

Title (en)

COMPUTER-IMPLEMENTED METHOD FOR THE IDENTIFICATION OF VARIANTS IN NUCLEIC ACID SEQUENCES

Title (de)

COMPUTERGESTÜTZTES VERFAHREN ZUR IDENTIFIZIERUNG VON VARIANTEN IN NUKLEINSÄURESEQUENZEN

Title (fr)

PROCÉDÉ INFORMATIQUE POUR L'IDENTIFICATION DE VARIANTES DANS DES SÉQUENCES D'ACIDE NUCLÉIQUE

Publication

EP 3210145 A1 20170830 (EN)

Application

EP 15784335 A 20151020

Priority

- EP 14189691 A 20141021
- EP 2015074253 W 20151020

Abstract (en)

[origin: WO2016062713A1] There is provided a computational method for the identification of nucleic acid variants between two cells, such as a normal cell vs. a pathological cell of a patient, or a cell at two different stages of development. The method is alignment-free, as it does not depend on the use of a reference genome, and accurately identifies all sorts of genetic variants, ranging from single nucleotide substitutions (SNVs) to large structural variants with great sensitivity and specificity. It thus allows to speed up in silico genomic analysis and personalized medicine.

IPC 8 full level

G16B 20/20 (2019.01); **G16B 30/00** (2019.01)

CPC (source: EP US)

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Citation (search report)

See references of WO 2016062713A1

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