

氏名	所属	職名	取得学位	専門分野	主な論文・著作・業績
清水 厚志	生体情報解析部門	教授	博士（理学）	ゲノム医学 人類遺伝学 分子生物学	①Sutoh Y, Hachiya T, Otsuka-Yamasaki Y, Komaki S, Minabe S, Ohmomo H, Tanno K, Hozawa A, Nakaya N, Noda A, Orui M, Ishikuro M, Obara T, Kuriyama S, Sasaki M, <u>Shimizu A.</u> : Genetic predisposition for immunoglobulin E production explains atopic risk in children: Tohoku Medical Megabank cohort study. Am J Hum Genet. (2025). Jul 15:S0002-9297(25)00246-0. doi: 10.1016/j.ajhg.2025.06.015. Epub ahead of print. ②Mishra, A., Malik, R., Hachiya, T., <u>Shimizu, A.</u> , et. al.: Stroke genetics informs drug discovery and risk prediction across ancestries. Nature. 611:115-123 (2022). ③Komaki, S., Nagata, M., Arai, E., Otomo, R., Ono, K., Abe, Y., Ohmomo, H., Umekage, S., Shinozaki, O, N., Hachiya, T., Sutoh, Y., Otsuka-Yamasaki, Y., Arai, Y., Hirose, N., Yoneyama, A., Okano, H., Sasaki, M., Kanai, Y. and <u>Shimizu, A.</u> : Epigenetic profile of Japanese supercentenarians: a cross-sectional study. Lancet Healthy Longev. 2:e83 (2023). ④清水厚志, 坊農秀雅 編. がんゲノムデータ解析, 東京：メディカルサイエンスインターナショナル, （2022） ⑤特許第7442221号「名称；生物学的年齢の計算方法、老化状態の評価方法、CpGサイトの評価方法、プログラム、およびコンピュータ可読記憶媒体」
大桃 秀樹	生体情報解析部門	特任准教授	博士 (神経科学)	ゲノム医学 分子生物学 解剖学一般 (含組織学・発生学)	①Harada S, <u>Ohmomo H</u> , Matsumoto M, Sata M, Iida M, Hirata A, Miyagawa N, Kuwabara K, Kato S, Toki R, Edagawa, S, Sugiyama D, Sato A, Hirayama A, Sugimoto M, Soga T, Tomita M, Shimizu A, Okamura T, and Takebayashi T: Metabolomics profiles alterations in cigarette smokers and heated tobacco product users, J Epidemiol. (2024) Online ahead of print. ②Taguchi Y-h, Komaki S, Sutoh Y, <u>Ohmomo H</u> , Yamasaki YO, and Shimizu A: Integrated analysis of human DNA methylation, gene expression, and genomic variation in iMETHYL database using kernel tensor decomposition-based unsupervised feature extraction, PLoS one. 18: e0289029 (2023). ③Komaki S, Nagata M, Arai E, Otomo R, Ono K, Abe Y, <u>Ohmomo H</u> , Umekage S, Shinozaki O-N, Hachiya T, Sutoh Y, Otsuka-Yamasaki Y, Arai Y, Hirose N, Yoneyama A, Okano H, Sasaki M, Kanai Y, Shimizu A. Epigenetic profile of Japanese supercentenarians: a cross-sectional study. Lancet Healthy Longev. 2:e83 (2023). ④ <u>Ohmomo H</u> , Komaki S, Sutoh Y, Hachiya T, Ono K, Arai E, Fujimoto H, Yoshida T, Kanai Y, Asahi K, Sasaki M, Shimizu A. Potential DNA methylation biomarkers for the detection of clear cell renal cell carcinoma identified by a whole blood-based epigenome-wide association study. Epigenetics Commun. 2:2 (2022) ⑤ <u>Ohmomo H</u> , Harada S, Komaki S, Ono K, Sutoh Y, Otomo R, Umekage S, Hachiya T, Katanoda K, Takebayashi T, Shimizu A. DNA Methylation Abnormalities and Altered Whole Transcriptome Profiles after Switching from Combustible Tobacco Smoking to Heated Tobacco Products. Cancer Epidemiol Biomarkers Prev. 31:269-279 (2022).

小巻 翔平	生体情報解析部門	講師	博士（理学）	バイオインフォマ ティクス エピジェネティクス 進化生態学	①Komaki S: Widespread misperception about a major East Asian biogeographic boundary exposed through bibliographic survey and biogeographic meta-analysis. <i>J Biogeogr</i> , 48:2375–2386 (2021). ②Komaki S, Ohmomo H, Hachiya T, Sutoh Y, Ono K, Furukawa R, Umekage S, Otsuka-Yamasaki Y, Minabe S, Takashima A, Tanno K, Sasaki M, and Shimizu A: Evaluation of short-term epigenetic age fluctuation. <i>Clin Epigenetics</i> . 14:76 (2022). ③Kanon KF, Jannat B, Komaki S, Alam MD, and Alam MS: Molecular differentiation between native and Vietnam originated striped snakeheads (<i>Channa striata</i>) in Bangladesh using mitochondrial <i>cytchrome b</i> gene. <i>J Bangladesh Agri Univ</i> . 20:467–476 (2022). ④Komaki S, Nagata M, Arai E, Otomo R, Ono K, Abe Y, Ohmomo H, Umekage S, Shinozaki-O N, Hachiya T, Sutoh Y, Otsuka-Yamasaki Y, Arai Y, Hirose N, Yoneyama A, Okano H, Sasaki M, Kanai Y, and Shimizu A: Epigenetic profile of Japanese supercentenarians: a cross-sectional study. <i>Lancet Healthy Longev</i> , 4:e83–e90 (2023). ⑤特許第7442221号「名称；生物学的年齢の計算方法、老化状態の評価方法、CpGサイトの評価方法、プログラム、およびコンピュータ可読記憶媒体」
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