# Seizo Koshiba

List of Publications by Year
in descending order

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|---|---|---|---|
| 40 papers | 2,027 citations | 393982<br>19 h-index | 288905<br>40 g-index |
| 43 all docs | 43 docs citations | 43 times ranked | 2332 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Maternal Baseline Characteristics and Perinatal Outcomes: The Tohoku Medical Megabank Project Birth and Three-Generation Cohort Study. Journal of Epidemiology, 2022, 32, 69-79. | 1.1 | 13 |
| 2 | Esterification promotes the intracellular accumulation of roxadustat, an activator of hypoxia-inducible factors, to extend its effective duration. Biochemical Pharmacology, 2022, 197, 114939. | 2.0 | 3 |
| 3 | Study Profile of the Tohoku Medical Megabank Community-Based Cohort Study. Journal of Epidemiology, 2021, 31, 65-76. | 1.1 | 81 |
| 4 | Identification of biomarkers to diagnose diseases and find adverse drug reactions by metabolomics. Drug Metabolism and Pharmacokinetics, 2021, 37, 100373. | 1.1 | 36 |
| 5 | Japonica Array NEO with increased genome-wide coverage and abundant disease risk SNPs. Journal of Biochemistry, 2021, 170, 399-410. | 0.9 | 17 |
| 6 | Molecular basis for the disruption of Keap1–Nrf2 interaction via Hinge &amp; Latch mechanism. Communications Biology, 2021, 4, 576. | 2.0 | 84 |
| 7 | Wide-Targeted Metabolome Analysis Identifies Potential Biomarkers for Prognosis Prediction of Epithelial Ovarian Cancer. Toxins, 2021, 13, 461. | 1.5 | 14 |
| 8 | Identification and Validation of Combination Plasma Biomarker of Afamin, Fibronectin and Sex Hormone-Binding Globulin to Predict Pre-eclampsia. Biological and Pharmaceutical Bulletin, 2021, 44, 804-815. | 0.6 | 10 |
| 9 | Machine learning approaches to predict gestational age in normal and complicated pregnancies via urinary metabolomics analysis. Scientific Reports, 2021, 11, 17777. | 1.6 | 7 |
| 10 | A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424. | 9.4 | 560 |
| 11 | Comparison of Kit-Based Metabolomics with Other Methodologies in a Large Cohort, towards Establishing Reference Values. Metabolites, 2021, 11, 652. | 1.3 | 10 |
| 12 | jMorp updates in 2020: large enhancement of multi-omics data resources on the general Japanese population. Nucleic Acids Research, 2021, 49, D536-D544. | 6.5 | 107 |
| 13 | dbTMM: an integrated database of large-scale cohort, genome and clinical data for the Tohoku Medical Megabank Project. Human Genome Variation, 2021, 8, 44. | 0.4 | 7 |
| 14 | Nrf2 plays a critical role in the metabolic response during and after spaceflight. Communications Biology, 2021, 4, 1381. | 2.0 | 10 |
| 15 | Cohort Profile: Tohoku Medical Megabank Project Birth and Three-Generation Cohort Study (TMM) Tj ETQq1 1 0.784314 rgBT /Overlock 2020, 49, 18-19m. | 0.9 | 107 |
| 16 | Identification of novel biomarkers of hepatocellular carcinoma by high-definition mass spectrometry: Ultrahigh-performance liquid chromatography quadrupole time-of-flight mass spectrometry and desorption electrospray ionization mass spectrometry imaging. Rapid Communications in Mass Spectrometry, 2020, 34, e8551. | 0.7 | 17 |
| 17 | O-Glycan-Altered Extracellular Vesicles: A Specific Serum Marker Elevated in Pancreatic Cancer. Cancers, 2020, 12, 2469. | 1.7 | 26 |
| 18 | Nrf2 contributes to the weight gain of mice during space travel. Communications Biology, 2020, 3, 496. | 2.0 | 27 |

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|---|---------|----|-----------|
| 19 | Identification of critical genetic variants associated with metabolic phenotypes of the Japanese population. Communications Biology, 2020, 3, 662. | 2.0 | 16 |
| 20 | Improved metabolomic data-based prediction of depressive symptoms using nonlinear machine learning with feature selection. Translational Psychiatry, 2020, 10, 157. | 2.4 | 24 |
| 21 | Amino-acid selective isotope labeling enables simultaneous overlapping signal decomposition and information extraction from NMR spectra. Journal of Biomolecular NMR, 2020, 74, 125-137. | 1.6 | 2 |
| 22 | Design and Progress of Oral Health Examinations in the Tohoku Medical Megabank Project. Tohoku Journal of Experimental Medicine, 2020, 251, 97-115. | 0.5 | 3 |
| 23 | Metabolic Profiling of the Cerebrospinal Fluid in Pediatric Epilepsy. Acta Medica Okayama, 2020, 74, 65-72. | 0.1 | 4 |
| 24 | 3.5KJPNv2: an allele frequency panel of 3552 Japanese individuals including the X chromosome. Human Genome Variation, 2019, 6, 28. | 0.4 | 115 |
| 25 | Estimating carrier frequencies of newborn screening disorders using a whole-genome reference panel of 3552 Japanese individuals. Human Genetics, 2019, 138, 389-409. | 1.8 | 7 |
| 26 | Maternity Log study: a longitudinal lifelog monitoring and multiomics analysis for the early prediction of complicated pregnancy. BMJ Open, 2019, 9, e025939. | 0.8 | 10 |
| 27 | Genome analyses for the Tohoku Medical Megabank Project towards establishment of personalized healthcare. Journal of Biochemistry, 2019, 165, 139-158. | 0.9 | 33 |
| 28 | Biallelic GALM pathogenic variants cause a novel type of galactosemia. Genetics in Medicine, 2019, 21, 1286-1294. | 1.1 | 40 |
| 29 | Omics research project on prospective cohort studies from the Tohoku Medical Megabank Project. Genes To Cells, 2018, 23, 406-417. | 0.5 | 38 |
| 30 | jMorp: Japanese Multi Omics Reference Panel. Nucleic Acids Research, 2018, 46, D551-D557. | 6.5 | 90 |
| 31 | Evaluation of reported pathogenic variants and their frequencies in a Japanese population based on a whole-genome reference panel of 2049 individuals. Journal of Human Genetics, 2018, 63, 213-230. | 1.1 | 35 |
| 32 | Detection of novel metabolite for roxadustat doping by global metabolomics. Journal of Biochemistry, 2018, 163, e1-e1. | 0.9 | 2 |
| 33 | Metabolomic changes in the mouse retina after optic nerve injury. Scientific Reports, 2018, 8, 11930. | 1.6 | 16 |
| 34 | The Tohoku Medical Megabank Project: Design and Mission. Journal of Epidemiology, 2016, 26, 493-511. | 1.1 | 236 |
| 35 | The structural origin of metabolic quantitative diversity. Scientific Reports, 2016, 6, 31463. | 1.6 | 18 |
| 36 | Establishment of Protocols for Global Metabolomics by LC-MS for Biomarker Discovery. PLoS ONE, 2016, 11, e0160555. | 1.1 | 56 |

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|---|---------|-----|-----------|
| 37 | Identification of key neoculin residues responsible for the binding and activation of the sweet taste receptor. Scientific Reports, 2015, 5, 12947. | 1.6 | 9 |
| 38 | Stable isotope labeling strategy based on coding theory. Journal of Biomolecular NMR, 2015, 63, 213-221. | 1.6 | 12 |
| 39 | A practical method for cell-free protein synthesis to avoid stable isotope scrambling and dilution. Analytical Biochemistry, 2011, 411, 223-229. | 1.1 | 53 |
| 40 | Improving cell-free protein synthesis for stable-isotope labeling. Journal of Biomolecular NMR, 2007, 37, 225-229. | 1.6 | 67 |