

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 A2 20101110 (EN)

Application

EP 09706204 A 20090203

Priority

- US 2009032970 W 20090203
- US 2503308 A 20080203
- 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

C12P 19/34 (2006.01); **C12Q 1/68** (2006.01)

CPC (source: EP)

C12Q 1/6869 (2013.01)

Designated contracting state (EPC)

AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO SE SI SK TR

Designated extension state (EPC)

AL BA RS

DOCDB simple family (publication)

WO 2009097626 A2 20090806; WO 2009097626 A3 20090924; EP 2247741 A2 20101110; EP 2247741 A4 20110223

DOCDB simple family (application)

US 2009032970 W 20090203; EP 09706204 A 20090203