



# QUALITY CONTROL for MOLECULAR DIAGNOSTICS

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**Cyprus**

**Lab Code: CY002**

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Dear Dr Leondios Kostrikis,

## QCMD 2008 ENVA8 HIV Drug Resistance Typing EQA Programme

Thank you for participating in this EQA Programme. Details of the panel characteristics and composition are shown below:

- The ENVA8 panel was based on characterised and cultured HIV virions diluted in HIV, HBV and HCV negative plasma.
- The ENVA8 panel contained various HIV subtypes:

Sample	Matrix <sup>1</sup>	Subtype	Release testing <sup>2</sup> Lyophilised samples Viral load (copies/ml)
ENVA8-01	Citrate Plasma	G	6.57 x 10 <sup>3</sup>
ENVA8-02	Citrate Plasma	C	2.63 x 10 <sup>4</sup>
ENVA8-03	Citrate Plasma	B	4.68 x 10 <sup>3</sup>
ENVA8-04	Negative Plasma	Negative	
ENVA8-05*	Citrate Plasma	C	1.51 x 10 <sup>4</sup>

1: All samples were diluted in HIV, HBV and HCV negative citrate plasma and lyophilised prior to distribution.

2: Release testing was performed using the Roche HIV-1 Monitor Test.

\* Two insertions (67-69) in Reverse transcriptase.

The data presented in this report shows the following for each of the panel samples:

- All codons considered BEING associated with HIV-1 drug resistance (according to the IAS-USA Drug Resistance table 2008).
- The consensus sequence at IAS codons containing a mutation.
- YOUR laboratory's result at all IAS codons.

Your personal performance score was 266. The maximum score achievable was 266. The full details of the scoring system and a full analysis of test results from all centres is provided in the final report.

If you have any queries concerning this programme, please contact the QCMD Neutral Office.

Yours faithfully,

**Dr Anton Van Loon, QCMD Executive Co-ordinator**

The QCMD programme is organised in collaboration with the European Society for Clinical Virology and the European Society for Clinical Microbiology & Infectious Diseases.



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The Protease and Reverse Transcriptase gene codons presented are those associated with clinical resistance to HIV. Information on these codons was published by the International AIDS Society-USA Drug Resistance Group (IAS) in the following article: Johnson VA et al. Update of the Drug Resistance Mutations in HIV-1: Spring 2008. Topics in HIV Medicine 2008: 16(1); 62 – 68.

**1) Results of the Protease drug mutation codon identification for CY002:**

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA8 -01	Your Result	ENVA8 -02	Your Result	ENVA8 -03	Your Result	ENVA8 -05	Your Result
		CS <sup>3</sup>	-01	CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-05
PR-10	CTC	CTA	CTA	TTT	TTT	ATC	ATC		CTC
PR-11	GTC		GTC		GTC		GTC		GTC
PR-13	ATA	GTA	GTA		ATA	GTA	GTA		ATA
PR-16	GGG		GGG	GAG	GAG		GGG		GGG
PR-20	AAG	ATA	ATA		AAG		AAG	AAA	AAA
PR-24	TTA		TTA		TTA		TTA		TTA
PR-30	GAT		GAT	AAC	AAC		GAT		GAT
PR-32	GTA		GTA		GTA		GTA		GTA
PR-33	TTA	TTG	TTG	CTA	CTA		TTA		TTA
PR-34	GAA		GAA		GAA		GAA		GAA
PR-35	GAA	GAC	GAC	GAC	GAC	GAC	GAC		GAA
PR-36	ATG	ATA	ATA	GTA	GTA	ATA	ATA	ATA	ATA
PR-43	AAA		AAA		AAA		AAA		AAA
PR-46	ATG		ATG		ATG	ATA	ATA		ATG
PR-47	ATA		ATA		ATA		ATA		ATA
PR-48	GGG		GGG	GGA	GGA		GGG	GGA	GGA
PR-50	ATT		ATT		ATT		ATT	ATA	ATA
PR-53	TTT		TTT		TTT		TTT		TTT
PR-54	ATC		ATC		ATC	GTC	GTC		ATC
PR-58	CAG		CAG		CAG		CAG	CAA	CAA
PR-60	GAT		GAT		GAT		GAT	GAG	GAG
PR-62	ATA		ATA	GTA	GTA	GTA	GTA		ATA
PR-63	CTC	CTT	CTT	CTT	CTT	CCC	CCC	CCT	CCT
PR-64	ATA		ATA		ATA		ATA		ATA
PR-69	CAT	AAA	AAA	AAA	AAA		CAT	AAA	AAA
PR-71	GCT		GCT		GCT	ACT	ACT	GCA	GCA
PR-73	GGT	GGG	GGG	GGC	GGC		GGT		GGT
PR-74	ACA		ACA	TCA	TCA		ACA		ACA
PR-76	TTA		TTA		TTA		TTA		TTA
PR-77	GTA	RTA	RTA		GTA		GTA	GTG	GTG
PR-82	GTC	ATC	ATC		GTC	GCC	GCC		GTC
PR-83	AAC		AAC		AAC		AAC		AAC
PR-84	ATA		ATA		ATA		ATA		ATA
PR-85	ATT		ATT		ATT		ATT		ATT
PR-88	AAT		AAT	GAT	GAT		AAT	AAC	AAC
PR-89	CTG	ATG	ATG	ATG	ATG		CTG	ATG	ATG
PR-90	TTG		TTG		TTG	ATG	ATG		TTG
PR-93	ATT		ATT	CTT	CTT	CTT	CTT	CTT	CTT

1. PR = Protease.      2. WT = Wild-type sequence pNL4-3.

The consensus sequence (CS) was created from the sequences submitted by all participating laboratories. An empty box signifies that the consensus sequence was in agreement with the wild type sequence pNL4-3. Panel sample ENVA8-04 was not considered in this analysis as it was a panel sample negative for HIV-1.

## 2) Results of the Reverse Transcriptase drug mutation codon identification for CY002:

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA8 -01	Your Result	ENVA8 -02	Your Result	ENVA8 -03	Your Result	ENVA8 -05	Your Result
		CS <sup>3</sup>	-01	CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-05
RT-41	ATG		ATG	TTG	TTG		ATG		ATG
RT-62	GCC		GCC		GCC		GCC		GCC
RT-65	AAA		AAA	AAG	AAG		AAA	AAG	AAG
RT-67	GAC		GAC	AAC	AAC		GAC	AAC	AAC
67-68	INSERT							TCT	TCT
68-69	INSERT							GAG	GAG
RT-69	ACT		ACT	GAT	GAT		ACT	TCT	TCT
RT-70	AAA		AAA	AAG	AAG		AAA	AAG	AAG
RT-74	TTA		TTA		TTA		TTA		TTA
RT-75	GTA		GTA		GTA		GTA		GTA
RT-77	TTC	TTT	TTT	TTT	TTT		TTC		TTC
RT-90	GTT	GTC	GTC		GTT		GTT		GTT
RT-98	GCA	GCG	GCG	GGA	GGA		GCA		GCA
RT-100	TTA		TTA		TTA		TTA		TTA
RT-101	AAA		AAA		AAA		AAA	GAG	GAG
RT-103	AAA		AAA		AAA		AAA		AAA
RT-106	GTA		GTA	GTG	GTG		GTA	ATG	ATG
RT-108	GTA		GTA		GTA		GTA		GTA
RT-115	TAT		TAT		TAT		TAT		TAT
RT-116	TTT		TTT		TTT		TTT		TTT
RT-151	CAG		CAG		CAG		CAG		CAG
RT-179	GTC	GTG	GTG	GTT	GTT	GTT	GTT		GTC
RT-181	TAC	TAC	TAC		TAT		TAT		TAT
RT-184	ATG		ATG	GTA	GTA		ATG		ATG
RT-188	TAT		TAT		TAT		TAT		TAT
RT-190	GGA		GGA		GGA		GGA	GCA	GCA
RT-210	TTG		TTG	TGG	TGG		TTG	TGG	TGG
RT-215	ACC		ACC	TAC	TAC		ACC	TAC	TAC
RT-219	AAA		AAA	AAG	AAG		AAA	AAG	AAG
RT-225	CCT		CCT	CCC	CCC		CCT	CCC	CCC

1. RT = Reverse Transcriptase.

2. WT = Wild-type sequence pNL4-3.

The consensus sequence (CS) was created from the sequences submitted by all participating laboratories. An empty box signifies that the consensus sequence was in agreement with the wild type sequence pNL4-3. Panel sample ENVA8-04 was not considered in this analysis as it was a panel sample negative for HIV-1.

**Genotypic mixtures are indicated using the IUB nucleotide ambiguity code system.**

IUB Code	K	M	R	S	W	Y	B	D	H	V	N
Mixture of	G or T	A or C	A or G	G or C	A or T	C or T	C, G or T	A, G or T	A, C or T	A, C or G	Any Base