

Name of Journal: *World Journal of Gastroenterology*

Manuscript NO: 49124

Manuscript Type: MINIREVIEWS

Exploring the hepatitis C virus genome using single molecule real-time sequencing

Takeda H *et al.* Exploring HCV genome by SMRT sequencing

Haruhiko Takeda, Taiki Yamashita, Yoshihide Ueda, Akihiro Sekine

Match Overview

1	Internet 49 words crawled on 06-Dec-2016 genomebiology.biomedcentral.com	1%
2	Crossref 41 words "UEG Week 2018 Oral Presentations", United European Gastroenterology Journal, 2018	1%
3	Crossref 36 words Yoshihide Ueda. "New sequencing technology, third-generation Nanopore sequencing, for hepatitis C virus research",	1%
4	Crossref 28 words Haruhiko Takeda, Yoshihide Ueda, Tadashi Inuzuka, Yukitaka Yamashita et al. "Evolution of multi-drug resistant HCV clo	1%
5	Internet 21 words crawled on 20-Sep-2017 www.nature.com	1%
6	Crossref 16 words Kazuma Nakano, Akino Shiroma, Makiko Shimoji, Hinako Tamotsu et al. "Advantages of genome sequencing by long-re...	<1%
7	Crossref 15 words Bull, Rowena A., Auda A. Eltahla, Chaturaka Rodrigo, Sylvie M. Koekkoek, Melanie Walker, Mehdi R. Pirozyan, Brigid Betz	<1%



All

Images

Videos

翻译成中文

关闭取词

30,300 Results

Any time ▾

Exploring viral infection using single-cell sequencing ...

<https://www.sciencedirect.com/science/article/pii/S0168170216303884>

Jul 15, 2017 · **Single-cell sequencing** (SCS) has emerged as a valuable tool to study cellular heterogeneity in diverse fields, including virology. By studying the viral and cellular **genome** and/or transcriptome, the dynamics of viral infection can be investigated at **single** cell level.

Cited by: 8

Author: Sylvie Rato, Monica Golumbeanu, Amalia...

Publish Year: 2017

Analysis of hepatitis C NS5A resistance associated ...

<https://www.sciencedirect.com/science/article/pii/S0166354215300449>

The aim of the study was to do an evaluation with single molecule real time (**SMRT**) sequencing on the **PacBio RSII instrument** to detect very **low levels of NS5A RAVs** (the RAVs are classified in Table 1). Another objective was to study in detail minor variants not associated with NS5A resistance (non-RAVs) within a limited sample range.

Cited by: 8

Author: Assar Bergfors, Daniël Leenheer, Daniël L...

Publish Year: 2016

Multiplexed highly-accurate DNA sequencing of closely ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4787755>

Nov 16, 2015 · Single genome amplification. **Cycling conditions** for both reactions are 98 ° C for 30 s, followed by 30 cycles of 98 ° C for 10 s, 72 ° C for 7.5 min, with a final extension at 72 ° C for 10 min. PCR reactions were visualized by **electrophoresis** through 1% agarose lithium acetate at 300 V for 25 min.

Cited by: 17

Author: Dario A. Dilemnia, Jung-Ting Chien, Daniel...

Publish Year: 2015

[PDF] Characterization of Hepatitis C Virus (HCV) Envelope ...

evolve.zoo.ox.ac.uk/Evolve/Oliver_Pybus_files/CharacterisationOfHCVUsingSMRTSequencing.pdf

Characterization of **Hepatitis C Virus (HCV)** Envelope Diversification from Acute to Chronic Infection within a Sexually Transmitted HCV Cluster by **Using Single-Molecule, Real-Time Sequencing**
Cynthia K. Y. Ho, aJayna Raghwani, b Sylvie Koekkoek, Richard H. Liang, c Jan T. M. Van der Meer, dMarc Van Der Valk, Menno De Jong, a Oliver G. Pybus, b

Analysis of hepatitis C NS5A resistance ... - PacBio

<https://www.pacb.com/publications/analysis-of-hepatitis-c-ns5a-resistance-associated...> ▾

Ultra-deep **single molecule real time (SMRT) sequencing** with the Pacific Biosciences (PacBio) RSII instrument was used to detect these RAVs. The **SMRT sequencing** was conducted on ten samples; three of them positive with **Sanger sequencing** (GT1a Q30H and Y93N, and GT3a Y93H), five GT1a



All

Images

Videos

翻译成中文

关闭取词

33,900 Results

Any time ▾

Analysis of hepatitis C NS5A resistance associated ...

<https://www.sciencedirect.com/science/article/pii/S0166354215300449>

Analysis of hepatitis C NS5A resistance associated polymorphisms **using** ultra deep **single molecule real time (SMRT) sequencing** Author links open overlay panel Assar Bergfors a 1 Daniël Leenheer a b 1 2 Anders Bergqvist a Adam Ameur c Johan Lennerstrand a

Cited by: 8

Author: Assar Bergfors, Daniël Leenheer, Daniël L...

Publish Year: 2016

A method for near full-length amplification and sequencing ...

<https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-016-2575-8>

Mar 17, 2016 · The **assay** was shown to have a detection limit of 1–3 cDNA copies per reaction. The method was tested with both **Illumina and PacBio single molecule, real-time (SMRT) sequencing** technologies. Illumina sequencing resulted in deep coverage and allowed detection of rare variants as well as HCV co-infection with multiple genotypes.

Published in: BMC Genomics · 2016

Authors: Rowena A Bull · Auda A Eltahla · Chaturaka Rodrigo · Sylvie M Koekkoek · Melanie W...

Affiliation: University of New South Wales · Pacific Biosciences

About: Viral load · Genotype · Hepacivirus · Proteomics · Phylogenetics · Detection limit

Multiplexed highly-accurate DNA sequencing of closely ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4787755>

Nov 16, 2015 · Multiplexed highly-accurate **DNA sequencing** of closely-related HIV-1 variants **using** continuous long reads from **single molecule, real-time sequencing** Dario A. Dilemnia , 1 Jung-Ting Chien , 1 Daniela C. Monaco , 1 Michael P.S. Brown , 2 Zachary Ende , 1 Martin J. Deymier , 1 Ling Yue , 1 Ellen E. Paxinos , 2 Susan Allen , 3 Alfredo Tirado-Ramos ...

Cited by: 18

Author: Dario A. Dilemnia, Jung-Ting Chien, Daniel...

Publish Year: 2015

Determining the Cellular Diversity of Hepatitis C Virus ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3838117>

We describe for the first time a system to investigate **RNA virus quasispecies** diversity at the cellular level utilizing hepatitis C virus (HCV) replicons. A high-fidelity nested reverse transcription (RT)-PCR assay was developed, and validation using control transcripts of known copy number indicated a detection limit of 3 copies of viral RNA/reaction.



国内版 国际版

Exploring the hepatitis C virus genome using single molecule real-time sequencin



All

Images

Videos

翻译成中文

关闭取词

26,700 Results

Any time ▼

Analysis of hepatitis C NS5A resistance associated ...

<https://www.sciencedirect.com/science/article/pii/S0166354215300449>

Analysis of hepatitis C NS5A resistance associated polymorphisms using ultra deep single molecule real time (SMRT) sequencing Author links open overlay panel Assar Bergfors a 1 Daniël Leenheer a b 1 2 Anders Bergqvist a Adam Ameur c Johan Lennerstrand a

Cited by: 8

Author: Assar Bergfors, Daniël Leenheer, Daniël ...

Publish Year: 2016

[PDF] Characterization of Hepatitis C Virus (HCV) Envelope ...

evolve.zoo.ox.ac.uk/Evolve/Oliver_Pybus_files/CharacterisationOfHCVUsingSMRTSequencing.pdf

Characterization of Hepatitis C Virus (HCV) Envelope Diversification from Acute to Chronic Infection within a Sexually Transmitted HCV Cluster by Using Single-Molecule, Real-Time Sequencing Cynthia K. Y. Ho, aJayna Raghwani, b Sylvie Koekkoek, Richard H. Liang, c Jan T. M. Van der Meer, dMarc Van Der Valk, Menno De Jong, a Oliver G. Pybus, b

Multiplexed highly-accurate DNA sequencing of closely ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4787755>

Nov 16, 2015 · Multiplexed highly-accurate DNA sequencing of closely-related HIV-1 variants using continuous long reads from single molecule, real-time sequencing Dario A. Dilemnia , 1 Jung-Ting Chien , 1 Daniela C. Monaco , 1 Michael P.S. Brown , 2 Zachary Ende , 1 Martin J. Deymier , 1 Ling Yue , 1 Ellen E. Paxinos , 2 Susan Allen , 3 Alfredo Tirado-Ramos ...

Cited by: 18

Author: Dario A. Dilemnia, Jung-Ting Chien, Danie...

Publish Year: 2015

A method for near full-length amplification and sequencing ...

<https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-016-2575-8> ▼

Mar 17, 2016 · Hepatitis C virus (HCV) is a rapidly evolving RNA virus that has been classified into seven genotypes. All HCV genotypes cause chronic hepatitis, which ultimately leads to liver diseases such as cirrhosis. The genotypes are unevenly distributed across the globe, with genotypes 1 and 3 being the most prevalent. Until recently, molecular epidemiological studies of HCV evolution within the host ...

Published in: BMC Genomics · 2016

Authors: Rowena A Bull · Auda A Eltahla · Chaturaka Rodrigo · Sylvie M Koekkoek · Melanie W...

Affiliation: University of New South Wales · Pacific Biosciences

About: Viral load · Genotype · Hepacivirus · Proteomics · Phylogenetics · Detection limit

Clinical and biological insights from viral genome sequencing