

研究成果の刊行に関する一覧表 (平成 27-29 年度)

雑誌

発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
Kayali AY, Escalante-Maldonado O, Vuddhakul V, Seto K, Nakaguchi Y, Nishibuchi M	Development of a method for detection of Shigatoxin-producing <i>Escherichia coli</i> belonging to clinically important twelve O serotypes based on the combination of PickPen-assisted immuno-magnetic separation and loop-mediated isothermal amplification.	Int. J. Immunol. Immunother.	2	1	2015
Harada T, Iguchi A, Iyoda S, Seto K, Taguchi M, Kumeda Y	Multiplex real-time PCR assays for screening of Shiga toxin 1 and 2 genes, including all known subtypes, and <i>Escherichia coli</i> O26-, O111-, and O157-specific genes in beef and sprout enrichment cultures.	J. Food Prot.	78	1800-1811	2015
Kawahara R, Seto K, Taguchi M, Nakajima C, Kumeda Y, Suzuki Y	Characterization of third-generation-cephalosporin-resistant Shiga toxin-producing strains of <i>Escherichia coli</i> O157:H7 in Japan.	J. Clin. Microbiol.	53	3035-3038	2015
Komoto S, Tacharoenmuang R, Guntapong R, Ide T, Haga K, Katayama K, Kato T, Ouchi Y, Kurahashi H, Tsuji T, Sangkitporn S, Taniguchi K.	Emergence and Characterization of Unusual DS-1-Like G1P[8] Rotavirus Strains in Children with Diarrhea in Thailand.	PLoS One.	10	e0141739	2015
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Matsushima Y, Ishikawa M, Shimizu T, Komane A, Kasuo S, Shinohara M, Nagasawa K, Kimura H, Ryo A, Okabe N, Haga K, Doan HY, Katayama K, Shimizu H.	Genetic analyses of GII.17 norovirus strains in diarrheal disease outbreaks from December 2014 to March 2015 in Japan reveal a novel polymerase sequence and amino acid substitutions in the capsid region.	Euro Surveill.	20	21173	2015

Wu FT, Chen HC, Yen C, Wu CY, Katayama K, Park Y, Hall AJ, Vinjé J, Huang JC, Wu HS.	Epidemiology and molecular characteristics of norovirus GII.4 Sydney outbreaks in Taiwan, January 2012–December 2013.	J Med Virol.	87	1462–1470	2015
Ide T, Komoto S, Higo-Moriguchi K, Htun KW, Myint YY, Myat TW, Thant KZ, Thu HM, Win MM, Oo HN, Htut T, Wakuda M, Dennis FE, Haga K, Fujii Y, Katayama K, Rahman S, Nguyen SV, Umeda K, Oguma K, Tsuji T, Taniguchi K.	Whole Genomic Analysis of Human G12P[6] and G12P[8] Rotavirus Strains that Have Emerged in Myanmar.	PLoS One.	10	e0124965	2015
Nguyen VH, Pham HT, Diep TT, Phan CD, Nguyen TQ, Nguyen NT, Ngo TC, Nguyen TV, DO QK, Phan HC, Nguyen BM, Ehara M, Ohnishi M, Yamashiro T, Nguyen LT, Izumiya H.	<i>Vibrio cholerae</i> O1 El Tor from southern Vietnam in 2010 was molecularly distinct from that present from 1999 to 2004.	Epidemiol Infect.	144	1241–1247	2016
Nguyen DT, Ngo TC, Le TH, Nguyen HT, Morita M, Arakawa E, Ohnishi M, Nguyen BM, Izumiya H.	Molecular epidemiology of <i>Vibrio cholerae</i> O1 in northern Vietnam (2007–2009), using multilocus variable-number tandem repeat analysis.	J Med Microbiol.	65	1007–1012	2016
Iguchi A, Iyoda S, Seto K, Nishii H, Ohnishi M, Mekata H, Ogura Y, Hayashi T	Six novel O genotypes from Shiga toxin-producing <i>Escherichia coli</i> .	Front. Microbiol.	7	765	2016

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Suzuki Y, Doan H. Y., Kimura H, Shinomiya H, Shirabe K, Katayama K.	Predicting genotype compositions in norovirus seasons in Japan.	Microbiol and Immunol.	60	418-426	2016

Doan HY, Haga K, Fujimoto A, Fujii Y, Takai-Todaka R, Oka T, Kimura H, Yoshizumi S, Shigemoto N, Okamoto-Nakagawa R, Shirabe K, Shinomiya H, Sakon-Tanaka N, and Katayama K.	Genetic analysis of human rotavirus C: the appearance of Indian-Bangladeshi strain in Far East Asian countries.	Infect Genet Evol.	41	160-173	2016
Ito M, Tsuchiaka S, Naoi Y, Otomaru K, Sato M, Masuda T, Haga K, Oka T, Yamasato H, Omatsu T, Sugimura S, Aoki H, Furuya T, Katayama Y, Oba M, Shirai J, Katayama K, Mizutani T, Nagai M.	Whole genome analysis of Japanese bovine toroviruses reveals natural recombination between porcine and bovine toroviruses.	Infect Genet Evol.	38	90-95	2016
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Yumiketa Y, Narita T, Inoue Y, Sato G, Kamitani W, Oka T, Katayama K, Sakaguchi T and Tohya Y.	Nonstructural protein p39 of feline calicivirus suppresses host innate immune response by preventing IRF-3 activation.	Veterinary Microbiology.	185	62-67	2016

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<p>Ogura Y, Gotoh Y, Itoh T, Sato MP, Seto K, Yoshino S, Isobe J, Etoh Y, Kurogi M, Kimata K, Maeda E, Piérard D, Kusumoto M, Akiba M, Tominaga K, Kirino Y, Kato Y, Shirahige K, Ooka T, Ishijima N, Lee KI, Iyoda S, Mainil JG, Hayashi T</p>	<p>Population structure of <i>Escherichia coli</i> O26 : H11 with recent and repeated <i>stx2</i> acquisition in multiple lineages.</p>	<p>Microbial Genomics</p>	<p>3</p>		<p>2017</p>
<p>Motoya T, Nagasawa K, Matsushima Y, Nagata N, Ryo A, Sekizuka T, Yamashita A, Kuroda M, Morita Y, Suzuki Y, Sasaki N, Katayama K, Kimura H.</p>	<p>Molecular Evolution of the VP1 Gene in Human Norovirus GII.4 Variants in 1974–2015.</p>	<p>Front Microbiol.</p>	<p>8</p>	<p>2399</p>	<p>2017</p>

Kuroda M, Masuda T, Ito M, Naoi Y, Doan YH, Haga K, Tsuchiaka S, Kishimoto M, Sano K, Omatsu T, Katayama Y, Oba M, Aoki H, Ichimaru T, Sunaga F, Mukono I, Yamasato H, Shirai J, Katayama K, Mizutani T, Oka T, Nagai M.	Genetic diversity and intergenogroup recombination events of sapoviruses detected from feces of pigs in Japan.	Infect Genet Evol.	55	209-217	2017
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Doan YH, Suzuki Y, Fujii Y, Haga K, Fujimoto A, Takai-Todaka R, Someya Y, Nayak MK, Mukherjee A, Imamura D, Shinoda S, Chawla-Sarkar M, Katayama K.	Complex reassortment events of unusual G9P[4] rotavirus strains in India between 2011 and 2013.	Infect Genet Evol.	54	417-428	2017
Kitamoto T, Takai-Todaka R, Kato A, Kanamori K, Takagi H, Yoshida K, Katayama K, Nakanishi A.	Viral population changes during murine norovirus propagation in RAW 264.7 cells	Front Microbiol.	8	1091	2017

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Mizukoshi F, Nagasawa K, Doan YH, Haga K, Yoshizumi S, Ueki Y, Shinohara M, Ishikawa M, Sakon N, Shigemoto N, Okamoto-Nakagawa R, Ochi A, Murakami K, Ryo A, Suzuki Y, Katayama K, Kimura H.	Molecular Evolution of the RNA-Dependent RNA Polymerase and Capsid Genes of Human Norovirus Genotype GII.2 in Japan during 2004-2015.	Front Microbiol.	8	705	2017
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泉谷秀昌、石原朋子、 伊豫田淳、大西真	2014年に分離された腸管出血性大 腸菌 0157、026 および 0111 株の MLVA 解析について	IASR	36	83-84	2015
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泉谷秀昌、黒木俊郎、林賢一、齊藤志保子、八柳潤、今野貴之、大西真	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar 4:b:-株の解析	日本感染症学雑誌	90	652-656	2016
泉谷秀昌、石原朋子、伊豫田淳、大西真	2015年に分離された腸管出血性大腸菌 0157、026 および 0111 株の MLVA 解析について	IASR	37	93-95	2016
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石原朋子、伊豫田淳、泉谷秀昌、大西真	腸管出血性大腸菌 non-0157/026/0111 広域感染事例の分子疫学解析	IASR	38	101-102	2017
李謙一、石原朋子、泉谷秀昌、伊豫田淳、大西真	全ゲノム配列解析を用いた腸管出血性大腸菌の分子疫学解析	化学療法の領域	33	1467-1471	2017
上野詩歩子、黒岩祥子、若松倫子、熊本サチ子、永岡貴美子、長岡章次、寺松孝二、畔野征子、梅崎みどり、吉田まり子、松尾美智代、濱崎光宏、中山志幸、世良暢之	保育所で発生した腸管出血性大腸菌 026 : H11 による集団感染事例-福岡県	IASR	38	148-149	2017
吉田弘、高橋雅輝、濱崎光宏、山下育孝、四宮博人、山下照夫、皆川洋子、岸本剛、調恒明	エンテロウイルス検査の信頼性確保について	IASR	38	199-200	2017