



**Supplementary Information:** *In addition to this statement, each candidate is requested to provide the following information:*

*The candidate's academic and honorary degrees;*

- B.A. Biology and Religion
- Ph.D. Molecular, Cellular and Developmental Biology

*The candidate's current occupation;*

- Professor in the Department of Microbiology and Immunology

*The candidate's current and past academic, societal, governmental, or commercial offices held;*

- 2017-present Co-founder, Koonkie Cloud Services
- 2015-present Director, ECOSCOPE training program
- 2012-present Primary Advisor, International Genetically Engineered Machine Team
- 2009-present JGI Microbial Genomics and Metagenomics User Advisory Committee
- 2013-2014 Co-founder and Secretary, MetaMixis Biologics
- 2012-2017 Associate Professor, Microbiology & Immunology
- 2011-2018 PNNL User Advisory Committee
- 2006-2012 Assistant Professor, Microbiology & Immunology

*The candidate's current professional or business interests;*

As ECOSCOPE Director I am engaged in outreach efforts to the biotechnology sector here in Canada and in the United States. I have participated in both Lean Launchpad and StartX incubator programs and have co-founded two companies that compliment my research interests. I am actively involved in building a high-throughput screening facility here on campus leveraging CFI funding through the BioProducts Institute to support enzyme discovery efforts related to biomass deconstruction, mine tailings and pulp and paper mill sludge remediation. I have also developed collaborative research partnerships with Metro Vancouver focused on optimizing their reactor process for biogas production and with AlgaBloom focused on the production of platform chemicals using cyanobacterial host strains. I actively mentor students interested in biotechnology development and commercialization opportunities based on microbial ecology and biological engineering research themes. I am very interested in seeing Vancouver become a hub for biotechnology innovation focused on sustainability themes such as biorefining and carbon capture.



*The candidate's list of publications (if any).*

### **RESEARCH PUBLICATIONS IN PEER-REVIEWED JOURNALS (91 Total)**

1. *Metagenomes Reveal Global Distribution of Bacterial Steroid Catabolism in Natural, Engineered, and Host Environments.* Holert J, Cardenas E, Bergstrand LH, Zaikova E, Hahn AS, **Hallam SJ**, Mohn WW. MBio. 2018 Jan 30;9(1). pii: e02345-17. doi: 10.1128/mBio.02345-17. PMID: 29382738
2. *Structural and mechanistic analysis of a  $\beta$ -glycoside phosphorylase identified by screening a metagenomic library.* Macdonald SS, Patel A, Larmour VLC, Morgan-Lang C, **Hallam SJ**, Mark BL, Withers SG. J Biol Chem. 2018 Mar 2;293(9):3451-3467. doi: 10.1074/jbc.RA117.000948. PMID: 29317495
3. *An Improved Whole-Cell Biosensor for the Discovery of Lignin-Transforming Enzymes in Functional Metagenomic Screens.* Ho JCH, Pawar SV, **Hallam SJ\***, Yadav VG\*. ACS Synth Biol. 2018 Feb 16;7(2):392-398. doi: 10.1021/acssynbio.7b00412. PMID: 29182267
4. *Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation.* Pachiadaki MG, Sintes E, Bergauer K, Brown JM, Record NR, Swan BK, Mathyer ME, **Hallam SJ**, Lopez-Garcia P, Takaki Y, Nunoura T, Woyke T, Herndl GJ, Stepanauskas R. Science. 2017 Nov 24;358(6366):1046-1051. doi: 10.1126/science.aan8260. PMID: 29170234
5. *Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along ecothermodynamic gradients.* Hawley AK, Nobu MK, Wright JJ, Durno WE, Morgan-Lang C, Sage B, Schwientek P, Swan BK, Rinke C, Torres-Beltrán M, Mewis K, Liu WT, Stepanauskas R, Woyke T, **Hallam SJ**. Nat Commun. 2017 Nov 15;8(1):1507. doi: 10.1038/s41467-017-01376-9. PMID: 29142241
6. *A communal catalogue reveals Earth's multiscale microbial diversity.* Thompson LR, Sanders JG, McDonald D, Amir A, Ladau J, Locey KJ, Prill RJ, Tripathi A, Gibbons SM, Ackermann G, Navas-Molina JA, Janssen S, Kopylova E, Vázquez-Baeza Y, González A, Morton JT, Mirarab S, Zech Xu Z, Jiang L, Haroon MF, Kanbar J, Zhu Q, Jin Song S, Kosciulek T, Bokulich NA, Lefler J, Brislawn CJ, Humphrey G, Owens SM, Hampton-Marcell J, Berg-Lyons D, McKenzie V, Fierer N, Fuhrman JA, Clauset A, Stevens RL, Shade A, Pollard KS, Goodwin KD, Jansson JK, Gilbert JA, Knight R; Earth Microbiome Project Consortium. Nature. 2017 Nov 23;551(7681):457-463. doi: 10.1038/nature24621. PMID: 29088705
7. *Monitoring microbial responses to ocean deoxygenation in a model oxygen minimum zone.* **Hallam SJ**, Torres-Beltrán M, Hawley AK. Sci Data. 2017 Oct 31;4:170158. doi: 10.1038/sdata.2017.158. PMID: 29087370



8. *A compendium of geochemical information from the Saanich Inlet water column.* Torres-Beltrán M, Hawley AK, Capelle D, Zaikova E, Walsh DA, Mueller A, Scotfield M, Payne C, Pakhomova L, Kheirandish S, Finke J, Bhatia M, Shevchuk O, Gies EA, Fairley D, Michiels C, Suttle CA, Whitney F, Crowe SA, Tortell PD, **Hallam SJ**. *Sci Data*. 2017 Oct 31;4:170159. doi: 10.1038/sdata.2017.159. PMID: 29087371
9. *A compendium of multi-omic sequence information from the Saanich Inlet water column.* Hawley AK, Torres-Beltrán M, Zaikova E, Walsh DA, Mueller A, Scotfield M, Kheirandish S, Payne C, Pakhomova L, Bhatia M, Shevchuk O, Gies EA, Fairley D, Malfatti SA, Norbeck AD, Brewer HM, Pasa-Tolic L, Del Rio TG, Suttle CA, Tringe S, **Hallam SJ**. *Sci Data*. 2017 Oct 31;4:170160. doi: 10.1038/sdata.2017.160. PMID: 29087368
10. *Single cell genomics of uncultured marine alveolates shows parphyly of basal dinoflagellates.* Strassert JFH, Karnkowska A, Hehenberger E, Del Campo J, Kolisko M, Okamoto N, Burki F, Janouškovec J, Poirier C, Leonard G, **Hallam SJ**, Richards TA, Worden AZ, Santoro AE, Keeling PJ. *ISME J*. 2018 Jan;12(1):304-308. doi: 10.1038/ismej.2017.167. PMID: 28994824
11. *Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea.* Bowers RM, Kyrpides NC, Stepanauskas R, Harmon-Smith M, Doud D, Reddy TBK, Schulz F, Jarett J, Rivers AR, Eloe-Fadrosh EA, Tringe SG, Ivanova NN, Copeland A, Clum A, Becraft ED, Malmstrom RR, Birren B, Podar M, Bork P, Weinstock GM, Garrity GM, Dodsworth JA, Yooseph S, Sutton G, Glöckner FO, Gilbert JA, Nelson WC, **Hallam SJ**, Jungbluth SP, Ettema TJG, Tighe S, Konstantinidis KT, Liu WT, Baker BJ, Rattei T, Eisen JA, Hedlund B, McMahon KD, Fierer N, Knight R, Finn R, Cochrane G, Karsch-Mizrachi I, Tyson GW, Rinke C; Genome Standards Consortium, Lapidus A, Meyer F, Yilmaz P, Parks DH, Eren AM, Schriml L, Banfield JF, Hugenholtz P, Woyke T. *Nat Biotechnol*. 2017 Aug 8;35(8):725-731. doi: 10.1038/nbt.3893. PMID: 28787424
12. *A metagenomic survey of forest soil microbial communities more than a decade after timber harvesting.* Wilhelm RC, Cardenas E, Leung H, Maas K, Hartmann M, Hahn AS, **Hallam SJ**, Mohn WW. *Sci Data*. 2017 Jul 25;4:170092. doi: 10.1038/sdata.2017.92. eCollection 2017. PMID: 28765786
13. *Nutrient Acquisition and the Metabolic Potential of Photoferrotrophic Chlorobi.* Thompson KJ, Simister RL, Hahn AS, **Hallam SJ**, Crowe SA. *Front Microbiol*. 2017 Jul 6;8:1212. doi: 10.3389/fmicb.2017.01212. eCollection 2017. PMID: 28729857
14. *Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae.* Collingro A, Köstlbacher S, Musmann M, Stepanauskas R, **Hallam**



- SJ**, Horn M. ISME J. 2017 Oct;11(10):2334-2344. doi: 10.1038/ismej.2017.95. PMID: 28644443
15. *A geographically-diverse collection of 418 human gut microbiome pathway genome databases.* Hahn AS, Altman T, Konwar KM, Hanson NW, Kim D, Relman DA, Dill DL, **Hallam SJ**. Sci Data. 2017 Apr 11;4:170035. doi: 10.1038/sdata.2017.35. PMID: 28398290
  16. *Draft Genome Sequence of the Pelagic Photoferrotroph Chlorobium phaeoferrooxidans.* Crowe SA, Hahn AS, Morgan-Lang C, Thompson KJ, Simister RL, Llorós M, Hirst M, **Hallam SJ**. Genome Announc. 2017 Mar 30;5(13). pii: e01584-16. doi: 10.1128/genomeA.01584-16. PMID: 28360175
  17. *IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses.* Paez-Espino D, Chen IA, Palaniappan K, Ratner A, Chu K, Szeto E, Pillay M, Huang J, Markowitz VM, Nielsen T, Huntemann M, K Reddy TB, Pavlopoulos GA, Sullivan MB, Campbell BJ, Chen F, McMahon K, **Hallam SJ**, Denev V, Cavicchioli R, Caffrey SM, Streit WR, Webster J, Handley KM, Salekdeh GH, Tsesmetzis N, Setubal JC, Pope PB, Liu WT, Rivers AR, Ivanova NN, Kyrpides NC. Nucleic Acids Res. 2017 Jan 4;45(D1):D457-D465. doi: 10.1093/nar/gkw1030. PMID: 27799466
  18. *Integrating biogeochemistry with multiomic sequence information in a model oxygen minimum zone.* Louca S, Hawley AK, Katsev S, Torres-Beltran M, Bhatia MP, Kheirandish S, Michiels CC, Capelle D, Lavik G, Doebeli M, Crowe SA\*, **Hallam SJ\***. Proc Natl Acad Sci U S A. 2016 Oct 4;113(40):E5925-E5933. PMID: 27655888 Dr. Crowe and I share corresponding author status (\*)
  19. *Ammonium and nitrite oxidation at nanomolar oxygen concentrations in oxygen minimum zone waters.* Bristow LA, Dalsgaard T, Tiano L, Mills DB, Bertagnolli AD, Wright JJ, **Hallam SJ**, Ulloa O, Canfield DE, Revsbech NP, Thamdrup B. Proc Natl Acad Sci U S A. 2016 Sep 20;113(38):10601-6. doi: 10.1073/pnas.1600359113. PMID: 27601665
  20. *LCA\*: an entropy-based measure for taxonomic assignment within assembled metagenomes.* Hanson NW, Konwar KM, **Hallam SJ**. Bioinformatics. 2016 Dec 1;32(23):3535-3542. PMID: 27515739
  21. *High-resolution phylogenetic microbial community profiling.* Singer E, Bushnell B, Coleman-Derr D, Bowman B, Bowers RM, Levy A, Gies EA, Cheng JF, Copeland A, Klenk HP, **Hallam SJ**, Hugenholtz P, Tringe SG, Woyke T. ISME J. 2016 Aug;10(8):2020-32. doi: 10.1038/ismej.2015.249.
  22. *Synthesis and evaluation of a series of 6-chloro-4-methylumbelliferyl glycosides as fluorogenic reagents for screening metagenomic libraries for glycosidase activity.* Chen



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23. *Phylogeny and physiology of candidate phylum 'Atribacteria' (OP9/JS1) inferred from cultivation-independent genomics.* Nobu MK, Dodsworth JA, Murugapiran SK, Rinke C, [Gies EA](#), Webster G, Schwientek P, Kille P, Parkes RJ, Sass H, Jørgensen BB, Weightman AJ, Liu WT, **Hallam SJ**, Tsiamis G, Woyke T, Hedlund BP. ISME J. 2016 Feb;10(2):273-86. doi: 10.1038/ismej.2015.97. PMID: 26090992
24. *Patterns of Endemism and Habitat Selection in Coalbed Microbial Communities.* [Lawson CE](#), [Strachan CR](#), [Williams DD](#), Koziel S, **Hallam SJ**, Budwill K. Appl Environ Microbiol. 2015 Nov;81(22):7924-37. doi: 10.1128/AEM.01737-15. PMID: 26341214
25. *Assembly independent functional annotation of short-read data using SOFA: Short-ORF functional annotation.* [Hahn A. S.](#), [N. W. Hanson](#), [D. Kim](#), [K. M. Konwar](#) and **S. J. Hallam**. 2015. Computational Intelligence in Bioinformatics and Computational Biology (**CIBCB**), 2015 IEEE Conference on. doi: 10.1109/CIBCB.2015.7300324
26. *FragGeneScan-plus for scalable high-throughput short-read open reading frame prediction.* [Kim D.](#), [A. S. Hahn](#), [S. Wu](#), [N. W. Hanson](#), [K. M. Konwar](#) and **S. J. Hallam**. 2015. Computational Intelligence in Bioinformatics and Computational Biology (**CIBCB**), 2015 IEEE Conference on. doi: 10.1109/CIBCB.2015.7300341
27. *Viral dark matter and virus-host interactions resolved from publicly available microbial genomes.* Roux S, **Hallam SJ**, Woyke T, Sullivan MB. Elife. 2015 Jul 22;4. doi: 10.7554/eLife.08490. PMID: 26200428
28. *In Silico Analysis of the Metabolic Potential and Niche Specialization of Candidate Phylum "Latescibacteria" (WS3).* Youssef NH, Farag IF, Rinke C, **Hallam SJ**, Woyke T, Elshahed MS. PLoS One. 2015 Jun 3;10(6):e0127499. doi: 10.1371/journal.pone.0127499. eCollection 2015. PMID: 26039074
29. *MetaPathways v2.5: quantitative functional, taxonomic and usability improvements.* [Konwar KM](#), [Hanson NW](#), [Bhatia MP](#), [Kim D](#), [Wu SJ](#), [Hahn AS](#), [Morgan-Lang C](#), [Cheung HK](#), **Hallam SJ**. Bioinformatics. 2015 Oct 15;31(20):3345-7. doi: 10.1093/bioinformatics/btv361. PMID: 26076725
30. *Previously unknown evolutionary groups dominate the ssDNA gokushoviruses in oxic and anoxic waters of a coastal marine environment.* Labonté JM, **Hallam SJ**, Suttle CA. Front Microbiol. 2015 Apr 22;6:315. doi: 10.3389/fmicb.2015.00315. eCollection 2015. PMID: 25954254



31. *Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions.* Chow CE, Winget DM, White RA 3rd, **Hallam SJ**, Suttle CA. *Front Microbiol.* 2015 Apr 10;6:265. doi: 10.3389/fmicb.2015.00265. eCollection 2015. PMID: 25914678
32. *Forest harvesting reduces the soil metagenomic potential for biomass decomposition.* Cardenas E, Kranabetter JM, Hope G, Maas KR, **Hallam SJ**, Mohn WW. *ISME J.* 2015 Nov;9(11):2465-76. doi: 10.1038/ismej.2015.57. PMID: 25909978
33. *Non-symbiotic Bradyrhizobium ecotypes dominate North American forest soils.* VanInsberghe D, Maas KR, Cardenas E, Strachan CR, **Hallam SJ**, Mohn WW. *ISME J.* 2015 Nov;9(11):2435-41. doi: 10.1038/ismej.2015.54. PMID: 25909973
34. *Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton.* Labonté JM, Swan BK, Poulos B, Luo H, Koren S, **Hallam SJ**, Sullivan MB, Woyke T, Wommack KE, Stepanauskas R. *ISME J.* 2015 Nov;9(11):2386-99. doi: 10.1038/ismej.2015.48. PMID: 25848873
35. *The microbial community of a passive biochemical reactor treating arsenic, zinc, and sulfate-rich seepage.* Baldwin SA, Khoshnoodi M, Rezadehbashi M, Taupp M, **Hallam SJ**, Mattes A, Sanei H. *Front Bioeng Biotechnol.* 2015 Mar 6;3:27. doi: 10.3389/fbioe.2015.00027. eCollection 2015. PMID: 25798439
36. *Rare taxa have potential to make metabolic contributions in enhanced biological phosphorus removal ecosystems.* Lawson CE, Strachan BJ, Hanson NW, Hahn AS, Hall ER, Rabinowitz B, Mavinic DS, Ramey WD, **Hallam SJ**. *Environ Microbiol.* 2015 Dec;17(12):4979-93. doi: 10.1111/1462-2920.12875. PMID: 25857222
37. Baldwin S.A., M. Khoshnoodi, M. Rezadehbashi, M. Taupp, **S. J. Hallam**, A. Mattes and H. Sanei. *The microbial community of a passive biochemical reactor treating arsenic, zinc, and sulfate-rich seepage.* 2015. *Frontiers in Bioengineering and Biotechnology* 3:27 doi: 10.3389/fbioe.2015.00027.
38. *Microbes don't play solitaire: how cooperation trumps isolation in the microbial world.* **Hallam SJ**, McCutcheon JP. *Environ Microbiol Rep.* 2015 Feb;7(1):26-8. doi: 10.1111/1758-2229.12248. PMID: 25721597
39. *Koonkie: An Automated Software Tool for Processing Environmental Sequence Information using Hadoop.* Kim, D., K. M. Kishori, N. W. Hanson, and **S. J. Hallam**. 2014. *Academy of Science and Engineering 2104 ASE Conference on BigData and Social Informatics.*



40. *Illuminating microbial dark matter in meromictic Sakinaw Lake.* Gies EA, Konwar KM, Beatty JT, Hallam SJ. *Appl Environ Microbiol.* 2014 Nov;80(21):6807-18. doi: 10.1128/AEM.01774-14. PMID: 25172853
41. *Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics.* Roux S, Hawley AK, Torres Beltran M, Scofield M, Schwientek P, Stepanauskas R, Woyke T, Hallam SJ\*, Sullivan MB\*. *Elife.* 2014 Aug 29;3:e03125. doi: 10.7554/eLife.03125. PMID: 25171894 Dr. Sullivan and I share corresponding author status (\*).
42. ¥ *Metagenomic scaffolds enable combinatorial lignin transformation.* Strachan CR, Singh R, VanInsberghe D, Ievdokymenko K, Budwill K, Mohn WW, Eltis LD, Hallam SJ. *Proc Natl Acad Sci U S A.* 2014 Jul 15;111(28):10143-8. doi: 10.1073/pnas.1401631111. Epub 2014 Jun 30. PMID: 24982175
43. ¥ *Metabolic pathways for the whole community.* Hanson NW, Konwar KM, Hawley AK, Altman T, Karp PD, Hallam SJ. *BMC Genomics.* 2014 Jul 22;15:619. doi: 10.1186/1471-2164-15-619. PMID: 25048541
44. ¥ *Metaproteomics reveals differential modes of metabolic coupling among ubiquitous oxygen minimum zone microbes.* Hawley AK, Brewer HM, Norbeck AD, Paša-Tolić L, Hallam SJ. *Proc Natl Acad Sci U S A.* 2014 Aug 5;111(31):11395-400. doi: 10.1073/pnas.1322132111. PMID: 25053816
45. *Metapathways 2.0: A master-worker model for environmental Pathway/Genome Database construction on grids and clouds.* Hanson, N.W., K. M. Konwar, S. Wu, Hallam SJ. 2014. *Computational Intelligence in Bioinformatics and Computational Biology, 2014 IEEE Conference on.* doi: 10.1109/CIBCB.2014.6845516
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47. *Thioploca spp. sheaths as niches for bacterial and protistan assemblages.* Buck, K.R., J.P. Barry, Hallam SJ. 2013. *Marine Ecology.* doi:10.1111/maec.12076
48. *Genomic properties of Marine Group A bacteria indicate a role in the marine sulfur cycle.* Wright JJ, Mewis K, Hanson NW, Konwar KM, Maas KR, Hallam SJ. *ISME J.* 2014 Feb;8(2):455-68. doi: 10.1038/ismej.2013.152. PMID: 24030600



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50. *Metagenomics of hydrocarbon resource environments indicates aerobic taxa and genes to be unexpectedly common.* An D, Caffrey SM, Soh J, Agrawal A, Brown D, Budwill K, Dong X, Dunfield PF, Foght J, Gieg LM, **Hallam SJ**, Hanson NW, He Z, Jack TR, Klassen J, Konwar KM, Kuatsjah E, Li C, Larter S, Leopatra V, Nesbø CL, Oldenburg T, Pagé AP, Ramos-Padron E, Rochman FF, Saidi-Mehrabad A, Sensen CW, Sipahimalani P, Song YC, Wilson S, Wolbring G, Wong ML, Voordouw G. *Environ Sci Technol.* 2013 Sep 17;47(18):10708-17. doi: 10.1021/es4020184. PMID: 23889694
51. *MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information.* Konwar KM, Hanson NW, Pagé AP, **Hallam SJ**. *BMC Bioinformatics.* 2013 Jun 21;14:202. doi: 10.1186/1471-2105-14-202. PMID: 23800136
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54. *Insights into the phylogeny and coding potential of microbial dark matter.* Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson IJ, Cheng JF, Darling A, Malfatti S, Swan BK, Gies EA, Dodsworth JA, Hedlund BP, Tsiamis G, Sievert SM, Liu WT, Eisen JA, **Hallam SJ**, Kyrpides NC, Stepanauskas R, Rubin EM, Hugenholtz P, Woyke T. *Nature.* 2013 Jul 25;499(7459):431-7. doi: 10.1038/nature12352. PMID: 23851394
55. *Sequencing platform and library preparation choices impact viral metagenomes.* Solonenko SA, Ignacio-Espinoza JC, Alberti A, Cruaud C, **Hallam SJ**, Konstantinidis K, Tyson G, Wincker P, Sullivan MB. *BMC Genomics.* 2013 May 10;14:320. doi: 10.1186/1471-2164-14-320. PMID: 23663384 input on the manuscript.]
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58. *Genomic and transcriptomic studies of an RDX (hexahydro-1,3,5-trinitro-1,3,5-triazine)-degrading actinobacterium.* Chen HP, Zhu SH, Casabon I, **Hallam SJ**, Crocker FH, Mohn WW, Indest KJ, Eltis LD. Appl Environ Microbiol. 2012 Nov;78(21):7798-800. doi: 10.1128/AEM.02120-12. Epub 2012 Aug 24. PMID: 22923396.
59. *Microbial community structure across fluid gradients in the Juan de Fuca Ridge hydrothermal system.* Anderson RE, Beltrán MT, **Hallam SJ**, Baross JA. FEMS Microbiol Ecol. 2013 Feb;83(2):324-39. doi: 10.1111/j.1574-6941.2012.01478.x. PMID: 22928928
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62. *Activity and abundance of denitrifying bacteria in the subsurface biosphere of diffuse hydrothermal vents of the Juan de Fuca Ridge.* Bourbonnais, A., S. K. Juniper, D. A. Butterfield, A. H. Devol, M. M. M. Kuypers, G. Lavik, **S. J. Hallam**, C. B. Wenk, B. X. Chang, S. A. Murdock, and M. F. Lehmann. 2012. Biogeosciences Discussions, 9:4177–4223
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64. *Methanotrophic communities of Saanich Inlet: a microcosm perspective.* Sauter LM, Latypova E, Smalley NE, Lidstrom ME, **Hallam SJ**, Kalyuzhnaya MG. Syst Appl Microbiol. 2012 May;35(3):198-203. doi: 10.1016/j.syapm.2011.10.006. Epub 2012 Mar 9. PMID: 22406542
65. *V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets.* Hartmann M, Howes CG,



Veldre V, Schneider S, Vaishampayan PA, Yannarell AC, Quince C, Johansson P, Björkroth KJ, Abarenkov K, **Hallam SJ**, Mohn WW, Nilsson RH. *FEMS Microbiol Lett.* 2011 Jun;319(2):140-5. doi: 10.1111/j.1574-6968.2011.02274.x. PMID: 21453324

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Dr. Schulze-Makuch and I are co-corresponding authors (\*).
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#### **BOOK CHAPTERS AND INVITED REVIEW ARTICLES (11)**

##### *(a) Chapters*

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4. Taupp, M. and **Hallam SJ.** 2010. *The “meta-methanoxgenome”* Part 23 in the Handbook of Hydrocarbon Microbiology, doi: 10.1007/978-3-540-77587-4\_162
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