Curriculum Vitae

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Education:

2011	MD	Medicine	Faculty of Medicine, The University of Tokyo, Tokyo, Japan
2020	PhD	Internal Medicine (Prof. Kazuhiko Yamamoto)	Graduate School of Medicine, The University of Tokyo, Tokyo, Japan

Academic Appointments

04/2020-09/2020	Assistant Professor	Department of Statistical Genetics	Osaka University, Japan
09/2020-present	Postdoctoral Research Fellow	Division of Genetics	Brigham & Women's Hospital in the Raychaudhuri Laboratory and at Harvard Medical School

Professional Societies:

2018- American Society of Human Genetics

Honors and Prizes:

2010	Otsubo Tetsumon Fellowship Award	The University of Tokyo	Academic achievements
2017	Finalist of Meeting Award	the 62th Annual Meeting of the Japan Society of Human Genetics	Research
2018	Semifinalist	American Society of Human Genetics/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research	Research
2019	Finalist	American Society of Human Genetics/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research	Research
2020	The President's Award	The University of Tokyo	Academic achievements
2020	L'Oréal-UNESCO For Women in Science International Award		Academic achievements
2020	Young Investigator's Award	The Japan Society of Human Genetics	Academic achievements

Local Invited Presentations:

2019 Integration of GWAS summary statistics and miRNA-target gene network with tissue-specific miRNA expression profile identified novel pathogenesis of complex human traits implicated in tissue specificity.
Osaka University, Osaka, Japan

International Invited Presentations:

2020 East Asian genomic data elucidates how the population-specific natural selection shaped phenotypic variation and survival outcome of modern humans. American Society of Human Genetics 2020 (Invited Session, Virtual conference)

National Abstract Oral Presentations

2018 Integration of GWAS summary statistics and miRNA-target gene network with tissue-specific miRNA expression profile identified novel pathogenesis of complex human traits implicated in tissue specificity.
the 62th Annual Meeting of the Japan Society of Human Genetics, Kobe, Japan.

2019 Integration of GWAS summary statistics and miRNA-target gene network with tissue-specific miRNA expression profile identified novel pathogenesis of complex human traits implicated in tissue specificity.
the 62th Annual General Assembly and Scientific Meeting of the Japan College of Rheumatology, Yokohama, Japan.

International Abstract Oral Presentations

2018 Integration of GWAS summary statistics and miRNA-target gene network with tissue-specific miRNA expression profile identified novel pathogenesis of complex human traits implicated in tissue specificity.
American Society of Human Genetics, San Diego, CA.

2019 Trans-ethnic mega-biobank polygenic risk score analysis involving 676,000 individuals identified blood pressure and obesity as causal drivers affecting human longevity.
American Society of Human Genetics, Houston, Tx.

2019 Machine-learning based deconvolution of biobank-driven GWAS data with 170,000 individuals enlightens the finest-scale genetic, evolutional, and polygenic risk score divergence within Japanese population.
American Society of Human Genetics, Houston, Tx.

Current Licensure and Certification:

2011- Japanese Medical License
2019-2024 Japanese Board of Rheumatology

Publications (Selected publication is highlighted in blue)

1. **Sakaue S**, Kanai M, Tanigawa Y, Karjalainen J, Kurki M, Yamamoto K, Konuma T, FinnGen, Biobank Japan, Kamatani Y, Palotie A, Rivas M, Daly MJ, Matsuda K, Okada Y. A cross-population atlas of genetic associations for 220 human phenotypes. *Nat Genet.* (In press)
2. **Sakaue S**, Yamaguchi E, Inoue Y, Takahashi M, Hirata J, Suzuki K, Ito S, Arai T, Hirose M, Tanino Y, Nikaido T, Ichiwata T, Ohkouchi S, Hirano T, Takada T, Miyawaki S, Dofuku S, Maeda Y, Nii T, Kishikawa T, Ogawa K, Masuda T, Yamamoto K, Sonehara K, Tazawa R, Morimoto K, Takaki M, Konno S, Suzuki M, Tomii K, Nakagawa A, Handa T, Tanizawa K, Ishii H, Ishida M, Kato T, Takeda N, Yokomura K, Matsui T, Watanabe M, Inoue H, Imaizumi K, Goto Y, Kida H, Fujisawa T, Suda T, Yamada T, Satake Y, Ibata H, Hizawa N, Mochizuki H, Kumanogoh A, Matsuda F, Nakata K, Hirota T, Tamari M, Okada Y. Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. *Nat Commun.* 2021 Feb 15;12(1):1032.
3. Lin BM, Grinde KE, Brody JA, Breeze CE, Raffield LM, Mychaleckyj JC, Thornton TA, Perry JA, Baier LJ, de Las Fuentes L, Guo X, Heavner BD, Hanson RL, Hung YJ, Qian H, Hsiung CA, Hwang SJ, Irvin MR, Jain D, Kelly TN, Kobes S, Lange L, Lash JP, Li Y, Liu X, Mi X, Musani SK, Papanicolaou GJ, Parsa A, Reiner AP, Salimi S, Sheu WH, Shuldiner AR, Taylor KD, Smith AV, Smith JA, Tin A, Vaidya D, Wallace RB, Yamamoto K, **Sakaue S**, Matsuda K, Kamatani Y, Momozawa Y, Yanek LR, Young BA, Zhao W, Okada Y, Abecasis G, Psaty BM, Arnett DK, Boerwinkle E, Cai J, Yii-Der Chen I, Correa A, Cupples LA, He J, Kardia SL, Kooperberg C, Mathias RA, Mitchell BD, Nickerson DA, Turner ST, Vasan RS, Rotter JI, Levy D, Kramer HJ, Köttgen A, Nhlbi Trans-Omics For Precision Medicine TOPMed Consortium, TOPMed Kidney Working Group, Rich SS, Lin DY, Browning SR, Franceschini N. Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. *EBioMedicine.* 2021 Jan;63:103157.
4. Sargurupremraj M, Suzuki H, Jian X, Sarnowski C, Evans TE, Bis JC, Eiriksdottir G, **Sakaue S**, Terzikhan N, Habes M, Zhao W, Armstrong NJ, Hofer E, Yanek LR, Hagenaars SP, Kumar RB, van den Akker EB, McWhirter RE, Trompet S, Mishra A, Saba Y, Satizabal CL, Beaudet G, Petit L, Tsuchida A, Zago L, Schilling S, Sigurdsson S, Gottesman RF, Lewis CE, Aggarwal NT, Lopez OL, Smith JA, Valdés Hernández MC, van der Grond J, Wright MJ, Knol MJ, Dörr M, Thomson RJ, Bordes C, Le Grand Q, Duperron MG, Smith AV, Knopman DS, Schreiner PJ, Evans DA, Rotter JI, Beiser AS, Maniega SM, Beekman M, Trollor J, Stott DJ, Vernooij MW, Wittfeld K, Niessen WJ, Soumaré A, Boerwinkle E, Sidney S, Turner ST, Davies G, Thalamuthu A, Völker U, van Buchem MA, Bryan RN, Dupuis J, Bastin ME, Ames D, Teumer A, Amouyel P, Kwok JB, Bülow R, Deary IJ, Schofield PR, Brodaty H, Jiang J, Tabara Y, Setoh K, Miyamoto S, Yoshida K, Nagata M, Kamatani Y, Matsuda F, Psaty BM, Bennett DA, De Jager PL, Mosley TH, Sachdev PS, Schmidt R, Warren HR, Evangelou E, Trégouët DA; International Network against Thrombosis (INVENT) Consortium; International Headache Genomics Consortium (IHGC), Ikram MA, Wen W, DeCarli C, Srikanth VK, Jukema JW, Slagboom EP, Kardia SLR, Okada Y, Mazoyer B, Wardlaw JM, Nyquist PA, Mather KA, Grabe HJ, Schmidt H, Van Duijn CM, Gudnason V, Longstreth WT Jr, Launer LJ, Lathrop M, Seshadri S, Tzourio C, Adams HH, Matthews PM, Fornage M, Debette S. Cerebral small vessel disease genomics and its implications across the lifespan. *Nat Commun.* 2020 Dec 8;11(1):6285.

5. Masuda T, Ito H, Hirata J, **Sakaue S**, Ueda Y, Kimura T, Takeuchi F, Murakami Y, Matsuda K, Matsuo K, Okada Y. Fine Mapping of the Major Histocompatibility Complex Region and Association of the HLA-B*52:01 Allele With Cervical Cancer in Japanese Women. *JAMA Netw Open.* 2020 Oct 1;3(10):e2023248.
6. Vuckovic D, Bao EL, Akbari P, Lareau CA, Mousas A, Jiang T, Chen MH, Raffield LM, Tardaguila M, Huffman JE, Ritchie SC, Megy K, Ponstingl H, Penkett CJ, Albers PK, Wigdor EM, **Sakaue S**, Moscati A, Manansala R, Lo KS, Qian H, Akiyama M, Bartz TM, Ben-Shlomo Y, Beswick A, Bork-Jensen J, Bottinger EP, Brody JA, van Rooij FJA, Chitrala KN, Wilson PWF, Choquet H, Danesh J, Di Angelantonio E, Dimou N, Ding J, Elliott P, Esko T, Evans MK, Felix SB, Floyd JS, Broer L, Grarup N, Guo MH, Guo Q, Greinacher A, Haessler J, Hansen T, Howson JMM, Huang W, Jorgenson E, Kacprowski T, Kähönen M, Kamatani Y, Kanai M, Karthikeyan S, Koskeridis F, Lange LA, Lehtimäki T, Linneberg A, Liu Y, Lyytikäinen LP, Manichaikul A, Matsuda K, Mohlke KL, Mononen N, Murakami Y, Nadkarni GN, Nikus K, Pankratz N, Pedersen O, Preuss M, Psaty BM, Raitakari OT, Rich SS, Rodriguez BAT, Rosen JD, Rotter JI, Schubert P, Spracklen CN, Surendran P, Tang H, Tardif JC, Ghanbari M, Völker U, Völzke H, Watkins NA, Weiss S; VA Million Veteran Program, Cai N, Kundu K, Watt SB, Walter K, Zonderman AB, Cho K, Li Y, Loos RJF, Knight JC, Georges M, Stegle O, Evangelou E, Okada Y, Roberts DJ, Inouye M, Johnson AD, Auer PL, Astle WJ, Reiner AP, Butterworth AS, Ouwehand WH, Lettre G, Sankaran VG, Soranzo N. The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell.* 2020 Sep 3;182(5):1214-1231.e11.
7. Chen MH, Raffield LM, Mousas A, **Sakaue S**, Huffman JE, Moscati A, Trivedi B, Jiang T, Akbari P, Vuckovic D, Bao EL, Zhong X, Manansala R, Laplante V, Chen M, Lo KS, Qian H, Lareau CA, Beaudoin M, Hunt KA, Akiyama M, Bartz TM, Ben-Shlomo Y, Beswick A, Bork-Jensen J, Bottinger EP, Brody JA, van Rooij FJA, Chitrala K, Cho K, Choquet H, Correa A, Danesh J, Di Angelantonio E, Dimou N, Ding J, Elliott P, Esko T, Evans MK, Floyd JS, Broer L, Grarup N, Guo MH, Greinacher A, Haessler J, Hansen T, Howson JMM, Huang QQ, Huang W, Jorgenson E, Kacprowski T, Kähönen M, Kamatani Y, Kanai M, Karthikeyan S, Koskeridis F, Lange LA, Lehtimäki T, Lerch MM, Linneberg A, Liu Y, Lyytikäinen LP, Manichaikul A, Martin HC, Matsuda K, Mohlke KL, Mononen N, Murakami Y, Nadkarni GN, Nauck M, Nikus K, Ouwehand WH, Pankratz N, Pedersen O, Preuss M, Psaty BM, Raitakari OT, Roberts DJ, Rich SS, Rodriguez BAT, Rosen JD, Rotter JI, Schubert P, Spracklen CN, Surendran P, Tang H, Tardif JC, Trembath RC, Ghanbari M, Völker U, Völzke H, Watkins NA, Zonderman AB; VA Million Veteran Program, Wilson PWF, Li Y, Butterworth AS, Gauchat JF, Chiang CWK, Li B, Loos RJF, Astle WJ, Evangelou E, van Heel DA, Sankaran VG, Okada Y, Soranzo N, Johnson AD, Reiner AP, Auer PL, Lettre G. Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell.* 2020 Sep 3;182(5):1198-1213.e14.
8. Ishigaki K, Akiyama M, Kanai M, Takahashi A, Kawakami E, Sugishita H, **Sakaue S**, Matoba N, Low SK, Okada Y, Terao C, Amariuta T, Gazal S, Kochi Y, Horikoshi M, Suzuki K, Ito K, Koyama S, Ozaki K, Niida S, Sakata Y, Sakata Y, Kohno T, Shiraishi K, Momozawa Y, Hirata M, Matsuda K, Ikeda M, Iwata N, Ikegawa S, Kou I, Tanaka T, Nakagawa H, Suzuki A, Hirota T, Tamari M, Chayama K, Miki D, Mori M, Nagayama S, Daigo Y, Miki Y, Katagiri T, Ogawa O, Obara W, Ito H, Yoshida T, Imoto I, Takahashi T, Tanikawa C, Suzuki T, Sinozaki N, Minami S, Yamaguchi H, Asai S, Takahashi Y, Yamaji K, Takahashi K, Fujioka T, Takata R, Yanai H, Masumoto A, Koretsune Y, Kutsumi H, Higashiyama M, Murayama S, Minegishi N, Suzuki K, Tanno K, Shimizu A, Yamaji T, Iwasaki M, Sawada N, Uemura H, Tanaka K, Naito M, Sasaki M, Wakai K, Tsugane S, Yamamoto M, Yamamoto K, Murakami Y, Nakamura Y, Raychaudhuri S, Inazawa J,

Yamauchi T, Kadowaki T, Kubo M, Kamatani Y. Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. *Nat Genet.* 2020 Jul;52(7):669-679.

9. Matsunaga H, Ito K, Akiyama M, Takahashi A, Koyama S, Nomura S, Ieki H, Ozaki K, Onouchi Y, **Sakaue S**, Suna S, Ogishima S, Yamamoto M, Hozawa A, Satoh M, Sasaki M, Yamaji T, Sawada N, Iwasaki M, Tsugane S, Tanaka K, Arisawa K, Ikezaki H, Takashima N, Naito M, Wakai K, Tanaka H, Sakata Y, Morita H, Sakata Y, Matsuda K, Murakami Y, Akazawa H, Kubo M, Kamatani Y, Komuro I. Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. *Circ Genom Precis Med.* 2020 Jun;13(3):e002670.
10. **Sakaue S**, Kanai M, Karjalainen J, Akiyama M, Kurki M, Matoba N, Takahashi A, Hirata M, Kubo M, Matsuda K, Murakami Y, FinnGen, Daly MJ, Kamatani Y, Okada Y. Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. *Nat Med.* 2020 Apr;26(4):542-548.
11. **Sakaue S**, Hirata J, Kanai M, Suzuki K, Akiyama M, Too CL, Arayssi T, Hammoudeh M, Emadi SA, Masri BK, Halabi H, Badsha H, Uthman IW, Saxena R, Padyukov L, Hirata M, Matsuda K, Murakami Y, Kamatani Y, Okada Y. Dimensionality reduction enlightens the finest-scale genetic, evolutional, and phenotypic structure within the Japanese population. *Nat Commun.* 2020 Mar 26;11(1):1569.
12. Yamamoto K, **Sakaue S**, Matsuda K, Murakami Y, Kamatani Y, Ozono K, Momozawa Y, Okada Y. Genetic and phenotypic landscape of the mitochondrial genome in the Japanese population. *Commun Biol.* 2020 Mar 5;3(1):104.
13. Yasumizu Y*, **Sakaue S***, Konuma T, Suzuki K, Matsuda K, Murakami Y, Kubo M, Palamara PF, Kamatani Y, Okada Y. Genome-wide natural selection signatures are linked to genetic risk of modern phenotypes in the Japanese population. *Mol Biol Evol.* 2020 Jan 20. pii: msaa005.
14. Akiyama M, Ishigaki K, **Sakaue S**, Momozawa Y, Horikoshi M, Hirata M, Matsuda K, Ikegawa S, Takahashi A, Kanai M, Suzuki S, Matsui D, Naito M, Yamaji T, Iwasaki M, Sawada N, Tanno K, Sasaki M, Hozawa A, Minegishi N, Wakai K, Tsugane S, Shimizu A, Yamamoto M, Okada Y, Murakami Y, Kubo M, Kamatani Y. Characterizing rare and low-frequency height-associated variants in the Japanese population. *Nat Commun.* 2019 Sep 27;10(1):4393.
15. **Sakaue S**, Akiyama M, Hirata M, Matsuda K, Murakami Y, Kubo M, Kamatani Y, Okada Y. Functional variants in ADH1B and ALDH2 are non-additively associated with all-cause mortality in Japanese population. *Eur J Hum Genet.* 2020 Mar;28(3):378-382.
16. Ogawa K, Okuno T, Hosomichi K, Hosokawa A, Hirata J, Suzuki K, **Sakaue S**, Kinoshita M, Asano Y, Miyamoto K, Inoue I, Kusunoki S, Okada Y, Mochizuki H. Next-generation sequencing identifies contribution of both class I and II HLA genes on susceptibility of multiple sclerosis in Japanese. *J Neuroinflammation.* 2019 Aug 5;16(1):162.
17. Shungin D, Haworth S, Divaris K, Agler CS, Kamatani Y, Keun Lee M, Grinde K, Hindy G, Alaraudanjoki V, Pesonen P, Teumer A, Holtfreter B, **Sakaue S**, Hirata J, Yu YH, Ridker PM, Giulianini F, Chasman DI, Magnusson PKE, Sudo T, Okada Y, Völker U, Kocher T, Anttonen V, Laitala ML, Orho-Melander M, Sofer T, Shaffer JR, Vieira A, Marazita ML, Kubo M, Furuichi Y, North KE, Offenbacher S, Ingelsson E, Franks PW, Timpson NJ, Johansson I. Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. *Nat Commun.* 2019 Jun 24;10(1):2773.
18. **Sakaue S** and Okada Y. GREP: genome for REPositioning drugs. *Bioinformatics.* 2019 Oct 1;35(19):3821-3823.
19. Hirata J, Hosomichi K, **Sakaue S**, Kanai M, Nakaoka H, Ishigaki K, Suzuki K, Akiyama M,

Kishikawa T, Ogawa K, Masuda T, Yamamoto K, Hirata M, Matsuda K, Momozawa Y, Inoue I, Kubo M, Kamatani Y, Okada Y. Genetic and phenotypic landscape of the major histocompatibility complex region in the Japanese population. *Nat Genet.* 2019 Mar;51(3):470-480.

20. **Sakaue S**, Hirata J, Maeda Y, Kawakami E, Nii T, Kishikawa T, Ishigaki K, Terao C, Suzuki K, Akiyama M, Suita N, Masuda T, Ogawa K, Yamamoto K, Saeki Y, Matsushita M, Yoshimura M, Matsuoka H, Ikari K, Taniguchi A, Yamanaka H, Kawaji H, Lassmann T, Itoh M, Yoshitomi H, Ito H, Ohmura K, R Forrest AR, Hayashizaki Y, Carninci P, Kumanogoh A, Kamatani Y, de Hoon M, Yamamoto K, Okada Y. Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. *Nucleic Acids Res.* 2018 Dec 14;46(22):11898-11909.
21. Okada Y, Momozawa Y, **Sakaue S**, Kanai M, Ishigaki K, Akiyama M, Kishikawa T, Arai Y, Sasaki T, Kosaki K, Suematsu M, Matsuda K, Yamamoto K, Kubo M, Hirose N, Kamatani Y. Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. *Nat Commun.* 2018 Apr 24;9(1):1631.
22. Malik R, Chauhan G, Traylor M, Sargurupremraj M, Okada Y, Mishra A, Rutten-Jacobs L, Giese AK, van der Laan SW, Gretarsdottir S, Anderson CD, Chong M, Adams HHH, Ago T, Almgren P, Amouyel P, Ay H, Bartz TM, Benavente OR, Bevan S, Boncoraglio GB, Brown RD Jr, Butterworth AS, Carrera C, Carty CL, Chasman DI, Chen WM, Cole JW, Correa A, Cotlarciuc I, Cruchaga C, Danesh J, de Bakker PIW, DeStefano AL, den Hoed M, Duan Q, Engelter ST, Falcone GJ, Gottesman RF, Grewal RP, Gudnason V, Gustafsson S, Haessler J, Harris TB, Hassan A, Havulinna AS, Heckbert SR, Holliday EG, Howard G, Hsu FC, Hyacinth HI, Ikram MA, Ingelsson E, Irvin MR, Jian X, Jiménez-Conde J, Johnson JA, Jukema JW, Kanai M, Keene KL, Kissela BM, Kleindorfer DO, Kooperberg C, Kubo M, Lange LA, Langefeld CD, Langenberg C, Launer LJ, Lee JM, Lemmens R, Leys D, Lewis CM, Lin WY, Lindgren AG, Lorentzen E, Magnusson PK, Maguire J, Manichaikul A, McArdle PF, Meschia JF, Mitchell BD, Mosley TH, Nalls MA, Ninomiya T, O'Donnell MJ, Psaty BM, Pulit SL, Rannikmäe K, Reiner AP, Rexrode KM, Rice K, Rich SS, Ridker PM, Rost NS, Rothwell PM, Rotter JI, Rundek T, Sacco RL, **Sakaue S**, Sale MM, Salomaa V, Sapkota BR, Schmidt R, Schmidt CO, Schminke U, Sharma P, Slowik A, Sudlow CLM, Tanislav C, Tatlisumak T, Taylor KD, Thijs VNS, Thorleifsson G, Thorsteinsdottir U, Tiedt S, Trompet S, Tzourio C, van Duijn CM, Walters M, Wareham NJ, Wassertheil-Smoller S, Wilson JG, Wiggins KL, Yang Q, Yusuf S; AFGen Consortium; Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium; International Genomics of Blood Pressure (iGEN-BP) Consortium; INVENT Consortium; STARNET, Bis JC, Pastinen T, Ruusalepp A, Schadt EE, Koplev S, Björkegren JLM, Codoni V, Civelek M, Smith NL, Trégouët DA, Christophersen IE, Roselli C, Lubitz SA, Ellinor PT, Tai ES, Kooner JS, Kato N, He J, van der Harst P, Elliott P, Chambers JC, Takeuchi F, Johnson AD; BioBank Japan Cooperative Hospital Group; COMPASS Consortium; EPIC-CVD Consortium; EPIC-InterAct Consortium; International Stroke Genetics Consortium (ISGC); METASTROKE Consortium; Neurology Working Group of the CHARGE Consortium; NINDS Stroke Genetics Network (SiGN); UK Young Lacunar DNA Study; MEGASTROKE Consortium, Sanghera DK, Melander O, Jern C, Strbian D, Fernandez-Cadenas I, Longstreth WT Jr, Rolfs A, Hata J, Woo D, Rosand J, Pare G, Hopewell JC, Saleheen D, Stefansson K, Worrall BB, Kittner SJ, Seshadri S, Fornage M, Markus HS, Howson JMM, Kamatani Y, Debette S, Dichgans M. Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nat Genet.* 2018 Apr;50(4):524-537.
23. **Sakaue S** and Okada Y. Human genetics contributes to the understanding of disease pathophysiology and drug discovery. *J Orthop Sci.* 2017 Nov;22(6):977-981.

24. Okada Y, Kishikawa T, **Sakaue S**, Hirata J. Future Directions of Genomics Research in Rheumatic Diseases. *Rheum Dis Clin North Am.* 2017 Aug;43(3):481-487.
25. **Sakaue S** and Hagino N. IMAGES IN CLINICAL MEDICINE. Takayasu's Arteritis. *N Engl J Med.* 2016 Aug 18;375(7):675.
26. **Sakaue S**, Sumitomo S, Fujio K, Yamamoto K. Unilateral proptosis in a woman with asthma. *BMJ Case Rep.* 2015 Feb 12;2015.
27. **Sakaue S**, Sumitomo S, Kubo K, Fujio K, Yamamoto K. Tocilizumab-induced leucocytoclastic vasculitis in a patient with rheumatoid arthritis. *Rheumatology.* 2014 Aug;53(8):1529-30.

***** Equal contribution

Thesis:

Sakaue S, Yamamoto K, Okada Y, Fujio K. Elucidation of novel disease pathogenesis through integrative analysis of genome-wide association studies and tissue-specific expression profile of miRNAs [dissertation]. The University of Tokyo; 2020.