Profile

安水 良明 / Yoshiaki Yasumizu, M.D.

Education and Employment

• 2013 Apr - 2019 March Faculty of Medicine, Osaka University

MD Researcher Education Program (Shimon Sakaguchi's Lab)

- 2019 2021 Junior Resident, Osaka University Hospital
- 2019 2022 Visiting Academic Staff, Department of Neurology, Graduate School of Medicine, Osaka University
- 2020 Junior Researchers, Institute for Poen and Transdisciplinary Research Initiatives (OTRI)
 Integrated Frontier Research for Medical Science Division, Osaka University
- 2021- Ph.D. Experimental Immunology, Immunology Frontier Research Center, Osaka University

Transdisciplinary Program for Biomedical Entrepreneurship and Innovation

Programming and Computation

Python, R, bash, CWL, Docker, GCP, git

Bioinformatics

- Single-cell RNA-seq / spatial transcriptome data analysis
- Bulk RNA-seq / ATAC-seq / ChIP-seq / WGBS
- Human Genome Analysis
- Machine Learning (deep learning, gradient boosting, MCMC and others)

Wet Lab Skills

- Cell preparation, Immunofluorescence labeling and cell-sorting
- Immunohisto chemistry
- T-cell culture
- Mice experiments
- Library preparation for RNA-seq
- Library preparation and sequence using Nanopore Sequencers

Selected Publications

- Yasumizu Yoshiaki, Ohkura Naganari, Murata Hisash, Kinoshita Makoto ... Morii Eiichi, Shintani Yasushi, Sakaguchi Shimon, Okuno Tatsusada, Mochizuki, Hideki Myasthenia gravis-specific aberrant neuromuscular gene expression by medullary thymic epithelial cells in thymoma. Nat. Commun. 13, 4230 (2022). 10.1038/s41467-022-31951-8 Press
- Yujiro Kidani, Wataru Nogami, Yoshiaki Yasumizu, Atsunari Kawashima, Atsushi Tanaka, ... Yuichiro Doki, Naganari Ohkura, Shimon Sakaguchi. CCR8-targeted specific depletion of clonally expanded

Treg cells in tumor tissues evokes potent tumor immunity with long-lasting memory. *Proceedings of the National Academy of Sciences* Feb 2022, 119 (7) e2114282119; DOI: 10.1073/pnas.2114282119.

- Yoshiaki Yasumizu, Atsushi Hara, Shimon Sakaguchi, Naganari Ohkura, VIRTUS: a pipeline for comprehensive virus analysis from conventional RNA-seq data, *Bioinformatics*, (2020), btaa859, https://doi.org/10.1093/bioinformatics/btaa859
- Naganari Ohkura, Yoshiaki Yasumizu (co-first), Yohko Kitagawa, Atsushi Tanaka, Yamami Nakamura, Daisuke Motooka, Shota Nakamura, Yukinori Okada, Shimon Sakaguchi, Regulatory T cell-specific epigenomic region variants are a key determinant of susceptibility to common autoimmune diseases. *Immunity*, 52(6), 1119-1132.e4. https://doi.org/10.1016/j.immuni.2020.04.006

Honors and Awards

- 2022 Japan Society for the Promotion of Science Ikushi Prize
- 2021 Best Presentation Award, 50th Annual Meeting of the Japanese Society for Immunology
- 2021 Young Neuroimmunologist Award, 33rd Annual Meeting of the Japanese Society for Neuroimmunology
- 2021 Encouragement Award for Junior Residents, Osaka University Hospital
- 2020 Best Presentation Award at the Meeting of Young Virologists 2020 "VIRTUS: A comprehensive viral quantification method using multicellular and single cell RNA-seq
- 2018 Kaggle "Home Credit Default Risk" Silver medal
- 2018 Bioinformatics Contest 2018 (hosted by ITMO University, Russia) 18th prize, Honorable Mention
- 2017 Bioinformatics Technician Certification Examination (Best score)
- 2017 Oral presentation at the "2017 National Retreat for the Project for the Development and Training of the Next Generation of World-Leading MD Researchers" (Best Oral Presentation Award)
- 2017 19th Immunology Summer School 2017 in Shonan, Best Presentation Award, "Regulatory T Cell-Specific Epigenome and Its Association with Autoimmune Diseases"
- 2017 National Taiwan University Exchange Meeting (Excellent Presentation Award)

Softwares

- VIRTUS: a pipeline for comprehensive virus analysis from conventional RNA-seq data. Manuscript in preparation. [github]
- Hiraoka, Yu, Yamada, Kohki, Kawasaki, Yusuke, Hirose, Haruka, Matsumoto, Yasunari, Ishikawa, Kaito, & Yasumizu, Yoshiaki. (2019, July 27). ikra: RNAseq pipeline centered on Salmon. (Version v1.2.1). Zenodo. http://doi.org/10.5281/zenodo.3352573 [github]



Internship

- 2019 Bono Lab at Database Center for Life Science
- 2018 Genomics and Immunoregulation (J. Schultze Lab), Bonn University
- 2018 Statistical Genetics (Y. Okada Lab), Osaka University

Leadership Experience

- Osaka University Python Society founded (link)
- AIMS AI Medical Research Society Executive (link)

Community

- Japanese Society for Immunology
- Japanese Society of Neurology
- Japanese Society for Neuroimmunology

Publications

- Yasumizu Yoshiaki, Ohkura Naganari, Murata Hisash, Kinoshita Makoto ... Morii Eiichi, Shintani Yasushi, Sakaguchi Shimon, Okuno Tatsusada, Mochizuki, Hideki Myasthenia gravis-specific aberrant neuromuscular gene expression by medullary thymic epithelial cells in thymoma. Nat. Commun. 13, 4230 (2022). 10.1038/s41467-022-31951-8 Press
- Murata, Hisashi, Makoto Kinoshita, Yoshiaki Yasumizu, Daisuke Motooka, Shohei Beppu, Naoyuki Shiraishi, Yasuko Sugiyama, et al. 2022. "Cell-Free DNA Derived From Neutrophils Triggers Type 1 Interferon Signature in Neuromyelitis Optica Spectrum Disorder." Neurology Neuroimmunology Neuroinflammation 9 (3): e1149. https://doi.org/10.1212/NXI.000000000001149.
- Yujiro Kidani, Wataru Nogami, Yoshiaki Yasumizu, Atsunari Kawashima, Atsushi Tanaka, Yudai Sonoda, Yumi Tona, Kunitaka Nashiki, Reimi Matsumoto, Masaki Hagiwara, Motonao Osaki, Keiji Dohi, Takayuki Kanazawa, Azumi Ueyama, Mai Yoshikawa, Tetsuya Yoshida, Mitsunobu Matsumoto, Kanji Hojo, Satomi Shinonome, Hiroshi Yoshida, Michinari Hirata, Miya Haruna, Yamami Nakamura, Daisuke Motooka, Daisuke Okuzaki, Yasuko Sugiyama, Makoto Kinoshita, Tatsusada Okuno, Taigo Kato, Koji Hatano, Motohide Uemura, Ryoichi Imamura, Kazunori Yokoi, Atsushi Tanemura, Yasushi Shintani, Tadashi Kimura, Norio Nonomura, Hisashi Wada, Masaki Mori, Yuichiro Doki, Naganari Ohkura, Shimon Sakaguchi. CCR8-targeted specific depletion of clonally expanded Treg cells in tumor tissues evokes potent tumor immunity with long-lasting memory. *Proceedings of the National Academy of Sciences* Feb 2022, 119 (7) e2114282119; DOI: 10.1073/pnas.2114282119.
- Yoshiaki Yasumizu, Naganari Ohkura, Hisashi Murata, Makoto Kinoshita, Soichiro Funaki, Satoshi Nojima, Kansuke Kido, Masaharu Kohara, Daisuke Motooka, Daisuke Okuzaki, Shuji Suganami, Eriko Takeuchi, Yamami Nakamura, Yusuke Takeshima, Masaya Arai, Satoru Tada, Meinoshin Okumura, Eiichi Morii, Yasushi Shintani, Shimon Sakaguchi, Tatsusada Okuno, Hideki Mochizuki. Myasthenia gravis-specific aberrant neuromuscular gene expression by medullary thymic epithelial cells in thymoma. bioRxiv 2021.12.19.473411; doi: https://doi.org/10.1101/2021.12.19.473411
- Abdelhamid, Rehab F, Kotaro Ogawa, Goichi Beck, Yoshiaki Yasumizu, Jyunki Jinno, Kousuke Baba, Yoshitaka Nagai, et al. 2021. "PiRNA/ PIWI Protein Complex as Potential Biomarkers in Sporadic Amyotrophic Lateral Sclerosis." Molecular Neurobiology, January. https://doi.org/10.1007/s12035-021-02686-2.
- Beppu, Shohei, Makoto Kinoshita, Jan Wilamowski, Tadahiro Suenaga, Yoshiaki Yasumizu, Kotaro Ogawa, Teruyuki Ishikura, et al. 2022. "High Cell Surface Expression and Peptide Binding Affinity of HLA-DQA1*05:03, a Susceptible Allele of Neuromyelitis Optica Spectrum Disorders (NMOSD)."
 Scientific Reports 12 (1): 1–12. https://doi.org/10.1038/s41598-021-04074-1.
- Akikazu Harada, Shinji Matsumoto, Yoshiaki Yasumizu, Toshiyuki Akama, Hidetoshi Eguchi, Akira Kikuchi. Recruitment of KRAS downstream target ARL4C to membrane protrusions accelerates pancreatic cancer cell invasion. eLife, (2021), e66721. doi: https://doi.org/10.7554/eLife.66721 Press
- Ishikura, Teruyuki, Makoto Kinoshita, Mikito Shimizu, Yoshiaki Yasumizu, Daisuke Motooka, Daisuke Okuzaki, Kazuya Yamashita, et al. 2021. "Anti-AQP4 Autoantibodies Promote ATP Release from Astrocytes and Induce Mechanical Pain in Rats." Journal of Neuroinflammation 18 (1): 181. https://doi.org/10.1186/s12974-021-02232-w.

Yoshiyuki Matsuo, Shinnosuke Komiya, Yoshiaki Yasumizu, Yuki Yasuoka, Katsura Mizushima,
Tomohisa Takagi, Kirill Kryukov, Aisaku Fukuda, Yoshiharu Morimoto, Yuji Naito, Hidetaka Okada,
Hidemasa Bono, So Nakagawa, Kiichi Hirota. Full-Length 16S RRNA Gene Amplicon Analysis of
Human Gut Microbiota Using MinIONTM Nanopore Sequencing Confers Species-Level Resolution.

BMC Microbiology, (2021), 1–13. https://doi.org/10.1101/2020.05.06.078147.

- Yoshiaki Yasumizu, Atsushi Hara, Shimon Sakaguchi, Naganari Ohkura, VIRTUS: a pipeline for comprehensive virus analysis from conventional RNA-seq data, *Bioinformatics*, (2020), btaa859, https://doi.org/10.1093/bioinformatics/btaa859
- Hiroaki Shime, Mizuyu Odanaka, Makoto Tsuiji, Takuma Matoba, Masaki Imai, Yoshiaki Yasumizu,
 Ryuta Uraki, Kiyoshi Minohara, Maiko Watanabe, Anthony John Bonito, Hidehiro Fukuyama, Naganari
 Ohkura, Shimon Sakaguchi, Akimichi Morita, Sayuri Yamazaki. Proenkephalin + regulatory T cells
 expanded by ultraviolet B exposure maintain skin homeostasis with a healing function. Proceedings of
 the National Academy of Sciences. (2020), 202000372. https://doi.org/10.1073/pnas.2000372117

 Press
- Naganari Ohkura, Yoshiaki Yasumizu, Yohko Kitagawa, Atsushi Tanaka, Yamami Nakamura, Daisuke Motooka, Shota Nakamura, Yukinori Okada, Shimon Sakaguchi, Regulatory T cell-specific epigenomic region variants are a key determinant of susceptibility to common autoimmune diseases. *Immunity*, 52(6), 1119-1132.e4. https://doi.org/10.1016/j.immuni.2020.04.006
- Yoshiaki Yasumizu, Saori Sakaue, Takahiro Konuma, Ken Suzuki, Koichi Matsuda, Yoshinori Murakami, Michiaki Kubo, Pier Francesco Palamara, Yoichiro Kamatani, Yukinori Okada, Genome-wide natural selection signatures are linked to genetic risk of modern phenotypes in the Japanese population. *Molecular Biology and Evolution*. (2020) https://doi.org/10.1093/molbev/msaa005 Press
- Innate Myeloid Cell Subset-Specific Gene Expression Patterns in the Human Colon are Altered in Crohn's Disease Patients. *Digestion* (2018). (co-first)

Presentations

- 2022 AJACS online 14, Lectuer for RNAseq analysis on browser (120min, 283participants) https://biosciencedbc.jp/event/ajacs/ajacs95.html
- 2022 NGS EXPO 2022 oral presentation, poster presentation, chair
- 2022 Nagoya Neurology Summer School
- 2022 63rd Annual Meeting of the Japanese Society of Neurology, Symposium
- 2022 Japanese Society of Neurology "Bioinformatics Hands-on for Neurologists 2021" Planning, Hands-on, Lecture. https://www.neurology-jp.org/news/pdf/news_20211202_01_01.pdf
- 2021 Single-cell 2021 Osaka Online seminar
 https://www2.aeplan.co.jp/singlecell2021_osaka/profile.html#CV03
- 2020 The 2nd Japanese Medical Al Contest 2020
- 2019 The 48th Annual Meeting of the Japanese Society for Immunology, Oral presentation "Single-cell transcriptomic atlas of thymic Treg development"
- 2017 The 46th Annual Meeting of the Japanese Society for Immunology Oral presentation "Significance of the regulatory T cell-specific epigenetics in autoimmune disease susceptibility"
- 2017 The 5th NGS field meeting Poster presentation

Publications (Japanese)

● 安水良明, 大倉永也 「制御性T細胞のシングルセル解析」 炎症と免疫 vol.30 no.6 p486-489(2022)

• **安水良明** 「ブラウザで完結するRNA-seq解析」「10. iDEP, BioJupies, RaNA-seq - ウェブブラウザで完結するRNA-seq解析ツール」 実験医学増刊 vol.40 no.17 バイオDBとウェブツール ラボで使える最新70選知る・学ぶ・使う、バイオDX時代の羅針盤 (2022)(link)

- **安水良明**, 大倉永也 「シングルセル解析」 皮膚科 vol.2 no.4 p427-432(2022)
- **安水良明**, 小河浩太郎, 望月秀樹 「バイオインフォマティクス」 CLINICAL NEUROSCIENCE vol.39 no.9 p1133-1138(2021)
- 安水良明, 大倉永也 「制御性T細胞特異的エピゲノムは, 自己免疫疾患感受性に強く影響する」臨床免疫・アレルギー科第75巻第3号 p253-258 (2021)
- **安水良明**, 大倉永也 「免疫制御,免疫寛容,免疫記憶」 日本医師会雑誌 第149巻・特別号(2) pS61-65 (2020)
- **安水良明**, 岡田随象 「大規模ヒトゲノム解析による日本人集団の適応進化の解明」 腎臓内科・泌尿器科 Vol.10 No.6 p566-571 (2019)
- 大田達郎, 石井学, 末竹裕貴, 丹生智也, 山田航輝, 安水良明 「CWL(Common Workflow Language)があれば, DRY解析はもう怖くない」 次世代シーケンサー DRY解析教本 改訂第2版 p331-338 (2019)
- **安水良明**, 中村やまみ, 大倉永也 「T細胞におけるシングルセル解析」 実験医学増刊 「シングルセルゲノミクス」 Vol.37 No.20 p3421-3427 (2019)
- **安水良明** 「Chapter 1 まずはこれだけ! 解析環境を整える〜Mac+Biocondaを中心に」 実験医学別冊 RNA-Segデータ解析 WETラボのための鉄板レシピ p10-27 (2019)(link)
- 大倉永也、安水良明「Treg分化におけるエピゲノムの役割」 医学のあゆみ Vol. 268 No. 13 p1030-1035 (2019)
- 安水良明 「Pythonで医学に貢献を」 実験医学 Vol. 37 No. 4 p621 (2019) (link)