

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	<p>①Sutoh Y, Komaki S, Yamaji T, Suzuki S, Katagiri R, Sawada N, Ono K, Ohmomo H, Hachiya T, Otsuka-Yamasaki Y, Takashima A, Umekage S, Iwasaki M, <u>Shimizu A</u>. Low MICA Gene Expression Confers an Increased Risk of Graves' Disease: A Mendelian Randomization Study. <i>Thyroid</i>. 32:188-195 (2022).</p> <p>②Mishra, A., Malik, R., Hachiya, T., <u>Shimizu, A.</u>, et. al.: Stroke genetics informs drug discovery and risk prediction across ancestries. <i>Nature</i>. 611:115-123 (2022).</p> <p>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. <i>Lancet Healthy Longev</i>. 2:e83 (2023).</p> <p>④<u>清水厚志</u>, 坊農秀雅 編. <u>がんゲノムデータ解析</u>, 東京：メディカルサイエンスインターナショナル, (2022)</p> <p>⑤特許6716143号「名称；脳梗塞発症リスクの予測モデル作成方法および予測方法」</p>
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)	<p>①Komaki 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. <i>Lancet Healthy Longev</i>. 2:e83 (2023).</p> <p>②Nishida Y, Hara M, <u>Ohmomo H</u>, Ono K, Shimizu A, Horita M, Shimano C, Taguchi N, Higaki Y, Tanaka K. Epigenome-wide Association Study Identified VT11A DNA Methylation Associated with Accelerometer-assessed Physical Activity. <i>Med. Sci. Sports. Exerc</i>. 54:1879-1888 (2022).</p> <p>③<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. <i>Epigenetics Commun</i>. 2:2 (2022)</p> <p>④<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. <i>Cancer Epidemiol Biomarkers Prev</i>. 31:269-279 (2022).</p> <p>⑤<u>Ohmomo H</u>, Komaki S, Ono K, Sutoh Y, Hachiya T, Arai E, Fujimoto H, Yoshida T, Kanai Y, Sasaki M, Shimizu A. Evaluation of clinical formalin-fixed paraffin-embedded tissue quality for targeted-bisulfite sequencing. <i>Pathol Int</i>. 71:135-140 (2021).</p>

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 テイクス エピジェネティク ス 進化生態学	<p>①Komaki 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).</p> <p>②Ogata S, Doi H, Igawa T, Komaki S, and Takahara T: Environmental DNA methods for detecting two invasive alien species (American bullfrog and red swamp crayfish) in Japanese ponds. <i>Ecol Res</i>. 37:701–710 (2022).</p> <p>③Saito S, Saito T C, Igawa T, Takeda N, Komaki S, Ohta T, and Tominaga M: Evolutionary tuning of Transient Receptor Potential Ankyrin 1 underlies the variation in heat avoidance behaviors among frog species inhabiting diverse thermal niches. <i>Mol Biol Evol</i>. msac180 (2022).</p> <p>④Kanon 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).</p> <p>⑤Komaki 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).</p>
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