

Title (en)

PAIRED-END READS IN SEQUENCING BY SYNTHESIS

Title (de)

AUSLESUNG GEPAARTER ENDEN IN EINER SEQUENZIERUNG DURCH SYNTHESE

Title (fr)

ÉLÉMENTS DE LECTURE À EXTRÉMITÉS APPARIÉES DANS LE SÉQUENÇAGE PAR SYNTHÈSE

Publication

EP 2247741 A4 20110223 (EN)

Application

EP 09706204 A 20090203

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- US 4739708 P 20080423
- US 9891008 P 20080922

Abstract (en)

[origin: WO2009097626A2] The disclosure provides methods of generating paired reads in sequencing-by-synthesis process, particularly, in systems with relatively short read lengths (e.g., 15-35 bases), such as for example, in single molecule sequencing by synthesis. Several implementations of the methods are provided. Of particular advantage are the methods that permit re-sequencing of the template, which yields lower error rates. The invention further provides methods of using paired reads, for example, for positioning them over repeats or for assembly into large sequences, including whole genome assembly.

IPC 8 full level

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CPC (source: EP)

C12Q 1/6869 (2013.01)

Citation (search report)

- [A] ZAJAC ET AL: "Expression profiling of signature gene sets with trinucleotide threading", GENOMICS, ACADEMIC PRESS, SAN DIEGO, US, vol. 91, no. 2, 3 December 2007 (2007-12-03), pages 209 - 217, XP022426734, ISSN: 0888-7543, DOI: 10.1016/J.YGENO.2007.10.012
- See references of WO 2009097626A2

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