

GENETICS

# HOW TO GET CLOSER TO THE TARGET

27.11.2007 1 COMMENT

Attending last week another Illumina sequencer course, I still have the question how to enrich the target sequence. A colleague calling me this morning (thanks TB!) had a pointer to a new [nature methods](#) editorial covering three different methods- a 100-mer capture probe for each exon sized segment with the need of extremely deep resequencing and two other methods using direct hybridization of segments onto commercially oligo arrays. Aren't there any other protocols?

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## NACHTRAG

admin

20.02.2008 AT 11:46

Laborwelt 2008;9:6 has the description by a Roche employee how high density capture arrays by NimbleGen were used to enrich some 6726 exon carrying fragments of 0.5-2 Mb length that covered 660 genes. More on <http://www.nature.com/nmeth/journal/v4/n11/abs/nmeth1109.html> and <http://bioinformatics.oxfordjournals.org/cgi/content/full/22/2/134> This lead to an 400-fold enrichment of target sites.

COMMENTS ARE CLOSED.

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