**Supplementary information**

Table S1. Systematic review of the literature using Scopus. Search was done within the Title, Abstract, Keywords’ field using ‘Antarctic’ with the terms ‘e\*DNA’, ‘environmental DNA’ ‘Next Generation Sequencing’ (NGS), ‘High Throughput Sequencing’ (HTS), ‘barcoding’ and ‘Metagenomics’. Papers were excluded where the sampling was not done in Antarctica, the sub-Antarctic or the Southern Ocean or where genetic data were not collected from environmental samples. Papers were assessed and divided by the environmental source of DNA (water, soil, sediment, ice/snow and other). References in bold are repeats within the same environmental source but different search terms. Studies that targeted vertebrate DNA are marked with \*.

|  |  |  |  |
| --- | --- | --- | --- |
| **Sample** | **Search Term** | **Hits** | **References** |
| **Water** | *Seawater* | **Total** | **38** |   |
| *e\*DNA* | 4 | **Cowart et al. 2018\*; Flaviani et al. 2018;** Fuentes et al. 2019; **Mariani et al. 2019\*** |
| *Environmental DNA* | 5 | Rich et al. 2008; Rodríguez-Martínez et al. 2009; **Cowart et al. 2018\*; Flaviani et al. 2018; Mariani et al. 2019\*** |
| *\*barcoding* | 2 | **Zoccarato et al. 2016; Mariani et al. 2019\*** |
| *NGS* | 10 | Ghiglione et al. 2012; Wolf et al. 2013a; Wolf et al. 2013b; **Lee et al. 2015;** Millard et al. 2016; **Moreno-Pino et al. 2016; Flaviani et al. 2018; De Corte et al. 2019;** Moss et al. 2020; **Sadaiappan et al. 2020** |
| *HTS* | 11 | Alonso-Sáez et al. 2011; **Lee et al. 2015;** Yu et al. 2015; **Moreno-Pino et al. 2016; Zoccarato et al. 2016;** Lin et al. 2017; **Cowart et al. 2018\*;** Gast et al. 2018; Lin et al. 2019; Liu and Jiang 2020; **Zhang et al. 2020** |
| *Metagenomics* | 19 | Alonso-Sáez et al. 2012; Grzymski et al. 2012; Wilkins et al. 2013; Williams et al. 2013, 2014; Bertrand et al. 2015; Delmont et al. 2015; **Lee et al. 2015;** Brum et al. 2016; Gionfriddo et al. 2016; Miranda et al. 2016; Alcamán-Arias et al. 2018; **Cowart et al. 2018\*;** Alarcón-Schumacher et al. 2019; **De Corte et al. 2019;** Kim et al. 2019; Yang et al. 2019a; Yang et al. 2019b; **Sadaiappan et al. 2020; Zhang et al. 2020** |
| *Terrestrial water bodies* | **Total** | **27** |   |
| *e\*DNA* | 1 | Fröls et al. 2012 |
| *Environmental DNA* | 1 | Karr et al. 2005 |
| *\*barcoding* | 0 |  |
| *NGS* | 4 | Lagkouvardos et al. 2014; Li et al. 2020b; Picazo et al. 2019; Weisleitner et al. 2019 |
| *HTS* | 5 |  Archer et al. 2014; Quiroga et al. 2015 Archer et al. 2016; Schiaffino et al. 2016; Cho et al. 2020 |
| *Metagenomics* | 17 | Ng et al. 2010; Lauro et al. 2011; Yau et al. 2011; Durso et al. 2012; Demaere et al. 2013; Huang et al. 2013; Yau et al. 2013; **Lagkouvardos et al. 2014;** Lõpez-Bueno et al. 2015; Simmons et al. 2015; Tschitschko et al. 2015; de Cárcer et al. 2016; Cornet et al. 2018; Tschitschko et al. 2018; Hamm et al. 2019; Yang et al. 2019; Li et al. 2020b |
| **Soil** |  | **Total** | **43** |   |
| *e\*DNA* | 1 | **Fraser et al. 2018** |
| *Environmental  DNA* | 8 | **Cieśliński et al. 2009b; Cieśliński et al. 2009a;** Rao et al. 2012; Teasdale et al. 2013; **Pansu et al. 2015; Czechowski et al. 2016b; Czechowski et al. 2016a; Fraser et al. 2018** |
| *\*barcoding* | 6 | **Pansu et al. 2015; Czechowski et al. 2016a; Fraser et al. 2018; Khomich et al. 2018;** Rippin et al. 2018; Canini et al. 2020 |
| *NGS* | 6 | Bergstrom et al. 2015; Pessi et al. 2015; **Baeza et al. 2017;** Yan et al. 2017; **Borsetto et al. 2019;** Weisleitner et al. 2019 |
| *HTS* | 12 | van Dorst et al. 2014; Cox et al. 2016; **Czechowski et al. 2016a; Czechowski et al. 2016b;** Tahon et al. 2016; Wei et al. 2016; Cong et al. 2017; Kleinteich et al. 2017; Chua et al. 2018; **Khomich et al. 2018;** Han et al. 2019; Rego et al. 2019 |
| *Metagenomics* | 25 | Berlemont et al. 2009; **Cieśliński et al. 2009a; Cieśliński et al. 2009b;** Heath et al. 2009; Berlemont et al. 2011; Hu et al. 2012; Pearce et al. 2012; Bartasun et al. 2013; Berlemont et al. 2013; Chan et al. 2013; Winsley et al. 2014; Amos et al. 2015; Anderson et al. 2015; **Baeza et al. 2017;** Goordial et al. 2017b; Ji et al. 2017; Pulschen et al. 2017; Santamans et al. 2017; Donovan et al. 2018; Van Goethem et al. 2018; **Borsetto et al. 2019;** Li et al. 2019a; Molina-Montenegro et al. 2019; Oh et al. 2019; Yuan et al. 2019 |
| **Sediment** |   | **Total** | **22** |  |
| *e\*DNA* | 0 |  |
| *Environmental DNA* | 7 | Gordon et al. 2000; Habura et al. 2004; Karr et al. 2005; Pawlowski et al. 2005; Jaraula et al. 2010; Pawlowski et al. 2011; Ficetola et al. 2018\* |
| *\*barcoding* | 3 | **Fonseca et al.  2017;** Brannock et al. 2018; Vause et al. 2019 |
| *NGS* | 1 | Weisleitner  2019 |
| *HTS* | 6 | Emil Ruff et al. 2014; Archer et al. 2015; Fonseca et al.  2017; Li et al. 2019a; Cho et al. 2020; Li et al. 2020a |
| *Metagenomics* | 6 | Huang et al. 2013; Hopkins et al.  2014; Matos et al. 2016; Vishnivetskaya et al. 2018; Centurion et al. 2019; Millán-Aguiñaga et al. 2019 |
| **Ice/Snow** |   | **Total** | **12** |   |
| *e\*DNA* | 0 |   |
| *Environmental DNA* | 0 |   |
| *\*barcoding* | 2 | Davey et al. 2019; Soto et al. 2020 |
| *NGS* | 1 | Weisleitner et al. 2019 |
| *HTS* | 7 | Webster-Brown et al. 2015; **Lopatina et al. 2016;** Sommers et al. 2018; Gast et al. 2018; Campen et al. 2019; Lutz et al. 2019; Sommers et al. 2019a |
| *Metagenomics* | 5 | Shtarkman et al. 2013; Antony et al. 2016; Gionfriddo et al. 2016; **Lopatina et al. 2016;** Sommers et al. 2019b |
|  **Other** | *Air* | **Total** | **3** |   |
| *e\*DNA* | 0 |   |
| *Environmental DNA* | 0 |   |
| *\*barcoding* |  |  |
| *NGS* | 2 | Weisleitner et al. 2019; Kobayashi et al. 2016 |
| *HTS* | 1 | Bottos et al. 2014 |
| *Metagenomics* | 1 |   |
| *Rock* | **Total** | **13** |   |
| *e\*DNA* | 1 | Vause et al. 2019 |
| *Environmental DNA* | 1 | De la Torre et al. 2003 |
| *\*barcoding* | 4 | Coleine et al. 2018; Coleine et al. 2019; Coleine et al. 2020a; **Coleine et al. 2020b** |
| *NGS* | 0 |  |
| *HTS* | 4 | Archer et al. 2017; Lacap-Bugler et al. 2017; Rego et al. 2019; **Coleine et al. 2020b** |
| *Metagenomics* | 4 | Chan et al. 2013; Le et al. 2016; Guerrero et al. 2017; Li et al. 2019b |
| *Microbial Mat* | **Total** | **14** |   |
| *e\*DNA* | 0 |   |
| *Environmental DNA* | 1 | Callejas et al. 2011 |
| *\*barcoding* | 0 |  |
| *NGS* | 3 | **Zawar-Reza et al. 2014; Koo et al. 2017a;** Koo et al. 2017b |
| *HTS* | 7 | Tytgat et al. 2014; Pessi et al. 2016; Johnson et al. 2017; **Koo et al. 2017a;** Pessi et al. 2018; Almela et al. 2019; Lezcano et al. 2019 |
| *Metagenomics* | 6 | **Zawar-Reza et al. 2014;** Koo et al. 2016; Velázquez et al. 2016; **Koo et al. 2017a;** Zaikova et al. 2019; Dillon et al. 2020 |
| *Bio film* | **Total** | **1** |   |
| *e\*DNA* | 0 |   |
| *Environmental DNA* | 0 |   |
| *\*barcoding* | 0 |   |
| *NGS* | 0 |   |
| *HTS* | 0 |   |
| *Metagenomics* | 1 | Tighe et al. 2017 |
| *Faeces* | **Total** | **7** |   |
| *e\*DNA* | 0 |   |
| *Environmental DNA* | 0 |   |
| *\*barcoding* | 0 |  |
| *NGS* | 2 | Varsani et al. 2014; McInnes et al. 2016\* |
| *HTS* | 4 | Medeiros et al. 2016; Neira et al. 2017; Yew et al. 2017; Morandini et al. 2019 |
| *Metagenomics* | 1 | Grzesiak et al. 2020 |

**References**

Alarcón-Schumacher T, Guajardo-Leiva S, Antón J, Díez B. 2019. Elucidating viral communities during a phytoplankton bloom on the west Antarctic Peninsula. Frontiers in Microbiology. 10:1014.

Alcamán-Arias ME, Farías L, Verdugo J, Alarcón-Schumacher T, Díez B. 2018. Microbial activity during a coastal phytoplankton bloom on the Western Antarctic Peninsula in late summer. FEMS Microbiology Letters. 365(10):1-51.

Almela P, Velázquez D, Rico E, Justel A, Quesada A. 2019. Carbon pathways through the food web of a microbial mat from Byers Peninsula, Antarctica. Frontiers in Microbiology. 10:628.

Alonso-Sáez L, Andersson A, Heinrich F, Bertilsson S. 2011. High archaeal diversity in Antarctic circumpolar deep waters. Environmental Microbiology Reports. 3(6):689-697.

Alonso-Sáez L, Waller AS, Mende DR, Bakker K, Farnelid H, Yager PL, Lovejoy C, Tremblay JE, Potvin M, Heinrich F, Estrada M, Riemann L, Bork P, Pedrós-Alió C, Bertilsson S. 2012. Role for urea in nitrification by polar marine Archaea. Proceedings of the National Academy of Sciences of the United States of America. 109(44):17989-17994.

Amos GCA, Borsetto C, Laskaris P, Krsek M, Berry AE, Newsham KK, Calvo-Bado L, Pearce DA, Vallin C, Wellington EMH. 2015. Designing and implementing an assay for the detection of rare and divergent NRPS and PKS clones in European, Antarctic and Cuban soils. PLoS ONE. 10(9):e0138327.

Anderson D, Ferreras E, Trindade M, Cowan D. 2015. A novel bacterial water Hypersensitivity-like protein shows in vivo protection against cold and freeze damage. FEMS Microbiology Letters. 362(15):fvn110.

Antony R, Sanyal A, Kapse N, Dhakephalkar PK, Thamban M, Nair S 2016. Microbial communities associated with Antarctic snowpack and their biogeochemical implications. Microbiological Research. 192:192-202.

Archer SDJ, McDonald IR, Herbold CW, Cary SC. 2014. Characterisation of bacterioplankton communities in the meltwater ponds of Bratina Island, Victoria Land, Antarctica. FEMS Microbiology Ecology. 89(2):451-464.

Archer SDJ, McDonald IR, Herbold CW, Lee CK, Cary CS. 2015. Benthic microbial communities of coastal terrestrial and ice shelf Antarctic meltwater ponds. Frontiers in Microbiology. 6:485.

Archer SDJ, McDonald IR, Herbold CW, Lee CK, Niederberger TS, Cary C. 2016. Temporal, regional and geochemical drivers of microbial community variation in the melt ponds of the Ross Sea region, Antarctica. Polar Biology. 39(2):267-282.

Archer SDJ, de los Ríos A, Lee KC, Niederberger TS, Cary SC, Coyne KJ, Douglas S, Lacap-Bugler DC, Pointing SB. 2017. Endolithic microbial diversity in sandstone and granite from the McMurdo Dry Valleys, Antarctica. Polar Biology. 40(5):997-1006.

Baeza M, Barahona S, Alcaíno J, Cifuentes V. 2017. Amplicon-metagenomic analysis of fungi from Antarctic terrestrial habitats. Frontiers in Microbiology. 8:2235.

Bartasun P, Cieśliński H, Bujacz A, Wierzbicka-Woś A, Kur J. 2013. A study on the interaction of Rhodamine B with methylthioadenosine phosphorylase protein sourced from an Antarctic soil metagenomic library. PLoS ONE. 8(1):55697.

Bergstrom DM, Bricher PK, Raymond B, Terauds A, Doley D, McGeoch MA, Whinam J, Glen M, Yuan Z, Kiefer K, Shaw JD, Bramely-Alves J, Rudman T, Mohammed C, Lucieer A, Visoiu M, Jansen van Vuuren B, Ball MC. 2015. Rapid collapse of a sub-Antarctic alpine ecosystem: The role of climate and pathogens. Journal of Applied Ecology. 52(3):774-783.

Berlemont R, Delsaute M, Pipers D, D'Amico S, Feller G, Galleni M, Power P. 2009. Insights into bacterial cellulose biosynthesis by functional metagenomics on Antarctic soil samples. ISME Journal. 3(9):1070-1081.

Berlemont R, Pipers D, Delsaute M, Angiono F, Feller G, Galleni M, Power P. 2011. Exploring the Antarctic soil metagenome as a source of novel cold-adapted enzymes and genetic mobile elements. Rev Argent Microbiol. 43(2):94-103.

Berlemont R, Jacquin O, Delsaute M, La Salla M, Georis J, Verté F, Galleni M, Power P. 2013. Novel cold-adapted esterase MHlip from an Antarctic soil metagenome. Biology. 2(1):177-188.

Bertrand EM, McCrow JP, Moustafa A, Zheng H, McQuaid JB, Delmont TO, Post AF, Sipler RE, Spackeen JL, Xu K. 2015. Phytoplankton–bacterial interactions mediate micronutrient colimitation at the coastal Antarctic sea ice edge. Proceedings of the National Academy of Sciences. 112(32):9938-9943.

Borsetto C, Amos GCA, Da Rocha UN, Mitchell AL, Finn RD, Laidi RF, Vallin C, Pearce DA, Newsham KK, Wellington EMH. 2019. Microbial community drivers of PK/NRP gene diversity in selected global soils. Microbiome. 7(1):78.

Bottos EM, Woo AC, Zawar-Reza P, Pointing SB, Cary SC. 2014. Airborne bacterial populations above desert soils of the McMurdo Dry Valleys, Antarctica. Microbial Ecology. 67(1):120-128.

Brannock PM, Learman DR, Mahon AR, Santos SR, Halanych KM. 2018. Meiobenthic community composition and biodiversity along a 5500 km transect of Western Antarctica: A metabarcoding analysis. Marine Ecology Progress Series. 603:47-60.

Brum JR, Hurwitz BL, Schofield O, Ducklow HW, Sullivan MB. 2016. Seasonal time bombs: Dominant temperate viruses affect Southern Ocean microbial dynamics. ISME Journal. 10(2):437-449.

Callejas C, Gill PR, Catalán AI, Azziz G, Castro-Sowinski S, Batista S. 2011. Phylotype diversity in a benthic cyanobacterial mat community on King George Island, maritime Antarctica. World Journal of Microbiology and Biotechnology. 27(6):1507-1512.

Campen R, Kowalski J, Lyons WB, Tulaczyk S, Dachwald B, Pettit E, Welch KA, Mikucki JA. 2019. Microbial diversity of an Antarctic subglacial community and high-resolution replicate sampling inform hydrological connectivity in a polar desert. Environmental Microbiology. 21(7):2290-2306.

Canini F, Geml J, D'Acqui LP, Selbmann L, Onofri S, Ventura S, Zucconi L. 2020. Exchangeable cations and pH drive diversity and functionality of fungal communities in biological soil crusts from coastal sites of Victoria Land, Antarctica. Fungal Ecology. 45:100923.

Centurion VB, Delforno TP, Lacerda-Júnior GV, Duarte AWF, Silva LJ, Bellini GB, Rosa LH, Oliveira VM. 2019. Unveiling resistome profiles in the sediments of an Antarctic volcanic island. Environmental Pollution. 255:113240.

Chan Y, Van Nostrand JD, Zhou J, Pointing SB, Farrell RL. 2013. Functional ecology of an Antarctic Dry Valley. Proceedings of the National Academy of Sciences of the United States of America. 110(22):8990-8995.

Cho H, Hwang CY, Kim JG, Kang S, Knittel K, Choi A, Kim SH, Rhee SK, Yang EJ, Lee S, Hyun JH. 2020. A unique benthic microbial community underlying the phaeocystis Antarctica-dominated Amundsen Sea polynya, Antarctica: A Proxy for Assessing the Impact of Global Changes. Frontiers in Marine Science. 6:797.

Chua CY, Yong ST, González MA, Lavin P, Cheah YK, Tan GYA, Wong CMVL. 2018. Analysis of bacterial communities of King George and Deception Islands, Antarctica using high-throughput sequencing. Current Science. 115(9):1701-1705.

Cieśliński H, Długołcka A, Kur J, Turkiewicz M. 2009a. An MTA phosphorylase gene discovered in the metagenomic library derived from Antarctic top soil during screening for lipolytic active clones confers strong pink fluorescence in the presence of rhodamine B. FEMS Microbiology Letters. 299(2):232-240.

Cieśliński H, Białkowska A, Tkaczuk K, Długołȩcka A, Kur J, Turkiewicz M. 2009b. Identification and molecular modelling of a novel lipase from an Antarctic soil metagenomic library. Polish Journal of Microbiology. 58(3):199-204.

Coleine C, Zucconi L, Onofri S, Pombubpa N, Stajich JE, Selbmann L. 2018. Sun exposure shapes functional grouping of fungi in cryptoendolithic Antarctic communities. Life. 8(2):19.

Coleine C, Stajich JE, Pombubpa N, Zucconi L, Onofri S, Canini F, Selbmann L. 2019. Altitude and fungal diversity influence the structure of Antarctic cryptoendolithic Bacteria communities. Environmental Microbiology Reports. 11(5):718-726.

Coleine C, Stajich JE, Pombubpa N, Zucconi L, Onofri S, Selbmann L. 2020a. Sampling strategies to assess microbial diversity of Antarctic cryptoendolithic communities. Polar Biology. 43(3):225-235.

Coleine C, Pombubpa N, Zucconi L, Onofri S, Stajich JE, Selbmann L. 2020b. Endolithic fungal species markers for harshest conditions in the McMurdo Dry Valleys, Antarctica. Life 10(2):13.

Cong B, Wang N, Liu S, Liu F, Yin X, Shen J. 2017. Isolation, characterization and transcriptome analysis of a novel Antarctic *Aspergillus sydowii* strain MS-19 as a potential lignocellulosic enzyme source. BMC Microbiology. 17(1):1-14.

Cornet L, Bertrand AR, Hanikenne M, Javaux EJ, Wilmotte A, Baurain D. 2018. Metagenomic assembly of new (Sub)polar cyanobacteria and their associated microbiome from non-axenic cultures. Microbial Genomics. 4(9):212.

Cowart DA, Murphy KR, Cheng CHC. 2018. Metagenomic sequencing of environmental DNA reveals marine faunal assemblages from the West Antarctic Peninsula. Marine Genomics. 37:148-160.

Cox F, Newsham KK, Bol R, Dungait JAJ, Robinson CH. 2016. Not poles apart: Antarctic soil fungal communities show similarities to those of the distant Arctic. Ecology Letters. 19(5):528-536.

Czechowski P, White D, Clarke L, McKay A, Cooper A, Stevens MI. 2016b. Age-related environmental gradients influence invertebrate distribution in the prince Charles mountains, east Antarctica. Royal Society Open Science. 3(12):160296.

Czechowski P, Clarke LJ, Cooper A, Stevens MI. 2017. A primer to metabarcoding surveys of Antarctic terrestrial biodiversity. Antarctic Science. 29(1):3-15.

Davey MP, Norman L, Sterk P, Huete-Ortega M, Bunbury F, Loh BKW, Stockton S, Peck LS, Convey P, Newsham KK, Smith AG. 2019. Snow algae communities in Antarctica: metabolic and taxonomic composition. New Phytologist. 222(3):1242-1255.

De Cárcer DA, López-Bueno A, Alonso-Lobo JM, Quesada A, Alcamí A. 2016. Metagenomic analysis of lacustrine viral diversity along a latitudinal transect of the Antarctic Peninsula. FEMS Microbiology Ecology. 92(6):1-10.

De Corte D, Martínez JM, Cretoiu MS, Takaki Y, Nunoura T, Sintes E, Herndl GJ, Yokokawa T. 2019. Viral communities in the global deep ocean conveyor belt assessed by targeted viromics. Frontiers in Microbiology. 10:1801.

De la Torre JR, Goebel BM, Friedmann EI, Pace NR. 2003. Microbial diversity of cryptoendolithic communities from the McMurdo Dry Valleys, Antarctica. Applied and Environmental Microbiology. 69(7):3858-3867.

Delmont TO, Murat Eren A, Vineis JH, Post AF. 2015. Genome reconstructions indicate the partitioning of ecological functions inside a phytoplankton bloom in the Amundsen Sea, Antarctica. Frontiers in Microbiology. 6:1090.

Demaere MZ, Williams TJ, Allen MA, Brown MV, Gibson JAE, Rich J, Lauro FM, Dyall-Smith M, Davenport KW, Woyke T, Kyrpides NC, Tringe SG, Cavicchioli R. 2013. High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. Proceedings of the National Academy of Sciences of the United States of America. 110(42):16939-16944.

Dillon ML, Hawes I, Jungblut AD, MacKey TJ, Eisen JA, Doran PT, Sumner DY. 2020. Environmental control on the distribution of metabolic strategies of benthic microbial mats in Lake Fryxell, Antarctica. PLoS ONE. 15(4):e0231053.

Donovan PD, Gonzalez G, Higgins DG, Butler G, Ito K. 2018. Identification of fungi in shotgun metagenomics datasets. PLoS ONE. 13(2):e0192898.

Durso LM, Miller DN, Wienhold BJ. 2012. Distribution and quantification of antibiotic resistant genes and bacteria across agricultural and non-agricultural Metagenomes. PLoS ONE. 7(11):e48325.

Emil Ruff S, Probandt D, Zinkann AC, Iversen MH, Klaas C, Würzberg L, Krombholz N, Wolf-Gladrow D, Amann R, Knittel K. 2014. Indications for algae-degrading benthic microbial communities in deep-sea sediments along the Antarctic Polar Front. Deep-Sea Research Part II: Topical Studies in Oceanography. 108:6-16.

Ficetola GF, Poulenard J, Sabatier P, Messager E, Gielly L, Leloup A, Etienne D, Bakke J, Malet E, Fanget B, Støren E, Reyss JL, Taberlet P, Arnaud F. 2018. DNA from lake sediments reveals long-term ecosystem changes after a biological invasion. Science Advances. 4(5):4292.

Flaviani F, Schroeder DC, Lebret K, Balestreri C, Highfield AC, Schroeder JL, Thorpe SE, Moore K, Pasckiewicz K, Pfaff MC, Rybicki EP. 2018. Distinct oceanic microbiomes from viruses to protists located near the Antarctic Circumpolar current. Frontiers in Microbiology. 9:1474.

Fröls S, Dyall-Smith M, Pfeifer F. 2012. Biofilm formation by haloarchaea. Environmental Microbiology. 14(12):3159-3174.

Fraser CI, Connell L, Lee CK, Cary SC. 2018. Evidence of plant and animal communities at exposed and subglacial (cave) geothermal sites in Antarctica. Polar Biology. 41(3):417-421.

Fuentes S, Arroyo JI, Rodríguez-Marconi S, Masotti I, Alarcón-Schumacher T, Polz MF, Trefault N, De la Iglesia R, Díez B. 2019. Summer phyto- and bacterioplankton communities during low and high productivity scenarios in the Western Antarctic Peninsula. Polar Biology. 42(1):159-169.

Gast RJ, Fay SA, Sanders RW. 2018. Mixotrophic activity and diversity of Antarctic marine protists in austral summer. Frontiers in Marine Science. 5:13.

Ghiglione JF, Galand PE, Pommier T, Pedrós-Alió C, Maas EW, Bakker K, Bertilson S, Kirchman DL, Lovejoy C, Yager PL, Murray AE. 2012. Pole-to-pole biogeography of surface and deep marine bacterial communities. Proceedings of the National Academy of Sciences of the United States of America. 109(43):17633-17638.

Gionfriddo CM, Tate MT, Wick RR, Schultz MB, Zemla A, Thelen MP, Schofield R, Krabbenhoft DP, Holt KE, Moreau JW. 2016. Microbial mercury methylation in Antarctic sea ice. Nature Microbiology. 1(10):16127.

Goordial J, Davila A, Greer CW, Cannam R, DiRuggiero J, McKay CP, Whyte LG. 2017b. Comparative activity and functional ecology of permafrost soils and lithic niches in a hyper-arid polar desert. Environmental Microbiology. 19(2):443-458.

Gordon DA, Priscu J, Giovannoni S. 2000. Origin and phylogeny of microbes living in permanent Antarctic lake ice. Microbial Ecology. 39(3):197-202.

Grzesiak J, Kaczyńska A, Gawor J, Żuchniewicz K, Aleksandrzak-Piekarczyk T, Gromadka R, Zdanowski MK. 2020. A smelly business: Microbiology of Adélie penguin guano (Point Thomas rookery, Antarctica). Science of the Total Environment. 714:136714.

Grzymski JJ, Riesenfeld CS, Williams TJ, Dussaq AM, Ducklow H, Erickson M, Cavicchioli R, Murray AE. 2012. A metagenomic assessment of winter and summer bacterioplankton from Antarctica Peninsula coastal surface waters. ISME Journal. 6(10):1901-1915.

Guerrero LD, Vikram S, Makhalanyane TP, Cowan DA 2017. Evidence of microbial rhodopsins in Antarctic Dry Valley edaphic systems. Environmental Microbiology. 19(9):3755-3767.

Habura A, Pawlowski J, Hanes SD, Bowser SS. 2004. Unexpected foraminiferal diversity revealed by small-subunit rDNA analysis of Antarctic sediment. Journal of Eukaryotic Microbiology. 51(2):173-179.

Hamm JN, Erdmann S, Eloe-Fadrosh EA, Angeloni A, Zhong L, Brownlee C, Williams TJ, Barton K, Carswell S, Smith MA, Brazendale S, Hancock AM, Allen MA, Raftery MJ, Cavicchioli R. 2019. Unexpected host dependency of Antarctic Nanohaloarchaeota. Proceedings of the National Academy of Sciences of the United States of America. 116(29):14661-14670.

Heath C, Xiao PH, Cary SC, Cowan D. 2009. Identification of a novel alkaliphilic esterase active at low temperatures by screening a metagenomic library from Antarctic desert soil. Applied and Environmental Microbiology. 75(13):4657-4659.

Hopkins M, Kailasan S, Cohen A, Roux S, Tucker KP, Shevenell A, Agbandje-Mckenna M, Breitbart M. 2014. Diversity of environmental single-stranded DNA phages revealed by PCR amplification of the partial major capsid protein. ISME Journal. 8(10):2093-2103.

Hu XP, Heath C, Taylor MP, Tuffin M, Cowan D. 2012. A novel, extremely alkaliphilic and cold-active esterase from Antarctic desert soil. Extremophiles. 16(1):79-86.

Jaraula CMB, Brassell SC, Morgan-Kiss RM, Doran PT, Kenig F. 2010. Origin and tentative identification of tri to pentaunsaturated ketones in sediments from Lake Fryxell, East Antarctica. Organic Geochemistry. 41(4):386-397.

Ji M, Greening C, Vanwonterghem I, Carere CR, Bay SK, Steen JA, Montgomery K, Lines T, Beardall J, Van Dorst J, Snape I, Stott MB, Hugenholtz P, Ferrari B. 2017. Atmospheric trace gases support primary production in Antarctic desert surface soil. Nature. 552(7685):400-403.

Johnson SS, Zaikova E, Goerlitz DS, Bai Y, Tighe SW. 2017. Real-time DNA sequencing in the Antarctic Dry Valleys using the Oxford nanopore sequencer. Journal of Biomolecular Techniques. 28(1):2-7.

Karr EA, Sattley WM, Rice MR, Jung DO, Madigan MT, Achenbach LA. 2005. Diversity and distribution of sulfate-reducing bacteria in permanently frozen Lake Fryxell, McMurdo Dry Valleys, Antarctica. Applied and Environmental Microbiology. 71(10):6353-6359.

Khomich M, Cox F, Andrew CJ, Andersen T, Kauserud H, Davey ML. 2018. Coming up short: Identifying substrate and geographic biases in fungal sequence databases. Fungal Ecology. 36:75-80.

Kim SJ, Kim JG, Lee SH, Park SJ, Gwak JH, Jung MY, Chung WH, Yang EJ, Park J, Jung J, Hahn Y, Cho JC, Eugene ML, Rodriguez-Valera F, Hyun, JH

Rhee, Sung-Keun. 2019. Genomic and metatranscriptomic analyses of carbon remineralization in an Antarctic polynya. Microbiome. 7(1):15p.

Kleinteich J, Hildebrand F, Bahram M, Voigt AY, Wood SA, Jungblut AD, Küpper FC, Quesada A, Camacho A, Pearce DA, Convey P, Vincent WF, Zarfl C, Bork P, Dietrich DR. 2017. Pole-to-Pole connections: Similarities between arctic and Antarctic microbiomes and their vulnerability to environmental change. Frontiers in Ecology and Evolution. 5:137.

Kobayashi F, Maki T, Kakikawa M, Noda T, Mitamura H, Takahashi A, Imura S, Iwasaka Y. 2016. Atmospheric bioaerosols originating from Adélie penguins (*Pygoscelis adeliae*): Ecological observations of airborne bacteria at Hukuro Cove, Langhovde, Antarctica. Polar Science. 10(1):71-78.

Koo H, Hakim JA, Fisher PRE, Grueneberg A, Andersen DT, Bej AK. 2016. Distribution of cold adaptation proteins in microbial mats in Lake Joyce, Antarctica: Analysis of metagenomic data by using two bioinformatics tools. Journal of Microbiological Methods. 120:23-28.

Koo H, Mojib N, Hakim JA, Hawes I, Tanabe Y, Andersen DT, Bej AK. 2017a. Microbial communities and their predicted metabolic functions in growth laminae of a unique large conical mat from Lake Untersee, East Antarctica. Frontiers in Microbiology. 8:1347.

Koo H, Hakim JA, Morrow CD, Eipers PG, Davila A, Andersen DT, Bej AK. 2017b. Comparison of two bioinformatics tools used to characterize the microbial diversity and predictive functional attributes of microbial mats from Lake Obersee, Antarctica. Journal of Microbiological Methods. 140:15-22.

Lacap-Bugler DC, Lee KK, Archer S, Gillman LN, Lau MCY, Leuzinger S, Lee CK, Maki T, McKay CP, Perrott JK, de Los Rios-Murillo A, Warren-Rhodes KA, Hopkins DW, Pointing SB. 2017. Global diversity of desert hypolithic cyanobacteria. Frontiers in Microbiology. 8:867.

Lagkouvardos I, Weinmaier T, Lauro FM, Cavicchioli R, Rattei T, Horn M. 2014. Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the Chlamydiae. ISME Journal. 8(1):115-125.

Lauro FM, Demaere MZ, Yau S, Brown MV, Ng C, Wilkins D, Raftery MJ, Gibson JA, Andrews-Pfannkoch C, Lewis M, Hoffman JM, Thomas T, Cavicchioli R. 2011. An integrative study of a meromictic lake ecosystem in Antarctica. ISME Journal. 5(5):879-895.

Le PT, Makhalanyane TP, Guerrero LD, Vikram S, De Peer YV, Cowan DA. 2016. Comparative metagenomic analysis reveals mechanisms for stress response in hypoliths from extreme hyperarid deserts. Genome Biology and Evolution. 8(9):2737-2747.

Lee J, Lee HT, Hong WY, Jang E, Kim J. 2015. FCMM: A comparative metagenomic approach for functional characterization of multiple metagenome samples. Journal of Microbiological Methods. 115:121-128.

Lezcano MA, Moreno-Paz M, Carrizo D, Prieto-Ballesteros O, Fernández-Martínez MÁ, Sánchez-García L, Blanco Y, Puente-Sánchez F, De Diego-Castilla G, García-Villadangos M, Fairén AG, Parro V. 2019. Biomarker profiling of microbial mats in the geothermal band of Cerro Caliente, Deception Island (Antarctica): life at the edge of heat and cold. Astrobiology. 19(12):1490-1504.

Li AZ, Han XB, Zhang MX, Zhou Y, Chen M, Yao Q, Zhu HH. 2019a. Culture-dependent and -independent analyses reveal the diversity, structure, and assembly mechanism of benthic bacterial community in the Ross Sea, Antarctica. Frontiers in Microbiology. 10:2523.

Li Y, Cha QQ, Dang YR, Chen XL, Wang M, McMinn A, Espina G, Zhang YZ, Blamey JM, Qin QL. 2019b. Reconstruction of the functional ecosystem in the high light, low temperature Union Glacier region, Antarctica. Frontiers in Microbiology. 10:2408.

Li J, Gu X, Gui Y. 2020a. Prokaryotic diversity and composition of sediments from Prydz Bay, the Antarctic Peninsula Region, and the Ross Sea, Southern Ocean. Frontiers in Microbiology. 11:783.

Li W, Dore JE, Steigmeyer AJ, Cho YJ, Kim OS, Liu Y, Morgan-Kiss RM, Skidmore ML, Priscu JC. 2020b. Methane production in the oxygenated water column of a perennially ice-covered Antarctic lake. Limnology and Oceanography. 65(1):143-156.

Lin Y, Cassar N, Marchetti A, Moreno C, Ducklow H, Li Z. 2017. Specific eukaryotic plankton are good predictors of net community production in the Western Antarctic Peninsula. Scientific Reports. 7(1):14845.

Lin Y, Gifford S, Ducklow H, Schofield O, Cassara N. 2019. Towards quantitative microbiome community profiling using internal standards. Applied and Environmental Microbiology. 85(5):e02634-18.

Liu Q, Jiang Y. 2020. Application of microbial network analysis to discriminate environmental heterogeneity in Fildes Peninsula, Antarctica. Marine Pollution Bulletin. 156:111244.

Lopatina A, Medvedeva S, Shmakov S, Logacheva MD, Krylenkov V, Severinov K. 2016. Metagenomic analysis of bacterial communities of Antarctic surface snow. Frontiers in Microbiology. 7:398.

Lõpez-Bueno A, Rastrojo A, Peirõ R, Arenas M, Alcamí A. 2015. Ecological connectivity shapes quasispecies structure of RNA viruses in an Antarctic lake. Molecular Ecology. 24(19):4812-4825.

Lutz S, Ziolkowski LA, Benning LG. 2019. The biodiversity and geochemistry of cryoconite holes in Queen Maud Land, East Antarctica. Microorganisms. 7(6):160.

Mariani S, Baillie C, Colosimo G, Riesgo A. 2019. Sponges as natural environmental DNA samplers. Current Biology. 29(11):401-402.

Matos MN, Lozada M, Anselmino LE, Musumeci MA, Henrissat B, Jansson JK, Mac Cormack WP, Carroll J, Sjöling S, Lundgren L, Dionisi HM. 2016. Metagenomics unveils the attributes of the alginolytic guilds of sediments from four distant cold coastal environments. Environmental Microbiology. 18(12):4471-4484.

Medeiros AW, Giongo A, Valdez FP, De Amorin DB, Tavares M, D'Azevedo PA, Franco AC, Frazzon J, Frazzon APG. 2016. Characterization of the faecal bacterial community of wild young South American (*Arctocephalus australis*) and Subantarctic fur seals (*Arctocephalus tropicalis*). FEMS Microbiology Ecology. 92(3):fiw029.

Millán-Aguiñaga N, Soldatou S, Brozio S, Munnoch JT, Howe J, Hoskisson PA, Duncan KR. 2019. Awakening ancient polar actinobacteria: Diversity, evolution and specialized metabolite potential. Microbiology. 165(11):1169-1180.

Millard AD, Pearce D, Zwirglmaier K. 2016. Biogeography of bacteriophages at four hydrothermal vent sites in the Antarctic based on g23 sequence diversity. FEMS Microbiology Letters. 363(7):fnw043.

Miranda JA, Culley AI, Schvarcz CR, Steward GF. 2016. RNA viruses as major contributors to Antarctic virioplankton. Environmental Microbiology. 18(11):3714-3727.

Molina-Montenegro MA, Ballesteros GI, Castro-Nallar E, Meneses C, Gallardo-Cerda J, Torres-Díaz C. 2019. A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomic. Polar Biology. 42(10):1825-1835.

Morandini V, Dugger KM, Ballard G, Elrod M, Schmidt A, Ruoppolo V, Lescroël A, Jongsomjit D, Massaro M, Pennycook J Kooyman GL, Schmidlin K, Kraberger S, Ainley DG, Varsani A. 2019. Identification of a novel Adélie penguin circovirus at Cape Crozier (Ross Island, Antarctica). Viruses. 11(12):1088.

Moreno-Pino M, De la Iglesia R, Valdivia N, Henríquez-Castilo C, Galán A, Díez B, Trefault N. 2016. Variation in coastal Antarctic microbial community composition at sub-mesoscale: Spatial distance or environmental filtering? FEMS Microbiology Ecology. 92(7):fiw088.

Moss JA, Henriksson NL, Pakulski JD, Snyder RA, Jeffrey WH. 2020. Oceanic microplankton do not adhere to the latitudinal diversity gradient. Microbial Ecology. 79(2):511-515.

Ng C, Demaere MZ, Williams TJ, Lauro FM, Raftery M, Gibson JAE, Andrews-Pfannkoch C, Lewis M, Hoffman JM, Thomas T, Cavicchioli R. 2010. Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. ISME Journal. 4(8):1002-1019.

Oh HN, Park D, Seong HJ, Kim D, Sul WJ. 2019. Antarctic tundra soil metagenome as useful natural resources of cold-active lignocelluolytic enzymes. Journal of Microbiology. 57(10):865-873.

Pansu J, Winkworth RC, Hennion F, Gielly L, Taberlet P, Choler P. 2015. Long-lasting modification of soil fungal diversity associated with the introduction of rabbits to a remote sub-Antarctic archipelago. Biology Letters. 11(9):20150408.

Pawlowski J, Fahrni JF, Guiard J, Conlan K, Hardecker J, Habura A, Bowser SS. 2005. Allogromiid foraminifera and gromiids from under the Ross Ice Shelf: Morphological and molecular diversity. Polar Biology. 28(7):514-522.

Pawlowski J, Fontaine D, da Silva AA, Guiard J. 2011. Novel lineages of Southern Ocean deep-sea foraminifera revealed by environmental DNA sequencing. Deep-Sea Research Part II: Topical Studies in Oceanography. 58(19-20):1996-2003.

Pearce DA, Newsham KK, Thorne MAS, Calvo-Bado L, Krsek M, Laskaris P, Hodson A, Wellington EM. 2012. Metagenomic analysis of a southern maritime Antarctic soil. Frontiers in Microbiology. 3:403.

Pessi IS, Osorio-Forero C, Gálvez EJ, Simões FL, Simões JC, Junca H, Macedo AJ. 2015. Distinct composition signatures of archaeal and bacterial phylotypes in the Wanda Glacier forefield, Antarctic Peninsula. FEMS Microbiology Ecology. 91(1):1-10.

Pessi IS, Maalouf PDC, Laughinghouse HDI, Baurain D, Wilmotte A. 2016. On the use of high-throughput sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. Journal of Phycology. 52(3):356-368.

Pessi IS, Lara Y, Durieu B, de Maalouf PC, Verleyen E, Wilmotte A. 2018. Community structure and distribution of benthic cyanobacteria in Antarctic lacustrine microbial mats. FEMS Microbiology Ecology. 94(5):fiy042.

Picazo A, Rochera C, Villaescusa JA, Miralles-Lorenzo J, Velázquez D, Quesada A, Camacho A. 2019. Bacterioplankton community composition along environmental gradients in lakes from Byers Peninsula (Maritime Antarctica) as determined by next-generation sequencing. Frontiers in Microbiology. 10:908.

Pulschen AA, Bendia AG, Fricker AD, Pellizari VH, Galante D, Rodrigues F. 2017. Isolation of uncultured bacteria from antarctica using long incubation periods and low nutritional media. Frontiers in Microbiology. 8:1346.

Quiroga MV, Valverde A, Mataloni G, Cowan D. 2015. Understanding diversity patterns in bacterioplankton communities from a sub-Antarctic peatland. Environmental Microbiology Reports. 7(3):547-553.

Rao S, Chan Y, Lacap DC, Hyde KD, Pointing SB, Farrell RL. 2012. Low-diversity fungal assemblage in an Antarctic Dry Valleys soil. Polar Biology. 35(4):567-574.

Rego A, Raio F, Martins TP, Ribeiro H, Sousa AGG, Séneca J, Baptista MS, Lee CK, Craig Cary S, Ramos V, Carvalho MF, Leão PN, Magalhães C. 2019. Actinobacteria and cyanobacteria diversity in terrestrial Antarctic microenvironments evaluated by culture-dependent and independent methods. Frontiers in Microbiology. 10:1018.

Rich VI, Konstantinidis K, DeLong EF. 2008. Design and testing of 'genome-proxy' microarrays to profile marine microbial communities. Environmental Microbiology. 10(2):506-521.

Rippin M, Lange S, Sausen N, Becker B. 2018. Biodiversity of biological soil crusts from the Polar Regions revealed by metabarcoding. FEMS Microbiology Ecology. 94(4):fiy036.

Rodríguez-Martínez R, Labrenz M, Del Campo J, Forn I, Jürgens K, Massana R. 2009. Distribution of the uncultured protist MAST-4 in the Indian Ocean, Drake Passage and Mediterranean Sea assessed by real-time quantitative PCR. Environmental Microbiology. 11(2):397-408.

Sadaiappan B, Kannan S, Palaniappan S, Manikkam R, Ramasamy B, Anilkumar N, Subramanian M. 2020. Metagenomic 16S rDNA amplicon data of microbial diversity and its predicted metabolic functions in the Southern Ocean (Antarctic). Data in Brief. 28:104876.

Santamans AC, Boluda R, Picazo A, Gil C, Ramos-Miras J, Tejedo P, Pertierra LR, Benayas J, Camacho A. 2017. Soil features in rookeries of Antarctic penguins reveal sea to land biotransport of chemical pollutants. PLoS ONE. 12(8):e0181901.

Schiaffino MR, Lara E, Fernández LD, Balagué V, Singer D, Seppey CC, Massana R, Izaguirre I. 2016. Microbial eukaryote communities exhibit robust biogeographical patterns along a gradient of Patagonian and Antarctic lakes. Environmental Microbiology. 18(12):5249-5264.

Shtarkman YM, Koçer ZA, Edgar R, Veerapaneni RS, D'Elia T, Morris PF, Rogers SO. 2013. Subglacial Lake Vostok (Antarctica) Accretion Ice Contains a Diverse Set of Sequences from Aquatic, Marine and Sediment-Inhabiting Bacteria and Eukarya. PLoS ONE. 8(7):e67221.

Simmons MP, Bachy C, Sudek S, Van Baren MJ, Sudek L, Ares M, Worden AZ. 2015. Intron invasions trace algal speciation and reveal nearly identical Arctic and Antarctic micromonas populations. Molecular Biology and Evolution. 32(9):2219-2235.

Sommers P, Darcy JL, Gendron E, Stanish LF, Bagshaw EA, Porazinska DL, Schmidt SK. 2018. Diversity patterns of microbial eukaryotes mirror those of bacteria in Antarctic cryoconite holes. FEMS Microbiology Ecology. 94(1):fix167.

Sommers P, Porazinska DL, Darcy JL, Zamora F, Fountain AG, Schmidt SK. 2019a. Experimental cryoconite holes as mesocosms for studying community ecology. Polar Biology. 42(11):I973-1984.

Sommers P, Fontenele RS, Kringen T, Kraberger S, Porazinska DL, Darcy JL, Schmidt SK, Varsani A. 2019b. Single-stranded DNA viruses in Antarctic cryoconite holes. Viruses. 11(11):1022.

Soto DF, Fuentes R, Huovinen P, Gómez I. 2020. Microbial composition and photosynthesis in Antarctic snow algae communities: Integrating metabarcoding and pulse amplitude modulation fluorometry. Algal Research. 45:101738

Tahon G, Tytgat B, Willems A. 2016. Diversity of phototrophic genes suggests multiple bacteria may be able to exploit sunlight in exposed soils from the Sør Rondane Mountains, East Antarctica. Frontiers in Microbiology. 7:2026

Teasdale SE, Beulke AK, Guy PL, Orlovich DA. 2013. Environmental barcoding of the ectomycorrhizal fungal genus Cortinarius. Fungal Diversity. 58(1):299-310.

Tighe S, Afshinnekoo E, Rock TM, McGrath K, Alexander N, McIntyre A, Ahsanuddins S, Bezdan D, Green SJ, Joye S, Stewart Johnson S, Baldwin DA, Bivens N, Ajami N, Carmical JR, Herriott IC, Colwell R, Donia M, Foox J, Greenfield N, Hunter T, Hoffman J, Hyman J, Jorgensen E, Krawczyk D, Lee J, Levy S, Garcia-Reyero N, Settles M, Thomas K, Gómez F, Schriml L, Kyrpides N, Zaikova E, Penterman J, Mason CE. 2017. Genomic methods and microbiological technologies for profiling novel and extreme environments for the extreme microbiome project (XMP). Journal of Biomolecular Techniques. 28(1):31-39.

Tschitschko B, Williams TJ, Allen MA, Páez-Espino D, Kyrpides N, Zhong L, Raftery MJ, Cavicchioli R. 2015. Antarctic archaea-virus interactions: Metaproteome-led analysis of invasion, evasion and adaptation. ISME Journal. 9(9):2094-2107.

Tschitschko B, Erdmann S, DeMaere MZ, Roux S, Panwar P, Allen MA, Williams TJ, Brazendale S, Hancock AM, Eloe-Fadrosh EA, Emiley A, Cavicchioli R. 2018. Genomic variation and biogeography of Antarctic haloarchaea. Microbiome. 6(1):113.

Tytgat B, Verleyen E, Obbels D, Peeters K, De Wever A, D'Hondt S, De Meyer T, Van Criekinge W, Vyverman W, Willems A. 2014. Bacterial diversity assessment in Antarctic terrestrial and aquatic microbial mats: A comparison between bidirectional pyrosequencing and cultivation. PLoS ONE. 9(6):e97564.

Van Dorst J, Bissett A, Palmer AS, Brown M, Snape I, Stark JS, Raymond B, McKinlay J, Ji M, Winsley T, Ferrari BC. 2014. Community fingerprinting in a sequencing world. FEMS Microbiology Ecology. 89(2):316-330.

Van Goethem MW, Pierneef R, Bezuidt OKI, Van De Peer Y, Cowan DA, Makhalanyane TP. 2018. A reservoir of 'historical' antibiotic resistance genes in remote pristine Antarctic soils. Microbiome. 6(1):40.

Varsani A, Kraberger S, Jennings S, Porzig EL, Julian L, Massaro M, Pollard A, Ballard G, Ainley DG. 2014. A novel papillomavirus in Adélie penguin (Pygoscelis adeliae) faeces sampled at the Cape Crozier colony, Antarctica. Journal of General Virology. 95(6):1352-1365.

Vause BJ, Morley SA, Fonseca VG, Jazdzewska A, Ashton GV, Barnes DKA, Giebner H, Clark MS, Peck LS. 2019. Spatial and temporal dynamics of Antarctic shallow soft-bottom benthic communities: Ecological drivers under climate change. BMC Ecology. 19(1):27.

Velázquez D, López-Bueno A, Aguirre De Cárcer D, De Los Ríos A, Alcamí A, Quesada A. 2016. Ecosystem function decays by fungal outbreaks in Antarctic microbial mats. Scientific Reports. 6:22954.

Vishnivetskaya TA, Buongiorno J, Bird J, Krivushin K, Spirina EV, Oshurkova V, Shcherbakova VA, Wilson G, Lloyd KG, Rivkina EM. 2018. Methanogens in the Antarctic Dry Valley permafrost. FEMS Microbiology Ecology. 94(8):fiy109.

Webster-Brown JG, Hawes I, Jungblut AD, Wood SA, Christenson HK. 2015. The effects of entombment on water chemistry and bacterial assemblages in closed cryoconite holes on Antarctic glaciers. FEMS Microbiology Ecology. 91(12):fiv144.

Wei STS, Lacap-Bugler DC, Lau MCY, Caruso T, Rao S, de los Rios A, Archer SK, Chiu JMY, Higgins C, Van Nostrand JD, Zhou J, Hopkins DW., Pointing SB. 2016. Taxonomic and functional diversity of soil and hypolithic microbial communities in Miers Valley, McMurdo Dry Valleys, Antarctica. Frontiers in Microbiology. 7:1642.

Weisleitner K, Perras A, Moissl-Eichinger C, Andersen DT, Sattler B. 2019. Source environments of the microbiome in perennially ice-covered lake Untersee, Antarctica. Frontiers in Microbiology. 10:1019.

Wilkins D, Lauro FM, Williams TJ, Demaere MZ, Brown MV, Hoffman JM, Andrews-Pfannkoch C, McQuaid JB, Riddle MJ, Rintoul SR, Cavicchioli R. 2013. Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. Environmental Microbiology. 15(5):1318-1333.

Williams TJ, Wilkins D, Long E, Evans F, Demaere MZ, Raftery MJ, Cavicchioli R. 2013. The role of planktonic Flavobacteria in processing algal organic matter in coastal East Antarctica revealed using metagenomics and metaproteomics. Environmental Microbiology. 15(5):1302-1317.

Williams TJ, Allen MA, DeMaere MZ, Kyrpides NC, Tringe SG, Woyke T, Cavicchioli R. 2014. Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. The ISME journal. 8(8):1645-1658.

Winsley TJ, Snape I, McKinlay J, Stark J, van Dorst JM, Ji M, Ferrari BC, Siciliano SD. 2014. The ecological controls on the prevalence of candidate division TM7 in polar regions. Frontiers in Microbiology. 5:345.

Wolf C, Frickenhaus S, Kilias ES, Peeken I, Metfies K. 2013a. Regional variability in eukaryotic protist communities in the Amundsen Sea. Antarctic Science. 25(6):741-751.

Wolf C, Frickenhaus S, Kilias ES, Peeken I, Metfies K. 2013b. Protist community composition in the Pacific sector of the Southern Ocean during austral summer 2010. Polar Biology. 37(3):375-389.

Yan W, Ma H, Shi G, Li Y, Sun B, Xiao X, Zhang Y. 2017. Independent shifts of abundant and rare bacterial populations across East Antarctica glacial foreland. Frontiers in Microbiology. 8:1534.

Yang Q, Gao C, Jiang Y, Wang M, Zhou X, Shao H, Gong Z, McMinn A. 2019a. Metagenomic characterization of the viral community of the South Scotia Ridge. Viruses. 11(2):95.

Yang Y, Li Z, Song W, Du L, Ye C, Zhao B, Liu W, Deng D, Pan Y, Lin H, Cao X. 2019b. Metagenomic insights into the abundance and composition of resistance genes in aquatic environments: Influence of stratification and geography. Environment International. 127:371-380.

Yau S, Lauro FM, DeMaere MZ, Brown MV, Thomas T, Raftery MJ, Andrews-Pfannkoch C, Lewis M, Hoffman JM, Gibson JA, Cavicchioli R. 2011. Virophage control of Antarctic algal host-virus dynamics. Proceedings of the National Academy of Sciences of the United States of America. 108(15):6163-6168.

Yau S, Lauro FM, Williams TJ, Demaere MZ, Brown MV, Rich J, Gibson JAE, Cavicchioli R. 2013. Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. ISME Journal. 7(10):1944-1961.

Yew WC, Pearce DA, Dunn MJ, Samah AA, Convey P. 2017. Bacterial community composition in Adélie (*Pygoscelis adeliae*) and Chinstrap (*Pygoscelis antarctica*) Penguin stomach contents from Signy Island, South Orkney Islands. Polar Biology. 40(12):2517-2530.

Yu Z, Yang J, Liu L, Zhang W, Amalfitano S. 2015. Bacterioplankton community shifts associated with epipelagic and mesopelagic waters in the Southern Ocean. Scientific Reports. 5:12897.

Zaikova E, Goerlitz DS, Tighe SW, Wagner NY, Bai Y, Hall BL, Bevilacqua JG, Weng MM, Samuels-Fair MD, Johnson SS. 2019. Antarctic relic microbial mat community revealed by metagenomics and metatranscriptomics. Frontiers in Ecology and Evolution. 7:1.

Zawar-Reza P, Argüello-Astorga GR, Kraberger S, Julian L, Stainton D, Broady PA, Varsani A. 2014. Diverse small circular single-stranded DNA viruses identified in a freshwater pond on the McMurdo Ice Shelf (Antarctica). Infection, Genetics and Evolution. 26:132-138.

Zhang W, Cao S, Ding W, Wang M, Fan S, Yang B, McMinn A, Wang M, Xie BB, Qin QL, Chen XL, He J, Zhang YZ. 2020. Structure and function of the Arctic and Antarctic marine microbiota as revealed by metagenomics. Microbiome. 8(1):77.

Zoccarato L, Pallavicini A, Cerino F, Umani SF, Celussi M. 2016. Water mass dynamics shape Ross Sea protist communities in mesopelagic and bathypelagic layers. Progress in Oceanography. 149:16-26.