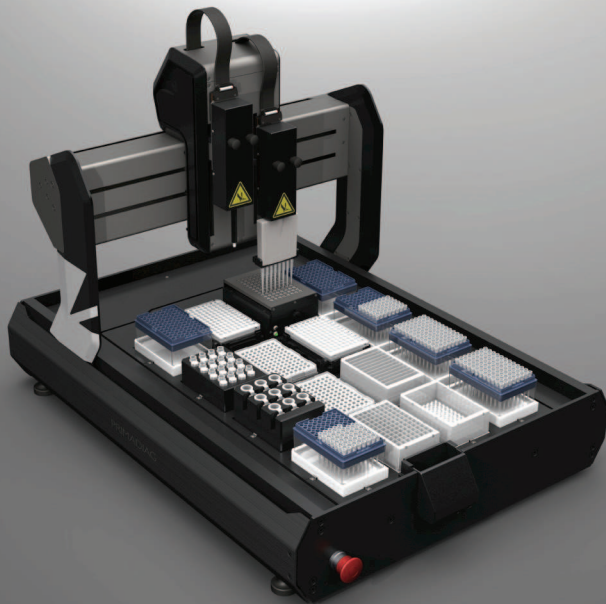# PRIMADIAG

The easiest way to automation

ACSIA NGS^Capture Edition
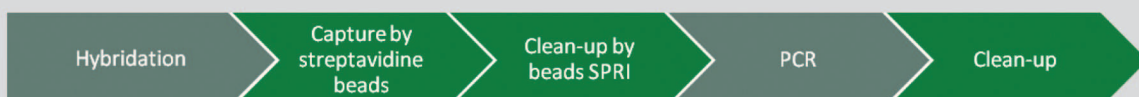
Performs from 1 to 96 samples

Save your reagents and consumables

Create a wide diversity of exome libraries at the end of the protocol

ACSIA NGS^Capture Edition allows you to **perform 48 samples without human intervention** or **96 samples with one intervention** during the target enrichment step. To do so, it operates from just after **the hybridization up through the final PCR amplification.** It is in this last step at the end of the process that a sufficient quantity of interesting fragments is obtained. Moreover, with our software and its **innovative SMT technology,** it ensures lower process costs by **reducing the quantity of tips used during your manipulations. ACSIA NGS^Capture Edition minimizes the use of your reagents and consumables** during your process and prevents waste. It also ensures minimal sample loss during treatment. At the end of your processes **ACSIA NGS^Capture Edition** offers **a greater diversity of newly created exome libraries and highly reduced process costs.**
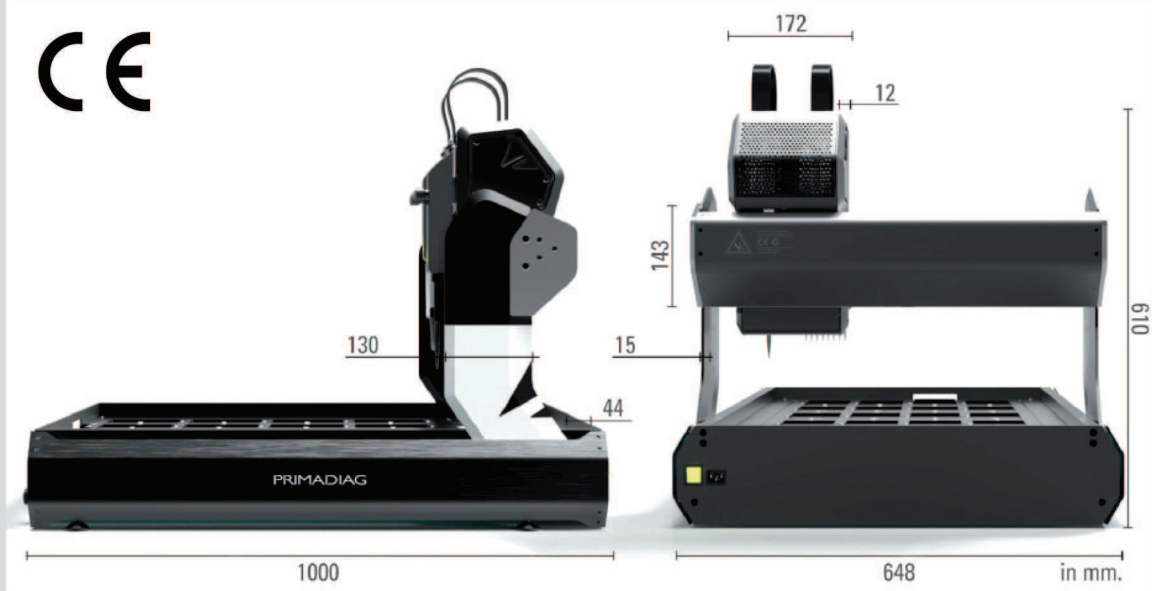
© Q.Instruments

- Magnetic Work Unit based on **our patented APIM technology (Attraction Point by Induced Magnetization)**
- Pipetting heads are **interchangeable within seconds**
- **High efficiency** automated platform managed by **innovative, smart software**
- Easy and User-Friendly programming
- Pre-programmed protocols for target enrichment step
- **Add-in our protective enclosure** for better safety during your processes
- **One of the market's best quality/price values**

PRIMACONTROLLER II

Hybridation	Capture by streptavidine beads	Clean-up by beads SPRI	PCR	Clean-up

Target Enrichment workflow

ACSIA NGS^{Capture} Edition consumes 3 tip boxes to perform 48 samples during the enrichment step whereas you will **use 16 tip boxes manually.** This edition is also **able to automate the libraries preparation** for next-generation sequencing and **offers a greater diversity of newly created exomes libraries.**

	Manual	ACSIA NGS-Capture-Edition
Couverture (%)	98,5	98,13
Alignment (%)	88,42	89,47
≥ Q30 bases (%)	84,97	85,17
Mean quality Score	33,4	33,5
Mismatch rate (%)	0,8	0,76
Number of detected SNPs	36011	35637
Number of detected insertions	1309	1287
Number of detected deletions	1352	1329

Table of results done by IntegraGen, EVRY, France
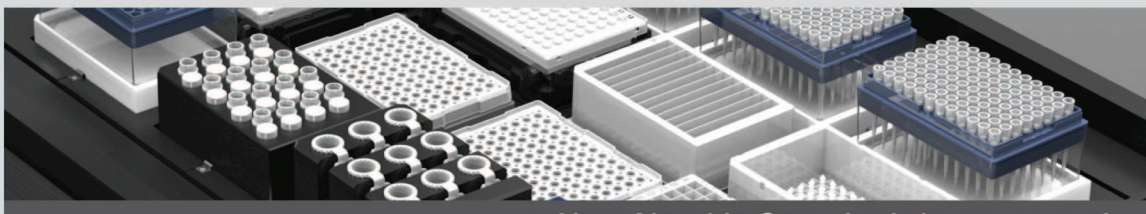
Your Need is Ours. Let's be partners !