

# HIV-1 subtyping

## 1- Use of HIV BLAST :

[http://www.hiv.lanl.gov/content/sequence/BASIC\\_BLAST/basic\\_blast.html](http://www.hiv.lanl.gov/content/sequence/BASIC_BLAST/basic_blast.html)

Sequences should be in a FASTA format

NB : It is important to respect the ">" symbol before the name of the sequence. Avoid any spaces in the name of the sequence.

Example :

>U455

```
ATGGGTGCGAGAGCGTCAGTATTAAGCGGGAAAAAATTAGATTCATGGGA
GAAAATTCGGTTAAGGCCAGGGGGAAACAAAAATATAGACTGAAACATT
TAGTATGGGCAAGCAGGGAGCTGGAAAAATTCACACTTAACCCTGGCCTT
TTAGAAACAGCAGAAGGATGTCAGCAATACTGGGACAATTACAACCAGC
TCTCCAGACAGGAACAGAAGAACTTAGATCATTATATAATACAGTAGCAG
```

## HIV BLAST

**Purpose:** Find the HIV database sequences most similar to your query(s).

### Input

Paste your sequence(s)  
[\[Sample Input\]](#)

or upload a file  Aucun fichier sélectionné.

or enter accession number(s)

### Options

Output style  [See examples.](#)

Number of BLAST matches to display

Run BLAST against   
all subtyped sequences  
subtype A

or a background set of sequences you upload  
 Aucun fichier sélectionné.

E-mail  Always email results

Show location of match in genome  Only matters for nucleotide input; **unchecked to speed the job**

After clicking "Submit", the result will be returned to you in this form

Query: U455

Download sequences fasta Align NCBI Blast Result Geography

Download	Accession	Name	Subtype	Country	Year	Description	Score	E value	Identities	Location of match in genome
<input type="checkbox"/>										
<input checked="" type="checkbox"/>	<a href="#">M62320</a>	U455_U455A	A1	UG	1985	Human immunodeficiency virus type 1 Ugandan isolate U455, complete proviral genome	<a href="#">374</a>	3e-102	250/250 (100%)	
<input checked="" type="checkbox"/>	<a href="#">EF164134</a>	ML274_16_10_97b_2	A1	KE	1997	HIV-1 isolate ML274-16.10.97b(2) from Kenya gag protein (gag) gene, partial cds	<a href="#">325</a>	1e-87	237/250 (95%)	
<input checked="" type="checkbox"/>	<a href="#">EF164133</a>	ML274_16_10_97b	A1	KE	1997	HIV-1 isolate ML274-16.10.97b from Kenya gag protein (gag) gene, partial cds	<a href="#">325</a>	1e-87	237/250 (95%)	
<input checked="" type="checkbox"/>	<a href="#">GQ429919</a>	clone_55	A1	KE	1995	HIV-1 clone 55 from Kenya gag protein (gag) gene, complete cds	<a href="#">323</a>	4e-87	236/249 (95%)	
<input checked="" type="checkbox"/>	<a href="#">EF164490</a>	ML1138_13_12_94_2	A1	KE	1994	HIV-1 isolate ML1138-13.12.94(2) from Kenya gag protein (gag) gene, partial cds	<a href="#">323</a>	4e-87	236/249 (95%)	
<input checked="" type="checkbox"/>	<a href="#">KR781623</a>	ML0313.1988	A1	KE	1988	HIV-1 clone ML0313_1 from Kenya gag protein (gag) and pol protein (pol) genes, partial cds	<a href="#">323</a>	4e-87	236/249 (95%)	
<input checked="" type="checkbox"/>	<a href="#">EF164489</a>	ML1138_13_12_94	A1	KE	1994	HIV-1 isolate ML1138-13.12.94 from Kenya gag protein (gag) gene, partial cds	<a href="#">323</a>	4e-87	236/249 (95%)	
<input checked="" type="checkbox"/>	<a href="#">EF164149</a>	ML313_13_5_96	A1	KE	1996	HIV-1 isolate ML313-13.5.96 from Kenya gag protein (gag) gene, partial cds	<a href="#">320</a>	3e-86	235/249 (94%)	
<input checked="" type="checkbox"/>	<a href="#">EF164492</a>	ML1138_21_9_95_2	A1	KE	1995	HIV-1 isolate ML1138-21.9.95(2) from Kenya gag protein (gag) gene, partial cds	<a href="#">320</a>	3e-86	235/249 (94%)	
<input checked="" type="checkbox"/>	<a href="#">EF164171</a>	ML361_6_8_87	A1	KE	1987	HIV-1 isolate ML361-6.8.87 from Kenya gag protein (gag) gene, partial cds	<a href="#">320</a>	3e-86	235/249 (94%)	

## 2-Use of REGA HIV-1 subtyping tool-version 3.0 :

<http://dbpartners.stanford.edu:8080/RegaSubtyping/stanford-hiv/typingtool/>

Sequences should be in a FASTA format

Paste into the window your nucleotide sequence in the following format (format "fasta")

```
>IDsequence  
ccaattagtcctattgacact....
```

**Sequences**

**FASTA Input**  
Paste your sequence(s) in the input field in FASTA format or upload a FASTA file.

>IDsequence  
ccaattagtcctattgacact....

Choose File No file chosen

RESET ANALYZE

After clicking "ANALYZE" you switch on this page (the analysis can sometimes take several minutes):

You may bookmark this page to revisit these results later.

Analysis in progress... (Showing partial results).

This page will be automatically updated every 5 seconds... [Cancel job](#)

[Submit analysis](#)

[How to cite](#)

[Tutorial](#)

[Decision trees](#)


[Subtyping process](#)

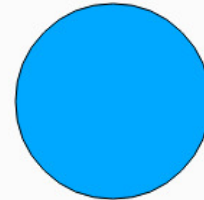
[Example sequences](#)

[Contact us](#)

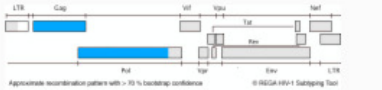
## The result will be returned to you in this form

### Summary

Rega Assignment	Number of sequences	Percentage	Legend
<a href="#">HIV-1 Subtype B</a>	1	100%	
<i>Total</i>	1	100%	



You may bookmark this page to revisit these results later.

Name	Length	Report	Assignment	Support	Genome
AF033819 AF033819	4080	<a href="#">Report</a>	HIV-1 Subtype B	100.0	

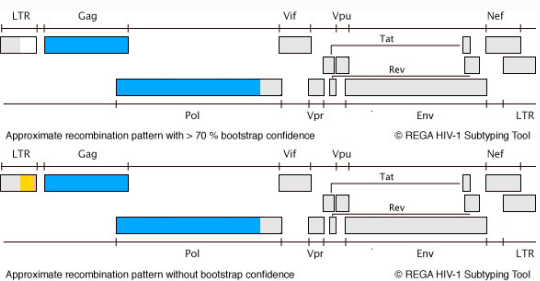
Download results: [Table \(Excel format\)](#) [Table \(CSV format\)](#) [XML File](#) [Sequences \(Fasta format\)](#)

- You have the possibility of obtaining a detailed report especially for complex recombinant after clicking on "report"

**Sequence Assignment**

Name: AF033819|AF033819    Length: 4080

Assignment: HIV-1 Subtype B    Bootstrap: 100.0%



Legend:

- A
- B
- C
- D
- F
- G
- H
- J
- K
- < 70%
- NA

Your sequence starts at position 454 and finishes at position 4534 relative to the reference sequence.

Motivation: Subtype assigned based on sequence > 800 bps clustering with a pure subtype and CRF or sub-subtype with bootstrap > 70% without recombination in the bootscan.

**Be careful : Subtype for short sequences are often NA (not available)**

You can find the subtype results in several forms:

Download results: [Table \(Excel format\)](#) [Table \(CSV format\)](#) [XML File](#) [Sequences \(Fasta format\)](#)

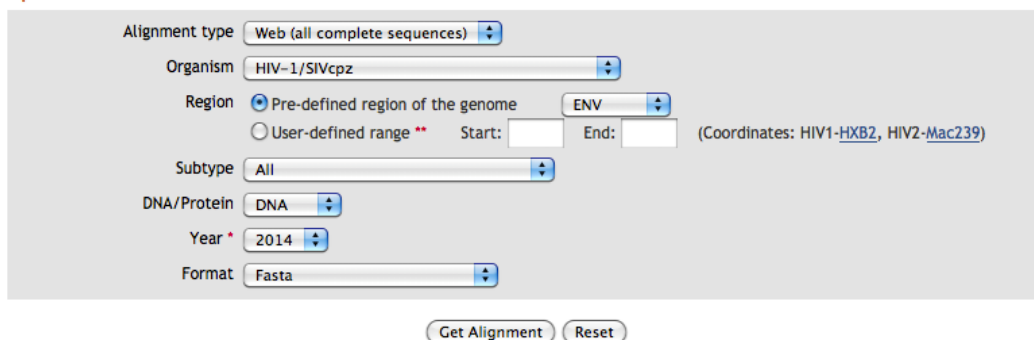
### 3-Phylogenetic tree:

You can download a set of reference sequences.

<http://www.hiv.lanl.gov/content/sequence/NEWALIGN/align.html>

You can choose the entire genome sequences or select a portion of the genome (ENV, POL ...)

#### Options



The screenshot shows a web form for selecting HIV-1/SIVcpz sequences. The form includes the following fields and options:

- Alignment type:** Web (all complete sequences)
- Organism:** HIV-1/SIVcpz
- Region:** Pre-defined region of the genome (selected), ENV (dropdown menu). Below this, there are radio buttons for "User-defined range \*\*" with "Start:" and "End:" input fields, and a note "(Coordinates: HIV1-HXB2, HIV2-Mac239)".
- Subtype:** All
- DNA/Protein:** DNA
- Year \*:** 2014
- Format:** Fasta

At the bottom of the form are two buttons: "Get Alignment" and "Reset".