



Block 4, Kelvin Campus,  
West of Scotland Science Park,  
Glasgow, G20 0SP  
Scotland

Tel: +44 (0) 141 945 6474

Fax: +44 (0) 141 945 5795

www.qcmd.org

info@qcmd.org

# QUALITY CONTROL for MOLECULAR DIAGNOSTICS

Dr Leondios Kostrikis  
Biological Sciences/Lab of Biotechnology & Molecular Virology  
University of Cyprus  
75 Kallipoleos Avenue  
1678 Nicosia  
Cyprus

**Lab Code:** CY002

Dear Dr Leondios Kostrikis,

## QCMD 2009 ENVA9 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 ENVA9 panel was based on characterised and cultured HIV virions diluted in HIV, HBV and HCV negative plasma.
- The ENVA9 panel contained various HIV subtypes:

Sample	Matrix <sup>1</sup>	Subtype	Release testing <sup>2</sup> Lyophilised samples Viral load (copies/ml)
ENVA9-02	Citrate Plasma	G	1.13 x 10 <sup>4</sup>
ENVA9-03	Citrate Plasma	B	1.06 x 10 <sup>4</sup>
ENVA9-05	Citrate Plasma	C	2.79 x 10 <sup>4</sup>
ENVA9-06	Citrate Plasma	C	1.21 x 10 <sup>4</sup>
ENVA9-07	Citrate Plasma	A	1.13 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 COBAS TaqMan HIV-1 Test.

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 **339**. The maximum score achievable was **340**. 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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Edinburgh EH2 3AH



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. (2008). Update of the Drug Resistance Mutations in HIV-1: December 2008. Topics in HIV Medicine, 16(5):138-145

### 1. Results of the Protease drug mutation codon identification for CY002:

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA9 -02	Your Result	ENVA9 -03	Your Result	ENVA9 -05	Your Result	ENVA9 -06	Your Result	ENVA9 -07	Your Result
	CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-05	CS <sup>3</sup>	-06	CS <sup>3</sup>	-07	
PR-10	CTC	CTA	CTA	ATC	ATC	TTT	TTT	CTT	CTT	TTA	TTA
PR-11	GTC		GTC		GTC		GTC		GTC		GTC
PR-13	ATA	GTA	GTA	GTA	GTA		ATA		ATA	GTA	GTA
PR-16	GGG		GGG		GGG	GAG	GAG		GGG		GGG
PR-20	AAG	ATA	ATA		AAG		AAG	AGG	AGG	ATA	ATA
PR-24	TTA		TTA		TTA		TTA	CTA	CTA		TTA
PR-30	GAT		GAT		GAT	AAC	AAC		GAT		GAT
PR-32	GTA		GTA		GTA		GTA		GTA		GTA
PR-33	TTA	TTG	TTG		TTA	CTA	CTA		TTA		TTA
PR-34	GAA		GAA		GAA		GAA		GAA		GAA
PR-35	GAA	GAC	GAC	GAC	GAC	GAC	GAC	GAT	GAT	GAC	GAC
PR-36	ATG	ATA	ATA	ATA	ATA	GTA	GTA	ATA	ATA	ATA	ATA
PR-43	AAA		AAA		AAA		AAA		AAA		AAA
PR-46	ATG		ATG	ATA	ATA		ATG		ATG		ATG
PR-47	ATA		ATA		ATA		ATA		ATA		ATA
PR-48	GGG		GGG		GGG	GGA	GGA	GGA	GGA		GGG
PR-50	ATT		ATT		ATT		ATT		ATT		ATT
PR-53	TTT		TTT		TTT		TTT		TTT		TTT
PR-54	ATC		ATC	GTC	GTC		ATC		ATC		ATC
PR-58	CAG		CAG		CAG		CAG	CAA	CAA	CAA	CAA
PR-60	GAT		GAT		GAT		GAT		GAT		GAT
PR-62	ATA		ATA	GTA	GTA	GTA	GTA		ATA		ATA
PR-63	CTC	CTT	CTT	CCC	CCC	CTT	CTT	CTT	CTT	CCT	CCT
PR-64	ATA		ATA		ATA		ATA		ATA		ATA
PR-69	CAT	AAA	AAA		CAT	AAA	AAA	AAG	AAG	AAA	AAA
PR-71	GCT		GCT	ACT	ACT		GCT		GCT	GCC	GCC
PR-73	GGT	GGG	GGG		GGT	GGC	GGC		GGT		GGT
PR-74	ACA		ACA		ACA	TCA	TCA		ACA		ACA
PR-76	TTA		TTA		TTA		TTA		TTA		TTA
PR-77	GTA	RTA	RTA		GTA		GTA	GTG	GTG	GTG	GTG
PR-82	GTC	ATC	ATC	GCC	GCC		GTC		GTC		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		AAT		AAT	GAT	GAT	AAC	AAC		AAT
PR-89	CTG	ATG	ATG		CTG	ATG	ATG	ATG	ATG	ATG	ATG
PR-90	TTG		TTG	ATG	ATG		TTG		TTG		TTG
PR-93	ATT		ATT	CTT	CTT	CTT	CTT	CTT	CTT		ATT

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.

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

Amino Acid position <sup>1</sup>	WT <sup>2</sup>	ENVA9 -02	Your Result	ENVA9 -03	Your Result	ENVA9 -05	Your Result	ENVA9 -06	Your Result	ENVA9 -07	Your Result
		CS <sup>3</sup>	-02	CS <sup>3</sup>	-03	CS <sup>3</sup>	-05	CS <sup>3</sup>	-06	CS <sup>3</sup>	-07
RT-41	ATG		ATG		ATG	<b>TTG</b>	<b>TTG</b>		ATG		ATG
RT-62	GCC		GCC		GCC		GCC	<b>GYC</b>	<b>GYC</b>		GCC
RT-65	AAA		AAA		AAA	<b>AAG</b>	<b>AAG</b>	<b>ARG</b>	<b>ARG</b>		AAA
RT-67	GAC		GAC		GAC	<b>AAC</b>	<b>AAC</b>	<b>RAC</b>	<b>RAC</b>	<b>GAT</b>	<b>GAT</b>
RT-69	ACT		ACT		ACT	<b>GAT</b>	<b>GAT</b>	<b>AYT</b>	<b>AYT</b>	<b>ACC</b>	<b>ACC</b>
RT-70	AAA		AAA		AAA	<b>AAG</b>	<b>AAG</b>	<b>AAG</b>	<b>AAG</b>		AAA
RT-74	TTA		TTA		TTA		TTA		TTA		TTA
RT-75	GTA		GTA		GTA		GTA	<b>RYA</b>	<b>RYA</b>		GTA
RT-77	TTC	<b>TTT</b>	<b>TTT</b>		TTC	<b>TTT</b>	<b>TTT</b>		TTC		TTC
RT-90	GTT	<b>GTC</b>	<b>GTC</b>		GTT		GTT		GTT	<b>GTC</b>	<b>GTC</b>
RT-98	GCA	<b>GCG</b>	<b>GCG</b>		GCA	<b>GGA</b>	<b>GGA</b>		GCA	<b>GCG</b>	<b>GCG</b>
RT-100	TTA		TTA		TTA		TTA		TTA		TTA
RT-101	AAA		AAA		AAA		AAA	<b>CAA</b>	<b>CAA</b>		AAA
RT-103	AAA		AAA		AAA		AAA	<b>AAC</b>	<b>AAC</b>		AAA
RT-106	GTA		GTA		GTA	<b>GTG</b>	<b>GTG</b>	<b>ATG</b>	<b>ATG</b>		GTA
RT-108	GTA		GTA		GTA		GTA		GTA		GTA
RT-115	TAT		TAT		TAT		TAT		TAT		TAT
RT-116	TTT		TTT		TTT		TTT		TTT		TTT
RT-138	GAG		GAG		GAG		GAG	<b>GCA</b>	<b>GCA</b>		GAG
RT-151	CAG		CAG		CAG		CAG		CAG	<b>CAA</b>	<b>CAA</b>
RT-179	GTC	<b>GTG</b>	<b>GTG</b>	<b>GTT</b>	<b>GTT</b>	<b>GTT</b>	<b>GTT</b>	<b>GTT</b>	<b>GTT</b>	<b>GTG</b>	<b>GTG</b>
RT-181	TAC		TAY	<b>TAT</b>	<b>TAT</b>	<b>TAT</b>	<b>TAT</b>	<b>TAT</b>	<b>TAT</b>		TAC
RT-184	ATG		ATG		ATG	<b>GTA</b>	<b>GTA</b>	<b>GTR</b>	<b>GTR</b>		ATG
RT-188	TAT		TAT		TAT		TAT		TAT		TAT
RT-190	GGA		GGA		GGA		GGA		GGA		GGA
RT-210	TTG		TTG		TTG	<b>TGG</b>	<b>TGG</b>		TTG	<b>CTG</b>	<b>CTG</b>
RT-215	ACC		ACC		ACC	<b>TAC</b>	<b>TAC</b>		ACC		ACC
RT-219	AAA		AAA		AAA	<b>AAG</b>	<b>AAG</b>	<b>AAR</b>	<b>AAR</b>		AAA
RT-225	CCT		CCT		CCT	<b>CCC</b>	<b>CCC</b>	<b>CCA</b>	<b>CCA</b>	<b>CCC</b>	<b>CCC</b>
RT-230	ATG		ATG		ATG		ATG		ATG		ATG

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.

**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