

Recent patent applications in genomic mapping

Patent number	Description	Assignee	Inventor	Priority application date	Publication date
US 20120064521	A method for detecting DNA hydroxymethylation in a DNA sample comprising mammalian genomic DNA involving contacting a DNA sample comprising a glycosylated hydroxymethylcytosine with a DNA endonuclease to cleave the DNA and detecting at least one DNA sequence from sample not cleaved by the DNA endonuclease to determine the presence of hydroxymethylation in the DNA sequence.	Jia X, Yen J	Jia X, Yen J	9/9/2010	3/15/2012
US 20120053082	A method for chromosomal mapping comprising providing a sample of a nucleic acid and exposing the sample to a physical genomic analysis composition comprising oligonucleotides of different sequences.	Barrett MT, Caren MP	Barrett MT, Caren MP	4/7/2006	3/1/2012
US 20120035354	A polynucleotide isolated from <i>Eucalyptus grandis</i> and <i>Pinus radiata</i> , useful for modifying content, structure and composition of lignin in target organisms such as plants; useful for wood processing for producing paper, genome mapping, physical mapping, positional cloning of genes, and designing oligonucleotide probes and primers.	ArborGen (Summerville, SC, USA), Rubicon Forests Holdings (Auckland, NZ)	Bloksberg LN, Havukkala I	9/11/1996	2/9/2012
US 20120030602	A kit comprising a computer-readable storage medium comprising a program for producing a graphical user interface used for viewing genomic array data produced by array-based comparative genome hybridization and cytogenetic data for cytogenetic assays.	Barrett MT, Caren MP	Barrett MT, Caren MP	6/23/2006	2/2/2012
WO 2012008831	Ordering of sequence tags from part of a genome by generating clone aliquots from a genomic clone library, generating sequence tags and ordering the sequence tags based on the combined presence of sequence tags in the clone aliquots; useful for generating a physical map of part of a genome and detecting genomic variation between two samples.	Keygene (Wageningen, NL)	Michiels A, van Eijk MJT, van Oeveren AJ	7/13/2010	1/19/2012
US 20120016595	A method of transcript mapping by identifying an occurring segment from a 5' and 3' terminal tag from a transcript of a gene, and identifying feasible gene location, which has a sequence length not exceeding a predefined gene length.	Agency for Science, Technology and Research (Singapore)	Ruan Y, Sung WKK	9/13/2004	1/19/2012
WO 2010099301, US 20110311506, EP 2401376	A transposon comprising at least one hyperactive piggyBac nucleic acid sequence or its variant(s), derivative(s) or fragment(s) that retains transposon activity; useful in gene transfer systems for gene therapy, insertional mutagenesis, gene tagging and gene discovery, e.g., genome mapping.	Johns Hopkins University (Baltimore)	Craig NL	2/25/2009	9/2/2010, 12/22/2011, 1/4/2012
WO 2010091248, US 20100204921, EP 2399214	A method of selecting one or more markers associated with a trait of interest in a species of interest, comprising identifying markers associated with the trait of interest in a population of the species using a suitably programmed computer to perform genome-wide association mapping.	Syngenta Participations (Basel)	Byrum J, Clarke JDV, Guo Z, Gutierrez RLA, Kishore VK, Li M, Wang D	2/6/2009	8/12/2010, 8/12/2010, 12/28/2011
WO 2008112754, US 20080228457	A computer-accessible medium including a processing arrangement that obtains one detectable oligonucleotide probe hybridized to at least one double-stranded nucleic acid molecule cleaved with one restriction enzyme. The location of the detectable oligonucleotide probe is detected to generate a genome wide probe map.	New York University (New York)	Anantharaman T, Lim S, Mishra B	3/12/2007	9/18/2008, 9/18/2008

Source: Thomson Scientific Search Service. The status of each application is slightly different from country to country. For further details, contact Thomson Scientific, 1800 Diagonal Road, Suite 250, Alexandria, Virginia 22314, USA. Tel: 1 (800) 337-9368 (<http://www.thomson.com/scientific>).

