



HIV sequence database

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Intra-patient Sequence Search

Purpose

This interface retrieves sets of sequences containing more than N sequences per patient.

Tips

- Click or mouse over the field name for specific tips.
- Before using, please read [About the intra-patient search interface](#).

Restrictions

- ☐ [Longitudinal](#) samples only
- ☐ Known [timeline](#)
 - ☐ Known time since [start/end of treatment](#)
 - ☐ Known time since [infection/seroconversion](#) OR [Fiebig stage](#)
 - ☐ Known [sampling year](#)
 - ☐ Known number of [days since first sample](#)
- ☒ [Untreated only](#) ☐ [Treated only](#) ☐ [Report treatment status in output](#)

Search for

[Sets containing at least](#) sequences per patient

[Author last name](#)

[PubMed ID](#)

<u>Project name</u>	<div>Any ACTG 229 ACTG 359 ACTG 5211 ACTG 5241</div>		
<u>Organism</u>	<div>Any HIV-1 HIV-2 SIV</div>	<u>Subtype</u>	<div>Any no subtype A A1 A2 B</div>
<u>Genomic region</u>	<div>Any complete genome 5' LTR 5' LTR R 5' LTR U3 5' LTR U5 TAR Gag-Pol Gag p17 (matrix) p24 (capsid) p7 (nucleocapsid) p6 Pol CDS</div>	Or define <u>start</u> <input type="text" value="2253"/> and <u>end</u> <input type="text" value="3869"/> <input checked="" type="checkbox"/> Include fragments of minimum length <input type="text" value="100"/>	
<div>SearchReset</div>			

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Questions or comments? Contact us at seq-info@lanl.gov.