

# ViroScore-Suite

Integrated Medical Record and Clinical Decision Support System

**Mutation list**

Reverse transcriptase: I2I, T7P, V35T, T39A, M41L, E44D, K49R, V60I, D67N, T69D, L74\*, V90I, Q102K, K103N, K122E, D123S, C152D, S163S, E169A, K173A, Q174K, V178L, V179\*, Y181C, Q207E, L210W, R211K, T215Y, K223\*, V241V, V245G, E249D, A272P, R277K, L278L, T286A, A288T, E291D, V292I, E297A, E302E, D324D

Protease: V3I, L10I, I15V, K20R, L24I, L33F, E35D, M36I, S37N, R41K, K43\*, M46L, G46G, I50\*, I54V, R57K, Q58E, O61N, I62V, L63Q, H69\*, V75V, V82A, L89M

(\*): ambiguous codon

**Compare algorithms**

Drug	ANRS 09/03	Detroit Medical Center 01/03	Grupo de Aconselhamento Viroológico 10/03	Centre Hospitalier de Luxembourg v4.4, 02/03	Rega v5.5, 06/02
Zidovudine	R	R	R	R	R
Zalcitabine	not defined	R	R	R	R
Didanosine	R	R	R	R	R
Stavudine	R	R	R	R	R
Lamivudine	S	R	J	J	J
Abacavir	R	R	J	S	R
Tenofovir	R	R	R	R	J
Nevirapine	R	R	R	R	R
Delavirdine	not defined	R	R	R	R
Etravirenz	R	R	R	R	R
Indinavir	R	R	R	R	R
Saquinavir*	R	J	R	J	R
Ritonavir	R	R	R	R	R
Nelfinavir	J	R	R	J	R
Amprenavir*	R	R	R	R	R
Lopinavir	R	J	R	R	R
Atazanavir	R	S	R	R	R
Tipranavir*	S	not defined	not defined	I	not defined

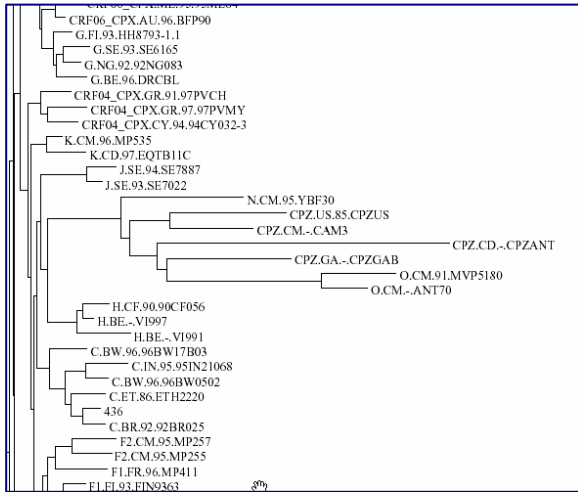
Legend: ■ Susceptible ■ Possible resistance ■ Resistance

**Reported resistance mutations**

NRTI: M41L, E44D, D67N, T69D, L74\*, L74V\*, L210W, T215Y  
 NNRTI: K103N, V179\*, Y181C  
 PI: L10I, I15V, K20R, L24I, L33F, E35D, M36I, R41K, K43T\*, M46L, I50\*, I50V\*, I54V, Q58E, I62V, V82A, L89M

(\*): ambiguous codon

ViroScorer resistance data report



Subtype characterization using phylogenetic analysis

mutation	number	%	zdv	ddc	ddi	3tc	d4t	abc	tdf
M41L	92	24.9							
E44D	23	6.2							
A62V	6	1.6							
K65R	3	0.8							
D67N	89	24.1							
T69D	24	6.5							
I15S69	3	0.8							
K70R	61	16.5							
L74V	18	4.9							

Real time table of IAS-USA experts' group mutations list for selected sequences in the database

About the ViroScore Suite:

ViroScore Suite is a HIV resistance system (interpretation and subtyping) with a sequence database and built in analysis and reporting tools.

Who is using the ViroScore Suite:

The ViroScore Suite is used by virologists and clinical experts in the field of HIV resistance:

- By Reference laboratories performing HIV resistance testing
  - Better sequence management
  - More advanced resistance reporting
- By the EU Spread trial ([www.spread-europe.org](http://www.spread-europe.org))
  - 4000 naïve patient sequences
  - Real-time interpretation and subtyping
  - Sharing information between European Centers
- By pharmaceutical companies to gather clinical cohort and drug utilization data
- By researchers to collect, manage and analyze their patient sequence data and link it to clinical information

Why they are using it:

- Resistance reports are often difficult to understand and use properly
- Trained clinicians can relate mutations to drugs and clinical patient data.
- Straight forward color coding
- Listing of relevant mutations
- Virologists and physicians need accurate, up to date tools to manage HIV infection
- Standard genotypic assay provide only one test interpretation based on a single expert group. ViroScorer offers 5 algorithms for resistance interpretation from opinion leader groups throughout the world.

*"I 'm impressed by the technology ABL developed, robust and efficient, having the patients as the central focus point of this plat form technology... as it is used already in the last 12 months to support successfully the enrolment of 500 patients from 16 European countries in SPREAD."*

- Charles Boucher, the Spread Project coordinator.

**Algorithms**

Desired algorithms:

- ANRS
- Detroit Medical Center
- Grupo de Aconselhamento Viroológico
- Centre Hospitalier de Luxembourg
- Rega institute

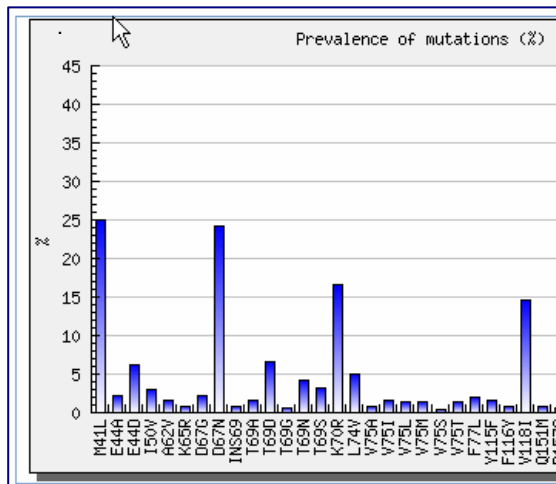
Include quality control process

Include PDF report generation

Include phylogenetic-based subtype characterization

Include Retrogram format generation

Previous Next Clear



**Corresponding graphic based on selected mutations patterns**

Class	Group	Previous treatment	Current treatment
EE-GP41	120	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	nrv	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	dv	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	efv	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	zfv	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	dsu	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	ddi	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	dai	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	3tc	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	efv	<input type="checkbox"/>	<input type="checkbox"/>
NNRTI	138	<input type="checkbox"/>	<input type="checkbox"/>
PI	14u	<input type="checkbox"/>	<input type="checkbox"/>
PI	13n	<input type="checkbox"/>	<input type="checkbox"/>
PI	rtv	<input type="checkbox"/>	<input type="checkbox"/>
PI	rfv	<input type="checkbox"/>	<input type="checkbox"/>
PI	apv	<input type="checkbox"/>	<input type="checkbox"/>
PI	1p v	<input type="checkbox"/>	<input type="checkbox"/>
PI	162	<input type="checkbox"/>	<input type="checkbox"/>
PI	13v	<input type="checkbox"/>	<input type="checkbox"/>

**HIVLib Search on database matches using clinical and resistance data**

**The ViroScore Features:**

**ViroScorer or the HIV Resistance Assay Interpretations :**

- 16 marketed anti-HIV drugs are interpreted
- 5 international, up to date public algorithms from HIV resistance experts groups
- 3 coding regions of interest
  - Reverse transcriptase
  - Protease
  - gp 41 (soon gp 120)
- Upload sequence data using FASTA or other formats
- Fully compatible with TruGene® (Bayer) and ViroSeq® (Applied BioSystems) assays: just load the sequences
- Or introduce multiple mutations when full sequences are not available
- Embedded subtype characterization

**Sequence Database:**

- Storage of sequences as raw data
- Automated mutation detection
- Automated updating of viral resistance interpretations over time and generated by successive algorithm releases
- Quality control check on sequences
- Sequence contamination detection tool

**EpiVisor:**

- Real time prevalence of main HIV mutations in your patient population
- IAS-USA expert group mutation list to be displayed
- Easy to use interface for selecting mutation patterns
- Automated graphic display of selected mutations

**HIVLib:**

- Link clinical and resistance data
- Easy to use query tools
- No need to know SQL or other programming language
- Search for sequences and display in Fasta format

**Customization :**

- Automated:
  - From 1 to 5 algorithms can be displayed
  - Subtype characterization method (homology or phylogenetic analysis)
  - Email the resistance data report in PDF format
- Services:
  - Compute other algorithms
  - Adapt the resistance data report for local settings
  - Upload of a large sequences files or databases

**Import and Export Functionality:**

- Upload in batch all your previously performed HIV sequences
- Import data in multiple formats
- Export data to a structured XML format
- 7 algorithms available in the XML export
- Link to laboratory data systems

For more information, please visit our websites at [www.therapyedge.com](http://www.therapyedge.com) and [www.ablsa.com](http://www.ablsa.com)