

JCR 2022 ICW Excellent Abstract Award

Entry No.	Name	Abstract Title
20006	Yuichi Ishikawa	Estimation of short-term prognostic factors in hospitalized patients with herpes zoster, and the incidence of cerebro-cardiovascular events and the possible risk factors after hospitalization: a descriptive study using a national administrative inpatient database in Japan
20007	Mari Kamiya	Agonistic stimulation of Glucagon-like peptide-1 receptor ameliorates experimental polymyositis through inhibiting muscle fiber necroptosis
20010	Yosuke Kunishita	Efficacy and safety of abatacept in rheumatoid arthritis patients with prior malignancy
20020	Koji Sakuraba	Autoantibodies Against Malondialdehyde-modifications Promote Osteoclast Development by Reprogramming Cellular Metabolism
20030	Mitsuhiro Akiyama	A novel T cell population, IL-17RA+ITGB1+T cell, which shows immune suppression resistance and tissue homing, is involved in spondyloarthritis.
20032	Suguru Honda	Development and practical application of scoring system for the Sharp/van der Heijde score using convolutional neural network
20034	Chinatsu Takai	Perinatal clinical course of female patients with rheumatoid arthritis treated with bDMARDs
20036	Yasuyuki Todoroki	Nailfold microvascular abnormalities predict pulmonary arterial hypertension and can be improved by immunosuppressant treatment in patients with mixed connective tissue disease (MCTD)
20042	Ryu Watanabe	Drug retention of biologics or JAK inhibitors in patients with difficult-to-treat rheumatoid arthritis: Results from the ANSWER cohort
20049	Risa Yoshihara	Synovial phenotyping in Japanese RA patients using ultrasound-guided needle biopsy
20051	Yoshika Tsuji	Effect of smoking on serum IgG4 during health checkups in Nagasaki Island Study (NaIS)
20053	Masataka Umeda	Hypoxia Promotes the Expression of ADAM9 by Tubular Epithelial Cells which Enhances TGF- β 1 Activation and Promotes Tissue Fibrosis in Lupus Nephritis
20063	Takayuki Fujii	Contribution of PRIME cells to treatment response and long-term outcomes of biologics treatment in rheumatoid arthritis.
20068	Sotaro Nakajima	Synovial tissue heterogeneity and predominant inflammatory signals in rheumatoid arthritis
20071	Yuya Fujita	Characterization and pathogenicity of CD8+ T cells in patients with systemic lupus erythematosus - LOOPS/FLOW registry -
20079	Yusuke Miyazaki	Efficacy and safety of belimumab for maintenance therapy in patients with systemic lupus erythematosus
20083	Remi Sumiyoshi	Identification of pathways that discriminate between TAFRO type and NOS type in idiopathic multicentric Castleman's disease
20092	Masanobu Ueno	Risk estimation of difficult-to-treat (D2T) RA: FIRST registry
20099	Hachiro Konaka	Caspase-1-mediated secretion of mitochondrial DNA-rich exosomes causes pathological inflammation in a human chronic inflammatory disorder
20100	Masahiro Nakano	Large-scale immune cell-type-specific gene expression atlas revealed critical transcriptome architecture underlying the disease establishment and exacerbation of systemic lupus erythematosus
20102	Yoshihiko Tomofuji	Metagenome-wide association studies revealed the altered gut bacteriome and virome in autoimmune diseases.
20103	Yuto Takakura	Prediction of disease flare by biomarkers after discontinuing biologics in patients with rheumatoid arthritis achieving stringent remission
20111	Kodai Sakiyama	Dynamic functional connectivity associated with response to biologics in rheumatoid arthritis and spondyloarthritis
20116	Yoshino Inoue	Post-disease control by discontinuation of tofacitinib in patients with rheumatoid arthritis; a multicenter, prospective, randomized study (XANADU study)
20119	Ai Yaku	Regnase-1 regulates pulmonary arterial hypertension
20124	Naoaki Ohkubo	Immunophenotypes predicting flare of systemic lupus erythematosus (SLE) - using data from LOOPS/FLOW registry -
20127	Eri Katsuyama	CD38 promotes Ca ²⁺ flux and suppresses interleukin-2 production by promoting the expression of GM2 on the surface membrane of SLE T cells.
20134	Takahiro Itamiya	Transcriptome-wide association study of immune-related traits using a large-scale immune cell gene-expression database