

Publications

Bruch A*, Lazarova V*, Krueger T, Schaeuble S, Kelani AA, Lehenberger P, Kniemeyer O, Panagiotou G, Blango MG (2024) Mod5 mediates a molecular trade-off between optimal gene expression and antifungal resistance. *bioRxiv* [Preprint]

Chen J, Lu RS, Diaz-Canestro C, Song E, Jia X, Liu Y, Wang C, Cheung CKY, Panagiotou G#, Xu A# (2024) Distinct changes in serum metabolites and lipid species in the onset and progression of NAFLD in obese Chinese. *Comput Struct Biotechnol J* 23(2024), 791-800.

Garcia-Morena D, Fernandez-Cantos MV, Lopez Escalera S, Lok J, Iannone V, Cancellieri P, Maathuis W, Panagiotou G, Aranzamendi C, El Aidy S, Kolehmainen M, El-Nezami H, Wellejus A, Kuipers OP (2024) *In-vitro* influence of specific Bacteroidales strains on gut and liver health related to Metabolic dysfunction-associated fatty liver disease. *Probiotics Antimicrob Proteins* [Epub ahead of print]

Heilig L, Fariha N, Trinks N, Aimaganianda V, Wong SSW, Fontaine T, Terpitz U, Strobel L, Lemauff F, Sheppard D, Schaeuble S, Kurzai O, Hünninger K, Weiss E, Vargas M, Howell PL, Panagiotou G, Wurster S, Einsele H, Löffler J (2024) CD56-mediated activation of human natural killer cells is triggered by *Aspergillus fumigatus* galactosaminogalactan. *PLOS Pathog* 20(6), e1012315.

Li H*, Zhang L*, Li J*, Wu Q*, Qian L, He J, Ni Y, Kovatcheva-Datchary P, Yuan R, Liu S, Shen L, Zhang M, Sheng B, Li P, Kang K, Wu L, Fang Q, Long X, Liu X, Wang X, Li Y, Ye Y, Ye J, Bao Y, Zhao Y, Xu G, Panagiotou G#, Xu A#, and Jia W# (2024) Resistant starch intake facilitates weight loss in humans by reshaping the gut microbiota. *Nat Metab* 6(3), 578-597.

Loos D*, Pereira da Costa Filho A*, Dutilh B E, Barber AE#, Panagiotou G# (2024) A global survey of host, aquatic, and soil microbiomes reveals shared abundance and genomic features between bacterial and fungal generalists. *Cell Rep* 43(4), 114046.

McIlroy SE#, Guibert I, Archana A, Chung WYH, Duffy JE, Gotama R, Hui J, Knowlton N, Leray M, Meyer C, Panagiotou G, Paulay G, Russell B, Thompson PD, Baker DM# (2024) Life goes on: Spatial heterogeneity promotes biodiversity in an urbanized coastal marine ecosystem. *Glob Chang Biol* 30(4), e17248.

Peng H, Schmiederer J, Chen X, Panagiotou G, Kries H# (2024) Controlling substrate- and stereospecificity of condensation domains in nonribosomal peptide synthetases. *ACS Chem Bio* 19(3), 599-606.

Senne de Oliveira Lino F*, Garg S*, Li SS, Misiakou MA, Kang K, Labate Vale da Costa B, Svend-Aage Beyer-Pedersen T, Guerra Giacon T, Basso TO, Panagiotou G, Sommer MOA# (2024) Strain dynamics of contaminating bacteria modulate the yield of ethanol biorefineries. *Nat Commun* 15(1), 5323.

Soll D*, Chu CF*, Sun S*, Lutz V, Arunkumar M, Gachechiladze M, Schäuble S, Alissa-Alkhalaf M, Nguyen T, Khalil MA, Garcia-Ribelles I, Mueller M, Buder K, Michalke B, Panagiotou G, Ziegler-Martin K, Benz P, Schatzlmaier P, Hiller K, Stockinger H, Luu M, Schober K, Moosmann C, Schamel WW, Huber M, Zielinski CE# (2024) Sodium chloride in the tumor microenvironment enhances T-cell metabolic fitness and cytotoxicity. *Nat. Immunol.* [Accepted]

Sprague JL, Schille TB, Allert S, Trümper V, Lier A, Großmann P, Priest EL, Tsavou A,

Panagiotou G, Naglik JR, Wilson D, Schäuble S, Kasper L^{*}, Hube B^{*#} (2024) *Candida albicans* translocation through the intestinal epithelial barrier is promoted by fungal zinc acquisition and limited by NFκB-mediated barrier protection. *PLoS Pathog* 20(3), e1012031.

Yuu EY, Bühner C, Eckmanns T, Fulde M, Herz M, Kurzai O, Lindstedt C, Panagiotou G, Piro VC, Radonic A, Renard BY, Reuss A, Leal Siliceo S, Thielemann N, Thürmer A, van Vorst K, Wieler LH, Haller S[#] (2024) The gut microbiome, resistome, and mycobiome in preterm newborn infants and mouse pups: lack of lasting effects by antimicrobial therapy or probiotic prophylaxis. *Gut Pathog* 16(1), 27.

Brandt P^{*}, Mirhakkak MH^{*}, Wagner L, Driesch D, Möslinger A, Fänder P, Schäuble S, Panagiotou G, Vylkova S[#] (2023) High-throughput profiling of *Candida auris* isolates reveals clade-specific metabolic differences. *Microbiol Spectr* 11(3), e0049823.

Chao YY, Puhach A, Frieser D, Arunkumar M, Lehner L, Seeholzer T, Garcia-Lopez A, van der Wal M, Fibi-Smetana S, Dietschmann A, Sommermann T, Ćiković T, Taher L, Gresnigt MS, Vastert SJ, van Wijk F, Panagiotou G, Krappmann D, Groß O, Zielinski CE (2023) Human TH17 cells engage gasdermin E pores to release IL-1α on NLRP3 inflammasome activation. *Nat Immunol* 24(2), 295-308.

Chen J^{*}, Leal Siliceo S^{*}, Ni Y, Nielsen HB, Xu A, Panagiotou G (2023) Identification of robust and generalizable biomarkers for microbiome-based stratification in lifestyle interventions. *Microbiome* 11(1), 178.

Csader S^{*}, Chen X^{*}, Leung H^{*}, Männistö V, Pentikäinen H, Tauriainen MM, Savonen K, El-Nezami H, Schwab U[#], Panagiotou G[#] (2023) Gut ecological networks reveal associations between bacteria, exercise and clinical profile in non-alcoholic fatty liver disease patients. *mSystems* 8(5), e0022423.

Häder A[#], Schäuble S[#], Gehlen J, Thielemann N, Buerfent BC, Schüller V, Hess T, Wolf T, Schröder J, Weber M, Hünninger K, Löffler J, Vylkova S, Panagiotou G, Schumacher J, Kurzai O (2023) Pathogen-specific innate immune response patterns are distinctly affected by genetic diversity. *Nat Commun* 14(1), 3239.

Kelani AA, Bruch A, Riviaccio F, Visser C, Krüger T, Weaver D, Pan X, Schaeuble S, Panagiotou G, Kniemeyer O, Bromley MJ, Bowyer P, Barber AE, Brakhage AA, Blango MG (2023) Disruption of the *A. fumigatus* RNA interference machinery alters the conidial transcriptome. *RNA* 29(7), 1033-1050.

Leung H, Xiong L, Ni Y, Busch A, Bauer M, Press AT, Panagiotou G (2023) Impaired flux of bile acids from the liver to the gut reveals microbiome-immune interactions associated with liver damage. *NPJ Biofilms and microbiomes* 9(1), 35.

Mirhakkak MH^{*}, Chen X^{*}, Heinekamp T, Sae-Ong T, Xu LL, Ni Y, Kurzai O, Barber AE, Brakhage AA, Boutin S, Schäuble S[#], Panagiotou G[#] (2023) Genome-scale Metabolic modeling of *Aspergillus fumigatus* strains reveals growth dependencies on the lung microbiome. *Nat Commun* 14(1), 4369.

Ni Y^{*}, Qian L^{*}, Leal Siliceo S^{*}, Long X^{*}, Nychas E, Liu Y, Ismaiah MJ, Leung H, Zhang L, Gao Q, Wu Q, Zhang Y, Jia Xi, Liu S, Yuan R, Zhou L, Wang X, Li Q, Zhao Y, El-Nezami H, Xu A, Xu G[#], Li H[#], Panagiotou G[#], Jia W[#] (2023) Resistant starch decreases intrahepatic triglycerides in NAFLD patients via gut microbiome alterations. *Cell Metab* 35(9), 1530-1547.

- Patumcharoenpol P, Kingkaw A, Nakphaichit M, Chatchatee P, Suratannon N[#], Panagiotou G, Vongsangnak W[#] (2023) Exploring longitudinal gut microbiome towards metabolic functional changes associated in atopic dermatitis in early childhood. *Biology (Basel)* 12(9), 1262-1277.
- Refisch A[#], Sen ZD, Klassert TE, Busch A, Besteher B, Danyeli LV, Helbing D, Schulze-Späte U, Stallmach A, Bauer M, Panagiotou G, Jacobsen ID, Slevogt H, Opel N, Walter M (2023) Microbiome and immuno-metabolic dysregulation in patients with major depressive disorder with atypical clinical presentation. *Neuropharmacology* 235, 109568. (Review)
- Schruefer S, Pschibul A, Wong SSW, Sae-Ong T, Wolf T, Schäuble S, Panagiotou G, Brakhage AA, Amanianda V, Kniemeyer O, Ebel F (2023) Distinct transcriptional responses to fludioxonil in *Aspergillus fumigatus* and its Δ tcsC and Δ skn7 mutants reveal a crucial role for Skn7 in the cell wall reorganizations triggered by this antifungal. *BMC Genomics* 24(1), 684.
- Seelbinder B[#], Lohinai Z^{*}, Vazquez-Urbe R, Brunke S, Chen X, Mirhakkak M, Lopez-Escalera S, Dome B, Megyesfalvi Z, Berta J, Galffy G, Dulka E, Wellejus A, Weiss GJ, Bauer M, Hube B, Sommer MOA, Panagiotou G (2023) *Candida* expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions. *Nat Commun* 14(1), 2673.
- Allert S, Schulz D, Kämmer P, Großmann P, Wolf T, Schäuble S, Panagiotou G, Brunke S, Hube B (2022) From environmental adaptation to host survival: Attributes that mediate pathogenicity of *Candida auris*. *Virulence* 13(1), 191-214.
- Alonso-Roman R, Last A, Mirhakkak MH, Sprague JL, Möller L, Großmann P, Graf K, Gratz R, Mogavero S, Vylkova S, Panagiotou G, Schäuble S, Hube B, Gresnigt MS (2022) *Lactobacillus rhamnosus* colonisation antagonizes *Candida albicans* by forcing metabolic adaptations that compromise pathogenicity. *Nat Commun* 13(1), 3192.
- Brandt P, Gerwien F, Wagner L, Krüger T, Ramírez-Zavala B, Mirhakkak MH, Schäuble S, Kniemeyer O, Panagiotou G, Brakhage AA, Morschhäuser J, Vylkova S (2022) *Candida albicans* SR-like protein kinases regulate different cellular processes: Sky1 is involved in control of ion homeostasis, while Sky2 is important for dipeptide utilization. *Front Cell Infect Microbiol* 12, 850531.
- Jia W, Panagiotou G (2022) Recent advances in diabetes and microbiota. *Sci Bull* 67(17), 1720-1723. (Review)
- Jurburg SD, Eisenhauer N, Buscot F, Chatzinotas A, Chaudhari NM, Heintz-Buschart A, Kallies R, Küsel K, Litchman E, Macdonald CA, Müller S, Reuben RC, Nunes da Rocha U, Panagiotou G, Rillig MC, Singh BK (2022) Potential of microbiome-based solutions for agrifood systems. *Nature Food* 3(8), 557-560. (Review)
- Leung H, Long X, Ni Y, Qian L, Nychas E, Siliceo SL, Pohl D, Hanhineva K, Liu Y, Xu A, Nielsen HB, Belda E, Clément K, Loomba R, Li H, Jia W, Panagiotou G (2022) Risk assessment with gut microbiome and metabolite markers in NAFLD development. *Sci Transl Med* 14(648), eabk0855.
- Russell TJ, De Silva EK, Crowley VM, Shaw-Saliba K, Dube N, Josling G, Pasaje CFA, Kouskoumvekaki I, Panagiotou G, Niles JC, Jacobs-Lorena M, Denise Okafor C, Gamo FJ, Llinás M[#] (2022) Inhibitors of ApiAP2 protein DNA binding exhibit multistage activity against *Plasmodium* parasites. *PLOS Pathog* 18(10), e1010887.

Tappe B, Lauruschkat C, Strobel L, Kurzai O, Rebhan S, Kraus S, Lauruschkat C, Garcia JP, Bussemer L, Possler L, Held M, Huenniger K, Kniemeyer O, Schäuble S, Brakhage AA, Panagiotou G, White L, Einsele H, Löffler J, Wurster S (2022) COVID-19 patients share common, corticosteroid-independent features of impaired host immunity to pathogenic molds. *Front Immunol* 13, 954985.

Zoran T, Seelbinder B, White PL, Price JS, Kraus S, Kurzai O, Linde J, Häder A, Loeffler C, Grigoleit GU, Einsele H, Panagiotou G, Loeffler J, Schäuble S (2022) Molecular profiling reveals characteristic and decisive signatures in patients after allogeneic stem cell transplantation suffering from invasive pulmonary aspergillosis. *J Fungi (Basel)* 8(2), 171.

Barber AE*, Sae-Ong T*, Kang K, Seelbinder S, Li J, Walther G, Panagiotou G# & Kurzai O# (2021) *Aspergillus fumigatus* pan-genome analysis identifies genetic variants associated with human infection. *Nat Microbiol* 6(12), 1526-1536.

Boysen JM, Saeed N, Wolf T, Panagiotou G, Hillmann F (2021) The peroxiredoxin asp f3 acts as redox sensor in *Aspergillus fumigatus*. *Genes* 12(5), 668.

Kang K, Imamovic L, Misiakou M, Sørensen MB, Heshiki Y, Ni Y, Zheng T, Li J, Ellabaan MMH, Colomer-Lluch M, Rode AA, Bytzer P, Panagiotou G#, Sommer MOA (corresponding author#) (2021) Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. *Gut Microbes* 13(1), 1-19.

Lauruschkat CD, Etter S, Schnack E, Ebel F, Schäuble S, Page L, Rümens D, Dragan M, Schlegel N, Panagiotou G, Kniemeyer O, Brakhage AA, Einsele H, Wurster S, Loeffler J (2021) Chronic occupational mold exposure drives expansion of *Aspergillus*-reactive type 1 and type 2 T-helper cell responses. *J Fungi* 7(9), 698.

Loos D*, Zhang L, Beemelmans C, Kurzai O, Panagiotou G# (2021) DANIEL: A user-friendly web server for fungal ITS amplicon sequencing data. *Front Microbiol* 12, 720513.

Marfil-Sanchez A*, Seelbinder B*, Ni Y, Varga J, Berta J, Hollosi V, Dome B, Megyesfalvi Z, Dulka E, Galffy G, Weiss GJ, Panagiotou G#, Zoltan Lohinai Z# (2021) Gut microbiome functionality might be associated with exercise tolerance and recurrence of resected early-stage lung cancer patients. *PLOS One* 16(11), e0259898.

Marfil-Sánchez A*, Zhang L*, Alonso-Pernas P, Mirhakkak M, Mueller M, Seelbinder B, Ni Y, Santhanam R, Busch A, Beemelmans C, Ermolaeva M, Bauer M#, Panagiotou G# (2021) An integrative understanding of the large metabolic shifts induced by antibiotics in critical illness. *Gut Microbes* 13(1), 1993598.

Mirhakkak M, Schäuble S, Klassert T, Brunke S, Brandt P, Loos D, Uribe R, de Oliveira Lino FS, Ni Y, Vylkova S, Slevogt H, Hube B, Weiss G, Sommer M, Panagiotou G# (2021) Metabolic modeling predicts specific gut bacteria as key determinants for *Candida albicans* colonization levels. *ISME J* 15(5), 1257-1270.

Ni Y*, Lohinai Z*, Heshiki Y, Dome B, Moldvay J, Dulka E, Galffy G, Berta J, Weiss GJ, Sommer MOA, Panagiotou G# (2021) Distinct composition and metabolic functions of human gut microbiota are associated with cachexia in lung cancer patients. *ISME J* 15(11), 3207-3220.

Nong W, Qu Z, Barton-Owen T, Wong YPA, Yin Yip H, Lee HT, Narayana S, Baril T, Swale T, Cao J, Chan TF, Kwan HS, Ming NS, Panagiotou G, Qian PY, Qiu JW, Yip KY, Ismail N, Pati S,

John A, Tobe ST, Bendena WG, Cheung SG, Hayward A, Hui JHL (2021) Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. *Commun Biol* 4(1), 83.

Patumcharoenpol P, Nakphaichit M, Panagiotou G, Senavongse A, Suratannon N, Vongsangnak W (2021) MetGEMs toolbox: Metagenome-scale models as integrative toolbox for uncovering metabolic functions and routes of human gut microbiome. *PLOS Comput Biol* 17(1), e1008487.

Zhang J, Ni Y, Qian L, Fang Q, Zheng T, Zhang M, Gao Q, Zhang Y, Ni J, Hou X, Bao Y, Kovatcheva-Datchary P, Xu A, Li H, Panagiotou G[#], Jia W (2021) Decreased abundance of *Akkermansia muciniphila* leads to the impairment of insulin secretion and glucose homeostasis in lean type 2 diabetes. *Adv Sci (Weinh)* 8(16), e2100536.

Barber AE, Riedel J, Sae-Ong T, Kang K, Brabetz W, Panagiotou G, Deising HB, Kurzai O (2020) Effects of agricultural fungicide use on *Aspergillus fumigatus* abundance, antifungal susceptibility, and population structure. *mBio* 11(6), e02213-20.

Blango MG, Pschibul A, Riviaccio F, Krüger T, Rafiq M, Jia L, Zheng T, Goldmann M, Voltersen V, Li J, Panagiotou G, Kniemeyer O, Brakhage AA (2020) Dynamic surface proteomes of allergenic fungal conidia. *J Proteome Res* 19(5), 2092-2104.

Cakir T, Uddin R, Panagiotou G, Durmuş S (2020) Novel approaches for systems biology of metabolism-oriented pathogen-human interactions: A mini-review *Front Cell Infect Microbiol* 10, 52. (Review)

Dissanayake TK, Schäuble S, Mirhakkak MH, Wu WL, Ng CK, Yip C-Y, García-López A, Wolf T, Yeung ML, Chan KH, Yuen KY, Panagiotou G, To KKW (2020) Comparative transcriptomic analysis of rhinovirus and influenza virus infection. *Front Microbiol* 11(1580), 1-13.

Gill H, Leung GMK, Yim R, Lee P, Pang HH, Ip HW, Leung RYY, Li J, Panagiotou G, Ma ESK, Kwong YL (2020) Myeloproliferative neoplasms treated with hydroxyurea, pegylated interferon alpha-2A or ruxolitinib: Clinicohematologic responses, quality-of-life changes and safety in the real-world setting. *Hematology* 25(1), 247-257.

Gill H, Yim R, Pang HH, Lee P, Chan TSY, Hwang YY, Leung GMK, Ip HW, Leung RYY, Yip SF, Kho B, Lee HKK, Mak V, Chan CC, Lau JSM, Lau CK, Lin SY, Wong RSM, Li W, Ma ESK, Li J, Panagiotou G, Sim JPY, Lie AKW, Kwong YL (2020) Clofarabine, cytarabine, and mitoxantrone in refractory/relapsed acute myeloid leukemia: High response rates and effective bridge to allogeneic hematopoietic stem cell transplantation. *Cancer Med* 9(10), 3371-3382.

Haange SB, Jehmlich N, Krügel U, Hintschich C, Wehrmann D, Hankir M, Seyfried F, Froment J, Hübschmann T, Müller S, Wissenbach DK, Kang K, Buettner C, Panagiotou G, Noll M, Rolle-Kampczyk U, Fenske W, von Bergen M (2020) Gastric bypass surgery in a rat model alters the community structure and functional composition of the intestinal microbiota independently of weight loss. *Microbiome* 8(1), 13.

Heshiki Y, Vazquez-Urbe R, Li J, Ni Y, Quainoo S, Imamovic L, Li J, Sørensen M, Chow BKC, Weiss GJ, Xu A, Sommer MOA, Panagiotou G (2020) Predictable modulation of cancer treatment outcomes by the gut microbiota. *Microbiome* 8(1), 28.

Khaliq W, Großmann P, Neugebauer S, Kleyman A, Domizi R, Calcinaro S, Brealey D, Gräler M, Kiehntopf M, Schäuble S, Singer M, Panagiotou G^{**}, Bauer M^{**} (corresponding authors^{**}) (2020)

Lipid metabolic signatures deviate in sepsis survivors compared to non-survivors. *Comput Struct Biotechnol J* 18, 3678-3691.

Liu Y, Wang Y, Ni Y, Cheung CKY, Lam KSL, Wang Y, Xia Z, Ye D, Guo J, Tse MA, Panagiotou G^{**}, Xu A^{**} (corresponding authors^{**}) (2020) Gut microbiome fermentation determines the efficacy of exercise for diabetes prevention. *Cell Metab* 31(1), 77-91.

Machata S, Müller MM, Lehmann R, Sieber P, Panagiotou G, Carvalho A, Cunha C, Lagrou K, Maertens J, Slevogt H, Jacobsen ID (2020) Proteome analysis of bronchoalveolar lavage fluids reveals host and fungal proteins highly expressed during invasive pulmonary aspergillosis in mice and humans. *Virulence* 11(1), 1337-1351.

Nie X, Chen J, Ma X, Ni Y, Shen Y, Yu H, Panagiotou G^{**}, Bao Y^{**} (corresponding authors^{**}) (2020) A metagenome-wide association study of gut microbiome and visceral fat accumulation. *Comput Struct Biotechnol J* 18, 2596-2609.

Seelbinder B, Chen J, Brunke S, Vazquez-Urbe R, Santhanam R, Meyer AC, de Oliveira Lino FS, Chan KF, Loos D, Imamovic L, Tsang CC, Lam RP, Sridhar S, Kang K, Hube B, Woo PCY, Sommer MOA, Panagiotou G (2020) Antibiotics create a shift from mutualism to competition in human gut communities with a longer-lasting impact on fungi than bacteria. *Microbiome* 8(1), 133.

Seelbinder B, Wallstabe J, Marischen L, Weiss E, Wurster S, Page L, Löffler C, Bussemer L, Schmitt AN, Wolf T, Linde J, Cicin-Sain L, Becker J, Kalinke U, Vogel J, Panagiotou G, Einsele H, Westermann AJ, Schauble S, Loeffler J (2020) Triple RNA-seq reveals synergy in a human virus-fungus co-infection model. *Cell Reports* 33(7), 108389.

Chen J^{*}, McIlroy SE, Archana A, Baker DM, Panagiotou G^{**} (2019) A pollution gradient contributes to the taxonomic, functional, and resistome diversity of microbial communities in marine sediments. *Microbiome* 7(1), 104.

Kang K, Bergdahl B, Machado D, Dato L, Han TL, Li J, Villas-Boas S, Herrgård MJ, Förster J, Panagiotou G (2019) Linking genetic, metabolic and phenotypic diversity among *S. cerevisiae* strains using multi-omics associations *Gigascience* 8(4), giz015.

Li J, Rettedal EA, van der Helm E, Ellabaan M, Panagiotou G^{**}, Sommer MOA^{**} (corresponding authors^{**}) (2019) Antibiotic treatment drives the diversification of the human gut resistome. *Genom Proteom Bioinf* 17(1), 39-51.

Zhang L, Ouyang Y, Li H, Shen L, Ni Y, Fang Q, Wu G, Qian L, Xiao Y, Zhang J, Yin P, Panagiotou G, Xu G, Ye J, Jia W (2019) Metabolic phenotypes and the gut microbiota in response to dietary resistant starch type 2 in normal-weight subjects: a randomized crossover trial. *Sci Rep* 9(1), 4736.

Zheng T, Li J, Ni Y, Kang K, Misiakou MA, Imamovic L, Chow BKC, Rode AA, Bytzer P, Sommer M, Panagiotou G^{**} (2019) Mining, analyzing, and integrating viral signals from metagenomic data. *Microbiome* 7(1), 42.

Gill H, Ip HW, Yim R, Tang WF, Pang HH, Lee P, Leung GMK, Li J, Tang K, So JCC, Leung RYY, Li J, Panagiotou G, Lam CCK, Kwong YL (2018) Next-generation sequencing with a 54-gene panel identified unique mutational profile and prognostic markers in Chinese patients with myelofibrosis. *Ann Hematol* 98(4), 869-879.

- Imamovic L, Misiakou MA, van der Helm E, Panagiotou G, Muniesa M, Sommer MOA (2018) Complete genome sequence of *Escherichia coli* strain WG5. *Genome Announc* 6(2), e01403-17.
- Kang K, Ni Y, Li J, Imamovic L, Sarkar C, Kobler MD, Heshiki Y, Zheng T, Kumari S, Wong JCY, Archana A, Wong CWM, Dingle C, Denizen S, Baker DM, Sommer MOA, Webster CJ, Panagiotou G^{**} (2018) The environmental exposures and inner- and intercity traffic flows of the metro system may contribute to the human skin microbiome and resistome. *Cell Reports* 24(5), 1190-1202.
- Lau SKP, Teng JLL, Chiu TH, Chan E, Tsang AKL, Panagiotou G, Zhai SL, Woo PCY (2018) Differential microbial communities of omnivorous and herbivorous cattle in Southern China. *Comput Struct Biotechnol J* 16, 54-60.
- Heshiki Y, Dissanayake T, Zheng T, Kang K, Yueqiong N, Xu Z, Sarkar C, Woo PCY, Chow BKC, Baker D, Yan A, Webster CJ, Panagiotou G^{**}, Li J^{**} (2017) Toward a Metagenomic Understanding on the Bacterial Composition and Resistome in Hong Kong Banknotes. *Front Microbiol* 8, 632.
- Ni Y, Jensen K, Kouskoumvekaki I^{**}, Panagiotou G^{**} (2017) NutriChem 2.0: exploring the effect of plant-based foods on human health and drug efficacy. *Database* (2017),
- Zheng T, Ni Y, Li J, Chow BKC, Panagiotou G^{**} (2017) Designing Dietary Recommendations Using System Level Interactomics Analysis and Network-Based Inference. *Front Physiol* 8, 753.
- Li J, Sung CY, Lee N, Ni Y, Pihlajamäki J, Panagiotou G, El-Nezami H (2016) Probiotics modulated gut microbiota suppresses hepatocellular carcinoma growth in mice. *Proc Natl Acad Sci U S A* 113(9), E1306-E1315.
- Jensen K, Ni Y, Panagiotou G, Kouskoumvekaki I (2015) Developing a molecular roadmap of drug-food interactions. *PLOS Comput Biol* 11(2), e1004048.
- Jensen K, Panagiotou G, Kouskoumvekaki I (2015) NutriChem: a systems chemical biology resource to explore the medicinal value of plant-based foods. *Nucleic Acids Res* 43(Database issue), D940-D945.
- Kang K, Li J, Lim BL, Panagiotou G (2015) MESSI: metabolic engineering target selection and best strain identification tool. *Database (Oxford)* 2015,
- Ni Y, Li J, Panagiotou G (2015) A Molecular-Level Landscape of Diet-Gut Microbiome Interactions: Toward Dietary Interventions Targeting Bacterial Genes. *MBio* 6(6), e01263.
- Udatha DB, Madsen KM, Panagiotou G, Olsson L (2015) Multiple nucleophilic elbows leading to multiple active sites in a single module esterase from *Sorangium cellulosum*. *J Struct Biol* 190(3), 314-327.
- Udatha DB, Topakas E, Salazar M, Olsson L, Andersen MR, Panagiotou G (2015) Deciphering the signaling mechanisms of the plant cell wall degradation machinery in *Aspergillus oryzae*. *BMC Syst Biol* 9, 77.
- Jensen K, Panagiotou G, Kouskoumvekaki I (2014) Integrated text mining and chemoinformatics analysis associates diet to health benefit at molecular level. *PLOS Comput Biol* 10(1), e1003432.
- Westergaard D, Li J, Jensen K, Kouskoumvekaki I, Panagiotou G (2014) Exploring mechanisms of diet-colon cancer associations through candidate molecular interaction networks. *BMC*

Genomics 15, 380.

Jacobsen UP, Nielsen HB, Hildebrand F, Raes J, Sicheritz-Ponten T, Kouskoumvekaki I, Panagiotou G (2013) The chemical interactome space between the human host and the genetically defined gut metabotypes. *ISME J* 7(4), 730-742.

Topakas E, Panagiotou G, Christakopoulos P (2013) Characteristics, sources, production and applications. Xylanases. In: Yang S-T, El Ensashy H, Thongchul N (eds.) *Bioprocessing Technologies in Biorefinery for Sustainable Production of Fuels, Chemicals, and Polymers* pp. 147-169. Wiley. ISBN: 978-0-470-54195.

Udatha DB, Rasmussen S, Sicheritz-Pontén T, Panagiotou G (2013) Targeted metabolic engineering guided by computational analysis of single-nucleotide polymorphisms (SNPs). *Methods Mol Biol* 985, 409-428.

Herrgård M, Panagiotou G (2012) Analyzing the genomic variation of microbial cell factories in the era of "New Biotechnology" *Comput Struct Biotechnol J* 3, e201210012.

Jensen K, Plichta D, Panagiotou G, Kouskoumvekaki I (2012) Mapping the genome of *Plasmodium falciparum* on the drug-like chemical space reveals novel anti-malarial targets and potential drug leads. *Mol Biosyst* 8(6), 1678-1685.

Panagiotou G, Taboureau O (2012) The impact of network biology in pharmacology and toxicology. *SAR QSAR Environ Res* 23(3-4), 221-235. (Review)

Kouskoumvekaki I, Panagiotou G (2011) Navigating the human metabolome for biomarker identification and design of pharmaceutical molecules. *J Biomed Biotechnol* 2011,

Madsen KM, Udatha GD, Semba S, Otero JM, Koetter P, Nielsen J, Ebizuka Y, Kushiro T, Panagiotou G (2011) Linking genotype and phenotype of *Saccharomyces cerevisiae* strains reveals metabolic engineering targets and leads to triterpene hyper-producers. *PLOS One* 6(3), e14763.

Panagiotou G, Topakas E, Moukouli M, Christakopoulos P, Olsson L (2011) Studying the ability of *Fusarium oxysporum* and recombinant *Saccharomyces cerevisiae* to efficiently cooperate in decomposition and ethanolic fermentation of wheat straw. *Biomass and Bioenergy* 35(8), 3727-3732.

Udatha DB, Kouskoumvekaki I, Olsson L, Panagiotou G (2011) The interplay of descriptor-based computational analysis with pharmacophore modeling builds the basis for a novel classification scheme for feruloyl esterases. *Biotechnol Adv* 29(1), 94-9110.

Panagiotou G, Topakas E, Olivares R, Christakopoulos P, Olsson L (2010) Feruloyl esterases as biosynthetic tools for the organic synthesis of nutraceutical compounds In: Heldman DR, Hoover DG, Wheeler MB (eds.) *Encyclopedia of Biotechnology in Agriculture and Food* CRC Press, Boca Raton, FL, USA. ISBN: 978-0849350276.

Panagiotou G, Andersen MR, Grotkjaer T, Regueira TB, Nielsen J, Olsson L (2009) Studies of the production of fungal polyketides in *Aspergillus nidulans* by using systems biology tools. *Appl Environ Microbiol* 75(7), 2212-2220.

Panagiotou G, Grotkjaer T, Hofmann G, Bapat PM, Olsson L (2009) Overexpression of a novel

endogenous NADH kinase in *Aspergillus nidulans* enhances growth. *Metab Eng* 11(1), 31-39.

Kouskoumvekaki I, Yang Z, Jónsdóttir SO, Olsson L, Panagiotou G (2008) Identification of biomarkers for genotyping *Aspergilli* using non-linear methods for clustering and classification. *BMC Bioinformatics* 9, 59.

Panagiotou G, Andersen MR, Grotkjaer T, Regueira TB, Hofmann G, Nielsen J, Olsson L (2008) Systems analysis unfolds the relationship between the phosphoketolase pathway and growth in *Aspergillus nidulans*. *PLOS One* 3(12), e3847.

Panagiotou G, Pachidou F, Petroutsos D, Olsson L, Christakopoulos P (2008) Fermentation characteristics of *Fusarium oxysporum* grown on acetate. *Bioresour Technol* 99(15), 7397-7401.

Panagiotou G, Papadakis MA, Topakas E, Olsson L, Christakopoulos P (2008) Identification of NADH kinase activity in filamentous fungi and structural modelling of the novel enzyme from *Fusarium oxysporum* *Process Biochemistry* 43(10), 1114-1120.

Meijer S, Panagiotou G, Olsson L, Nielsen J (2007) Physiological characterization of xylose metabolism in *Aspergillus niger* under oxygen-limited conditions. *Biotechnol Bioeng* 98(2), 462-475.

Otero JM, Panagiotou G, Olsson L (2007) Fueling industrial biotechnology growth with bioethanol. *Adv Biochem Eng Biotechnol* 108, 1-40.

Panagiotou G, Kouskoumvekaki I, Jónsdóttir SO, Olsson L (2007) Monitoring novel metabolic pathways using metabolomics and machine learning: induction of the phosphoketolase pathway in *Aspergillus nidulans* cultivations *Metabolomics* 3(4), 503-516.

Panagiotou G, Olavarria R, Olsson L (2007) *Penicillium brasilianum* as an enzyme factory; the essential role of feruloyl esterases for the hydrolysis of the plant cell wall. *J Biotechnol* 130(3), 219-228.

Panagiotou G, Christakopoulos P, Grotkjaer T, Olsson L (2006) Engineering of the redox imbalance of *Fusarium oxysporum* enables anaerobic growth on xylose. *Metab Eng* 8(5), 474-482.

Panagiotou G, Granouillet P, Olsson L (2006) Production and partial characterization of arabinoxylan-degrading enzymes by *Penicillium brasilianum* under solid-state fermentation. *Appl Microbiol Biotechnol* 72(6), 1117-1124.

Panagiotou G, Christakopoulos P, Olsson L (2005) The influence of different cultivation conditions on the metabolome of *Fusarium oxysporum*. *J Biotechnol* 118(3), 304-315.

Panagiotou G, Christakopoulos P, Olsson L (2005) Simultaneous saccharification and fermentation of cellulose by *Fusarium oxysporum* F3—growth characteristics and metabolite profiling *Enzyme and Microbial Technology* 36(5-6), 693-699.

Panagiotou G, Christakopoulos P, Villas-Boas SG, Olsson L (2005) Fermentation performance and intracellular metabolite profiling of *Fusarium oxysporum* cultivated on a glucose-xylose mixture. *Enzyme and Microbial Technology* 36, 100-106.

Panagiotou G, Villas-Bôas SG, Christakopoulos P, Nielsen J, Olsson L (2005) Intracellular

metabolite profiling of *Fusarium oxysporum* converting glucose to ethanol. *J Biotechnol* 115(4), 425-434.

Panagiotou G, Christakopoulos P (2004) NADPH-dependent D-aldose reductases and xylose fermentation in *Fusarium oxysporum*. *J Biosci Bioeng* 97(5), 299-304.

Panagiotou G, Kekos D, Macris BJ, Christakopoulos P (2003) Production of cellulolytic and xylanolytic enzymes by *Fusarium oxysporum* grown on corn stover in solid state fermentation. *Industrial Crops and Products* 18(1), 37-45.

Panagiotou G, Topakas E, Economou L, Kekos D, Macris BJ, Christakopoulos P (2003) Induction, purification, and characterization of two extracellular alpha-L-arabinofuranosidases from *Fusarium oxysporum*. *Can J Microbiol* 49(10), 639-644.

Panagiotou G, Kekos D, Macris BJ, Christakopoulos P (2002) Purification and characterisation of NAD⁺-dependent xylitol dehydrogenase from *Fusarium oxysporum* *Biotechnology Letters* 24(24), 2089-2092.

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