

1. Record Nr.	UNINA9910823391003321
Titolo	Tag-based next generation sequencing [[electronic resource] /] / edited by Matthias Harbers and Gunter Kahl
Pubbl/distr/stampa	Weinheim, : Wiley-Blackwell, c2012
ISBN	3-527-64457-1 3-527-64458-X 3-527-64477-6
Descrizione fisica	1 online resource (609 p.)
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Disciplina	572.8/633
Soggetti	Gene mapping Genomics - Methodology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	pt. 1. Tag-based nucleic acid analysis -- pt. 2. Next-generation tag-based sequencing -- pt. 3. Bioinformatics for tag-based technologies.
Sommario/riassunto	Tag-based approaches were originally designed to increase the throughput of capillary sequencing, where concatemers of short sequences were first used in expression profiling. New Next Generation Sequencing methods largely extended the use of tag-based approaches as the tag lengths perfectly match with the short read length of highly parallel sequencing reactions. Tag-based approaches will maintain their important role in life and biomedical science, because longer read lengths are often not required to obtain meaningful data for many applications. Whereas genome re-sequencing and de novo sequ