The natural B-cell receptor repertoire is a wealth of information on the immune state of an individual.
Applications

Library analysis
- Assess germline gene representation
- Assess CDR3 diversity

Hybridoma hit expansion
- Discover clonal lineage members
- Assess germline gene usage

Natural immune response characterization
- Track clones across time and tissue
- Analyze affinity maturation
Features

- Available for rabbit, llama, alpaca, and human
- Start from tissues including bone marrow, spleen, lymph node, and blood

- Full-length variable region amplification and sequencing
- Multiple isotypes from IgH, IgK, and IgL

- Automated repertoire construction and analysis
- Full data access on the cloud

Results available in as little as 3 weeks
Stage 1
Repertoire sequencing

Starting from tissue or cells

RNA extraction

PCR amplification of variable regions

Quality filtering and adaptor trimming

Next-generation sequencing
Stage 2

Repertoire construction

Read-pair stitching

Read collapsing

Error correction

Stage 3
VDJ labeling and CDR identification

V-D-J labeling

CDR identification

Clone clustering

IGHV3-9  IGHD4  IGHJ4

IGHV3-23  IGHD1  IGHJ4

Stage 4
Repertoire analysis

Accessible through the Reptor webportal

Germline gene usage

CDR3 length distribution

Somatic hypermutation distribution

Mutations by position
Contact us for a demo!

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