrity extracted from complex environmental samples. *Environmental Microbiology*, 21(2): 827-844, 2019.
DOI: [10.1111/1462-2920.14516](https://doi.org/10.1111/1462-2920.14516)
- [P7] J. De Vrieze, **U. Z. Ijaz**, A. M. Saunders, and S. Theuerl. Terminal restriction fragment length polymorphism as an "old school" but reliable technique for swift microbial community screening in anaerobic digestion. *Scientific Reports*, 8:16818, 2018.
DOI:[10.1038/s41598-018-34921-7](https://doi.org/10.1038/s41598-018-34921-7)
- [P8] A. Kostrytsia, S. Papirio, L. Morrison, **U. Z. Ijaz**, G. Collins, P. N. L. Lens, and G. Esposito. Biokinetics of microbial consortia using biogenic sulfur as a novel electron donor for sustainable denitrification. *Bioresource Technology*, 270:359-367, 2018.

DOI:[10.1016/j.biortech.2018.09.044](https://doi.org/10.1016/j.biortech.2018.09.044)

[Impact Factor: **5.807**, Journal Ranking: **1/14** (Agricultural Engineering); JCR 2017]

- [P9] I. Reich[#], U. Z. Ijaz[#], M. Gormally, and C. J. Smith[#]. 16S rRNA sequencing reveals likely beneficial core microbes within faecal samples of the EU protected slug *Geomalacus maculosus*. **Scientific Reports**, 8:10402, 2018.
#Joint corresponding authors
DOI: [10.1038/s41598-018-28720-3](https://doi.org/10.1038/s41598-018-28720-3)
- [P10] U. Z. Ijaz^{*}, L. Sivaloganathan^{*}, A. Mckenna^{*}, A. Richmond, C. Kelly, M. Linton, A. Stratakos, U. Lavery, A. Elmi, B. Wren, N. Dorell, N. Corcionivoschi, and O. Gundogdu. Comprehensive longitudinal microbiome analysis of chicken cecum reveals a shift from competitive to environmental drivers and a window of opportunity for *Campylobacter*. **Frontiers in Microbiology**, 9:2452, 2018.
DOI: [10.3389/fmicb.2018.02452](https://doi.org/10.3389/fmicb.2018.02452)
***Joint first authors**
- [P11] S. T. Calus, U. Z. Ijaz[#], and A. Pinto[#]. NanoAmpli-Seq: A workflow for amplicon sequencing from mixed microbial communities on the nanopore sequencing platform. **GigaScience**, giy140, 2018.
DOI:[10.1093/gigascience/giy140](https://doi.org/10.1093/gigascience/giy140)
#Joint corresponding authors
NanoAmpli-Seq - Sample processing and sequence library preparation workflow:
<https://www.protocols.io/view/nanoampli-seq-sample-processing-and-sequencing-lib-u26eyhe>
DOI: [10.17504/protocols.io.u26eyhe](https://doi.org/10.17504/protocols.io.u26eyhe)
NanoAmpli-Seq - Bioinformatics workflow:
<https://www.protocols.io/view/nanoampli-seq-bioinformatics-workflow-u25eyg6>
DOI: [10.17504/protocols.io.u25eyg6](https://doi.org/10.17504/protocols.io.u25eyg6)
Code: <https://github.com/umerijaz/nanopore>
[Impact Factor: **7.267**, Journal Ranking: **7/64** (Multidisciplinary Sciences); JCR 2017]
- [P12] O. Koci, M. Logan, V. Svolos, R. K. Russell, K. Gerasimidis, and U. Z. Ijaz[#]. An automated identification and analysis of ontological terms in gastrointestinal diseases and nutrition-related literature provides useful insights. **PeerJ**, 6:e5047, 2018.
DOI: [10.7717/peerj.5047](https://doi.org/10.7717/peerj.5047)
#Corresponding author
Accompanied software:
pyTag: <https://github.com/KociOrges/pytag>
- [P13] K. Gerasimidis, K. Zafeiropoulou, M. Mackinder, U. Z. Ijaz, H. Duncan, E. Buchanan, T. Cardigan, C. A. Edwards, P. McGrogan, and R. K. Russell. Comparison of clinical methods with the faecal gluten immunogenic peptide to assess gluten intake in coeliac disease. **Journal of Pediatric Gastroenterology & Nutrition**, 67(3):356-360, 2018.
DOI: [10.1097/MPG.0000000000002062](https://doi.org/10.1097/MPG.0000000000002062)
- [P14] C. Keating, D. Hughes, T. Mahony, D. Cysneiros, U. Z. Ijaz, C. J. Smith, and V. O'Flaherty. Cold adaptation and replicable microbial community development during long-term low temperature anaerobic digestion of synthetic sewage. **FEMS Microbiology Ecology**, 94(7):fiy095, 2018.
DOI: [10.1093/femsec/fiy095](https://doi.org/10.1093/femsec/fiy095)
- [P15] J. De Vrieze, A. J. Pinto, W. T. Sloan, and U. Z. Ijaz[#]. The active microbial community more accurately reflects the anaerobic digestion process: 16S rRNA (gene) sequencing as a predictive tool. **Microbiome**, 6:63, 2018.
DOI: [10.1186/s40168-018-0449-9](https://doi.org/10.1186/s40168-018-0449-9)
#Corresponding author
[Impact Factor: **9.133**, Journal Ranking: **10/125** (Microbiology); JCR 2017]

- [P16] X. Yuan, Y. Song, Y. Song, J. Xu, Y. Wu, A. Glidle, M. Cusack, **U. Z. Ijaz**, J. Cooper, W. Huang, and H. Yin. Effect of laser irradiation on cell function and its implications in Raman spectroscopy. *Applied and Environmental Microbiology*, 84:e02508-17, 2018.
DOI: [10.1128/AEM.02508-17](https://doi.org/10.1128/AEM.02508-17)
- [P17] C. Pedersen, **U. Z. Ijaz**, E. Gallagher, F. Horton, R. J. Ellis, E. Jaiyeola, T. Duparck, D. Russell-Jones, P. Hinton, P. D. Cani, R. M. La Ragione, and M. D. Robertson. Fecal *Enterobacteriales* enrichment is associated with increased in vivo intestinal permeability in humans. *Physiological Reports*, 6(6):e13649, 2018.
DOI: [10.14814/phy2.13649](https://doi.org/10.14814/phy2.13649)
- [P18] A. Joyce, **U. Z. Ijaz**, C. Nzeteu, A. Vaughan, S. L. Shirran, C. H. Botting, C. Quince, V. O'Flaherty, and F. Abram. Linking microbial community structure and function during the acidified anaerobic digestion of grass. *Frontiers in Microbiology*, 9:540, 2018.
DOI:[10.3389/fmicb.2018.00540](https://doi.org/10.3389/fmicb.2018.00540)
Code: <http://userweb.eng.gla.ac.uk/umer.ijaz/bioinformatics/Metaproteomics.html>
- [P19] B. N. Parsons*, **U. Z. Ijaz***, R. D'Amore, M. Burkitt, R. Eccles, L. Lenzi, C. A. Duckworth, A. R. Moore, L. Tizlavicz, A. Varro, N. Hall, and D. M. Pritchard. Comparison of the human gastric microbiota in hypochlorhydric states arising as a result of *Helicobacter pylori*-induced atrophic gastritis, autoimmune atrophic gastritis and proton pump inhibitor use. *PLoS Pathogens*, 13(11): e1006653, 2017.
DOI:[10.1371/journal.ppat.1006653](https://doi.org/10.1371/journal.ppat.1006653)
***Joint first authors**
[Press Release: Shifting bacterial communities in the stomach may influence cancer risk, 2 November 2017.
https://www.eurekalert.org/pub_releases/2017-11/p-sbc102417.php
<https://www.sciencedaily.com/releases/2017/11/171102140511.htm>
[Press Release: Stomach microbiome implicated in varying risk of stomach tumours, 3 November 2017.
<https://www.worldwidecancerresearch.org/news/stomachmicrobiome/>
[Impact Factor: 6.608, Journal Ranking: 2/36 (Parasitology); JCR 2016]
- [P20] M. Logan, **U. Z. Ijaz**, R. Hansen, K. Gerasimidis, and R. Russell. Letter: reproducible evidence shows that exclusive enteral nutrition significantly reduces faecal Calprotectin concentrations in children with active Crohn's disease. *Alimentary Pharmacology & Therapeutics*, 46: 1119–1120, 2017.
DOI: [10.1111/apt.14351](https://doi.org/10.1111/apt.14351)
[Impact Factor: 7.286, Journal Ranking: 9/79 (Gastroenterology & Hepatology); JCR 2016]
- [P21] N. D. Ritchie, **U. Z. Ijaz**, and T. J. Evans. IL-17 signalling restructures the nasal microbiome and drives dynamic changes following *Streptococcus pneumoniae* colonization. *BMC Genomics*, 18:807, 2017.
DOI: [10.1186/s12864-017-4215-3](https://doi.org/10.1186/s12864-017-4215-3)
- [P22] J. De Vrieze, M. E. Christiaens, D. Walraedt, A. Devooght, **U. Z. Ijaz**, and N. Boon. Microbial community redundancy in anaerobic digestion drives process recovery after salinity exposure. *Water Research*, 111:109-117, 2017.
DOI: [10.1016/j.watres.2016.12.042](https://doi.org/10.1016/j.watres.2016.12.042)
[Impact Factor: 6.942, Journal Ranking: 1/88 (Water Resources); JCR 2016]
- [P23] K. Harris, T. L. Parsons, **U. Z. Ijaz**, L. Lahti, I. Holmes, and C. Quince. Linking statistical and ecological theory: Hubbell's unified neutral theory of biodiversity as a hierarchical Dirichlet process. *Proceedings of the IEEE*, 105(3):516-529, 2017.
DOI: [10.1109/JPROC.2015.2428213](https://doi.org/10.1109/JPROC.2015.2428213)
Accompanied software:
NMGS: <https://github.com/microbiome/NMGS>
[Impact Factor: 9.237, Journal Ranking: 5/260 (Electrical & Electronic Engineering); JCR 2016]

- [P24] A. Z. Ijaz, T. Jeffries, **U. Z. Ijaz**, K. Hamonts, and B. K. Singh. Extending SEQenv: A taxa-centric approach to environmental annotations of 16S rDNA sequences. *PeerJ*, 5:e3827, 2017.
DOI: [10.7717/peerj.3827](https://doi.org/10.7717/peerj.3827)
Relevant Software:
SEQenv-Ext: <http://hie-pub.westernsydney.edu.au/0610b020-39fb-11e7-b55d-525400daae48/>
TaxaSE System: <http://hie-pub.westernsydney.edu.au/6a603c5e-35d6-11e7-b329-525400daae48/>
[Selected as Editors' Pick under Biogeography at PeerJ: <https://peerj.com/subjects/biogeography/>]
- [P25] S. -K. Cho, K. -W. Jung, D. -H. Kim, J. -C. Kwon, **U. Z. Ijaz**, and S. G. Shin. Bacterial community analysis in upflow multi-layer anaerobic reactor (UMAR) treating high-solids organic wastes. *Biotechnology Progress*, 2017.
DOI: [10.1002/btpr.2540](https://doi.org/10.1002/btpr.2540)
- [P26] S. Connelley, S. G. Shin, R. J. Dillon, **U. Z. Ijaz**, C. Quince, W. T. Sloan, and G. Collins. Bioreactor scalability: laboratory-scale idealisation influences performance, ecology and community physiology in expanded sludge bioreactors. *Frontiers in Microbiology*, 8:664, 2017.
DOI: [10.3389/fmicb.2017.00664](https://doi.org/10.3389/fmicb.2017.00664)
- [P27] **U. Z. Ijaz**, C. Quince, L. Hanske, N. Loman, S. T. Calus, M. Bertz, C. A. Edwards, D. R. Gaya, R. Hansen, P. McGrogan, R. K. Russell, and K. Gerasimidis. The microbial 'dysbiosis' of Crohn's disease patients do not occur in their unaffected, genetically linked kindred. *PLoS ONE*, 12(2): e0172605, 2017.
DOI: [10.1371/journal.pone.0172605](https://doi.org/10.1371/journal.pone.0172605)
- [P28] A. Ho*, **U. Z. Ijaz***, T. K. S. Janssens, R. Ruijs, S. Y. Kim, W. de Boer, A. Temorshuizen, W. H. van der Putten, and P. L. E. Bodelier. Effects of bio-based residue amendments on greenhouse gas emission from agricultural soil are stronger than effects of soil type with different microbial community composition. *Global Change Biology Bioenergy*, 2017.
DOI: [10.1111/gcbb.12457](https://doi.org/10.1111/gcbb.12457)
***Joint first authors**
[Impact Factor: 6.151, Journal Ranking: 1/83 (Agronomy); JCR 2015]
- [P29] M. Schirmer, R. D'Amore, **U. Z. Ijaz**, N. Hall, and C. Quince. Illumina error profiles: Resolving fine-scale variation in metagenomic sequencing data. *BMC Bioinformatics*, 17:125, 2016.
DOI: [10.1186/s12859-016-0976-y](https://doi.org/10.1186/s12859-016-0976-y)
Code: https://bitbucket.org/ms_research/ep_metagenomic
[Citations: ~105; Google Scholar 03/2019]
- [P30] R. D'Amore*, **U. Z. Ijaz***, M. Schirmer, J. Kenny, R. Gregory, A. C. Darby, M. Shakya, M. Podar, C. Quince, and N. Hall. A comprehensive benchmarking study of next-generation sequencing platforms for 16S rRNA community profiling. *BMC Genomics*, 17:55, 2016.
DOI: [10.1186/s12864-015-2194-9](https://doi.org/10.1186/s12864-015-2194-9)
***Joint first authors**
Code: <https://bitbucket.org/umerijaz/amplimock/src>
[Citations: ~125; Google Scholar 04/2019]
- [P31] J. L. Ray, J. Althammer, K. S. Skaar, P. Simonelli, A. Larsen, D. Stoecker, A. Sazhin, **U. Z. Ijaz**, C. Quince, J. C. Nejstgaard, M. Frischer, G. Pohnert, and C. Troedsson. Metabarcoding and metabolome analysis of copepod grazing reveals feeding preference and linkage to metabolite classes in dynamic microbial plankton communities. *Molecular Ecology*, 2016.
DOI: [10.1111/mec.13844](https://doi.org/10.1111/mec.13844)
[Impact Factor: 5.947, Journal Ranking: 5/46 (Evolutionary Biology); JCR 2015]
- [P32] L. Sinclair*, **U. Z. Ijaz***, L. J. Jensen, M. Coolen, C. Gubry-Rangin, A. Chronakova, A. Oulas, C. Pavloudi, J. Schnetzer, A. Weimann, A. Z. Ijaz, A. Eiler, C. Quince, and E. Pafilis. Seqenv: linking microbes to environments through text mining. *PeerJ*, 4:e2690, 2016.

DOI:[10.7717/peerj.2690](https://doi.org/10.7717/peerj.2690)

***Joint first authors**

Accompanied software:

seqenv: <https://github.com/xapple/seqenv>

- [P33] [C. Pedersen](#), E. Gallagher, F. Horton, R. J. Ellis, **U. Z. Ijaz**, H. Wu, E. Jaiyeola, O. Diribe, T. Duparc, P. D. Cani, G. R. Gibson, P. Hinton, J. Wright, D. Russell-Jones, R. La Ragione, and M. D. Robertson. Host-microbiome interactions in human type 2 diabetes following prebiotic dietary fibre (galacto-oligosaccharide) intake. *British Journal of Nutrition*, 116(11):1869-1877, 2016.
DOI:[10.1017/S0007114516004086](https://doi.org/10.1017/S0007114516004086)
- [P34] K. Gerasimidis, M. Bertz, C. Quince, K. Brunner, A. Bruce, E. Combet, [S. T. Calus](#), N. Loman, and **U. Z. Ijaz**[#]. The effect of DNA extraction methodology on gut microbiota research applications. *BMC Research Notes*, 9:365, 2016.
DOI:[10.1186/s13104-016-2171-7](https://doi.org/10.1186/s13104-016-2171-7)
#Corresponding author
- [P35] C. Varsos, T. Patkos, A. Oulas, C. Pavludi, A. Gougousis, **U. Z. Ijaz**, I. Filiopoulou, N. Pattakos, E. V. Berghe, A. Fernandez-Guerra, S. Faulwetter, E. Chatzinikolaou, E. Pafilis, C. Beikiari, M. Doerr, and C. Arvantidis. Optimized R functions for analysis of ecological community data using the R virtual laboratory (RvLab). *Biodiversity Data Journal*, 4: e8357, 2016.
DOI: [10.3897/BDJ.4.e8357](https://doi.org/10.3897/BDJ.4.e8357)
Accompanied software:
RvLab: <https://portal.lifewatchgreece.eu/>
- [P36] [Q. M. Bautista-do los Santos](#), J. L. Schroeder, M. C. Sevillano-Rivera, R. Sungthong, **U. Z. Ijaz**, W. T. Sloan, and A. J. Pinto. Microbial communities in full-scale drinking water distribution systems – A meta-analysis. *Environmental Science: Water Research & Technology*, 2:631-644, 2016.
DOI:[10.1039/C6EW00030D](https://doi.org/10.1039/C6EW00030D)
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<http://pubs.rsc.org/en/journals/articlecollectionlanding?sercode=ew&themeid=ce4b64a9-9ad4-4fdf-a030-c2d77578a813>]
- [P37] B. Torondel, J. H. J. Ensink, [O. Gundogdu](#), **U. Z. Ijaz**, A. W. Walker, J. Parkhill, F. Abdelahi, V. –A. Nguyen, S. Sudgen, W. Gibson, and C. Quince. Assessment of the influence of intrinsic environmental and geographical factors on the bacterial ecology of pit latrines. *Microbial Biotechnology*, 9(2):209-223, 2016.
DOI:[10.1111/1751-7915.12334](https://doi.org/10.1111/1751-7915.12334)
Code: <http://userweb.eng.gla.ac.uk/umer.ijaz/bioinformatics/ecological.html>
- [P38] K. Gerasimidis, **U. Z. Ijaz**, C. Edwards, R. K. Russell, C. Quince, and R. Hansen. Response to Kaakoush et al. *American Journal of Gastroenterology*, 111(7):1033-1034, 2016.
DOI: [10.1038/ajg.2016.169](https://doi.org/10.1038/ajg.2016.169)
[Impact Factor: **10.383**, Journal Ranking: **6/79** (Gastroenterology & Hepatology); JCR 2015]
- [P39] C. Quince*, **U. Z. Ijaz***, N. Loman, A. D. Eren, D. Saulnier, J. Russell, S. J. Haig, [S. T. Calus](#), J. Quick, A. Barclay, M. Bertz, M. Blaut, R. Hansen, P. McGrogan, R. K. Russell, C. Edwards, and K. Gerasimidis. Extensive modulation of the fecal metagenome in children with Crohn’s disease during exclusive enteral nutrition. *American Journal of Gastroenterology*, 110:1718–1729, 2015.
DOI:[10.1038/ajg.2015.357](https://doi.org/10.1038/ajg.2015.357)
***Joint first authors**
[One of the two articles selected by the editorial board for Continuing Medical Education (CME) credit in the current issue]

[Citations: >85; Google Scholar 03/2019]

[Impact Factor: 10.383, Journal Ranking: 6/79 (Gastroenterology & Hepatology); JCR 2015]

[P40] M. Schirmer, U. Z. Ijaz, L. D'Amore, N. Hall, W. T. Sloan, and C. Quince. Insights into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform. *Nucleic Acids Research*, 43(6):pp.e37, 2015.

DOI: [10.1093/nar/gku1341](https://doi.org/10.1093/nar/gku1341)

Code: https://bitbucket.org/ms_research/ep

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