

Shuang-Xia Zhao

List of Publications by Year in descending order

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26
papers

653
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933447

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1315
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| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | The mutation screening in candidate genes related to thyroid dysgenesis by targeted next-generation sequencing panel in the Chinese congenital hypothyroidism. <i>Clinical Endocrinology</i> , 2022, 96, 617-626. | 2.4 | 5 |
| 2 | Detection of BRAF V600E in Fine-Needle Aspiration Samples of Thyroid Nodules by Droplet Digital PCR. <i>International Journal of Endocrinology</i> , 2022, 2022, 1-8. | 1.5 | 2 |
| 3 | Tpo knockout in zebrafish partially recapitulates clinical manifestations of congenital hypothyroidism and reveals the involvement of TH in proper development of glucose homeostasis. <i>General and Comparative Endocrinology</i> , 2022, 323-324, 114033. | 1.8 | 2 |
| 4 | Molecular and clinical genetics of the transcription factor GLIS3 in Chinese congenital hypothyroidism. <i>Molecular and Cellular Endocrinology</i> , 2021, 528, 111223. | 3.2 | 5 |
| 5 | The expression of mimecan in adrenal tissue plays a role in an organism's responses to stress. <i>Aging</i> , 2021, 13, 13087-13107. | 3.1 | 2 |
| 6 | Genetic Manipulation on Zebrafish Recapitulate the Clinical Manifestations of Congenital Hypothyroidism. <i>Endocrinology</i> , 2021, 162, . | 2.8 | 4 |
| 7 | Upregulation of GBP1 in thyroid primordium is required for developmental thyroid morphogenesis. <i>Genetics in Medicine</i> , 2021, 23, 1944-1951. | 2.4 | 13 |
| 8 | A five-gene panel refines differential diagnosis of thyroid nodules. <i>Journal of Clinical Laboratory Analysis</i> , 2021, 35, e23920. | 2.1 | 2 |
| 9 | Correlation of DUOX2 residual enzymatic activity with phenotype in congenital hypothyroidism caused by biallelic DUOX2 defects. <i>Clinical Genetics</i> , 2021, 100, 713-721. | 2.0 | 3 |
| 10 | The effect of radioiodine treatment on the characteristics of TRAb in Graves' disease. <i>BMC Endocrine Disorders</i> , 2021, 21, 238. | 2.2 | 5 |
| 11 | The TPO mutation screening and genotype-phenotype analysis in 230 Chinese patients with congenital hypothyroidism. <i>Molecular and Cellular Endocrinology</i> , 2020, 506, 110761. | 3.2 | 11 |
| 12 | Candidate gene associations reveal sex-specific Graves' disease risk alleles among Chinese Han populations. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1249. | 1.2 | 3 |
| 13 | Genetic Study in a Large Cohort Supported Different Pathogenesis of Graves' Disease and Hashimoto's Hypothyroidism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e2600-e2608. | 3.6 | 15 |
| 14 | Mutation screening of the TSHR gene in 220 Chinese patients with congenital hypothyroidism. <i>Clinica Chimica Acta</i> , 2019, 497, 147-152. | 1.1 | 20 |
| 15 | A Weighted Genetic Risk Score Using Known Susceptibility Variants to Predict Graves Disease Risk. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 2121-2130. | 3.6 | 3 |
| 16 | Identification of three novel SRD5A2 mutations in Chinese patients with 5 α -reductase 2 deficiency. <i>Asian Journal of Andrology</i> , 2019, 21, 577. | 1.6 | 9 |
| 17 | The genetic characteristics of congenital hypothyroidism in China by comprehensive screening of 21 candidate genes. <i>European Journal of Endocrinology</i> , 2018, 178, 623-633. | 3.7 | 77 |
| 18 | A dense mapping study of six European AITD susceptibility regions in a large Chinese Han Cohort of Graves' disease. <i>Clinical Endocrinology</i> , 2018, 89, 840-848. | 2.4 | 7 |

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|----|--|------|-----------|
| 19 | ITM2A Expands Evidence for Genetic and Environmental Interaction in Graves Disease Pathogenesis. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 652-660. | 3.6 | 11 |
| 20 | Aromatase deficiency: a novel compound heterozygous mutation identified in a Chinese girl with severe phenotype and obvious maternal virilization. <i>Molecular and Cellular Endocrinology</i> , 2016, 433, 66-74. | 3.2 | 19 |
| 21 | Refined association of TSH receptor susceptibility locus to Graves' disease in the Chinese Han population. <i>European Journal of Endocrinology</i> , 2014, 170, 109-119. | 3.7 | 26 |
| 22 | Identification of BACH2 as a susceptibility gene for Graves' disease in the Chinese Han population based on a three-stage genome-wide association study. <i>Human Genetics</i> , 2014, 133, 661-671. | 3.8 | 24 |
| 23 | A Refined Study of FCRL Genes from a Genome-Wide Association Study for Graves' Disease. <i>PLoS ONE</i> , 2013, 8, e57758. | 2.5 | 20 |
| 24 | Robust evidence for five new Graves' disease risk loci from a staged genome-wide association analysis. <i>Human Molecular Genetics</i> , 2013, 22, 3347-3362. | 2.9 | 80 |
| 25 | A genome-wide association study identifies two new risk loci for Graves' disease. <i>Nature Genetics</i> , 2011, 43, 897-901. | 21.4 | 243 |
| 26 | Association of the CTLA4 Gene with Graves' Disease in the Chinese Han Population. <i>PLoS ONE</i> , 2010, 5, e9821. | 2.5 | 42 |