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QUALITY CONTROL for MOLECULAR DIAGNOSTICS

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Cyprus

Lab Code: CY002

Dear Dr Leondios Kostrikis,

QCMD 2010 ENVA 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 2010 ENVA panel was based on characterised and cultured HIV virions diluted in HIV, HBV and HCV negative plasma.
- The 2010 ENVA panel contained various HIV subtypes:

Sample	Matrix ¹	Subtype	Release testing ²
			Lyophilised samples Viral load (copies/ml)
ENVA10-02	Citrate Plasma	C	7.16×10^3
ENVA10-04	Citrate Plasma	A	3.02×10^3
ENVA10-05	Citrate Plasma	B	1.21×10^4
ENVA10-06	Citrate Plasma	B	1.46×10^4
ENVA10-07	Citrate Plasma	AG	1.34×10^4

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 2009).
- The consensus sequence at IAS codons containing a mutation.
- YOUR laboratory's result at all IAS codons.

Your personal performance score was **338**. 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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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 (2009). Update of the Drug Resistance Mutations in HIV-1: December 2009. Topics in HIV Medicine, 17(5):138-145.

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

Amino Acid position ¹	WT ²	ENVA10 -02	Your Result	ENVA10 -04	Your Result	ENVA10 -05	Your Result	ENVA10 -06	Your Result	ENVA10 -07	Your Result	
		CS ³	-02	CS ³	-04	CS ³	-05	CS ³	-06	CS ³	-07	
PR-10	CTC		CTT	CTT	TTA	TTA		CTC		CTC	ATA	ATA
PR-11	GTC						GTC		GTC			GTC
PR-13	ATA				GTA	GTA		ATA		ATA	GTA	GTA
PR-16	GGG						GGG	GAG	GAG	GAG	GAG	GAG
PR-20	AAG				ATA	ATA		AAG		AAG	ATA	ATA
PR-24	TTA						TTA		TTA			TTA
PR-30	GAT						GAT		GAT			GAT
PR-32	GTA						GTA		GTA			GTA
PR-33	TTA						TTA		TTA			TTA
PR-34	GAA						GAA		GAA			GAA
PR-35	GAA				GAC	GAC		GAA		GAA		GAA
PR-36	ATG	ATA	ATA	ATA	ATA	ATA		ATG	ATA	ATA	ATA	ATA
PR-43	AAA						AAA		AAA			AAA
PR-46	ATG						ATG		ATG			ATG
PR-47	ATA						ATA		ATA			ATA
PR-48	GGG	GGA	GGA	GGA	GGA	GGA		GGG		GGG		GGG
PR-50	ATT						ATT		ATT			ATT
PR-53	TTT						TTT		TTT			TTT
PR-54	ATC						ATC		ATC			ATC
PR-58	CAG				CAA	CAA		CAG		CAG		CAG
PR-60	GAT						GAT		GAT			GAT
PR-62	ATA						ATA		ATA	RTA	RTA	RTA
PR-63	CTC				CCT	CCT		CTC	GCC	GCC	YCT	YCT
PR-64	ATA						ATA		ATA	MTA	MTA	MTA
PR-69	CAT	AAA	AAA	AAA	AAA	AAA		CAT	AAA	AAA	AAA	AAA
PR-71	GCT				GCC	GCC		GCT		GCT	GCC	GCC
PR-73	GGT						GGT		GGT			GGT
PR-74	ACA						ACA		ACA			ACA
PR-76	TTA						TTA		TTA			TTA
PR-77	GTA				GTG	GTG		GTA	GTG	GTG		GTA
PR-82	GTC						GTC		GTC			GTC
PR-83	AAC						AAC		AAC			AAC
PR-84	ATA						ATA		ATA			ATA
PR-85	ATT						ATT		ATT			ATT
PR-88	AAT						AAT		AAT			AAT
PR-89	CTG	ATG	ATG	ATG	ATG	ATG		CTG	TTG	TTG	ATG	ATG
PR-90	TTG						TTG		TTG			TTG
PR-93	ATT	CTT	CTT	CTT	CTT	CTT		ATT	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 ¹	WT ²	ENVA10 -02	Your Result	ENVA10 -04	Your Result	ENVA10 -05	Your Result	ENVA10 -06	Your Result	ENVA10 -07	Your Result
		CS ³	-02	CS ³	-04	CS ³	-05	CS ³	-06	CS ³	-07
RT-41	ATG	TTG	TTG		ATG		ATG		ATG		ATG
RT-62	GCC		GCC		GCC		GCC		GCC		GCC
RT-65	AAA	AAG	AAG		AAA		AAA		AAA		AAA
RT-67	GAC	GAT	GAT	GAT	GAT	GAY	GAY		GAC	GAT	GAT
RT-69	ACT		ACT	ACC	ACC		ACT		ACT		ACT
RT-70	AAA	AAG	AAG		AAA		AAA		AAA		AAA
RT-74	TTA		TTA		TTA	CTA	CTA		TTA		TTA
RT-75	GTA	ACA	ACA		GTA		GTA		GTA	GTR	GTR
RT-77	TTC		TTC		TTC		TTC	TTT	TTT		TTC
RT-90	GTT	ATT	ATT	GTC	GTC		GTT	GTC	GTC	GTC	GTC
RT-98	GCA		GCA	GCG	GCG		GCA		GCA		GCA
RT-100	TTA		TTA		TTA		TTA		TTA		TTA
RT-101	AAA		AAA		AAA		AAA		AAA		AAA
RT-103	AAA		AAA		AAA		AAA		AAA		AAA
RT-106	GTA	ATG	ATG		GTA		GTA		GTA		GTA
RT-108	GTA		GTA		GTA		GTA		GTA		GTA
RT-115	TAT		TAT		TAT		TAT		TAT		TAT
RT-116	TTT		TTT		TTT		TTY		TTT		TTT
RT-138	GAG	GAA	GAA		GAG		GAG		GAG		GAG
RT-151	CAG		CAG	CAA	CAA		CAG		CAG		CAG
RT-179	GTC	GAC	GAC	GTG	GTG	GTT	GTT	GTT	GTT	GTG	GTG
RT-181	TAC	TAT	TAT		TAC	TAT	TAT	TAT	TAT		TAC
RT-184	ATG		ATG		ATG		ATG		ATG		ATG
RT-188	TAT		TAT		TAT		TAT		TAT		TAT
RT-190	GGA		GGA		GGA		GGA		GGR		GGA
RT-210	TTG	TTA	TTA	CTG	CTG		TTG		TTG	CTG	CTG
RT-215	ACC		ACC		ACC		ACC		ACC		ACC
RT-219	AAA		AAA		AAA		AAA		AAA		AAA
RT-225	CCT	CCC	CCC	CCC	CCC		CCT		CCT		CCT
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