



# QUALITY CONTROL for MOLECULAR DIAGNOSTICS

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Lab Code: CY002

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Dear Dr Leondios Kostrikis,

## QCMD 2007 ENVA7 HIV Drug Resistance Typing Proficiency Programme

Thank you for participating in the QCMD 2007 ENVA7 HIV Drug Resistance Typing Proficiency Programme. Details of the panel characteristics and composition are shown below:

- The ENVA7 panel was based on characterised and cultured HIV-1 virions diluted in HIV, HBV and HCV negative plasma.
- The ENVA7 panel contained various HIV-1 subtypes:

Sample	Matrix <sup>1</sup>	Subtype	Viral load (copies/ml) <sup>2</sup>	
			Pre-lyophilisation	Post-lyophilisation
ENVA7-01	Citrate Plasma	C	2.6 x 10 <sup>4</sup>	1.18 x 10 <sup>4</sup>
ENVA7-02*	Citrate Plasma	C	4.68 x 10 <sup>4</sup>	9.2 x 10 <sup>3</sup>
ENVA7-03	Citrate Plasma	B	4.6 x 10 <sup>3</sup>	3.29 x 10 <sup>3</sup>
ENVA7-04	Citrate Plasma	B	3 x 10 <sup>4</sup>	1.76 x 10 <sup>4</sup>
ENVA7-05	Citrate Plasma	F	2.6 x 10 <sup>4</sup>	2.23 x 10 <sup>4</sup>

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

2. In-process quantitative analysis performed using the Roche HIV-1 Monitor Test.

\* 6 bp insertion present after codon 67 of RT

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 2007).
- The consensus sequence at IAS codons containing a mutation.
- YOUR laboratory's result at all IAS codons.

Your personal performance score was **330**. The maximum score achievable was **332**. 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: 2007. Topics in HIV Medicine 2007; 15(4); 119 – 125.

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

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA7 -01	Your Result	ENVA7 -02	Your Result	ENVA7 -03	Your Result	ENVA7 -04	Your Result	ENVA7 -05	Your Result
		CS <sup>3</sup>	-01	CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-04	CS <sup>3</sup>	-05
PR-10	CTC	TTT	TTT		CTC	ATC	RTC	ATC	RTC	CTA	CTA
PR-11	GTC		GTC		GTC		GTC		GTC		GTC
PR-13	ATA		ATA		ATA		ATA		ATA		ATA
PR-16	GGG	GAG	GAG		GGG		GGG		GGG		GGG
PR-20	AAG		AAG	AAA	AAA	ARG	AGG	ARR	ARR	AGG	AGG
PR-24	TTA		TTA		TTA		TTA		TTA		TTA
PR-30	GAT	AAC	AAC		GAT		GAT		GAT		GAT
PR-32	GTA		GTA		GTA		GTA		GTA		GTA
PR-33	TTA	CTA	CTA		TTA		TTA		TTA		TTA
PR-34	GAA		GAA		GAA		GAA		GAA		GAA
PR-35	GAA	GAC	GAC		GAA	GAC	GAC	GAC	GAC	GAC	GAC
PR-36	ATG	GTA	GTA	ATA	ATA	ATA	ATA	ATA	ATA	ATA	ATA
PR-43	AAA		AAA		AAA	AMA	AAA	AMA	AAA		AAA
PR-46	ATG		ATG		ATG	ATA	ATA	ATA	ATA		ATG
PR-47	ATA		ATA		ATA		ATA		ATA		ATA
PR-48	GGG	GGA	GGA	GGA	GGA		GGG		GGG		GGG
PR-50	ATT		ATT	ATA	ATA		ATT		ATT		ATT
PR-53	TTT		TTT		TTT		TTT		TTT		TTT
PR-54	ATC		ATC		ATC	GTC	GTC	GTC	GTC		ATC
PR-58	CAG		CAG	CAA	CAA		CAG		CAG		CAG
PR-60	GAT		GAT	GAG	GAG		GAT		GAT		GAT
PR-62	ATA	GTA	GTA		ATA	GTA	GTA	GTA	GTA		ATA
PR-63	CTC	CTT	CTT	CCT	CCT	CCC	CCC	CCC	CCC	CTT	CTT
PR-64	ATA		ATA		ATA		ATA		ATA		ATA
PR-69	CAT	AAA	AAA	AAA	AAA		CAT		CAT	CAC	CAC
PR-71	GCT		GCT	GCA	GCA	ACT	ACT	ACT	ACT		GCT
PR-73	GGT	GGC	GGC		GGT		GGT		GGT		GGT
PR-74	ACA	TCA	TCA		ACA		ACA		ACA		ACA
PR-76	TTA		TTA		TTA		TTA		TTA	TTG	TTG
PR-77	GTA		GTA	GTG	GTG		GTA		GTA		GTA
PR-82	GTC		GTC		GTC	GCC	GCC	GCC	GCC		GTC
PR-83	AAC		AAC		AAC		AAC		AAC		AAC
PR-84	ATA		ATA		ATA		ATA		ATA		ATA
PR-85	ATT		ATT		ATT		ATT		ATT		ATT
PR-88	AAT	GAT	GAT	AAC	AAC		AAT		AAT	AAC	AAC
PR-89	CTG	ATG	ATG	ATG	ATG	YTG	YTG	YTG	YTG	ATG	ATG
PR-90	TTG		TTG		TTG	ATG	ATG	ATG	ATG		TTG
PR-93	ATT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT		ATT

1. PR = Protease.

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

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.

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

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA7 -01	Your Result	ENVA7 -02	Your Result	ENVA7 -03	Your Result	ENVA7 -04	Your Result	ENVA7 -05	Your Result
		CS <sup>3</sup>	-01	CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-04	CS <sup>3</sup>	-05
RT-41	ATG	TTG	TTG		ATG		ATG		ATG		ATG
RT-62	GCC		GCC		GCC		GCC		GCC		GCC
RT-65	AAA	AAG	AAG	AAG	AAG		AAA		AAA		AAA
RT-67	GAC	AAC	AAC	AAC	AAC		GAC		GAC		GAC
RT-67-68	INSERT			TCT	TCT						
RT-68-69	INSERT			GAG	GAG						
RT-69	ACT	GAT	GAT	TCT	TCT		ACT		ACT		ACT
RT-70	AAA	AAG	AAG	AAG	AAG		AAA		AAA		AAA
RT-74	TTA		TTA		TTA		TTA		TTA		TTA
RT-75	GTA		GTA		GTA		GTA		GTA		GTA
RT-77	TTC	TTT	TTT		TTC		TTC		TTC		TTC
RT-90	GTT		GTT		GTT		GTT		GTT		GTT
RT-98	GCA	GGA	GGA		GCA		GCA		GCA		GCA
RT-100	TTA		TTA		TTA		TTA		TTA		TTA
RT-101	AAA		AAA	GAG	GAG		AAA		AAA		AAA
RT-103	AAA		AAA		AAA		AAA		AAA		AAA
RT-106	GTA	GTG	GTG	ATG	ATG		GTA		GTA		GTA
RT-108	GTA		GTA		GTA		GTA		GTA		GTA
RT-115	TAT		TAT		TAT		TAT		TAT		TAT
RT-116	TTT		TTT		TTT		TTT		TTT	TTC	TTC
RT-151	CAG		CAG		CAG		CAG		CAG	CAA	CAA
RT-179	GTC	GTT	GTT		GTC	GTT	GTT	GTT	GTT	GTT	GTT
RT-181	TAC	TAT	TAT	TAT	TAT	TAT	TAT	TAT	TAT		TAC
RT-184	ATG	GTA	GTA		ATG		ATG		ATG		ATG
RT-188	TAT		TAT		TAT		TAT		TAT		TAT
RT-190	GGA		GGA	GCA	GCA		GGA		GGA	GGG	GGG
RT-210	TTG	TGG	TGG	TGG	TGG		TTG		TTG	CTG	CTG
RT-215	ACC	TAC	TAC	TAC	TAC		ACC		ACC	ACT	ACT
RT-219	AAA	AAG	AAG	AAG	AAG		AAG		AAA		AAA
RT-225	CCT	CCC	CCC	CCC	CCC		CCT		CCT	CCC	CCC

1. RT = Reverse Transcriptase.

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

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.

**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