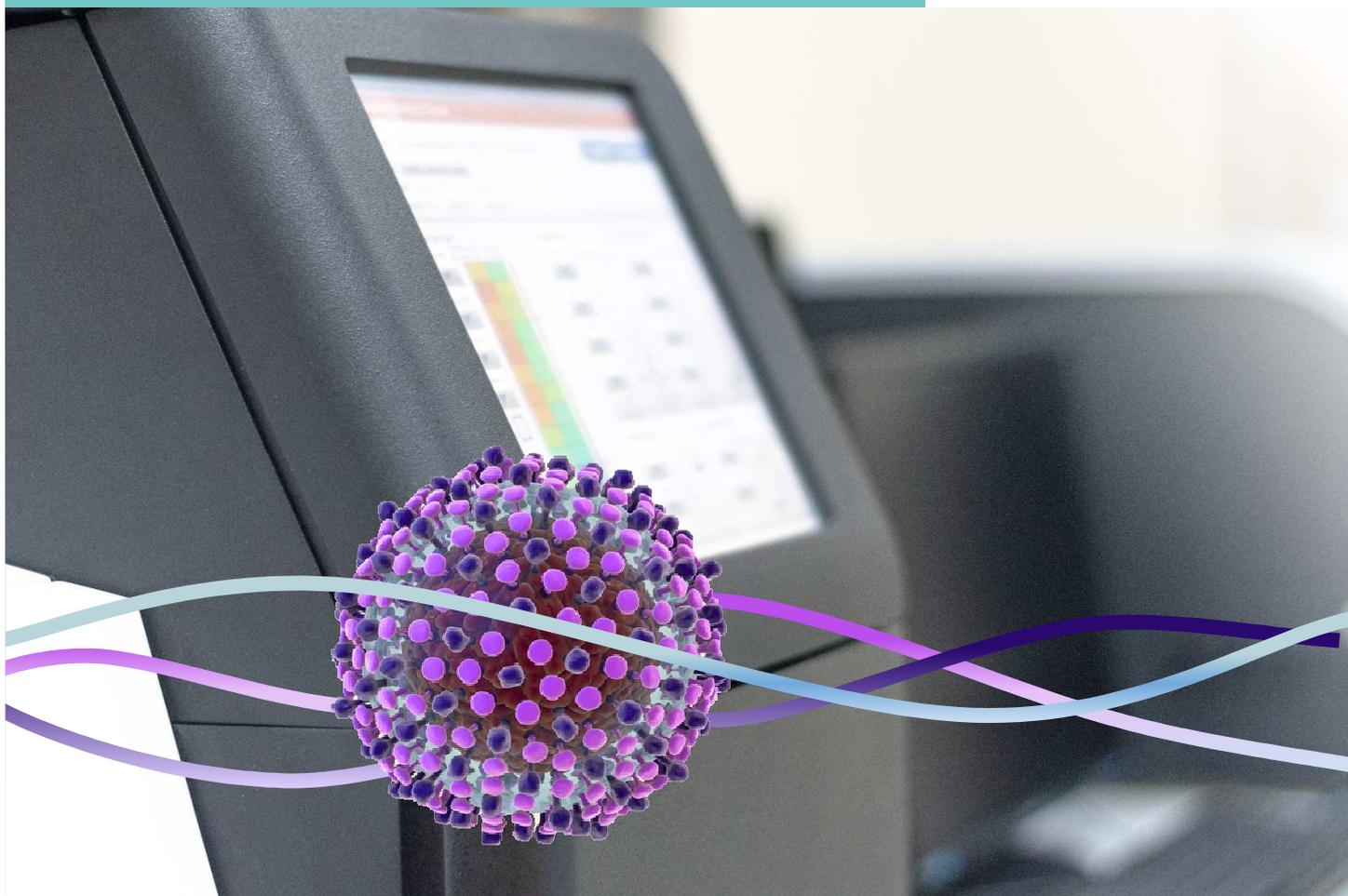


# V-Seq HCV

Kit for genotyping and detecting drug resistance associated substitution (RASs) in Hepatitis C virus, using Next Generation Sequencing (NGS)

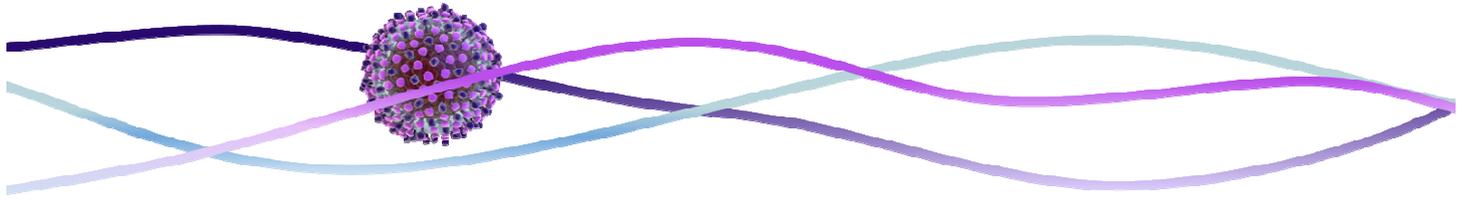


V-Seq HCV represents a relevant support for establishing a correct therapeutic approach to the treatment of HCV.

V-Seq HCV allows to identify both genotypes and presence of RASs in a single run.



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## DESCRIPTION

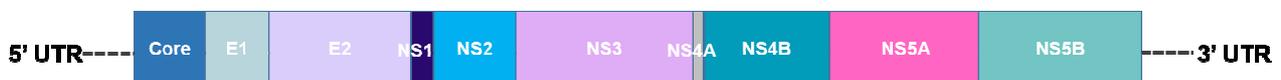
V-Seq HCV is a NGS assay that, in association with V-Seq HCV software, identifies genotypes 1-6 and detects RASs for the subtypes 1a and 1b in Hepatitis C virus as described in the latest HCV guidelines.

HCV Genotypes can respond differently to treatments, therefore HCV genotyping and RASs identification are considered crucial for a personalized therapy. The high rate of HCV genetic variability and the presence of RASs can inhibit the drug activity against target viral proteins (NS3, NS5A, NS5B). Other causes of therapeutic failure are the presence of recombinant genotypes or co-infections, not easily detected by classical genotyping methods.

V-Seq HCV kit contains all the reagents required for the target amplification and in association with the accessory kits generates NGS libraries compatible with the Illumina systems.

## V-Seq HCV TARGET GENES

Target genes	Identification
5'UTR	Genotype 1-6
Core	Genotype 1-6
NS3	RASs 1a and 1b
NS5A	RASs 1a and 1b
NS5B	Genotype 1-6 / RASs 1a and 1b

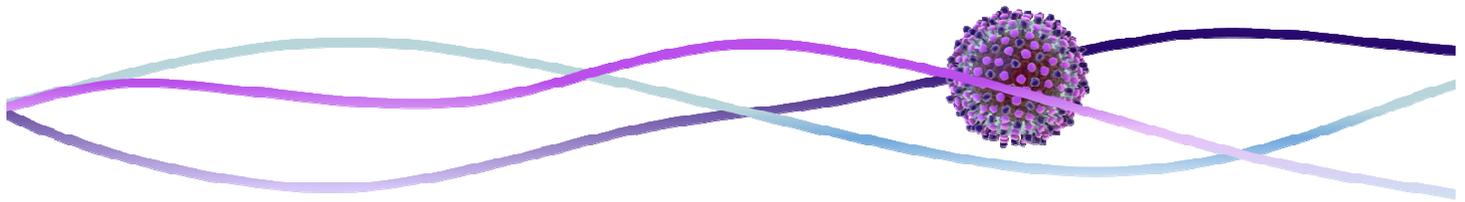


NS3, NS5A and NS5B are the target of the new antiviral drugs and the genes where the majority of RASs are localized.

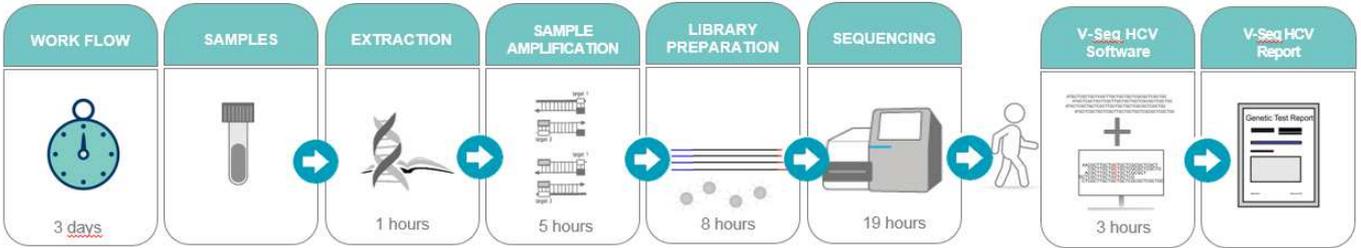
V-Seq HCV kit identifies genotypes and subtypes assessing the variability of 5'UTR, CORE and NS5B regions. The kit detects RASs for genotypes 1a and 1b through the analysis of NS3, NS5A and NS5B regions.

## SPECIFICATIONS

<b>Workflow:</b>	3 working days
<b>Starting material:</b>	Plasma and Serum
<b>Sample throughput:</b>	12 – 24 patient samples
<b>Shelf life:</b>	12 months
<b>V-Seq Software:</b>	For the bioinformatic analysis and results reporting



## PROTOCOL WORKFLOW



## COMPATIBLE INSTRUMENTS/CARTIDGES

Sequencing Platform	Cartridge	Samples (up to)
iSeq 100	iSeq 100 i1 Reagent Illumina (2x150 cycle)	24
MiSeq/MiSeqDx	MiSeq Reagent Micro Kit v2 (2x150 cycle)	24
MiSeq/MiSeqDx	MiSeq Reagent Nano Kit v2 (2x150 cycle)	12

## V-Seq HCV SOFTWARE

**Sample Result**

Sample Name: ZN4922\_10275\_A1\_1602  
 Date: 20190821-09:02:57  
 Bar: A810  
 Sample Name: ZN4922\_10275  
 Release: BQ2799-15-1801-5046  
 Identype: 1a  
 Clone Reference: H1919187180175  
 Phylogenetic analysis: From virus

**Amplicon Statistics**

Region	Base Pairs	Depth
5'UTR	95-281	373
	271-313	81
ORF2	171-761	111
	742-801	110
NS3	524-1011	376
	924-1002	371
NS5A	1471-1616	407
	1626-1810	373

**Runs**

Sample ID	Total Reads	Trimmed Reads	Mapped Reads	Filtered Reads	Genotype
Sample 1	51850	49156 (94.77%)	12911 (25.24%)	13238 (23.59%)	1a
Sample2	41500	40480 (97.52%)	10853 (26.39%)	10594 (23.25%)	6a
Sample3	270644	242370 (89.57%)	105667 (26.80%)	155106 (35.79%)	1a
Sample4	211916	217080 (102.44%)	88110 (41.58%)	85809 (21.48%)	3a
Sample5	77812	68862 (88.63%)	49251 (63.42%)	44754 (57.51%)	2a
Sample6	715484	157837 (22.06%)	107806 (24.84%)	68131 (44.51%)	4d
Sample7	61570	13674 (22.21%)	48957 (79.50%)	47694 (77.51%)	1b

V-Seq HCV Software is a proprietary software for bioinformatics analysis of sequencing results.

### Key features:

- Report including sample genotype/subtype, depth and percentage of coverage for each target region; RASs based on the latest guidelines and additional mutations for genotype 1a and 1b
- Results confirmation supported by a phylogenetic analysis
- Database for samples data storage
- Automated and user friendly data analysis
- Different user levels

## ORDER INFORMATION

Code	Product	Package
RUO-12-01	V-Seq HCV	24 tests

The device is to be used in association with the following accessory kits:

Code	Product	Package
RUO-12-20	V-Seq Library Prep	96 tests
RUO-12-21	V-Seq Library Purification	96 tests

## REFERENCES

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