



HYRAX

BIOSCIENCES

hyraxbio.com

At Hyrax Biosciences, we believe that precision medicine can, and should, be affordable for everyone. We create user-friendly, end-to-end software solutions that analyse DNA with unrivalled accuracy, reducing complex sequencing data to clear clinical reports.

Exatype (Sanger: sanger.exatype.com and NGS: exatype.com), our flagship product, currently enables analysis of HIV drug-resistance (HIVDR) data, and will soon be expanded to include drug-resistance testing for Mycobacterium tuberculosis and other pathogens.



Sanger Sequencing

Our Exatype Sanger sequencing solution combines the full WHO-recommended HIVDR data analysis method into a single, seamless step, which allows high-throughput data analysis through direct integration with the sequencing machine. Exatype Sanger uses the Stanford HIVDR algorithm for interpretation and reports can be viewed in an easy-to-use website or transferred directly to local LIMS/LIS systems.

Sample name: **S99m** | Sample ID: **527** [OPEN MAP](#)

(6) W	(7) Q	(8) R	(9) P	(10 key) P_L10	(11 key) P_V11	Reference Protein
W	Q	R	P	L	V	

T G G C A A C G A C C C C T C G T Standard
T G G C A G C G A C C C C T T G T Assembled

S99m-SeqR2 (reverse) **1**
T G G C A G C G A C C

S99m-SeqR3 (reverse) **T G G C A G C G A C**

JUMP TO LOCATION

Type a base number into the box below, and click Jump to base.

Type an amino acid number into the box below, and click Jump to amino acid.

Exatype integration of the chromatogram editing tool



Next Generation Sequencing (NGS)

The Exatype NGS solution supports the Illumina, Ion Torrent, PacBio CCS and Roche 454 sequencing platforms, and allows direct upload from sequencing machines as well as the ability to integrate with LIMS/LIS systems, thereby enabling true high-throughput use. Our software distinguishes sequencing errors, including homopolymer errors, from true mutations, enabling seamless, high-throughput analysis of full NGS plates, and mutation calling down to 1% prevalence.



HIV DRUG RESISTANCE REPORT

Sequencing Plate Information

Positive control: **Passed**

Negative control: **Passed**

Sample Name: **S5**

Exatype v2.4.3

Sequencing Platform: **Sanger**

Resistance Algorithm: **HIVdb 8.7**

Status: **Completed**

Analysis date: **2019-03-06**

● Susceptible ● Intermediate ● Resistant ● No Coverage

DRUG CLASS	DRUG	CALL ¹	MUTATIONS
NRTI	3TC	R	Mutations: [RT] L74V, [RT] Y115F, [RT] M184V
	ABC	R	
	AZT	S	
	D4T	S	
	DDI	R	
	FTC	R	
	TDF	S	
NNRTI	EFV	I	Mutations: [RT] Y181C, [RT] H221Y
	ETR	I	
	NVP	R	
	RPV	R	
	DOR	I	
PI	ATV/r	S	
	DRV/r	S	
	FPV/r	S	
	IDV/r	S	
	LPV/r	S	
	NFV	S	
	SQV/r	S	
	TPV/r	S	

¹These resistance calls are based on analysis of sequencing data and do not constitute medical advice. Further, no clinical decision should be based only on them. Please be sure to understand how these calls are made to ensure correct interpretation. For more information please view our terms and conditions at <https://sanger.exatype.com/terms-of-use> or contact us at support@hyraxbio.co.za.

Exatype HIV drug-resistance report