|  |  |  |  |
| --- | --- | --- | --- |
| **PATIENT DETAILS:**  **Name of the patient** | : XXX | **Reporting Date/Time** | : 22-04-2022; 15:46 |
| **Age** | : 24 YEARS | **Gender** | : MALE |
| **Referred by** | : DR ALOK VASHISHTHA | **Lab Code** | : WIP001 |

**TEST SAMPLE DETAILS:**

|  |  |
| --- | --- |
| **Type of clinical sample** | : EDTA PLASMA |
| **Sample received Date/Time** | : 11-04-2022; 12:15 |
| **Assay Code** | : **gDRI (GBL-17)** |

**Report**

# Summary Data

Sequence includes PR: codons 1 - 99 Sequence includes RT: codons 1 - 388 [Subtype:](https://hivdb.stanford.edu/page/hiv-subtyper/) C (95.35%)

# Technology

Reverse Transcription mediated Polymerase chain reaction and Automated DNA sequencing.

# Drug Resistance Interpretation: PR

PI Major Resistance Mutations: None

PI Accessory Resistance Mutations: None

Other Mutations: T12S, L19I, M36I, R41K, D60E, L63P, H69K, I93L

|  |  |
| --- | --- |
| **Protease Inhibitors** | |
| **atazanavir/r (ATV/r)** | Susceptible |
| **darunavir/r (DRV/r)** | Susceptible |
| **fosamprenavir/r (FPV/r)** | Susceptible |
| **indinavir/r (IDV/r)** | Susceptible |
| **lopinavir/r (LPV/r)** | Susceptible |
| **nelfinavir (NFV)** | Susceptible |
| **saquinavir/r (SQV/r)** | Susceptible |
| **tipranavir/r (TPV/r)** | Susceptible |

# PR Comments

None

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Mutation Scoring: PR** | | | | | | | | |
| **PI** | **ATV/r** | **DRV/r** | **FPV/r** | **IDV/r** | **LPV/r** | **NFV** | **SQV/r** | **TPV/r** |
| Total | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

# Drug Resistance Interpretation: RT

NRTI Resistance Mutations: None NNRTI Resistance Mutations: None

Other Mutations:K11Q, V35T, T39S, V60I, D121H, K122E, I142T, K173T, Q174R, D177E, I178L, G196E, T200A, Q207E, V245K, A2 72P, V276I, E291D, V292I, I293V, G335D, P345T, R356K, M357R, G359A, S379C

|  |  |
| --- | --- |
| **Nucleoside Reverse Transcriptase Inhibitors** | |
| **abacavir (ABC)** | Susceptible |
| **zidovudine (AZT)** | Susceptible |
| **stavudine (D4T)** | Susceptible |
| **didanosine (DDI)** | Susceptible |
| **emtricitabine (FTC)** | Susceptible |
| **lamivudine (3TC)** | Susceptible |
| **tenofovir (TDF)** | Susceptible |

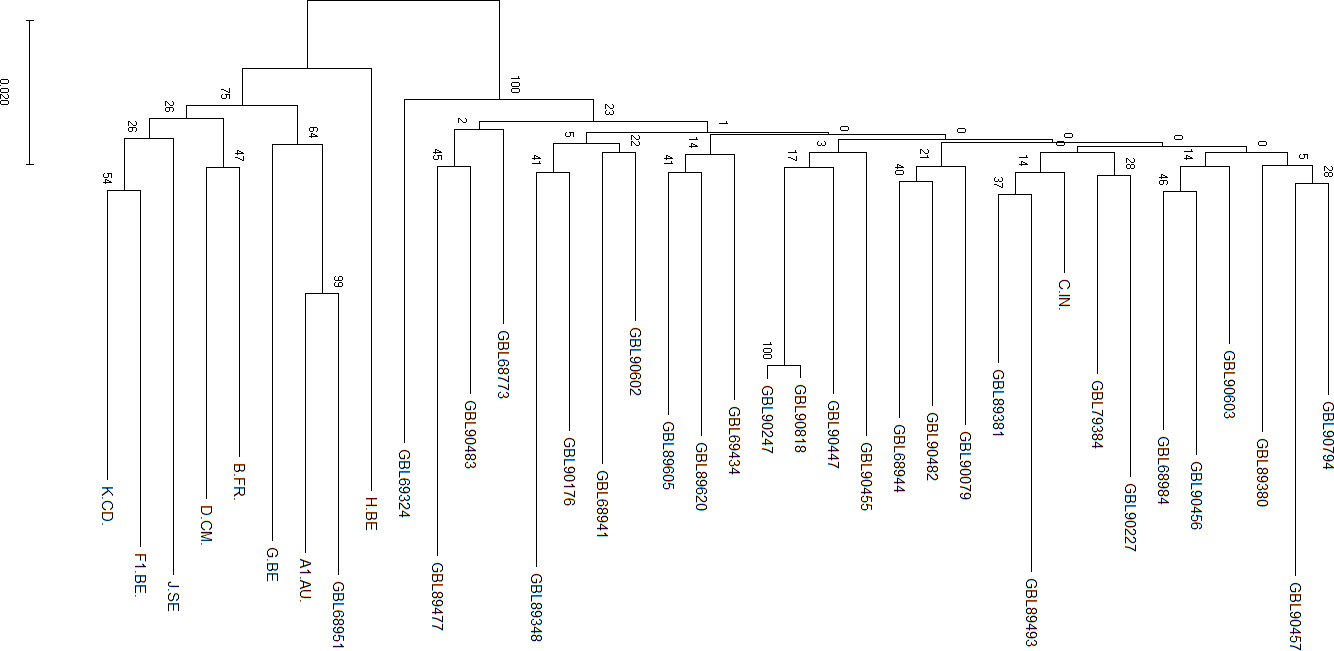
|  |  |
| --- | --- |
| **Non-nucleoside Reverse Transcriptase Inhibitors** | |
| **doravirine (DOR)** | Susceptible |
| **efavirenz (EFV)** | Susceptible |
| **etravirine (ETR)** | Susceptible |
| **nevirapine (NVP)** | Susceptible |
| **rilpivirine (RPV)** | Susceptible |

# RT Comments

None

# Mutation Scoring: RT

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **NRTI** | **ABC** | **AZT** | **D4T** | **DDI** | **FTC** | **3TC** | **TDF** |
| Total | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NNRTI** | **DOR** |  | **EFV** | **ETR** | **NVP** |  | **RPV** |
| Total | 0 |  | 0 | 0 | 0 |  | 0 |



**Phylogenetic Analysis to Verify Sequence Purity and Subtype Similarity**

Fig.1. The phylogenetic tree of the test sample **(GBL90818)** with the different HIV-1 subtype reference sequences and recent

test samples sequences. The numbers at the node represent the percent bootstrap support for 500 replicates. Bars at the base of the tree show genetic divergence. Description of Phylogeny: Subtype/Sample name; Sample: (Subtype C)

***Disclaimers:*** *‡The report represents only the specimen received in laboratory. ‡ PCR is a sensitive method, inconclusive and indeterminate results may be obtained due to presence of PCR inhibitory factors in the sample. Poor quality sample, delayed logistics and improper temperature conditions while sample transportation can affect the test results.*

|  |
| --- |
| *Interpretation algorithm: HIVdb Stanford.* |
| *This test has been developed at geneOmbio Technologies Pvt Ltd, Pune and its performance characteristics have been verified.* |
| *HIV-1 drug resistance interpretation assay from geneOmbio Technologies has successfully qualified EQAS from TreatAsia Bangkok ten*  *times since 2007.* |

-End of the report-