Chia Ling Chang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4101104/publications.pdf

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12 papers	72 citations	1937685 4 h-index	1588992 8 g-index
12 all docs	12 docs citations	12 times ranked	53 citing authors

#	Article	IF	Citations
1	Characterization of the novel <scp>HLAâ€C</scp>*03:294 allele by sequencingâ€based typing in a Taiwanese individual. Hla, 2022, 99, 215-216.	0.6	3
2	Identification of the novel <scp>HLAâ€C</scp>*07:446 allele in a volunteer bone marrow donor. Hla, 2022, 99, 397-399.	0.6	3
3	Identification of a novel <scp>HLAâ€DQB1</scp> allele, <scp>HLAâ€DQB1*03:168</scp>, by sequenceâ€based typing in a Taiwanese individual. Hla, 2020, 96, 546-547.	0.6	6
4	<scp>HLAâ€DQB1</scp>*05:02:12, an <scp>HLAâ€DQB1</scp>*05:02:01:01 variant, identified in a Taiwanese individual. Hla, 2020, 96, 551-552.	0.6	6
5	Different clinical features of patients with pulmonary disease caused by various Mycobacterium aviumâ€“intracellulare complex subspecies and antimicrobial susceptibility. International Journal of Infectious Diseases, 2020, 98, 33-40.	3.3	4
6	Enthesitis-related arthritis is the most common category of juvenile idiopathic arthritis in Taiwan and presents persistent active disease. Pediatric Rheumatology, 2019, 17, 58.	2.1	29
7	Detection of a novel HLAâ€B*46:01 variant, HLAâ€B*46:01:19, in a Taiwanese individual. Hla, 2018, 92, 414-415.	0.6	3
8	Identification of a novel HLAâ€DQB1 allele, DQB1*06:111, by sequenceâ€based typing in a Taiwanese individual. Hla, 2018, 92, 257-258.	0.6	4
9	<scp>HLA</scp>â€B*40:247, a novel <scp>HLA</scp>â€B*40 variant, identified by sequenceâ€based typing in a Taiwanese individual. Hla, 2017, 90, 121-122.	0.6	3
10	<scp>HLA</scp>â€A*33:<scp>74N</scp>, a novel <scp>HLA</scp>â€A*33 variant, identified by sequenceâ€based typing in a Taiwanese individual. Hla, 2017, 90, 365-366.	0.6	5
11	A novel allele, HLAâ€B*15:259, was identified in a Taiwanese individual by sequenceâ€based typing. Hla, 2016, 87, 103-104.	0.6	3
12	HLAâ€A*11:134, a novel HLAâ€A*11 variant, identified by sequenceâ€based typing in a Taiwanese individual. Hla, 2016, 88, 195-196.	0.6	3