PROJECT FINAL REPORT

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4.1 Final publishable summary report

EXECUTIVE SUMMARY

Major advances in HIV management and care have significantly improved quality of life for HIV-infected individuals. However, a number of important challenges remain, such as the continued emergence of resistance against new and existing classes of antiretroviral drugs. In addition, the rate of new HIV infections in Europe continues to rise, demanding effective surveillance and monitoring to ensure appropriate allocation of resources. Moreover, due to the close relationship of worldwide HIV epidemics, it is important to improve the conditions of antiretroviral rollout in resource-poor regions such as Africa.

The Collaborative HIV and Anti-HIV Drug Resistance Network (CHAIN) was established in 2009 to provide an integrated response to these challenges via pooling of knowledge, resources and tools on a pan-European scale and in partnership with African institutions in Senegal and Cameroon. The CHAIN consortium comprises 26 partners, each with a high level of relevant scientific expertise and access to an extended peer network. Over the past five years, a collaborative research effort has focused on delivering the overall mission of the CHAIN programme, to '*effectively and durably combat new and existing anti-HIV drug resistance in clinical settings, with special emphasis on Eastern Europe and heavily affected resource-poor regions in Africa*.'

In pursuit of this mission, seven work streams were formed to address seven interrelated challenges identified by the CHAIN consortium. The aims of the work streams were to:

1. Identify novel mechanisms of resistance to existing drug classes (reverse transcriptase inhibitors & protease inhibitors) and to new classes of antiretrovirals (integrase inhibitors & entry inhibitors e.g.CCR5 antagonists).
2. Develop and validate optimal laboratory methods for predicting response to antiretroviral therapies, particularly in the presence of drug-resistant viruses.
3. Coordinate a clinical/virological data management system enabling assessment of the clinical implications of resistance.
4. Maximize the utility of HIV gene sequences and follow-up data through development of a bioinformatics HIV Data Sharing System.
5. Develop paradigms for linking resistance data to existing national HIV reporting structures.
6. Assess and describe the potential risks for resistance development with rollout of antiretroviral therapy in resource-limited settings.
7. Define and implement minimally required standards of scientific and clinical expertise in HIV drug resistance in Europe (mainly Eastern) and Africa.

A number of valuable advances have been made towards preventing further development and spread of anti-HIV drug resistance. The CHAIN consortium has developed new laboratory tools to predict and measure anti-HIV drug resistance, and implemented management strategies to reduce its impact and incidence. HIV gene sequence data have been incorporated into national HIV reporting structures and evidence-based recommendations have been made for public health and regulatory authorities, to help limit the emergence and transmission of HIV drug resistance. Some of the most significant achievements of the seven CHAIN work packages are discussed herein.

PROJECT CONTEXT AND OBJECTIVES SUMMARY

Despite the huge advances made with HIV management and care, leading to a dramatic improvement in the quality of life for HIV infected individuals, there remain a number of significant challenges. Anti-HIV drug resistance represents a foremost threat to the effective use of HIV therapy in the developed and resource-poor regions of the world. Although the availability of new classes of antiretroviral drugs has dramatically reduced HIV-related mortality and morbidity, the emergence of HIV resistance in patients receiving Highly Active Anti-Retroviral Therapy (HAART), is now associated with increasing rates in disease progression.

As new classes of antiretroviral drugs are introduced, so the virus evolves new mechanisms to escape from inhibition. The implications of these genetic changes, both for the individual and the population, remain unknown. Insights into the susceptibility of viruses to antiretrovirals, and mechanisms underlying resistance development to both existing and novel drugs are essential to better clinically manage resistant viruses as these emerge, and to prevent further resistance development and spread. Antiviral therapy paradigms have been standardized during the last years, and remarkable results have been obtained. However the circulation of drug-resistant viral strains continues to be a major limitation of antiviral therapy. There are also major gaps in knowledge regarding drug resistance to existing drug classes, such as protease inhibitors. As continual virus escape from therapy occurs, there is a requirement to translate new knowledge of basic mechanisms into clinical practice. This requires the development of laboratory monitoring tools to best predict new resistance mechanisms, monitor resistance, and also ensure that clinical management of infected individuals remains optimal. The tools developed to investigate HIV resistance have historically been based on the B HIV-1 subtype (by far the most common HIV-1 strain circulating in North America). By contrast, non-B subtype viruses are responsible for more than 90% of worldwide HIV-1 infections and their prevalence is rising in Europe. Therefore, it is necessary to refine methodology, interpretation and the role of cross-resistance in B HIV-1 as well as in non-B HIV-1 and in HIV-2.

In addition to conducting studies to improve the treatment and care of infected individuals, it must be realised that the European epidemic is ever changing. The rate of new infections continues to rise, fuelled not only by within-Europe transmissions, but also through migration of infected individuals into Europe. Surveillance and monitoring of these shifts is essential in order that appropriate resources are allocated at country and European level to mitigate the adverse impact of the health of the population. New techniques of molecular epidemiology can be linked to established HIV surveillance structures, to optimise the real time monitoring of how the epidemic is changing. Of particular interest in this respect is the explosion of HIV amongst intravenous drug users and heterosexuals in Eastern Europe, and importation of infections from the endemic areas of sub-Saharan Africa. It requires the development of bioinformatics tools such as phylogenetic analysis to develop a global epidemiological model able to predict future trends. On a micro scale, the development of resistance within the host needs to be investigated, using tools such as data mining to predict the evolution of the virus under drug selective pressure. The most important information lacking is large pan-European datasets of temporal viral sequence and associated epidemiological and clinical data. Assimilation of real-time molecular epidemiology in the context of such national and international data provides a unique opportunity to map the growing epidemic, thus allowing for evidence-based interventions.

In view of the increasingly close relationship of worldwide HIV epidemics, it is important also to improve the conditions of antiretroviral rollout in the resource-poor regions of Africa. In particular the level of expensive laboratory monitoring required to optimise the World Health Organisation (WHO) rollout programme remains unclear. Modelling experiments, to advance understanding of the long-term impact of antiretroviral therapy rollout on treatment failure and drug-resistance in resource-poor regions, have the potential to produce highly informative data. Evidence-based recommendations can contribute to more effective strategies for public health and regulatory authorities. In the overall context of shifting epidemics, new interventions, and a European integrated approach to HIV therapy and drug resistance, there is an opportunity to guide new educational and drug licensing structures, in order to provide the optimal European response to the new HIV challenge. The degree of real-time monitoring itself will, in part, determine the likelihood of spread of drug resistance in the population. Further, the creation of a level playing field in the European and African scientific landscape in terms of scientific and clinical expertise in management of HIV drug resistance has been the ambitious focus of CHAIN.

The objectives of CHAIN:

- Identification of new mechanisms by which HIV escapes drug inhibition. This relates to new classes of drugs, such as integrase inhibitors, as well as existing classes of drugs.
- The development and validation of new and common laboratory tools for prediction and measurement of HIV drug resistance, particularly based on the mechanistic studies described above.
- Improved understanding of the clinical implications of drug resistance, with the development of optimal management strategies for transmitted and acquired HIV drug resistance, reducing the incidence and impact at population and patient level.
- A sustainable evidence base for better control of the epidemic and management of infected individuals. This requires new monitoring tools, and the development of systems for linking existing national HIV surveillance systems, together with the new science of molecular epidemiology, to better monitor HIV spread across Europe.
- Develop an evidence base to support antiretroviral rollout in Africa, and WHO initiated surveillance of HIV drug resistance in these settings.
- Provide an integrated educational framework for disseminating the findings from CHAIN research in an appropriate format. In addition, direct input into European Medicines Agency (EMA) post licensing surveillance guidance.

SCIENTIFIC AND TECHNICAL RESULTS/FOREGROUNDS

In pursuit of the CHAIN mission and in line with the above-mentioned challenges a range of main objectives and associated specific scientific, training and dissemination objectives were formulated and organised into seven work packages (WP1-7). The main objectives and key achievements and outputs of each work package are further detailed below.

WP1- NOVEL RESISTANCE MECHANISMS

Main objective: to complete gaps in our knowledge for resistance to existing drugs and identify novel resistance mechanisms to new drugs, preventing further development and spread.

Associated specific objectives:

- To identify novel mechanisms of resistance to existing drug classes (reverse transcriptase inhibitors (RTI) and protease inhibitors (PI)) and to new classes of antiretrovirals (integrase Inhibitors and CCR5 antagonists).
- To develop innovative and cost effective diagnostic approaches for measuring and monitoring susceptibility and resistance to CCR5 and integrase antagonists.
- To guide study on clinical relevance of newly identified drug resistance mechanisms.

The key achievements and outputs from WP1:

Drug-protein interactions

Due to its essential role in reverse transcription of HIV-1 RNA into DNA, the reverse transcriptase (RT) enzyme is a major target for antiretroviral therapy (ART). WP1 partners have reported novel findings on drug–protein interactions between HIV-1 RT and non-nucleoside RTI (NNRTI). The changes in protein conformation that occur following binding of the drug offer insights into the mechanisms underlying the development of drug resistance. Wright DW et al., J. Am. Chem. Soc., 2012;134:12885–12888; Wright DW et al., Biology 2012;1:222-244.

Genotypic and phenotypic assays for entry- RNAse H- and integrase inhibitors

A number of novel assays have been developed, including a drug susceptibility assay for HIV-2, and a genotypic assay to analyze the C-terminal domain of HIV-1 RT. A two-round phenotypic assay for protease inhibitor susceptibility testing of recombinant and primary HIV-1 isolates was developed (Puertas et al., 2012. J Clin Microbiol 3909–16), and a non-infectious cell-based phenotypic assay for the assessment of HIV-1 susceptibility to protease inhibitors (Buzon et al., J Antimicrob Chemother 2012; 67: 32–8). In addition, a quantitative Polymerase Chain Reaction (qPCR) method was developed to measure the viral load and replication capacity of mutant HIV-2 viruses, and a novel reverse-transcriptase (RT-PCR) strategy was established to sequence the connection and RNAse H domains of HIV-1 in plasma samples.

Novel HIV-1 resistance mutations

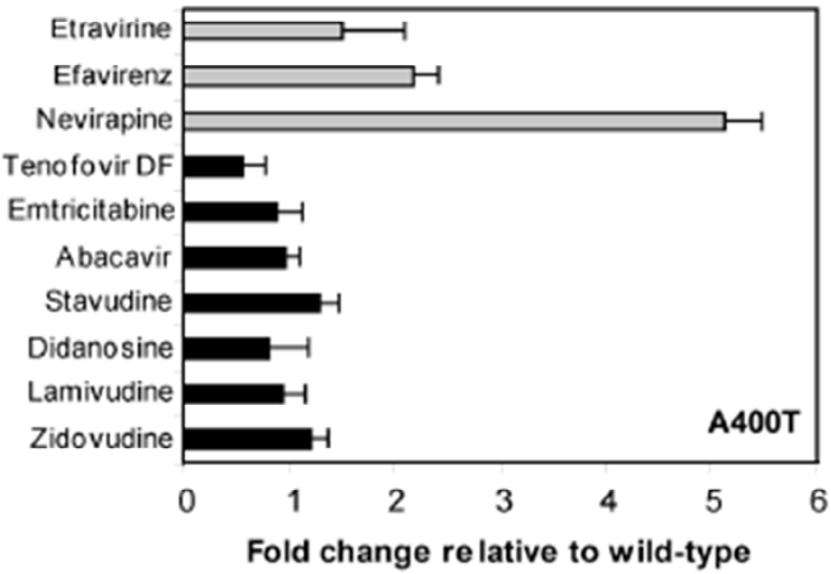
The majority of mutations conferring resistance to HIV-1 RTI have been identified within the polymerase domain of RT. Both the connection and RNAse H domains of RT contain key protein residues that are essential for RT structure and function, yet these are not routinely analysed in clinical samples. Partners

involved in WP1 have sequenced the entire RT gene from a cohort of HIV-1 patients who were failing therapy with zidovudine (AZT), lamivudine or duo therapy regimens incorporating AZT. This allowed identification of novel resistance mutations outside of the polymerase region of RT, which have subsequently been introduced into reference strains for analysis of their effects on drug susceptibility and replication. As a result, the mechanisms involved in the selection of HIV-1 reverse transcriptase thumb subdomain polymorphisms associated with nucleoside analogue therapy failure were described (Betancor et al., 2010. Antimicrob Agents Chemother 54: 4799-811). Further, the clinical, virological and biochemical evidence was shown supporting the association of HIV-1 reverse transcriptase polymorphism R284K and thymidine analogue resistance mutations M41L, L210W and T215Y in patients failing tenofovir/emtricitabine therapy (Betancor et al., 2009. Retrovirol 9:68).

The group also demonstrated the role of specific substitutions in RT in association with patterns of mutations to some nucleoside reverse transcriptase inhibitors. In this regard, specific substitutions have been described as having a regulatory role for Leu-214 in the emergence and phenotypic resistance of the TAM1 complex, which includes Leu-41, Trp-210, and Tyr-215 (Puertas et al., 2009. J Virol 83: 7434–9).

New mutations to non-nucleoside reverse transcriptase inhibitors have been identified. Thus, the A376S substitution in the connection subdomain of HIV-1 reverse transcriptase has been shown to confer increased risk of virological failure to nevirapine therapy (Paredes et al., 2011, J Infect Dis 204:741–52).

A threonine for alanine substitution at position 400 in the connection domain of RT was found to occur with high frequency in patients failing therapy with RTI compared with treatment-naïve patients (Wright DW et al, PLOS One 2013; 8:e74078). The T400 mutation was shown to confer resistance to the NNRTIs nevirapine and efavirenz (Figure). Furthermore, T400 was shown to reduce RNAse H activity both on its own and when combined with other mutations, through conformational changes to the primer grip domain. It is suggested that the slower degradation of the viral RNA genome provides more time for dissociation of the NNRTI from the stalled RT template/primer, allowing reverse transcription to resume.



Drug susceptibility of A400T virus. Susceptibility of the A400T virus to NNRTI (light grey) and NRTI (black) was measured using single-cycle drug susceptibility assays. The average of three independent experiments is plotted, and the standard deviation is shown (error bars). A400T substitution reduced susceptibility to nevirapine and efavirenz approximately 5-fold and 2-fold,respectively. From Wright DW et al, PloS One 2013;8:e74078

Within HIV-1 integrase, the group assessed raltegarvir susceptibility and fitness to progression of HIV-1 integrase in patients on long-term antiretroviral therapy (Buzon et al. 2008. Antivir Ther 13:881-93), and found that the HIV-1 integrase genotype strongly predicts raltegravir susceptibility but not viral fitness of primary virus isolates (Buzon et al. 2010. AIDS 24:17–25).

Novel HIV-2 resistance mutations

Using gene-sequencing techniques, a novel mutation – V111I – was identified in the polymerase region of RT in a cohort of patients with HIV-2 who were failing therapy with nucleoside RTI. This mutation was associated with mutations K65R and Q151M. Introduction of these mutations into reference strains showed that V111I both increases polymerase activity and increases the replication capacity of the K65R and Q151M viruses. Modelling experiments further revealed that V111I results in a catalytically competent RT enzyme that supports dNTP incorporation (Deuzing IP et al., manuscript in development).

Cell-based mechanisms of HIV-1 drug resistance

It has become increasingly apparent that the balance between drug influx and efflux transporter activity plays a critical role in the overall disposition of anti-HIV drugs in both cells and tissues. Thus, drug transporters directly influence the appearance of drug resistance and toxicity, and could also be related to persistence of HIV-1 (Minuesa et al., 2011. Pharmacol & Therap 132:268–79; Minuesa et al., 2008. J Pharmacol Exp Ther 324:558–67; Minuesa et al., 2009. J Pharmacol Exp Ther 329:252–61).

WP2- LABORATORY MONITORING TOOLS

Main objective: To develop and validate new and common laboratory tools for the prediction and measurement of HIV resistance.

Associated specific objectives:

- Develop and validate optimal laboratory methods for predicting response to antiretroviral therapies, particularly in the presence of drug resistant viruses.
- Identify appropriate uses for antiretroviral drug pharmacokinetics and resistance testing.
- Identify the clinical utility of HIV tropism and CCR5 antagonist resistance testing.
- Optimise interpretation algorithms of resistance data to guide therapy.
- Ensure optimal synergy of currently available quality assurance/quality control (QA/QC) systems for drug resistance testing.

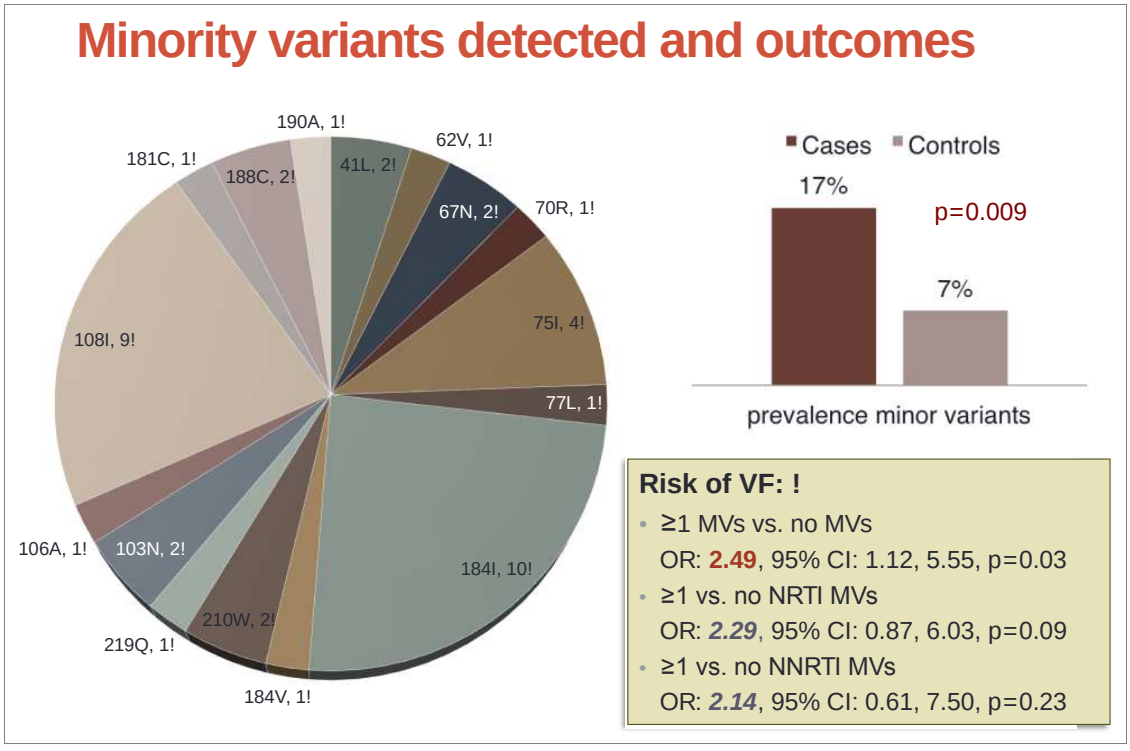
Work package 2 was divided into four research tracks and involved the collaborative efforts of thirteen European laboratories. Some of the important research arising from these collaborations is discussed below.

Track 1: Standardization of laboratory techniques, QA/QC and new technologies

Two novel and highly sensitive assays were developed and validated for amplification and genotyping of the protease and reverse transcriptase (RT) genes from dried blood spots, which will be of particular value in resource limited setting (RLS) (Aitken SC et al., J Clin Microbiol 2013; 51:1757-61; Aitken SC et al., submitted for review). Further, a novel strategy for protease inhibitor susceptibility testing, based on the ability of the HIV protease to cleave cellular translation factors such as eIF4GI and PABP, was evaluated and validated using HIV-1 proteases from 46 clinical isolates. The assay showed good correlation with the Virco TYPE HIV-1 assay and the Antivirogram assay (Puertas MC et al., J Clin Microbiol. 2012; 50:3909-16).

Track 2: Minority species

Studies were conducted to assess the clinical value of ultrasensitive genotyping. In partnership with EU and US groups, the EU-FP7-funded CHAIN consortium showed that low frequency drug-resistant HIV-1 more than doubles the risk of virological failure to first-line NNRTI-based ART (Figure). This is the first time this question has been addressed using state of the art Next Generation Sequencing (NGS) technology in a well designed, multi-cohort, case-controlled study (Li JZ et al, JAMA 2011; 305:1327-1335; Li JZ et al, J Infect Dis 2013; 207:893-897; Cozzi-Lepri A et al, Lancet Infect Dis; submitted for peer-review). Given the rapid developments in NGS technologies and their expected future clinical application, the CHAIN NGS Working Group was formed, which will serve as a platform for scientific discussions around NGS issues in Europe and work towards standardization of NGS analyses.



Minority variants (MVs) detected and outcomes. Distribution of minority drug-resistant HIV-1 variants (left), prevalence of minority variants in cases and controls (upper right), and association with risk of virological failure (VF) (right). NRTI, nucleoside reverse transcriptase inhibitor; NNRTI, non-nucleoside reverse transcriptase inhibitor. Unpublished data.

Track 3: Tropism

The EMA and FDA mandate testing for viral co-receptor usage, or viral tropism, prior to administration of new antiretrovirals such as the CCR5 antagonist maraviroc. Track 3 standardized and improved tropism prediction using sequence and phenotypic analysis of the HIV env-V3 region (V3). This novel approach to tropism prediction was shown to be highly effective and safe for diagnostic use. Further research demonstrated that proviral DNA can be sequenced and used to reliably predict tropism. This can guide a switch to CCR5 antagonist-based therapy in patients with suppressed plasma HIV-1 RNA who need to change their current regimen (Vandekerckhove L et al, Lancet 2011; Bellecave P et al, CROI 2012; Abstract 716).

Track 4: Algorithms, subtypes and HIV

For the first time, mutations associated with resistance to HIV-2 were identified based on criteria established by a panel of European experts, and are now freely available at http://www.hiv-grade.de (Charpentier, C et al, Clin Infect Dis. 2013; 56(11): 1654-8). In addition, a large cooperative study including CHAIN, COHERE and EUROCORD is underway to determine the contribution of different mutations to HIV-1 resistance to darunavir. Such studies are important to improve antiretroviral drug resistance-associated mutation interpretation and optimize combination therapy for HIV-infected individuals (Zazzi M et al, HIV Med 2011; Vercauteren, PLOS1 2013; e61436).

WP3- CLINICAL MANAGEMENT OF RESISTANCE

Main objective: to improve understanding of the clinical implications of drug resistance and develop optimal management strategies for transmitted and acquired HIV drug resistance, reducing the incidence and impact of resistance at a population and patient level.

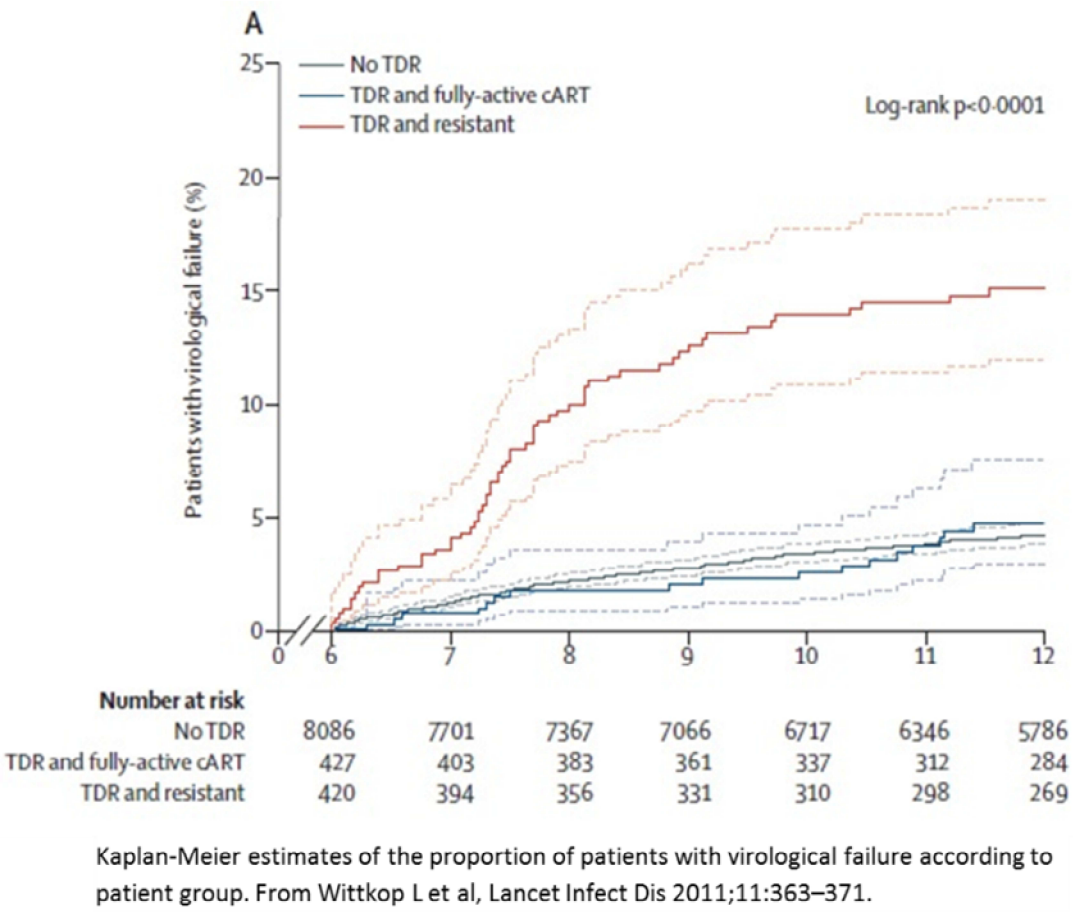
Associated specific objectives:

- Coordinate a clinical/virological data management system enabling assessment of the clinical implications of resistance.
- Determine the impact of HIV drug resistance on virological and immunological response in treatment-experienced patients.
- Identify optimal strategies for treatment of patients with multi drug-resistant HIV.
- Identify the impact of transmitted drug-resistance (TDR) on response to therapy.

Through a collaborative research effort involving numerous research centres in Europe, WP3 has incorporated several different data sources into multiple studies, resulting in numerous publications in high impact journals. Results from just a handful of these important studies are discussed below.

Transmitted drug resistance

The effect of TDR on outcomes in the first year of combination antiretroviral therapy (ART) was assessed in a multi-cohort study including 10,056 patients. TDR was detected in approximately 5% of subjects. Those with TDR and resistance to at least one drug in the ART regimen were shown to be three times more likely to develop virological failure than those without TDR (Figure, Wittkop et al., Lancet Infect Dis 2011; 11:363–371). These findings support current treatment guidelines for HIV, which recommend selection of initial treatment based on resistance testing in treatment-naive patients.



Kaplan-Meier estimates of the proportion of patients with virological failure according to patient group. From Wittkop L et al, Lancet Infect Dis 2011;11:363–371.

Kaplan-Meier estimates of the proportion of patients with virological failure according to patient group. TDR, transmitted drug resistance; cART, combination antiretroviral therapy. Reprinted from The Lancet Infectious Diseases, 11, Wittkop et al., Effect of transmitted drug resistance on virological and immunological response to initial combination antiretroviral therapy for HIV (EuroCoord – CHAIN joint project): a European multi-cohort study, 363-371, Copyright (2011), with permission from Elsevier.

Minority variants

A systematic review conducted by a multi-national group of researchers (including WP2 and WP3 members) led by Harvard University reported low-frequency drug resistance mutations in 14% of participants (Li et al., JAMA 2011; 305:1327–1335). The presence of minority variants was associated with 2.5–3 times the risk of virological failure. Importantly, a dose-dependent increase in the risk of virological failure was observed in

participants with a higher proportion or quantity of drug-resistant variants. A further study conducted in collaboration with WP2, WP4 and WP5, involving 6 European cohorts, found that the presence of at least one pre-existing minority variant in reverse transcriptase almost doubled the risk of virological failure to non-nucleoside reverse transcriptase inhibitor (NNRTI)-based ART. These data were presented at the 'International Workshop on HIV and Hepatitis Virus Drug Resistance and Curative Strategies' (Cozzi-Lepri et al., Antiviral Ther 2013; 18(Suppl1): A41) and have now been submitted for publication.

Viral subtype

Utilizing a large CHAIN cohort, the impact of viral subtype on responses to first-line therapy was assessed. Overall, HIV-1 subtype had no effect on virological and immunological responses. When restricting the analysis to adults, those without TDR had very similar responses to all patients combined (Wittkop et al., CROI 2013; poster presentation). In a collaborative project with EuroCoord and EPPICC, the prevalence of TDR in children was shown to be comparable to that found in adults. Younger age was associated with a higher risk of virological failure but not TDR (Wittkop et al. IAS 2013; poster TUPE306). Authors suggested that the effect of age may be related to fading of NNRTI resistance mutations in children exposed to single-dose nevirapine, Manuscripts discussing this data are currently being drafted.

WP4 - MOLECULAR EPIDEMIOLOGY AND BIOINFORMATICS OF RESISTANCE

Main objective: provide a sustainable knowledge base on HIV and HIV drug resistance for generation of data on a macro and a micro epidemiological scale to improve patient care, control the epidemic and prevent further spread of HIV drug resistance.

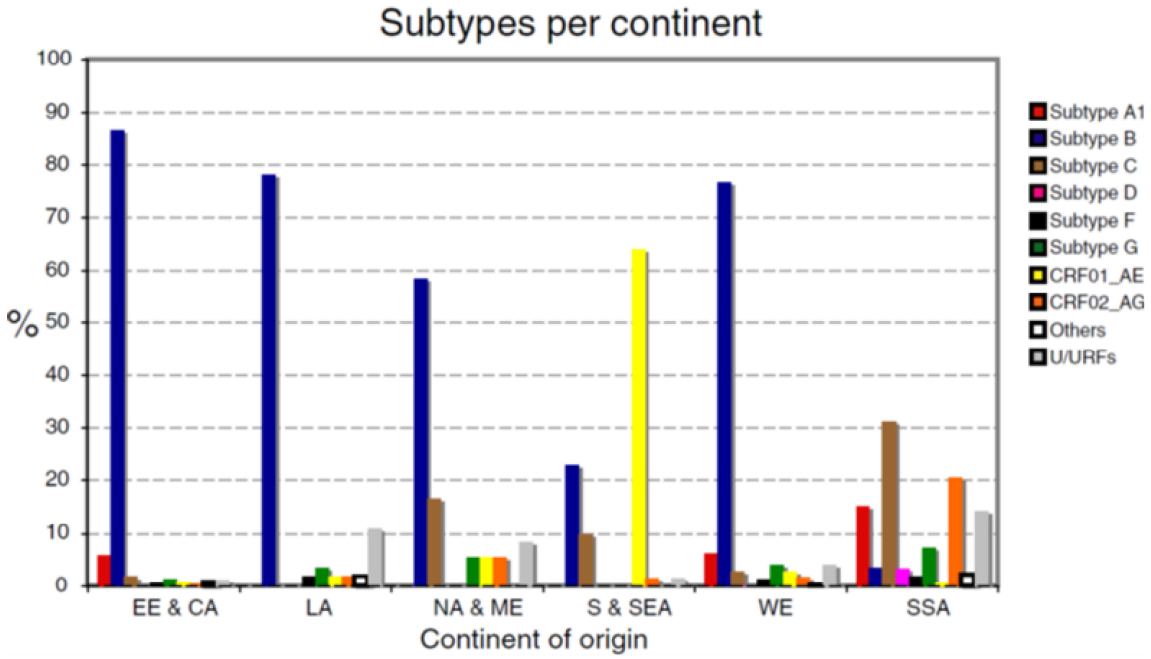
Associated specific objectives

- Maximize the utility of HIV gene sequences and follow-up data through development of a bioinformatics HIV Data Sharing System (HDSS).
- Improve clinical decision making for individuals with drug resistant viruses through web-based bioinformatics tools.
- Explain and predict the current and future spread of HIV variants throughout Europe and high prevalence areas such as Africa, with special attention to resistant virus variants.

Through expert collaboration on an international scale, partners involved in WP4 have developed a framework for merging large clinical HIV resistance databases such as EuResist, Eurosida and other national databases. These web-based 'super' datasets provide a tool to guide therapeutic decisions regarding optimal combination therapy for individual patients. These quality-checked datasets also provide a valuable resource for conducting molecular epidemiology and resistance studies.

Epidemiology

Large datasets have been generated for the most prevalent subtypes and recombinant HIV strains (subtypes A, B, C, D, G, and CRF01_AE, CRF02_AG) circulating in Europe and worldwide, including resource-limited settings (Abecasis et al, Retrovirology 2013; 10:7). Studies have shown that HIV epidemics are highly compartmentalized, and have also identified significant routes of HIV migration both within Europe and between Europe and other continents (Abecasis et al, Retrovirology 2013; 10:7; Lai et al, PLoS One 2012; 7:e42223; Lawyer et al, Med Microbiol Immunol 2012; 201:239-269, and several manuscripts in preparation). Another significant achievement of WP4 was the combined effort to analyse HIV subtypes in remote Russian regions and former Soviet Union (FSU) countries for the first time (Kazennova et al, Vopr Virusol 2013; 58:28-35; Laga et al, Vopr Virusol 2012; 57:26-32; Kazennova et al, Vopr Virusol 2011; 56:30-34). Several training programmes on HIV drug resistance have been developed and implemented in these regions.



Subtype distribution stratified by continent of origin of the patient. EE, Eastern Europe; CA, central Asia; LA, Latin America; NA, North America; ME, Middle East; S & SEA, South and South-East Asia; WE, Western Europe; SSA, Sub-Saharan Africa. From Abecasis AB et al. Retrovirology 2013; 10:7.

Resistance

Studies conducted as part of WP4 have significantly advanced viral genotype technology, allowing for accurate estimation of viral resistance in individual patients (Thielen et al, Intervirology 2012; 55:113-117; Bogojeska et al, Stat Appl Genet Mol Biol 2012; 11:Article 11). Importantly, treatment response prediction engines that work without genotypic information have also been developed, to facilitate therapy optimization in RLS (Prosperi et al, PLoS One 2010; 5:e13753). Moreover, an in-house HIV-1 resistance test has proven reliable also at low levels of viraemia (Santoro et al, Clin Infect Dis 2014). Our understanding of the

distribution and circulation of drug-resistant viral strains among B and non-B subtypes across Europe has vastly improved (Lai et al, PLoS One 2012; 7:e42223; Santoro M et al, AIDS Res Hum Retroviruses 2012;28:1285-1293), as has our awareness of the clinical implications of transmitted drug resistance (TDR). A study carried out in treatment-naïve patients indicated that TDR might increase, rather than decrease, viral fitness, leading to faster progression of disease in newly infected individuals (Theys et al, Retrovirology 2012; 9:81).

WP5 - EPIDEMIOLOGY AND SURVEILLANCE OF RESISTANCE

Main objective: incorporate HIV resistance data into national HIV reporting structures, creating a common surveillance system for monitoring HIV resistance and the dynamics of HIV spread in resource poor regions and Europe, enabling accurate defining and reporting of the emergence and transmission of HIV resistance.

Associated specific objectives:

- Develop paradigms for linking resistance data to existing national HIV reporting structures.
- Develop cost effective mechanisms for pooling HIV drug resistance data at national level.
- Demonstrate an ability to apply real time phylogenetics to assist in mapping local spread of resistant viruses.
- Determine the optimal laboratory methods for cost effective surveillance of HIV resistance in resource limited settings and algorithms for management of resistance.
- Develop implementation strategies for surveillance of HIV resistance in RLS.
- Estimate the burden of resistance within the population as a whole.

Surveillance of resistance

A key achievement of WP5 has been the development of structures and protocols for pooling clinical, HIV drug-resistance and socio-demographic data at a national level. Merging these datasets has allowed application of real-time phylogenetics to map the dynamics of HIV spread. In a Belgian cohort, cluster transmission analyses are currently being performed to evaluate the factors involved in the spread of resistance in local settings. In Russia, a national database of HIV drug resistance, including transmitted drug resistance mutations, has been constructed for the first time.

Resistance in treated populations

Progress has been made towards understanding the factors associated with virological and immunological failure following treatment with combination antiretroviral therapy (cART) in RLS. Adherence of <95%, as determined by pharmacy refill, was shown to predict both virological and immunological failure. This may help to identify patients for viral load monitoring and drug resistance testing in RLS.

Gupta RK et al., Lancet Infectious Diseases 2009; 9(7): 409-17; Ndembi N at al., J Infect Dis. 2010 Jan 1; 201(1): 106-13.

Several members of WP5 contributed to a report on retrospective prevalence and time-trends of HIV drug resistance in ART-exposed individuals in Western Europe between 1997 and 2008 (De Luca et al. J Infect Dis. 2013; 207:1216-1220). A significant reduction in HIV drug resistance was observed in more recent calendar years, despite increasing drug exposure. Whole ART sequencing strategies were thought to contribute significantly to these improvements.

A further key activity of WP5 was coordination a policy forum to determine how knowledge on HIV drug resistance can guide WHO HIV treatment guidelines for RLS. An expert workshop was organized to identify evidence-based strategies for minimizing the selection and transmission of resistance in RLS. These discussions have been summarized and published (Pillay D et al, Antiviral Therapy 2013; 18:831-6).

Transmission of resistance

As more people join antiretroviral therapy (ART) programmes in RLS, it is important to improve understanding of transmitted drug resistance (TDR) in these settings. With support from the Bill and Melinda Gates Foundation, a meta-analysis was published describing global trends in ART resistance in drug naïve individuals following ART rollout in RLS (Gupta et al, Lancet. 2012; 380:125–1258).

Estimates of TDR are based upon a consensus list developed by the WHO that includes mutations identified before ART became available. A higher prevalence of polymorphisms has been shown to reduce the likelihood of correctly estimating the prevalence of TDR (Frentz et al., J Acquir Immune Def Syndrome 2011; 58:e135-e137), which may lead to unnecessary adaptation of treatment regimens or implementation of costly steps to limit drug resistance. As such, an updated list of TDR mutations across viral subtypes is in development. A report detailing our current understanding of TDR mutations across subtypes is available: www.who.int/hiv/pub/drugresistance/report2012/en/

Through generation of a mathematical model, WP5 predicted the potential future impact of TDR on mortality and treatment outcomes in RLS. When TDR prevalence is low, the impact of its elimination was predicted to be small. However, when prevalence is high, the impact became substantial with increasing time of follow-up (Figure) (Cambiano V et al., Infect Dis 2013; 207:S57-S62). As such, it will be important to remain vigilant over transmission of drug-resistant HIV.

Years from baseline	Prevalence of NNRTI TDR at baseline				
	<10%	10%–20%	20%–30%	30%–40%	>40%
0–15	1 (1–2)	2 (2–2)	3 (3–4)	5 (5–5)	7 (6–7)
15–30	4 (3–5)	7 (6–7)	9 (9–10)	12 (12–13)	16 (15–16)
30–45	5 (3–8)	8 (7–9)	10 (10–11)	14 (14–15)	18 (17–19)

Predicted impact of TDR on mortality. Estimated percent reduction (95% confidence interval) in death rate in people on ART if new TDR is preventedbased on a modeling comparison of predicted long-term mortality after baseline between the predicted outcome and that under a counterfactual scenario where new TDR is prevented. Abbreviations: ART, antiretroviral therapy; NNRTI, nonnucleoside reverse transcriptase inhibitor; TDR, transmitted drug resistance.

WP6: EVIDENCE-BASED PUBLIC HEALTH

Main objective: Translate clinical evidence into effective strategies and evidence-based recommendations for public health and regulatory authorities.

Associated specific objectives

- Assess and describe the potential risks for resistance development with rollout of antiretroviral therapy (ART) in resource-limited settings (RLS).
- Develop public health approaches to minimize development of resistance and its clinical consequences.
- Make recommendations and support EMA efforts to optimize guidance and strategies for use of ART to minimize drug resistance.
- Utilize contemporary epidemiological information on drug resistance to identify the potential utility of new antiretroviral drugs.
- Develop guidelines and strategies for post marketing surveillance to evaluate the resistance consequences of newly approved therapies.

Assessing risk of resistance

Work package 6 has significantly advanced understanding of the long-term impact of ART rollout in RLS on treatment failure and drug resistance. Overall, the data have been promising. A study in India reported good responses to first-line therapy for nearly four years (Neogi Uet al., PLoS One. 2013; 8:e55421) while in Senegal, the risk of virological failure following first-line ART for >5 years was low compared with high-resource settings (De Beaudrap P et al., J Acquir Immune Defic Syndr 2013; 62:381–387). In both studies, lower adherence with therapy increased the risk for treatment failure and drug resistance. Understanding these

issues is important, as the risk of virological failure at 24 months was shown to be high in the Senegal cohort after switching to second-line therapy.

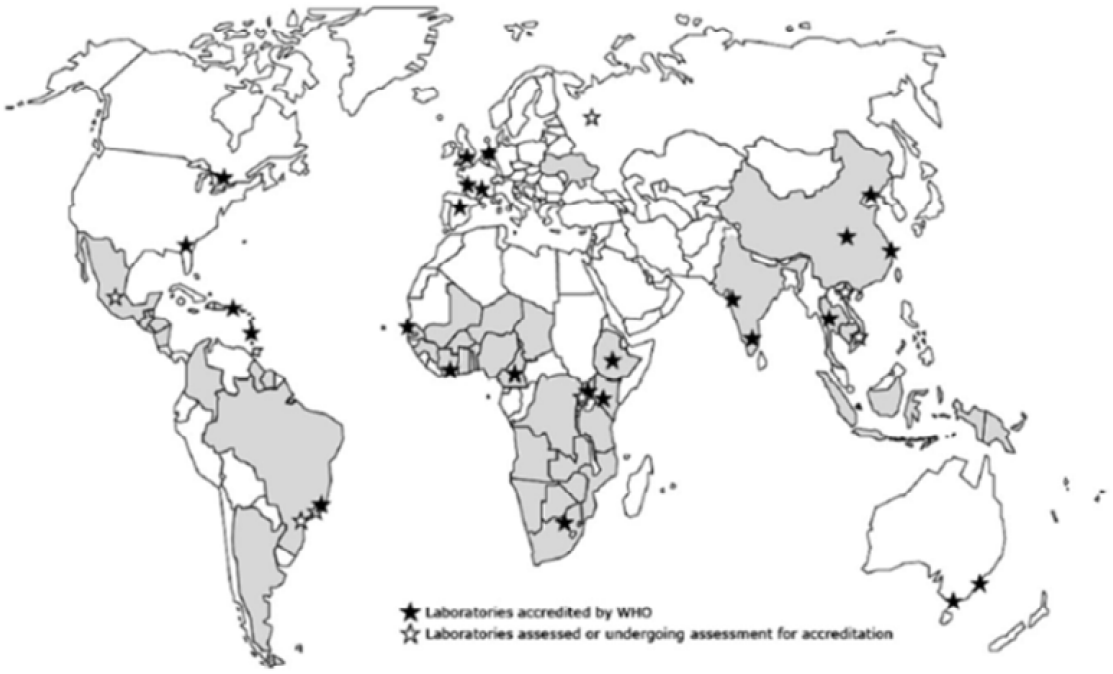
Modelling experiments have also produced highly informative data. A collaborative project with the WHO demonstrated that using tenofovir, rather than zidovudine, as a component of first-line therapy in RLS is cost-effective and more likely to preserve future treatment options in the absence of virological monitoring (von Wyl et al., PLoS One 2012; 7:e42834). Mathematical modelling further indicated that pre-exposure prophylaxis (PrEP) could be used as a cost-effective approach for preventing new HIV infections in RLS. Moreover, good adherence with therapy was predicted to reduce the risk of developing drug resistance if individuals became infected despite use of PrEP (Nichols et al, PloS One 2013; 8:e59549).

Public health approaches, guidelines and recommendations to minimize risk of resistance

A data and literature analysis carried out by WP6 concluded that detection of virologic failure within 12 months of initiating ART prevents the development of complex drug-resistance patterns and carries a low risk of compromising second-line treatment options in RLS. Since improved access to HIV drug resistance tests is clearly important in these settings, a simple and affordable assay was developed to detect phenotypic resistance to etravirine (ETR) and cross-resistance to other NNRTIs (Agneskog et al, J Med Virol 2013; 85:703-708).

Research carried out as part of WP6 contributed to a report on the WHO's HIV Drug Resistance Prevention and Assessment Strategy. As of June 2011, 52 countries had implemented at least 1 element of the strategy, and 27 laboratories had been accredited for HIV drug resistance genotyping to support assessment of acquired and transmitted HIV drug resistance in RLS (Figure) (Jordan et al, Clin Infect Dis 2012; 54:S245–249).

Based on data collated during the work programme, recommendations have been submitted to the EMA concerning the clinical development of medicinal products for the treatment of HIV, as well as the development of oral and topical HIV PrEP. In addition, numerous training events on HIV drug resistance have been developed and delivered to clinicians and epidemiologists in RLS.



Countries implementing at least 1 element of the World Health Organization (WHO) HIV drug resistance prevention and assessment strategy, and locations of laboratories undergoing assessment for HIV drug resistance genotyping accreditation, June 2011. From Jordan MR et al Clin Infect Dis, 2012;54:S245–249.

WP7- TRAINING AND CAPACITY BUILDING

Main objective: create a level playing field in the European and African scientific landscape in terms of scientific and clinical expertise in management of HIV drug resistance.

Associated specific objectives

- Define and implement minimally required standards of scientific and clinical expertise in HIV drug resistance in Europe (mainly Eastern) and Africa.
- Improve the scientific and clinical expertise of clinical practitioners, diagnosticians, epidemiologists and policy makers in HIV drug resistance, in order to reduce the adverse impact of HIV drug resistance.

Over the past 5 years, CHAIN partners have organized and implemented almost 40 workshops on HIV drug resistance throughout Europe and Africa, greatly exceeding the expectations of the work package. During this

time, partners involved in WP7 continually updated the training material for each of the training categories, to ensure inclusion of the latest developments and clinical data.

Highly regarded experts in the field of HIV drug resistance delivered courses in a variety of different formats, including face-to-face workshops, online presentations and discussion of clinical cases. Attendees included clinicians, epidemiologists, diagnosticians and policy makers.

Examples of workshops organized and successfully implemented as part of WP7

- Workshops in several African countries on ‘Early Infant Diagnosis of HIV’, including courses on ‘Clinical Management’, ‘Epidemiology and Surveillance’ and ‘Monitoring Tools’.
- Courses on ‘Advanced Diagnostics’ and ‘Antiviral Resistance in Europe’.
- Two- and four-day training courses on HIV resistance for clinicians, epidemiologists and medical officers in several Eastern European countries.
- Workshops on Drug Resistance in Africa, Asia and South America.
- A course on implementation of strategies for HIV RNA monitoring in resource-limited settings.

THE POTENTIAL IMPACT (INCLUDING THE SOCIO-ECONOMIC IMPACT AND THE WIDER SOCIETAL IMPLICATIONS OF THE PROJECT SO FAR) AND THE MAIN DISSEMINATION ACTIVITIES AND EXPLOITATION OF RESULTS

WP1- NOVEL RESISTANCE MECHANISMS

The focus of WP1 has been on expanding current knowledge on the mechanisms underlying resistance to existing and new antiviral drugs. The insight gained through WP1 research is essential to better clinically manage resistant viruses as they emerge, and to prevent further resistance development and spread. Understanding the genetic basis of resistance and cross-resistance is crucial for optimizing the use of existing drugs and for designing new antiviral agents and new therapeutic approaches.

The overall impact of the work package:

- Improved clinical management of drug resistant strains through improved understanding of drug-protein interactions.
- Detection of new resistance mutations using novel genotypic and phenotypic assays.
- Optimization of therapy and management of drug resistant strains via improved understanding of resistance mutations.

Remaining challenges and future research

- Continue to assess the effects of newly identified HIV-1 resistance mutations in combination with other NNRTI resistance mutations on drug susceptibility and replication.
- Determine the extent to which connection and RNase H domain mutations impact patient outcomes in HIV-1.
- Elucidate the impact of the polymerase V111I mutation in HIV-2.

WP2- LABORATORY MONITORING TOOLS

The general challenge of WP2 was to improve and validate new monitoring tools for the prediction and measurement of HIV resistance. Activities carried out as part of WP2 have helped to counter HIV drug resistance and impact the fight against HIV infection in RLS by:

- Developing simplified, cost-effective genotyping protocols and methods for handling clinical specimens, thereby improving access to HIV drug resistance genotyping information capable of optimizing therapeutic decisions.
- Extending knowledge on resistant minority species, providing the scientific basis for improved genotypic testing during the next decades.

- Standardizing genotypic tropism prediction and improving analysis of clinical samples with very low or undetectable viral load.
- Establishing rules for interpretation of genotypic HIV-2 resistance and providing free access to the list of identified HIV-2 resistance mutations.
- Refining the methods for establishing algorithms for genotype resistance interpretation.

Studies conducted to assess the clinical value of ultrasensitive genotyping showed that low frequency drug-resistant HIV-1 more than doubles the risk of virological failure to first-line NNRTI-based ART. This is the first time this question has been addressed using state of the art Next Generation Sequencing (NGS) technology in a well designed, multi-cohort; case-controlled study of several hundred HIV-1 infected individuals throughout Europe. It provides the scientific basis for improved genotypic testing during the decades to come. Further, work towards the standardization of NGS analyses (through establishing minimum technical and bioinformatics standards) should enable the development of tools to perform inter-laboratory QA/QC tests.

For the first time a list of mutations associated with HIV-2 resistance has been published and an automated tool for HIV-2 drug resistance analyses made freely available on the web: http://www.hiv-grade.de A panel of European experts voted on a rule set for interpretation of mutations in HIV-2 protease, reverse transcriptase, and integrase. The mutations listed here have been identified by 1 or more of the following criteria: (i) *in vitro* passage experiments or validation of contribution to resistance by using site-directed mutagenesis; (ii) susceptibility testing of laboratory or clinical isolates; (iii) nucleotide sequencing of viruses from patients in whom the drug is failing. This list of HIV-2 resistance mutations will be updated each year and a meeting in 2015 is planned.

In a broader context, the achievements of WP2 are many. They contribute to the possibility of generating and collecting HIV DR genotyping information from HIV-1 infected individuals in RLS, as has already been demonstrated in Uganda and South Africa. Having established a novel strategy for protease inhibitor susceptibility testing (using a cost-effective molecular-based assay) the potential is to optimise therapeutic decisions – particularly when the establishment of salvage regimens with protease inhibitors is required.

Future challenges for work related to WP2 are listed below:

- Update the list of HIV-2 resistance mutations on a yearly basis.
- Continue quality control assessment of the tropism prediction assay with a specific focus on non-B HIV subtypes.
- Continue the highly valuable activities of the NGS working group.

WP3- CLINICAL MANAGEMENT OF RESISTANCE

After five years of work the contribution of WP3 has improved our understanding of HIV drug resistance, particularly the clinical impact of transmitted drug resistant variants as well as the role of minority drug resistant variants on the virological outcomes of first-line and salvage ART. Tasks undertaken have set the clinical standard for drug resistance detection methodologies that have a direct impact on treatment strategies in high- and low-income settings. Also, studies undertaken in collaboration with WP2 and WP4 as well as with US research centres have allowed us to finally establish the relevance of the minority variants, which was an issue completely unknown when this grant started.

Work conducted as part of WP3 has facilitated the implementation of optimal therapeutic strategies that limit the spread of drug resistant variants in RLS and elsewhere by:

- Establishing a clinical standard for drug resistance detection methodologies in high- and low-income settings.
- Understanding of the clinical impact of TDR variants on the virological outcomes of first-line and salvage ART.
- Understanding, for the first time, the relevance of minority variants on the virological outcomes of first-line and salvage ART.
- Assessing the impact of viral subtype on responses to first-line therapy in adults and children.

A key future challenge in the fight against HIV and HIV drug resistance is to transfer expensive analytical systems to low-income settings. Improving or modifying technologies so that they can be implemented in a cost-effective manner may achieve this.

WP4 - MOLECULAR EPIDEMIOLOGY AND BIOINFORMATICS OF RESISTANCE

The main aim of WP4 is to provide a sustainable evidence base for better control of the HIV epidemic and management of infected individuals through development of comprehensive macro and micro-epidemiological bioinformatics tools that can be used to predict epidemiological trends and prevent any further expansion of HIV drug resistance.

Through the collaborative efforts of the work package a framework for merging large clinical databases into "super" datasets has been established. EuResist is already a very large resistance database, but can now be further expanded by clinical dataset like Eurosida and other national databases. These web-based "super" datasets provides Europe with a clear competitive advantage in large-scale research on several aspects of HIV infection, including resistance and epidemiology. They have paved the way forward for studies on HIV spread within Europe. The work is on going but has already provided new and deeper insights in to HIV epidemiology, which will ultimately lead to greater HIV prevention.

The overall impact of the work package:

- Provision of a platform for large-scale research on HIV drug resistance and epidemiology.
- New epidemiological information to guide design of HIV infection prevention programmes, in Europe as well as in RLS where these data were previously very limited.
- Improved understanding of how HIV resistance tests should be interpreted and availability of free, online treatment response prediction engines for everyday use in HIV clinics worldwide.
- Improved selection of the most effective drug combination therapies for individual patients using these web-based resources.
- Improved education and awareness of HIV drug resistance among doctors and epidemiologists through development and implementation of training programmes, particularly in former Soviet Union countries.

The impact and practical implications of WP4 findings can be summarized under the following subheadings:

Epidemiology

Large datasets have been generated for the most prevalent subtypes and recombinant HIV strains circulating in Europe and elsewhere in the world, including RLS. The results showed the global pattern of the spread of the epidemic e.g. areas acting as sources or sinks for viral infections, and in RLS. The expectation is that the data can be used to design interventions to prevent new infections. Other studies have shown that HIV epidemics are highly compartmentalized, and have also identified significant routes of HIV migration both within Europe and between Europe and other continents. Another significant achievement of WP4 was the combined effort to analyse HIV subtypes in remote Russian regions and former Soviet Union (FSU) countries for the first time. Several training programmes on HIV drug resistance have been developed and implemented in these regions.

In the broader context WP4 has aided in the development of improved tools for interpretation of HIV resistance that are freely accessible and thereby used all over the world. The development of a prototype system for predicting response to treatment in the absence of HIV genotype information is of significance in RLS where resistance testing might be difficult to incorporate in routine patient care. There is now better understanding of the predictors of adherence in RLS and the opportunity to build treatment response prediction engines that can work with or without genotypic information. The work programme was also first to combine the effort and expertise in HIV genotyping between all Russian-speaking FSU countries most of which are RLS.

Resistance

It has been seen that transmitted drug resistance of single mutations (especially NRTIs) originate predominantly from other TDR patients, rather than from treated patients. This could have a big influence on choices of first line regimen in the face of TDR. Evidence that transmission of drug resistance has the potential to increase viral fitness (rather than reduce it), due to preferential reversal of drug resistance mutations that reduce viral fitness, while compensatory mutations remain stable, is a valuable insight in to the mechanism of HIV resistance.

Future challenges

- Evaluate how progress in antiretroviral treatment and continuous human migration affect development and transmission of the different drug-resistant HIV strains worldwide.
- Use new data generating technology to track HIV spread and epidemiology to inform HIV education and prevention programmes.
- Use human genetic data to select candidates for HIV eradication pilot studies and to improve efficacy, safety and cost-effectiveness of antiretroviral treatment.
- Improve understanding of behaviour determinants of HIV transmission chains, to help guide prevention measures.
- Study the contribution of host factors on HIV infection treatment.
- Disseminate new knowledge effectively, including development of continuous medical education programmes for specialists in HIV/AIDS.

WP5 - EPIDEMIOLOGY AND SURVEILLANCE OF RESISTANCE

The focus of WP5 has been on assimilating the empiric data produced previously within the consortium to contribute to modelling. These approaches have been used to study the potential impact of transmitted drug resistance in the developing world, particularly regarding the trigger for change of antiretroviral guidance. Further, such approaches have been extended to consider the issue of treatment as prevention- a prevention paradigm that has rapidly gained credence during the existence of CHAIN. The work has focused not only on adults but also children. Despite major success in reducing mother to child transmission, the problem of treatment options for infected children remains high.

Finally, CHAIN has facilitated a number of country-wide studies on prevalence of resistance in treated and untreated individuals, which is reassurance that transmitted drug resistance is remaining low in a European context. This is not the case in the generalised epidemics in southern Africa, however.

Overall impact of the work package

- Improved selection of patients for viral load monitoring and drug resistance testing.
- Improved access to drug resistance testing in RLS.
- Identification of strategies to reduce drug resistance in RLS based on findings in developed countries.
- Potential to optimize treatment regimens using updated list of TDR mutations.
- Greater understanding of the potential impact of TDR in RLS.

Future challenges

- Continue to update the list of TDR mutations across viral subtypes.

- Introduce whole ART sequencing to RLS to help reduce prevalence of resistance to ART.
- Continue efforts to understand the dynamics of TDR spread, in an effort to reduce its prevalence and the associated mortality risk.

WP6: EVIDENCE-BASED PUBLIC HEALTH

The final year of CHAIN witnessed the increasing linkage of WP5 and WP6 activities, as the surveillance and epidemiology components of WP5 are utilised to develop epidemiological models that can inform public health. In particular, work with the World Health Organisation partner has taken CHAIN into the heart of international policy. 2013 witnessed the publication of the updated WHO guidelines for antiretroviral therapy. A number of questions remain, and we have directly addressed these. For instance, what level of transmitted drug resistance is needed to justify a change in policy from first line NRTI to first line PI therapy? What are the most cost effective means of monitoring antiviral rollout? CHAIN has led the world in such key analyses; the overall impact of the work package is outlined below:

- Optimization of initial therapy to help prevent further transmission of drug resistance.
- Improved strategies for the prevention and spread of HIV.
- Knowledge of the clinical value of PrEP in preventing new HIV infections in RLS, which can be used to inform prevention programmes.
- Improved access to drug resistance testing in RLS.
- Implementation of drug-resistance prevention strategies by numerous countries.
- New evidence-based recommendations to inform clinical practice guidelines.

Future challenges

- As access to ART expands, strengthen HIV drug resistance surveillance efforts in the face of increasing concern about HIV drug resistance emergence and transmission.
- Close gaps in knowledge on the impact of first-line resistance patterns on second-line outcomes through initiation of multi-centre trials.
- Improve knowledge regarding the impact of protease inhibitors and other ARTs on drug resistance.
- Continue surveillance of resistance at the time of treatment failure to allow optimal choice of ART and preservation of treatment options for life long therapy.

WP7- TRAINING AND CAPACITY BUILDING

Overall impact of the work package

- Improved management of HIV drug resistance among clinical practitioners and diagnosticians.
- Increased awareness among policy makers on the issue of HIV drug resistance.
- Development of a framework for implementing policies at the level of the National Health System.

Future challenges

The major challenge of the work programme was establishing a large network of courses in Eastern Europe and Africa and encouraging wide participation. Challenges moving forward include implementation of the remaining workshops and collection of pre- and post-test results of all courses organized in the framework of the CHAIN project.

4.2 Use and dissemination of foreground

Section A (public)

NO.	Title	Main author	Title of the periodical or the series	Number, date or frequency	Publisher	Year of publication	Relevant pages	Is/will open access be provided to this publication	Permanent identifiers (if avaiable)
1	Comparative performance of the REGA subtyping tool version 2 versus version 1.	Abecasis AB	Infections, Genetics and Evolution	10(3)	Elsevier	2009	380-5		
2	Effect of the human immunodeficiency virus type 1 reverse transcriptase polymorphism Leu-214 on Replication Capacity and Drug Susceptibility	Puertas MC	Journal of Virology	83(15)	Amercian Society for Microbiology	2009	1335-8	yes	10.1128/JVI.00487-09
3	Epidemiological and biological evidence for a compensatory effect of connection domain mutation N348	von Wyl V	J Infectious Diseases	201(7)	Pulsus Group	2009	647-56		

4	Factors associated with proviral DNA HIV-1 tropism in antiretroviral therapy-treated patients with fully suppressed plasma HIV viral load: implications for the clinical use of CCR5 antagonists	Soulie C	J Antimicrob Chemother	65(4)	Oxford University Press	2009	9094-101		
5	Molecular epidemiology reveals long-term changes in HIV type 1 subtype B transmission in Switzerland	Kouyos RD	J Infect Dis	201(10)	Chicago Journals	2009	1087-90		
6	Phylogenetic analysis of HIV sequences obtained in a respondent-driven sampling study of men who have sex with men.	Lepej SZ	AIDS Research and Human Retroviruses	25(12)	Mary Ann Liebert, Inc.	2009	2159-64	yes	doi: 10.1089/aid.2009.0130
7	Prevalence of etravirine mutations and impact on response to treatment in routine clinical care: the Swiss HIV Cohort Study (SHCS).	Scherrer AU	HIV Medicine	10(10)	Blackwell Publishing Ltd	2009	647-56	yes	doi: 10.1111/j.1468-1293.2009.00756

8	Gag determinants of fitness and drug susceptibility in protease inhibitor-resistant human immunodeficiency virus type 1.	Parry CM	J Virol	83(18)	Amercian Society for Microbiology	2009	9094-101	yes	doi: 10.1128/JVI.02356-08
9	The dynamics of appearance and disappearance of HIV-1 integrase mutations during and after withdrawal of raltegravir therapy.	Ferns RB	AIDS	23(16)	Lippincott Williams & Wilkins	2009	2159-64		doi:10.1097/QAD.0b013e32832ec4ae.
10	Virological monitoring and resistance to first-line highly active antiretroviral therapy in adults infected with HIV-1 treated under WHO guidelines: a systematic review and meta-analysis	Gupta RK	Lancet Infectious Diseases	9	Lancet	2009	409-417	no	
11	Prevalence of etravirine mutations and impact on response to treatment in routine clinical care: the Swiss	Scherrer AU	HIV Medicine	10	Blackwell Publishing Ltd	2009	647-656	yes	

	HIV Cohort Study								
12	Viral rebound and emergence of drug resistance in the absence of viral load testing: a randomized comparison between zidovudine-lamivudine plus Nevirapine and zidovudine-lamivudine plus Abacavir.	Ndembi N	Journal of Infectious Diseases	201(1)	Pulsus Group	2010	106-13		doi: 10.1086/648590
13	Determinants of HIV-1 transmission in men who have sex with men: a combined clinical, epidemiological and phylogenetic approach.	Fisher M	AIDS 2010	24(11)	Lippincott Williams & Wilkins	2010	1739-47		doi:10.1097/QAD.0b013e32833ac9e6.
14	Evolution of 2-long terminal repeat (2-LTR) episomal HIV-1 DNA in raltegravir-treated patients and in in vitro infected cells.	Reigadas S	J Antimicrob Chemother	65(3)	Oxford University Press	2010	106-13	yes	doi: 10.1093/jac/dkp473
15	Evolution of drug resistance during	Lyagoba F	J Aquir Immune	55(2)	Lippincott Williams &	2010	1739-47		

	48 weeks of zidovudine/lamivudine/tenofovir in the absence of real-time viral load monitoring		Defic Syndr		Wilkins				
16	Factors Associated with Virological Response to Etravirine in Nonnucleoside Reverse Transcriptase Inhibitor-Experienced HIV-1-Infected Patients	Marcelin AG	Antimicrob Agents Chemother	54(1)	Elsevier Science	2010	72-77		doi: 10.1128/AAC.01051-09
17	Full length HIV-1 gag determines protease inhibitor susceptability within in-vitro assays	Gupta RK	AIDS 2010	24	Lippincott Williams & Wilkins	2010	749-51		
18	High genetic barrier antiretroviral drugs in human immunodeficiency virus-positive pregnancy.	Zazzi M	Clin Infect Dis	50(6)	Infectious Diseases Society of America	2010	464-71	yes	doi: 10.1086/650748
19	HIV-1 replication and immune dynamics are affected by raltegravir intensification of HAART-	Buzon MJ	Nature Medicine	16(4)	Nature	2010	460-5	yes	doi: 10.1038/nm.2111

	suppressed subjects.								
20	Impact of Y143 HIV-1 integrase mutations on resistance to raltegravir in vitro and in vivo.	Delelis O	Antimicrob Agents Chemother	54(1)	Elsevier Science	2010	895-7		
21	Implementation of raltegravir in routine clinical practice: selection criteria for choosing this drug	Scherrer AU	J Acquir Immune Defic Syndr	53(4)	Lippincott Williams & Wilkins	2010	434-7		
22	In-vitro phenotypic susceptibility of HIV-2 clinical isolates to the integrase inhibitor S/GSK1349572.	Charpentier C	AIDS 2010	24(17)	Lippincott Williams & Wilkins	2010	2753-5		doi:10.1097/QAD.0b013e32833f9e36.
23	Partially active HIV-1 Vif alleles facilitate viral escape from specific antiretrovirals.	Fourati S	AIDS 2010	24(15)	Lippincott Williams & Wilkins	2010	2313-21	yes	doi:10.1097/QAD.0b013e32833e515a
24	Phylogenetic approach reveals that virus genotype largely determines HIV set-point viral load	Alizon S	PLoS Pathogens	6(9)		2010	1651-5		
25	Raltegravir has no residual antiviral activity in vivo	Wirden M	J Antimicrob	54(5)	Oxford University Press	2010	491-501		

	against HIV-1 with resistance-associated muta		Chemother						
26	Resistance analyses in highly experienced patients failing raltegravir, etravirine and darunavir/ritonavir regimen.	Charpentier, C	AIDS	24(17)	Lippincott Williams & Wilkins	2010	2651-6	yes	doi:10.1097/QAD.0b013e32833ed2a7
27	Secondary integrase resistance mutations found in HIV-1 minority quasispecies in integrase therapy-naive patients have little or no effect on susceptibility to integrase inhibitors	Ceccherini-Silberstein F	Antimicrob Agents Chemother	54(9)	American Society for Mircrobiology	2010	3938-3948	no	doi: 10.1128/AAC.01720-09
28	Changing patterns in HIV-1 non-B clade prevalence and diversity in Italy over three decades.	Lai A	HIV Med	11(9)	British HIV Association	2010	593-602	yes	doi: 10.1111/j.1468-1293.2010.00832.x
29	Comparative determination of HIV-1 co-receptor tropism by Enhanced Sensitivity Trofile, gp120 V3-loop	Prosperi MC	Retrovirology	07:56	BioMed Central Ltd.	2010		yes	doi: 10.1186/1742-4690-7-56

	RNA and DNA genotyping.								
30	Comparison of HIV-1 genotypic resistance test interpretation systems in predicting virological outcomes over time.	Frentz D	PLoS ONE	5(7)	Public Library of Science	2010	e11505	yes	doi: 10.1371/journal.pone.0011505
31	Different evolution of genotypic resistance profiles to emtricitabine versus lamivudine in tenofovir-containing regimens.	Svicher V	J Aquir Immune Defic Syndr	55(3)	Lippincott Williams & Wilkins	2010	336-44	yes	doi:10.1097/QAI.0b013e3181e6763f
32	Dihydrosphingomyelin impairs HIV-1 infection by rigidifying liquid-ordered membrane domains.	Vieira CR	Chem Biol.	17(7)	Cell Press	2010	766-75	yes	doi:10.1016/j.chembiol.2010.05.023
33	Dynamic escape of pre-existing raltegravir-resistant HIV-1 from raltegravir selection pressure.	Codoner FM	Antiviral Res.	88(3)	Elsevier Science	2010	281-6	yes	doi:10.1016/j.antiviral.2010.09.016
34	Dynamics of HIV-1 quasispecies during antiviral	Hedskog C	PLoS ONE	5(7)	Public Library of Science	2010	e11345	Is available open	

	treatment dissected using ultra-deep pyrosequencing.							access	
35	Efficacy and safety of ritonavir dose reduction based on the tipranavir inhibitory quotient in HIV-infected patients on salvage antiretroviral therapy with tipranavir/ritonavir.	Molto J	AIDS Res Hum Retroviruses	26(11)	Elsevier Science	2010	1191-6	yes	doi: 10.1089/aid.2009.0304
36	Evaluation of the genotypic prediction of HIV-1 coreceptor use versus a phenotypic assay and correlation with the virological response to maraviroc: the ANRS GenoTropism study	Recordon-Pinson P	Antimicrob Agents Chemother	54(8)	AAC	2010	3335-40	yes	doi: 10.1128/AAC.00148-10
37	Gag mutations can impact virological response to dual-boosted protease inhibitor combinations in	Larrouy L	Antimicrob Agents Chemother	54(7)	AAC	2010	2910-9	yes	doi: 10.1128/AAC.00194-10

	antiretroviral-naïve HIV-infected patients.								
38	HIV genetic diversity between plasma and cerebrospinal fluid in patients with HIV encephalitis.	Soulie, C	AIDS 2010	24(15)	Lippincott Williams & Wilkins	2010	2412-4	yes	doi:10.1097/QAD.0b013e32833e9245.
39	HIV type-1 drug resistance in antiretroviral treatment-naive adults infected with non-B subtype virus in the United Kingdom	Chilton DN	Antiviral Ther	15(7)		2010	985-91	no	doi: 10.3851/IMP1658
40	HIV-1 resistance patterns to integrase inhibitors in antiretroviral-experienced patients with virological failure on raltegravir-containing regimens.	da Silva D	J Antimicrob Chemother	65(6)	Oxford Journals	2010	1262-9	yes	doi: 10.1093/jac/dkq099
41	Impact of extensive HIV-1 variability on molecular diagnosis in the Congo basin	Bruzzone B	Journal of Clinical Virology	47(4)	Elsevier	2010	372-5	no	doi: 10.1016/j.jcv.2010.01.014
42	Impact of remote versus local	Balestrieri M	JCM	48(6)	JCM	2010	2321-2	yes	doi: 10.1128/JCM.02394-

	sampling on sensitivity of genotypic antiretroviral resistance testing.								09
43	Increasing prevalence of transmitted drug resistance mutations and non-B subtype circulation in antiretroviral-naive chronically HIV-infected patients from 2001 to 2006/2007 in France	Descamps D	J Antimicrob Chemother	65(12)	Oxford Journals	2010	2620-7	yes	doi: 10.1093/jac/dkq380
44	Low frequency of intermittent HIV-1 semen excretion in patients treated with darunavir-ritonavir at 600/100 milligrams twice a day plus two nucleoside reverse transcriptase inhibitors or monotherapy	Lambert-Niclot S	Antimicrob Agents Chemother	54(11)	AAC	2010	4910-3	yes	doi: 10.1128/AAC.00725-10
45	Low prevalence of transmitted drug resistance among newly diagnosed HIV-1 patients in Latvia.	Balode D	JMV	82(12)	WILEY PERIODICALS, INC.	2010	2013-8	yes	doi: 10.1002/jmv.21921

46	Mechanisms involved in the selection of HIV-1 reverse transcriptase thumb subdomain polymorphisms associated with nucleoside analogue therapy failure.	Betancor G	Antimicrob Agents Chemother	54(11)	AAC	2010	4799-811	yes	doi: 10.1128/AAC.00716-10
47	Minimal removal of raltegravir by hemodialysis in HIV-infected patients with end-stage renal disease.	Molto J	Antimicrob Agents Chemother	54(7)	AAC	2010	3047-8	yes	doi: 10.1128/AAC.00363-10
48	Performance of genotypic tropism testing in clinical practice using the enhanced sensitivity version of Trofile as reference assay: results from the OSCAR Study Group.	Svicher V	New Microbiol.	33(3)	New Microbiologica	2010	195-206	yes	
49	Permutation importance: a corrected feature importance measure.	Altmann A	Bioinformatics	26(10)	Oxford Journals	2010	1340-7	yes	doi:10.1093/bioinformatics/btq134
50	Pharmacokinetics, protein-binding-adjusted inhibitory	Lambert-Niclot S	HIV Med	11(10)	WILEY PERIODICALS, INC.	2010	666-9	yes	doi: 10.1111/j.1468-1293.2010.00839.x.

	quotients for atazanavir/ritonavir 300/100 mg in treatment-naïve HIV-infected patients.								
51	Prediction of the efficacy of bevirimat used for the treatment of HIV infection in Russia (article in Russian)	Kazennova EV	Vopr Virusol.	55(3		2010	37-41	no	
52	Resistance considerations in sequencing of antiretroviral therapy in low-middle income countries with currently available options.	De Luca A	Curr Opin HIV AIDS.	5(1)	Lippincott Williams & Wilkins	2010	27-37	yes	doi:10.1097/COH.0b013e328333ad45
53	Specific HIV-1 integrase polymorphisms change their prevalence in untreated versus antiretroviral-treated HIV-1-infected patients, all naive to integrase inhibitors.	Ceccherini-Silberstein F	J Antimicrob Chemother	65(11)	Oxford Journals	2010	2305-18	yes	doi: 10.1093/jac/dkq326
54	The risk of HIV drug resistance following	van de Vijver DA	Curr Opin Infect Dis	23(6)	Lippincott Williams & Wilkins	2010	621-7	yes	doi:10.1097/QCO.0b013e32833ff1e6

	implementation of pre-exposure prophylaxis.								
55	The use of human immunodeficiency virus resistance tests in clinical practice.	Ceccherini-Silberstein F	Clin Microbiol Infect.	16(10)	WILEY PERIODICALS, INC.	2010	1511-7	yes	doi: 10.1111/j.1469-0691.2010.03353.x.
56	Treatment simplification to once daily darunavir/ritonavir guided by the darunavir inhibitory quotient in heavily pretreated HIV-infected patients.	Molto J	Antiviral Ther	15(2)		2010	219-25	no	doi: 10.3851/IMP1519
57	Epidemiological and biological evidence for a compensatory effect of connection domain mutation N348I on M184V in HIV-1 reverse transcriptase	Von Wyl V	Journal of Infectious Diseases	201		2010	1054-1062		
58	Efficient suppression of minority quasispecies of drug-resistant viruses present at primary HIV-1 infection by RTV-boosted protease	Metzner KJ	Journal of Infectious Diseases	201		2010	1063-107		

	inhibitor containing antiretroviral therapy								
59	Implementation of raltegravir in routine clinical practice: selection criteria for choosing this drug, virological response rates and reasons for failure	Scherrer AU	Journal of the Acquired Immune Deficiency Syndromes	53		2010	464-471		
60	A novel methodology for large-scale phylogeny partition	Prosperi MC	Nat Commun	2	NPG	2011	321	no	doi: 10.1038/ncomms1325
61	A prognostic model for estimating the time to virologic failure in HIV-1 infected patients undergoing a new combination antiretroviral therapy regimen	Prosperi MC	BMC Med Inform Decis Mak	14;11		2011	40	yes	doi: 10.1186/1472-6947-11-40
62	A376S in the connection subdomain of HIV-1 reverse transcriptase confers increased risk of virological failure to nevirapine therapy	Parades R	J Infect Dis	204(5)	Pulsus Group	2011	741-52		

63	Added value of deep sequencing relative to population sequencing in heavily pre-treated HIV-1-infected subjects	Codoner FM	PLoS One	6(5)	Public Library of Science	2011	e19461		
64	Appearance of a single amino acid insertion at position 33 in HIV type 1 protease under a lopinavir-containing regimen, associated with reduced protease inhibitor susceptibility	Magiorkinis E	AIDS Res Hum Retroviruses	27(11)		2011	1223-9		
65	Assessing predicted HIV-1 replicative capacity in a clinical setting	Kouyos RD	PLoS Pathogens	7(11)		2011	e1002321		
66	Cellular HIV-1 DNA quantification and short-term and long-term response to antiretroviral therapy.	Masquelier B	J Antimicrob Chemother	66 (7)	Oxford Journals	2011	1582-9		
67	Characterization of human immunodeficiency virus type 1 (HIV-	Rieder P	Clin Infect Dis	53 (12)		2011	1271-9		

	1) diversity and tropism in 145 patients with primary HIV-1 infection								
68	Combined antiretroviral therapy and immune pressure lead to in vivo HIV-1 recombination with ancestral viral genomes.	Buzon MJ	J Aquir Immune Defic Syndr	57(2)	Lippincott Williams & Wilkins	2011	109-17		
69	Comparative antiviral activity of integrase inhibitors in human monocyte-derived macrophages and lymphocytes	Scopelliti F	Antiviral Res.	92(2)		2011	255-61		
70	Deep molecular characterization of HIV-1 dynamics under suppressive HAART.	Buzon MJ	PLoS Pathogens	7 (10)		2011	e1002314		
71	Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study	Prosperi MC	J Antimicrob Chemother	66 (8)	Oxford Journals	2011	1886-96	yes	doi: 10.1093/jac/dkr171

72	Docking analysis and resistance evaluation of clinically relevant mutations associated with the HIV-1 non-nucleoside reverse transcriptase inhibitors nevirapine, efavirenz and etravirine	Alcaro S	ChemMed Chem	6 (12)		2011	2203-13		
73	Drug resistance among drug-naive and first-line antiretroviral treatment-failing children in Cameroon	Fokam J	Pediatr Infect Dis J.	30 (12)		2011	1062-8		
74	Epidemiological network analysis in HIV-1 B infected patients diagnosed in Italy between 2000 and 2008	Callegaro A	Infection, Genetics and Evolution	11 (3)		2011	624-32		
75	Estimates of HIV transmitted drug resistance can be inflated due to natural sequence polymorphisms.	Frentz, D	J Acquir Immune Defic Syndr.	58 (5)		2011	e135-7		
76	HIV prevalence and route of transmission in Turkish	Schülter E	Med Microbiol Immunol	200 (4)		2011	219-23		

	immigrants living in North-Rhine Westphalia, Germany								
77	HIV Type 1 in a Rural Coastal Town in Kenya Shows Multiple Introductions with Many Subtypes and Much Recombination	Hue S	AIDS Research and Human Retroviruses	28(2)		2011	220-4		
78	HIV-1 dual/mixed tropic isolates show different genetic and phenotypic characteristics and response to maraviroc in vitro	Svicher V	Antiviral Res.	90 (1)		2011	42-53		
79	HIV-1 integrase: mechanisms of activity and inhibition (part II) (review in Russian)	M BOBKOVA	HIV-infection and immunosuppressions	3(3)		2011	13-23		
80	HIV-2 A-subtype gp125c_2-v_3-c_3 mutations and their association with CCR5 and CXCR4 tropism.	Dimonte S	Arch Virol.	156 (11)		2011	1943-51		

81	Identification and structural characterization of novel genetic elements in the HIV-1 V3 loop regulating coreceptor usage	Svicher V	Antiviral Ther	16(7)		2011	1035-45		
82	Impact of baseline HIV-1 tropism on viral response and CD4 cell count gains in HIV-infected patients receiving first-line antiretroviral therapy	Seclen E	J Infect Dis	204(1)	Pulsus Group	2011	139-44		
83	Improved virological outcome in White patients infected with HIV-1 non-B subtypes compared to subtype B	Scherrer, AU	Clin Infect Dis	53 (11)		2011	1143-52		
84	Interpretation of genotypic HIV-1 resistance to darunavir and virological response: validation of available systems and of a new score	De Luca A	Antiviral Ther	16 (4)		2011	489-97	yes	doi: 10.3851/IMP1799
85	Low frequency of HIV-1 tropism evolution in	Soulie C	AIDS 2011	25(4)	Lippincott Williams & Wilkins	2011	537-9	yes	doi:10.1097/QAD.0b013e32834345d3.

	patients successfully treated for at least 2 years.								
86	Molecular and epidemiology studies of HIV-1 prevalence in the Republic of Sakha (Yakutia) (article in Russian)	Kazennova EV	Vopr Virusol.	56(5)		2011	41759		
87	Molecular and structural aspects of clinically relevant mutations related to the approved non-nucleoside inhibitors of HIV-1 reverse transcriptase	Alcaro S	Drug Resist Updat.	14 (3)		2011	141-9		
88	Molecular characterization of HIV-1 CRF01_AE in Mekong Delta, Vietnam, and impact of T-cell epitope mutations on HLA recognition (ANRS 12159)	Lazaro E	PLoS One	6 (10)	Public Library of Science	2011	e26244		
89	Molecular epidemiology of HIV type 1 CRF02_AG in Cameroon and	Veras NM	AIDS Res Hum Retroviruses	27 (11)		2011	1173-82		

	African patients living in Italy								
90	On the problem of maternal and neonatal HIV drug resistance (article in Russian)	Bobkova MR	Vopr Virusol	56(5)		2011	47-9		
91	Performance evaluation of an in-house human immunodeficiency virus type-1 protease-reverse transcriptase genotyping assay in Cameroon	Fokam J	Arch Virol.	156 (7)		2011	1235-43		
92	Performance of ultra-deep pyrosequencing in analysis of HIV-1 pol gene variation	Mild M	PLoS One	6 (7)	Public Library of Science	2011	e22741		
93	Prediction of HIV-1 coreceptor usage (tropism) by sequence analysis using a genotypic approach	Sierra S	J Vis Exp	1 (58)		2011	3264	yes	doi: 10.3791/3264.
94	Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study)	Zazzi M	HIV Med	12 (4)		2011	211-8	yes	doi: 10.3851/IMP1799

95	Prevalence of resistance mutations related to integrase inhibitor S/GSK1349572 in HIV-1 subtype B raltegravir-naive and -treated patients	Malet I	J Antimicrob Chemother	66(7)	Oxford Journals	2011	1481-3		
96	Reappearance of minority K103N HIV-1 variants after interruption of ART initiated during primary HIV-1 infection.	Metzner KJ	PLoS One	6 (7)	Public Library of Science	2011	e21734		
97	Selected amino acid mutations in HIV-1 B subtype gp41 are associated with specific gp120v_3 signatures in the regulation of co-receptor usage	Dimonte S	Retrovirology	8(33)		2011		yes	doi:10.1186/1742-4690-8-33
98	Sentinel' mutations in standard population sequencing can predict the presence of HIV-1	Alteri C	J Antimicrob Chemother	66(11)	Oxford Journals	2011	2615-23		

	reverse transcriptase major mutations detectable only by ultra-deep pyrosequencing								
99	The estimation of personification influence upon HAART efficacy and safety: practical observations	Salamov, G	HIV-infection and immunosuppressions	3, N 3		2011	76-80		
100	The HIV-1 integrase G118R mutation confers raltegravir resistance to the CRF02_AG HIV-1 subtype	Malet I	J Antimicrob Chemother	66 (12)	Oxford Journals	2011	2827-30		
101	The role of migration and domestic transmission in the spread of HIV-1 non-B subtypes in Switzerland.	von Wyl V	J Infect Dis	204(7)	Pulsus Group	2011	1095-103		
102	Thymidine analogue excision and discrimination modulated by mutational complexes including single amino acid deletions of Asp-67 or Thr-69 in	Kisic M	J Biol Chem	286 (23)		2011	20615-24		dx.doi.org/10.1021/ja301565k

	HIV-1 reverse transcriptase								
103	Toward a quantitative understanding of viral phylogeography	Faria NR	Curr Opin Virol	1 (5)		2011	423-9		
104	Update on emergence of HIV-1 resistance to antiretroviral drug classes in an Italian national database: 2007-2009	Di Giambenedetto S	Clin Microbiol Infect	17 (9)		2011	1352-5		doi: 10.1111/j.1469-0691.2011.03563.x
105	Viral Suppression Rates in Salvage Treatment With Raltegravir Improved With the Administration of Genotypic Partially Active or Inactive Nucleoside/Tide Reverse Transcriptase Inhibitors	Scherrer A	J Acquir Immune Defic Syndr	57(1)		2011	24–31		
106	Resolution of Discordant HIV-1 Protease Resistance Rankings Using Molecular Dynamics Simulations	Wright, DW	Journal of Chemical Information and modelling	51	ACS Publications	2011	2636-2649		dx.doi.org/10.1021/ci200308r

107	Drug uptake transporters in antiretroviral therapy	Minuesa G	Pharmacol Ther	132 (3)		2011	268-79		
108	Residual activity of two HIV antiretroviral regimens prescribed without virological monitoring	Dunn, D.T	Antimicrobial agents and chemotherapy	55(10)	American Society for Mircrobiology	2011	4575-4580	no	doi: 10.1128/AAC.00580-11
109	Factors associated with virological failure in HIV-1-infected patients receiving darunavir/ritonavir monotherapy	Lambert-Niclot S	J Infect Dis	204(8)	Pulsus Group	2011	1211-6	yes	doi: 10.1093/infdis/jir518
110	Analysis of the prevalence of CCR5 coreceptor antagonist resistance mutations among HIV-1 variants in Russia (article in Russian)	Vasilyev A	Vopr Virusol	56(3)		2011	32-7	no	
111	Dynamics of two separate but linked HIV-1 CRF01_AE outbreaks among injection drug users in Stockholm, Sweden, and Helsinki, Finland.	Skar H	JVirol	85(1)	American Society for Mircrobiology	2011	510-8	No	

112	European Recommendations for the Clinical Use of HIV Drug Resistance Testing: 2011 Update	Vandamme AM	AIDS Rev	13(2)	Permanyer Publications	2011	77-108	yes	
113	Higher efficacy of nevirapine than efavirenz to achieve HIV-1 plasma viral load below 1 copy/ml.	Haim-boukobza, S	AIDS 2011	25(3)	Lippincott Williams & Wilkins	2011	341-4	yes	doi:10.1097/QAD.0b013e3283427de3
114	Impact of the N348I mutation in HIV-1 reverse transcriptase on nonnucleoside reverse transcriptase inhibitor resistance in non-subtype B HIV-1.	McCormick AL	Antimicrob Agents Chemother.	55(4)	AAC	2011	1806-9	yes	doi: 10.1128/AAC.01197-10
115	Low frequency HIV-1 drug resistance mutations and risk of NNRTI-based antiretroviral treatment failure	Li, J	JAMA	305(13)	JAMA	2011	1327-35	yes	doi: 10.1001/jama.2011.375
116	Molecular Epidemiological Analysis of Paired pol/env Sequences from Portuguese HIV Type 1 Patients.	Abecasis AB	AIDS Res Hum Retroviruses	27(7)	Mary Ann Liebert, Inc.	2011	803-5	yes	doi: 10.1089/AID.2010.0312

117	Plasma and intracellular (peripheral blood mononuclear cells) pharmacokinetics of once-daily raltegravir (800 milligrams) in HIV-infected patients.	Molto J	Antimicrob Agents Chemother	55(1)	AAC	2011	72-5	yes	doi: 10.1128/AAC.00789-10
118	Effect on transmission of HIV-1 resistance of timing of implementation of viral load monitoring to determine switches from first to second-line antiretroviral regimens in resource-limited settings	Phillips, A	AIDS	25	Lippincott Williams & Wilkins	2011	843–850	no	DOI:10.1097/QAD.0b013e328344037a
119	HIV-1 mutational pathways under multidrug therapy.	Lawyer G	AIDS Res Ther.	08:26	BioMed Central Ltd.	2011		yes	doi: 10.1186/1742-6405-8-26
120	Viral suppression rates in salvage treatment with raltegravir improved with the administration of genotypic partially active or inactive nucleoside/tide	Scherrer AU	Journal of Acquired Immune Deficiency Syndromes	57		2011	24–31		

	reverse transcriptase inhibitors								
121	Effect of transmitted drug resistance on virological and immunological response to initial combination antiretroviral therapy for HIV (EuroCoord-CHAIN joint project): a European multicohort study	The EuroCoord-CHAIN writing committee	Lancet Infectious Diseases	11(5)		2011	363-371		
122	Low-frequency HIV-1 Drug Resistance Mutations and the Risk of NNRTI-basedAntiretroviral Treatment Failure: A Systematic Review and Pooled Analysis	Li, J	Journal of the American Medical Association	305		2011	1327-1335		
123	Reappearance of minority K103N HIV-1 variants after interruption of ART initiated during primary HIV-1 infection	Metzner KJ	PLoS One	6(7)	Public Library of Science	2011	e21734		
124	The role of migration and	von Wyl V	Journal of Infectious	204(7)		2011	1095-1103		

	domestic transmission in the spread of HIV-1 non-B subtypes in Switzerland		Diseases						
125	Improved Virological Outcome in White Patients Infected With HIV-1 Non-B Subtypes Compared to Subtype B	Scherrer AU	Clinical Infectious Diseases	53(11)		2011	1143-1152		
126	Assessing predicted HIV-1 replicative capacity in a clinical setting	Kouyos RD	PLoS Pathogens	7(11)		2011	e1002321		
127	Characterization of Human Immunodeficiency Virus Type 1 (HIV-1) Diversity and Tropism in 145 Patients With Primary HIV-1 Infection	Rieder P	Clinical Infectious Diseases	53(12)		2011	1271-1279		
128	A non-infectious cell-based phenotypic assay for the assessment of HIV-1 susceptibility to protease inhibitors	Buzon MJ	J Antimicrob Chemother	67(1)	Oxford University Press	2012	32-8	no	doi:10.1093/jac/dkr433
129	Analysis of polymorphism of HIV-1 genome	Vasil'ev AV	Vopr Virusol	57(4)		2012			

	region coding for fusion protein								
130	Bioinformatical assistance of selecting anti-HIV therapies: where do we stand?	Lengauer T	Intervirology	55(2)	Karger	2012	108-12	yes	doi: 10.1159/000332000
131	Clinical, virological and biochemical evidence supporting the association of HIV-1 reverse transcriptase polymorphism R284K and thymidine analogue resistance mutations M41L, L210W and T215Y in patients failing tenofovir/emtricitabine therapy	Betancor G	Retrovirology	9: 68	BioMed Central Ltd.	2012		yes	doi: 10.1186/1742-4690-9-68
132	Comparative Analysis of Drug Resistance Among B and the Most Prevalent Non-B HIV Type 1 Subtypes (C, F, and CRF02_AG) in Italy.	Santoro, MM	AIDS Res Hum Retroviruses	28 (10)	Mary Ann Liebert, Inc.	2012	1285-93	yes	

133	Cost-effectiveness of tenofovir instead of zidovudine for use in first-line antiretroviral therapy in settings without virological monitoring	von Wyl V	PLoS One	7 (8)	Public Library of Science	2012	e42834	yes	doi:10.1371/journal.pone.0042834
134	Determinants of HIV drug resistance and public health implications in low- and middle-income countries.	Bertagnolio, S	Antivrial Ther	17 (6)		2012	941-53		doi: 10.3851/IMP2320
135	E138K and M184I mutations in HIV-1 reverse transcriptase coemerge as a result of APOBEC3 editing in the absence of drug exposure	Fourati S	AIDS	26	Lippincott Williams & Wilkins	2012	1619–1624		
136	E17A mutation in HIV-1 Vpr confers resistance to didanosine in association with thymidine analog mutations	Fourati S	Antiviral Res.	93 (1)		2012	167-74		
137	Effect of misclassification of antiretroviral treatment status on	Castro H	BMC Med Res Methodol.	12:30	BioMed Central Ltd.	2012		yes	doi: 10.1186/1471-2288-12-30

	the prevalence of transmitted HIV-1 drug resistance								
138	Efficacy of antiretroviral therapy switch in HIV-infected patients: a 10-year analysis of the EuResist Cohort	Oette M	Intervirology	55 (2)	Karger	2012	160-6		doi: 10.1159/000332018
139	Emerging mutations and associated factors in patients displaying treatment failure on an etravirine-containing regimen	Marcelin AG	Antiviral Ther	17 (1)		2012	119-23	no	doi: 10.3851/IMP1886.
140	Estimating the basic reproductive number from viral sequence data	Stadler T	Mol Biol Evol	29 (1)	Oxford Journals	2012	347-57		doi: 10.1093/molbev/msr217
141	Frequency and patterns of protease gene resistance mutations in HIV-infected patients treated with lopinavir/ritonavir as their first protease inhibitor	Barbar TJ	J Antimicrob Chemother	67 (4)	Oxford Journals	2012	995-1000		
142	Genetic and structural analysis of HIV-1 Rev responsive	Dimonte S	Intervirology	55 (5)		2012	385-90		

	element related to V38A and T18A enfuvirtide resistance mutations								
143	High frequency of antiviral drug resistance and non-B subtypes in HIV-1 patients failing antiviral therapy in Cuba	Kouri V	Journal of Clinical Virology	55		2012	348–355		
144	HIV-1 protease mutation 82M contributes to phenotypic resistance to protease inhibitors in subtype G	Palma AC	J Antimicrob Chemother	67 (5)	Oxford Journals	2012	1075-9		
145	HIV-1 Subtype F1 Epidemiological Networks among Italian Heterosexual Males Are Associated with Introduction Events from South America	Lai A	PLoS One	7 (8)	Public Library of Science	2012	e42223		
146	HIV-1 Molecular Epidemiology in the Balkans – A Melting Pot for High Genetic Diversity	M Stanojevic	AIDS Rev	14(1)		2012	28-36		
147	Impact of triplicate testing	Symons J	Clin Microbiol	18(6)		2012	606-12		

	on HIV genotypic tropism prediction in routine clinical practice		Infect						
148	In vitro phenotypic susceptibility of HIV-2 clinical isolates to CCR5 inhibitors	Visseaux B	Antimicrob Agents Chemother.	56 (1)		2012	137-9		
149	Incidence of HIV-1 drug resistance among antiretroviral treatment-naive individuals starting modern therapy combinations	von Wyl V	Clinical Infectious Diseases	54 (1)		2012	131-40		
150	Inferring epidemic contact structure from phylogenetic trees	Leventhal GE	PLoS Comput Biol	8 (3)		2012	e1002413		
151	Managing drug resistance in cancer: lessons from HIV therapy	Bock C	Nat Rev Cancer.	12 (7)		2012	494-501		doi: 10.1038/nrc3297
152	Molecular determinants of HIV-2 R5-X4 tropism in the V3 loop: development of a new genotypic tool	Visseaux B	J Infect Dis	205 (1)	Pulsus Group	2012	111-20		
153	Molecular Epidemiology of HIV-1 Subtypes	Neogi U	PLoS One	7 (6)	Public Library of Science	2012	e39819		

	in India: Origin and Evolutionary History of the Predominant Subtype C								
154	Naturally occurring hepatitis C virus (HCV) NS3/4A protease inhibitor resistance-related mutations in HCV genotype 1-infected subjects in Italy	Vicenti I	J Antimicrob Chemother	67 (4)	Oxford Journals	2012	984-7	yes	doi: 10.1093/jac/dkr581
155	Near full-length sequence analysis of HIV type 1 BF recombinants from Italy.	Saladini F	AIDS Res Hum Retroviruses	28 (3)		2012	299-303	yes	doi: 10.1089/aid.2011.0002
156	Persistent low-level HIV-1 RNA between 20 and 50 copies/mL in antiretroviral-treated patients: associated factors and virological outcome	Charpentier C	J Antimicrob Chemother.	67 (9)	Oxford Journals	2012	2231-5		
157	Phylodynamic and Phylogeographic Patterns of the HIV Type 1 Subtype F1 Parenteral Epidemic in Romania	Mbisa JL	AIDS Res Hum Retroviruses.	28 (9)		2012	1161-6		doi: 10.1089/AID.2011.0390.

158	Phylogenetic analysis of the Latvian HIV-1 epidemic	Balode D	AIDS Res Hum Retroviruses	28 (8)		2012	928-32		
159	Prevalence of HIV Type 1 Transmitted Drug Resistance in Slovenia: 2005–2010	Lunar MM	AIDS Res Hum Retroviruses.			2012	343-9		doi: 10.1089/AID.2012.0152
160	Prevalence of HIV-1 integrase mutations related to resistance to dolutegravir in raltegravir naı¨ve and pretreated patient	Saladini F	Clin Microbiol Infect.	18(10)		2012	E428-E430	no	doi: 10.1111/j.1469-0691.2012.03917.x
161	Prevalence of subtype-related polymorphisms associated with in vitro resistance to attachment inhibitor BMS-626529 in HIV-1 ‘non-B’-infected patients	Charpentier C	J Antimicrob Chemother	67(6)	Oxford Journals	2012	1459-61		
162	Quantized Water Access to the HIV-1 Protease Active Site as a Proposed Mechanism for Cooperative Mutations in Drug	Hall, BA	Biochemistry	52(33)	ACS Publications	2012	6487-6489		dx.doi.org/10.1021/bi300432u

	Affinity								
163	Resistance profiles of emtricitabine and lamivudine in tenofovir-containing regimens	Marcelin AG	J Antimicrob Chemother	67 (6)		2012	1475-8		
164	Resistance to antibody neutralization in HIV-2 infection occurs in late stage disease and is associated with X4 tropism	Marcelino, JM	AIDS	26(18)	Lippincott Williams & Wilkins	2012	2275-84		doi:10.1097/QAD.0b013e328359a89d
165	Resistant minority species are rarely observed in patients on darunavir/ritonavir monotherapy	Lambert-Niclot S	J Antimicrob Chemother	67 (6)	Oxford Journals	2012	1470-4		
166	Selected amino acid changes in HIV-1 subtype-C gp41 are associated with specific gp120V3 signatures in the regulation of co-receptor usage	Dimonte, S	Virus Res	168 (1-2)		2012	73-83		

167	Similar Evolution of Cellular HIV-1 DNA Level in Darunavir/Ritonavir Monotherapy versus Triple Therapy in MONOI – ANRS136 Trial over 96 Weeks	Lambert-Niclot S	PLoS One	7(7)	Public Library of Science	2012	e41390		
168	Standardized representation, visualization and searchable repository of antiretroviral treatment-change episodes	Rhee SY	AIDS Research and Therapy	9(1):13	BioMed Central Ltd.	2012		yes	doi: 10.1186/1742-6405-9-13.
169	Study of genotypic and phenotypic HIV-1 dynamics of integrase mutations during raltegravir treatment: a refined analysis by ultra-deep 454 pyrosequencing	Armenia D	J Infect Dis	205 (4)	Pulsus Group	2012	557-67		
170	Surveillance of HIV drug resistance in children receiving antiretroviral therapy: a pilot study of the World Health	Vaz P	Clinical Infectious Diseases	54 Suppl 4		2012	S369-74		doi:10.1093/cid/cis006

	Organization's generic protocol in Maputo, Mozambique.								
171	Targets for inhibition of HIV replication: entry, enzyme action, release and maturation	Sierra-Aragón, S	Intervirology	55 (2)		2012	84-97		
172	The HR2 polymorphism N140I in the HIV-1 gp41 combined with the HR1 V38A mutation is associated with a less cytopathic phenotype	Cunyat F	Retrovirology	9 (15)	BioMed Central Ltd.	2012		yes	doi: 10.1186/1742-4690-9-15.
173	The lowest X4 Geno2Pheno false-positive rate is associated with greater CD4 depletion in HIV-1 infected patients	Santoro, MM	Clin Microbiol Infect	18		2012	E289–E298		
174	Thumbs Down for HIV: Domain Level Rearrangements Do Occur in the NNRTI-Bound HIV-1 Reverse Transcriptase	Wright, DW	J Am Chem Soc	134(31)	ASC Publications	2012	12885-12888		
175	Time trends in drug resistant HIV-1 infections	Dolling D	BMJ	345		2012	e5253		doi: 10.1136/bmj

	in the United Kingdom up to 2009: multicentre observational study								
176	Transmitted HIV Drug Resistance Among Drug-Naive Subjects Recently Infected With HIV in Mexico City: A World Health Organization Survey to Classify Resistance and to Field Test Two Alternative Patient Enrollment Methods	Bertagnolio S	CID	54 Suppl 4		2012	S328-33		doi: 10.1093/cid/cir938
177	Treatment-associated polymorphisms inprotease are significantly associated withhigher viral load and lower CD4 count in newlydiagnosed drug-naive HIV-1 infected patients	Theys K	Retrovirology	9 (81)	BioMed Central Ltd.	2012		yes	doi: 10.1186/1742-4690-9-81
178	Update on World Health Organization HIV drug resistance prevention and	Jordan M	Clinical Infectious Diseases	54 Suppl 4		2012	S245-9		doi: 10.1093/cid/cis206

	assessment strategy: 2004-2011.								
179	World Health Organization generic protocol to assess drug-resistant HIV among children <18 months of age and newly diagnosed with HIV in resource-limited countries	Bertagnolio S	Clinical Infectious Diseases	54 Suppl 4		2012	S254-60		doi: 10.1093/cid/cis003
180	Global Conformational Dynamics of HIV-1 Reverse Transcriptase Bound to Non-Nucleoside Inhibitors	Wright, DW	Biology	1	www.mdpi.com/journal/biology	2012	222-244	Yes	doi:10.3390/biology1020222
181	Performance of genotypic tropism testing on proviral DNA in clinical practice: results from the DIVA study group	Svicher V	New Microbiologica	35 (1)		2012	17-25		
182	Global trends in antiretroviral resistance in treatment-naive individuals with HIV after rollout of antiretroviral treatment in	Gupta, RK	Lancet	380	Elsevier Science	2012	1250-8	yes	doi: 10.1016/S0140-6736(12)61038-1

	resource-limited settings: a global collaborative study and meta-regression analysis								
183	Polymorphic Mutations Associated With the Emergence of the Multinucleoside/Tide Resistance Mutations 69 Insertion and Q151M	Scherrer A	J Acquir Immune Defic Syndr	59(2)	Lippincott Williams & Wilkins	2012	105-12	yes	doi:10.1097/QAI.0b013e31823c8b69
184	The HIV-1 integrase genotype strongly predicts raltegravir susceptibility but not viral fitness of primaryvirus isolates	Buzon MJ	AIDS	24(1)	Lippincott Williams & Wilkins	2012	17-25	yes	doi:10.1097/QAD.0b013e328331c81e
185	Molecular-genetic characterization of the HIV-1 variants prevalent in Kyrghizia (article in Russian)	Laga V	Vopr Virusol.	57, N 5		2012	26-32		
186	Natural polymorphisms of HIV-1 IDU_A variant pol gene (article in Russian)	Kazennova E	HIV infection and immune disorders	4, N4		2012	44-51		

187	Molecular analysis of integrase coding HIV-1 pol gene region in patients from Russia and Uklraine (article in Russian)	Lapovok I	HIV infection and immune disorders	4, N4		2012	73-80		
188	Low Prevalence of Transmitted Drug Resistance in Patients Newly Diagnosed with HIV-1 Infection in Sweden 2003–2010	Karlsson, A	PLoS ONE	7(3)	Public Library of Science	2012	e33484	yes	doi:10.1371/journal.pone.0033484
189	Phylogenetic Analysis of the Latvian HIV-1 Epidemic	Balode, D	AIDS RESEARCH AND HUMAN RETROVIRUSES	28(8)	Mary Ann Liebert, Inc.	2012			DOI: 10.1089/aid.2011.0310
190	Incidence of HIV-1 Drug Resistance Among Antiretroviral Treatment - Naive Individuals Starting Modern Therapy Combinations	von Wyl V	Clinical Infectious Diseases	54(1)		2012	131-140		
191	Estimating the basic reproductive number from viral sequence data	Stadler T	Molecular Biology and Evolution	29(1)		2012	347–357		

192	Polymorphic mutations associated with the emergence of the multinucleoside/tide resistance mutations 69 insertion and Q151M	Scherrer AU	Journal of Acquired Immune Deficiency Syndromes	59		2012	105–112		
193	Inferring Epidemic Contact Structure from Phylogenetic Trees	Leventhal GE	PLOS Computational Biology	8(3)		2012	e1002413		
194	Minor protease inhibitor mutations at baseline do not increase the risk for a virological failure inHIV-1 subtype B infected patients	Scherrer AU	PLoS One	7(6)	Public Library of Science	2012	e37983		
195	Long-Lasting Protection of Activity of Nucleoside Reverse Transcriptase Inhibitors and Protease Inhibitors (PIs) by Boosted PI Containing Regimens	Scherrer AU	PLoS One	7(11)	Public Library of Science	2012	e50307		

196	The Prevalence of Transmitted Drug Resistance in Newly Diagnosed HIV-Infected Individuals in Croatia: The Role of Transmission Clusters of Men Who Have Sex with Men Carrying the T215S Surveillance Drug Resistance Mutation	Grgic I	AIDS Res Hum Retroviruses.	29(2)	Mary Ann Liebert, Inc.	2013	329-36	yes	doi: 10.1089/AID.2012.0191
197	A cohort study of treatment-experienced HIV-1-infected patients treated with raltegravir: factors associated with virological response and mutations selected at failure	Marcelin, AG	International Journal of Antimicrobial Agents	42(1)	Elsevier	2013	42-7		doi: 10.1016/j.ijantimicag
198	A Polymorphism at Position 400 in the Connection Subdomain of HIV-1 Reverse Transcriptase Affects Sensitivity to NNRTIs and RNaseH Activity	Wright, DW	PLOS ONE	8(10)	Public Library of Science	2013	e74078	yes	doi:10.1371/journal.pone.0074078
199	A Single Early	Murillo, W	Journal of	87(13)	American	2013	7463-	yes	doi:10.1128/JVI.01602

	Introduction of HIV-1 Subtype B into Central America Accounts for Most Current Cases		Virology		Society for Mircrobiology		7470		-12
200	An ancestral HIV-2/simian immunodeficiency virus peptide with potent HIV-1 and HIV-2 fusion inhibitor activity	Borrego, P	AIDS 2013	27(7)	Lippincott Williams & Wilkins	2013	1081–1090		
201	Antiretroviral Treatment Sequencing Strategies to Overcome HIV Type 1 Drug Resistance in Adolescents and Adults in Low-Middle-Income Countries	De Luca, A	The Journal of Infectious Diseases	207 (Suppl 2)	Pulsus Group	2013	S63-S69		
202	Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools	Pineda-Peña, A-C	Infection, Genetics and Evolution	19	Elsevier	2013	337–348		

203	Barriers to a cure for HIV: new ways to target and eradicate HIV-1 reservoirs.	Katlama C	Lancet, The	381(9883)	The Lancet	2013	2109-17	yes	doi: 10.1016/S0140-6736(13)60104-X
204	Circulation of HIV-1 CRF02_AG among MSM Population in Central Italy: A Molecular Epidemiology-Based Study	Giuliani, M	BioMed Research International		Hindawi Publishing Corporation	2013			Article ID 810617
205	Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response	Vercauteren, J	PLOS ONE	8(4)	Public Library of Science	2013	e61436		
206	Current Status of HIV-1 Diversity and Drug Resistance Monitoring In the Former USSR	Bobkova, M	AIDS Reviews. 2013	15(4)	Permanyer Publications	2013	204-12	yes	
207	Declining Prevalence of HIV-1 Drug Resistance in Antiretroviral Treatment-exposed	De Luca, A	The Journal of Infectious Diseases	207	Pulsus Group	2013	1216–20	yes	doi: 10.1093/infdis/jit017

	Individuals in Western Europe								
208	Differential impact of APOBEC3-driven mutagenesis on HIV evolution in diverse anatomical compartments	Fourati, S	AIDS 2014	28(4)	Lippincott Williams & Wilkins	2013	487–491		
209	Drug-resistance development differs between HIV-1-infected patients failing first-line antiretroviral therapy containing nonnucleoside reverse transcriptase inhibitors with and without thymidine analogues*	Santoro, MM	British HIV Association			2013	571–577	no	doi: 10.1111/hiv.12044
210	Dynamics of CD8 T-Cell Activation after Discontinuation of HIV Treatment Intensification.	Massanella, M	Journal of Acquired Immune Deficiency Syndromes	63(2)	Lippincott Williams & Wilkins	2013	152-60		doi:10.1097/QAI.0b013e318289439a.
211	Evolution of the human immunodeficiency virus type 2 envelope in the first years of	Rocha, C	Retrovirology	10:110	BioMed Central Ltd.	2013		yes	doi:10.1186/1742-4690-10-110

	infection is associated with the dynamics of the neutralizing antibody response								
212	Evolution of the K65R, K103N and M184V/I reverse transcriptase mutations in HIV-1-infected patients experiencing virological failure between 2005 and 2010	Charpentier, C	Journal of Antimicrobial Chemotherapy	68(10)	Oxford University Press	2013	2197-8	yes	doi: 10.1093/jac/dkt184
213	Evolving uses of oral reverse transcriptase inhibitors in the HIV-1 epidemic: from treatment to prevention	Gupta, RK	Retrovirology	10(82)	BioMed Central Ltd.	2013		yes	doi: 10.1186/1742-4690-10-82
214	Factors associated with a low HIV reservoir in patients with prolonged suppressive antiretroviral therapy	Fourati, S	Journal of Antimicrobial Chemotherapy	69	Oxford University Press	2013	753–756		
215	Functional conservation of HIV-1 Gag: implications for rational drug design	Li, G	Retrovirology	10:126	BioMed Central Ltd.	2013		yes	doi: 10.1186/1742-4690-10-126

216	Genetic barrier to the development of resistance to rilpivirine and etravirine between HIV-1 subtypes CRF02_AG and B	Fofana, DB	Journal of Antimicrobial Chemotherapy	68(11)	Oxford University Press	2013	2515-2	yes	doi:10.1093/jac/dkt251
217	Health benefits, costs, and cost-effectiveness of earlier eligibility for adult antiretroviral therapy and expanded treatment coverage: a combined analysis of 12 mathematical models	Eaton, JW	LancetGlobHealth2014;	2		2013	e23–34		
218	High Rate Of Antiretroviral Drug Resistance Mutations in HIV Type 1-Infected Senegalese Children in Virological Failure on First-Line Treatment According to the World Health Organization Guidelines	Kebe, K	AIDS RESEARCH AND HUMAN RETROVIRUSES	29(2)	Mary Ann Liebert, Inc.	2013	242-9	yes	doi:10.1089/aid.2011.0300
219	Highly multidrug-resistant HIV:	Todesco, E	Journal of Antimicro	68(12)	Oxford Journals	2013	2882-9	yes	doi: 10.1093/jac/dkt272

	clonal analysis and therapeutic strategies		bial Chemothe rapy						
220	HIV-1 drug resistance: where do polymorphisms fit in	Theys K	Future Microbiol ogy	8 (3)		2013	303-6		doi: 10.2217/fmb.13.10.
221	HIV-1 fitness landscape models for indinavir treatment pressure using observed evolution in longitudinal sequence data are predictive for treatment failure	Sangeda, RZ	Infection, Genetics and Evolution	19	Elsevier	2013	349–360		doi:10.1016/j.meegid.2013.03.014
222	HIV-1 genetic variation and drug resistance development	Megens, S	Expert-Reviews Anti Infect. Ther.	11(11)	Informa Ltd	2013	1159–1178		
223	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalize d epidemics	Abecasis, AB	Retrovirol ogy	10:07	BioMed Central Ltd.	2013			doi:10.1186/1742-4690-10-7
224	HIV-2EU: Supporting Standardized HIV-2 Drug Resistance Interpretation in	Charpentier, C	Clinical Infectious Diseases	56(11)	Oxford University Press	2013	1654-8	yes	doi: 10.1093/cid/cit104

	Europe								
225	Identification of a rare mutation at reverse transcriptase Lys65 (K65E) in HIV-1- infected patients failing on nucleos(t)ide reverse transcriptase inhibitors	Fourati, S	Journal of Antimicrobial Chemotherapy	68	Oxford University Press	2013	2199-2204		
226	Infections due to human immunodeficiency virus type 2 and human T-lymphotropic viruses in Spain	Trevin˜o, A	Medicina Clinica		Elsevier Espana	2013			
227	Influence of HIV infection on response to tenofovir in patients with chronic hepatitis B	Plaza, Z	AIDS 2013	27	Lippincott Williams & Wilkins	2013	2219–2224		
228	Inhibition of Dual/Mixed Tropic HIV-1 Isolates by CCR5-Inhibitors in Primary Lymphocytes and Macrophages	Surdo, M	PLOS ONE	8(7)	Public Library of Science	2013	e68076		
229	Limited cross-border infections in patients newly	Frentz, D	Retrovirology	10:36	BioMed Central Ltd.	2013		yes	doi: 10.1186/1742-4690-10-36

	diagnosed with HIV in Europe								
230	Low frequency of genotypic resistance in HIV-1-infected patients failing an atazanavir-containing regimen: a clinical cohort study	Dolling, DI	Journal of Antimicrobial Chemotherapy	68	Oxford University Press	2013	2339–2343		
231	National sentinel surveillance of transmitted drug resistance in antiretroviral-naive chronically HIV-infected patients in France over a decade: 2001 – 2011	Descamps, D	Journal of Antimicrobial Chemotherapy	68 (11)	Oxford University Press	2013	2626-31		
232	OPTIMISATION OF LABORATORY DIAGNOSTICS ALGORITHM AT THE CONFIRMATION STEPS OF HIV TESTING	Bobkova, M	ВИЧ□ИНФЕКЦИЯ И ИММУНОСУПРЕССИИ	ТОМ 5, No 2		2013			
233	Origin of Minority Drug-Resistant HIV-1 Variants in Primary HIV-1 Infection	Metzner, KJ	Journal of Infectious Diseases	208	Pulsus Group	2013			
234	Persistence of HIV-1	Castro, H	The Journal of	208	Pulsus Group	2013	1459-1463		

	Transmitted Drug Resistance Mutations		Infectious Diseases						
235	Predictors of Attrition and Immunological Failure in HIV- 1 Patients on Highly Active Antiretroviral Therapy from Different Healthcare Settings in Mozambique	Palladino, C	PLOS ONE	8(12)	Public Library of Science	2013	e82718		
236	Preexposure prophylaxis will have a limited impact on HIV-1 drug resistance in sub-Saharan Africa: a comparison of mathematical models	van de Vijver, DAMC	AIDS	27(18)	Lippincott Williams & Wilkins	2013	2943–2951		
237	RegaDB: community-driven data management and analysis for infectious diseases	Libin, P	BIOINFORMATICS	29(11)		2013	1477-1480		
238	Resistance to the most recent protease and non-nucleoside reverse transcriptase inhibitors across HIV-1 non-B	Anta, L	Journal of Antimicrobial Chemotherapy	68	Oxford University Press	2013	1994–2002		

	subtypes								
239	Rilpivirine resistance mutations in HIV patients failing non-nucleoside reverse transcriptase inhibitor-based therapies	Anta, L	AIDS	27	Lippincott Williams & Wilkins	2013	81–85		
240	Stability of unfrozen whole blood DNA for remote genotypic analysis of HIV-1 coreceptor tropism	Meini, G	BMC Infectious Diseases	13:508	BioMed Central Ltd.	2013		yes	doi: 10.1186/1471-2334-13-508
241	Structural modifications induced by specific HIV-1 protease-compensatory mutations have an impact on the virological response to the a first-line lopinavir/ritonavir-containing regimen	Alteri, C	Journal of Antimicrobial Chemotherapy		Oxford University Press	2013			
242	Superinfection with drug-resistant HIV is rare and does not contribute	Bartha, I	BMC Infectious Diseases		BioMed Central Ltd.	2013		yes	doi: 10.1186/1471-2334-13-537

	substantially to therapy failure in a large European cohort								
243	The Impact of HIV Drug Resistance on the Selection of First- and Second-Line ART in Resource-Limited Settings	Bertagnolio, S	Journal of Infectious Diseases	207(S2)	Pulsus Group	2013	S45-S48		
244	The impact of HIV-1 reverse transcriptase polymorphisms on responses to first-line nonnucleoside reverse transcriptase inhibitor-based therapy in HIV-1-infected adults	Mackie, NE	AIDS	27(14)	Lippincott Williams & Wilkins	2013	2245–2253		
245	The increasing genetic diversity of HIV-1 in the UK, 2002–2010	Dunn, D	AIDS	28(5)	Lippincott Williams & Wilkins	2013	773–780		
246	The Prevalence of Transmitted Drug Resistance in Newly Diagnosed HIV-Infected Individuals in Croatia: The Role of Transmission Clusters of Men Who Have Sex with Men	Grgic, I	AIDS RESEARCH AND HUMAN RETROVIRUSES	29(2)	Mary Ann Liebert, Inc.	2013	329-336		

	Carrying the T215S Surveillance Drug Resistance Mutation								
247	Towards Estimation of HIV-1 Date of Infection: A Time-Continuous IgG-Model Shows That Seroconversion Does Not Occur at the Midpoint between Negative and Positive Tests	Skar, H	PLOS ONE	8(4)	Public Library of Science	2013	e60906		
248	Transmitted drug resistance in French HIV-2-infected patients	Charpentier, C	AIDS 2013	27(10)	Lippincott Williams & Wilkins	2013	1671–1677		
249	Trends in Antiretroviral Therapy and Prevalence of HIV Drug Resistance Mutations in Sweden 1997–2011	Bontell, I	PLOS ONE	8(3)		2013			
250	Very late relapse after discontinuation of antiviral therapy for chronic hepatitis C	Soriano, V	Antiviral Therapy		International Medical Press	2013	1359-6535		

251	Drug Resistance Mutations and Genetic Diversity in Adults Treated for HIV Type 1 Infection in Mauritania	Fall-Malick, F-Zahra	Journal of Medical Virology		WILEY PERIODICALS, INC.	2013			
252	HIV-1 Subtype Is an Independent Predictor of Reverse Transcriptase Mutation K65R in HIV-1 Patients Treated with Combination Antiretroviral Therapy Including Tenofovir	Theys, K	Antimicrobial Agents and Chemotherapy	57(2)	American Society for Mircrobiology	2013	1053-6	yes	doi: 10.1128/AAC.01668-12
253	HIV-2 Susceptibility to Entry Inhibitors.	Borrego P	AIDS Reviews	15(1)		2013	49-61		
254	Antiretroviral Treatment Sequencing Strategies to Overcome HIV Type 1 Drug Resistance in Adolescents and Adults in Low-Middle-Income Countries	De Luca	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S63-S69	yes	doi: 10.1093/infdis/jit109.
255	Declining Prevalence of HIV-1 Drug Resistance in	De Luca A	Journal of Infectious Diseases	207(8)	Pulsus Group	2013	1216-20	yes	doi: 10.1093/infdis/jit017

	Antiretroviral Treatment-exposed Individuals in Western Europe								
256	Decreasing population selection rates of resistance mutation K65R over time in HIV-1 patients receiving combination therapy including tenofovir	Theys, K	Journal of Antimicrobial Chemotherapy	68(2)	Oxford Journals	2013	419-23	yes	doi: 10.1093/jac/dks380
257	Development of Antiretroviral Resistance in Children With HIV in Low- and Middle-Income Countries	Fitzgerald, F	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S85-S92	yes	doi: 10.1093/infdis/jit115
258	Emergence of HIV Drug Resistance During First- and Second-Line Antiretroviral Therapy in Resource-Limited Settings	Hosseinipour	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S49-S56	yes	doi: 10.1093/infdis/jit107
259	HIV-1 genetic variants in the Asian part of Russia: a study (2005-2010) (in	Kazennova EV	Vopr Virusol.	58(4)		2013	28-35		

	Russian)								
260	HIV-1 subtype distribution and its demographic determinants in newly diagnosed patients in Europe suggest highly compartmentalized epidemics	Abecasis AB	Retrovirology	10:07	BioMed Central Ltd.	2013			doi: 10.1186/1742-4690-10-7
261	Impact of Antiretroviral Drugs in Pregnant Women and Their Children in Africa: HIV Resistance and Treatment Outcomes	Paredes, R	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S93-S100	yes	doi: 10.1093/infdis/jit110
262	Low frequency of genotypic resistance in HIV-1-infected patients failing an atazanavir-containing regimen: a clinical cohort study	Dolling, DI	Journal of Antimicrobial Chemotherapy	68(10)	Oxford Journals	2013	2339-43	yes	doi: 10.1093/jac/dkt199
263	Mutations selected in HIV-2-infected patients failing a regimen including atazanavir	Cavaco-Silva J	JAC	68(1)	Oxford Journals	2013	190-2	yes	doi: 10.1093/jac/dks363
264	Nucleoside Reverse Transcriptase	Tang	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S70-S77	yes	doi: 10.1093/infdis/jit114

	Inhibitor Resistance Mutations Associated with First-Line Stavudine-Containing Antiretroviral Therapy: Programmatic Implications for Countries Phasing Out Stavudine								
265	Oral Antiretroviral Drugs as Public Health Tools for HIV Prevention: Global Implications for Adherence, Drug Resistance, and the Success of HIV Treatment Programs	Gupta, R	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S101-S106	yes	doi: 10.1093/infdis/jit108
266	Persistence of HIV-1 Transmitted Drug Resistance Mutations	Castro, H	Journal of Infectious Diseases	208(9)	Pulsus Group	2013	1459-63	yes	doi: 10.1093/infdis/jit345
267	Resistance at Virological Failure Using Boosted Protease Inhibitors Versus Nonnucleoside Reverse Transcriptase	Hill, A	Journal of Infectious Diseases	207 Suppl 2	Pulsus Group	2013	S78-S84	yes	doi: 10.1093/infdis/jit112.

	Inhibitors As First-Line Antiretroviral Therapy—Implications for Sustained Efficacy of ART in Resource-Limited Settings								
268	Transmission of Drug Resistant HIV and Its Potential Impact on Mortality and Treatment Outcomes in Resource-Limited Settings	Cambiano	Journal of Infectious Diseases	207, suppl 2	Pulsus Group	2013	S57-S62	no	doi: 10.1093/infdis/jit111
269	PCR-Induced Transitions Are the Major Source of Error in Cleaned Ultra-Deep Pyrosequencing Data	Brodin, J	PLoS ONE	8(7)	Public Library of Science	2013	e70388	Yes	doi:10.1371/journal.pone.0070388
270	Performance of ViroSeq HIV-1 genotyping system v2.0 on the HIV-1 strains circulating in Senegal	Thiam, M	Journal of Virological Methods	188	Elsevier	2013	97-103	yes	
271	HIV-1 genetic diversity and drug resistance and Senegalese patients in the	Thiam, M	Journal of Clinical Microbiology	51(2)	JournalsASM.org	2013	578-84		

	Public Health System								
272	Origin of minority drug-resistant HIV-1 variants in primary HIV-1 infection	Metzner KJ	The Journal of Infectious Diseases	208(7)		2013	1102-1112		
273	The Individualized Genetic Barrier Predicts Treatment Response in a Large Cohort of HIV-1 Infected Patients	Beerenwinkel N	PLOS Computational Biology	9(8)		2013	e1003203		
274	Adherence as a Predictor of the Development of Class-Specific Resistance Mutations: The Swiss HIV Cohort Study	von Wyl V	PLoS One	8(10)	Public Library of Science	2013	e77691		
275	Impact of Minority Nonnucleoside Reverse Transcriptase Inhibitor Resistance Mutations on Resistance Genotype After Virologic Failure	Li JZ	The Journal of Infectious Diseases	207		2013	893-897		

276	Changes in liver fibrosis in HIV/HCV-coinfected patients following different outcomes with peginterferon plus ribavirin therapy	Labarga, P	Journal of Viral Hepatitis	21(7)	John Wiley & Sons Ltd	2014	475-9		doi: 10.1111/jvh.12180
277	Cost-Effectiveness of PrEP in HIV/AIDS Control in Zambia - a Stochastic League Approach	Nichols, BE	JAIDS	66(2)	Lippincott Williams & Wilkins	2014	221-8	yes	doi:10.1097/QAI.0000000000000145
278	Longitudinal analysis of HIV-1 coreceptor tropism by single and triplicate HIV-1 RNA and DNA sequencing in patients undergoing successful first-line antiretroviral therapy	Meini, G	Journal of Antimicrobial Chemotherapy	69(3)	Oxford University Press	2014	735-41	yes	doi: 10.1093/jac/dkt426
279	Averted HIV infections due to expanded antiretroviral treatment eligibility offsets risk of transmitted drug resistance: a modeling study	Nichols, BE	AIDS 2014	28(1)	Lippincott Williams & Wilkins	2014	73–83		
280	Computing	Wright, DW	Journal of	10	ACS	2014	1228−12		doi.org/10.1021/ct4007

	Clinically Relevant Binding Free Energies of HIV-1 Protease Inhibitors		Chemical Theory and Computation		Publications		41		037
281	Discordances with HIV-1 RNA quantitative determinations by three commercial assays in Pointe Noire, Republic of Congo	Bruzzone, B	Journal of Virological Methods		Elsevier	2014		no	doi:10.1016/j.jviromet.2014.02.030
282	Dried Blood Spots for HIV-1 Drug Resistance Genotyping in Decentralized Settings in Senegal	Malick Diouara, AA	Journal of Medical Virology	86	WILEY PERIODICALS, INC.	2014	45–51		
283	Hepatitis Delta Is a Major Determinant of Liver Decompensation Events and Death in HIV-Infected Patients	Fernández-Montero, JV	Clinical Infectious Diseases	58(11)	Oxford University Press	2014	1549-53	yes	doi: 10.1093/cid/ciu167
284	HIV-2 Integrase Polymorphisms and Longitudinal Genotypic Analysis of HIV-2	Cavaco-Silva, J	PLOS ONE	9(3)	Public Library of Science	2014	e92747	yes	doi:10.1371/journal.pone.0092747

	Infected Patients Failing a Raltegravir-Containing Regimen								
285	HIV-2 viral tropism influences CD41 T cell count regardless of viral load	Trevino, A	Journal of Antimicrobial Chemotherapy		Oxford University Press	2014			
286	Longitudinal changes in viral RNA concentration in patients with chronic hepatitis C and/or HIV infection in the absence of antiviral therapy	Barreiro, P	Journal of Clinical Virology	58 (2013)	Elsevier	2014	391–395		
287	Patterns of Transmitted HIV Drug Resistance in Europe Vary by Risk Group	Frentz, D	PLOS ONE	9(4)	Public Library of Science	2014	e94495	yes	doi:10.1371/journal.pone.0094495
288	Residual HIV-1 Replication during CArt: The Role in Therapy Outcome	Lukashov, VV	Молекулярная диагностика	Том 1.	Коллектив авторов, 2014	2014			ISBN 978-5-906325-80-8
289	Spontaneous HCV clearance in HIV patients with chronic hepatitis C-bearing IL28B-CC alleles using antiretroviral therapy	Vispo, E	AIDS	28(10)	Lippincott Williams & Wilkins	2014	1473-8	yes	doi:10.1097/QAD.0000000000000275

290	The case for addressing primary resistance mutations to non-nucleoside reverse transcriptase inhibitors to treat children born from mothers living with HIV in sub-Saharan Africa	Ke´be, K	Journal of the International AIDS Society	17	PubMedCentral	2014	18526	yes	doi: 10.7448/IAS.17.1.18526
291	X4 tropic viruses are on the rise in recent HIV-1 seroconverters in Spain	Sierra-Enguita, R	AIDS	28	Lippincott Williams & Wilkins	2014			
292	Detection of low-frequency HIV type 1 reverse transcriptase drug resistance mutations by ultradeep sequencing in naive HIV type 1-infected individuals	Bellecave P	AIDS Res Hum Retroviruses	30(2)	Mary Ann Liebert, Inc.	2014	170-173	yes	doi: 10.1089/AID.2013.0130
293	Prevalence and evolution of low frequency HIV drug resistance mutations detected by ultra deep sequencing in patients experiencing first line antiretroviral	Vandenhende MA,	PLOS ONE	9(1)	Public Library of Science	2014	e86771	yes	doi:10.1371/journal.pone.0086771

	therapy failure.								
294	Treatment-naive individuals are the major source of transmitted HIV-1 drug resistance in men who have sex with men in the Swiss HIV Cohort Study	Drescher SM	Clinical Infectious Diseases	58(2)		2014	285-294		
295	Using an epidemiological model for phylogenetic inference reveals density dependence in HIV transmission	Leventhal GE	Molecular Biology and Evolution	31(1)		2014	6–17		
296	HIV 1 INTEGRASE: MECHANISMS OF ITS ACTIVITY AND INHIBITION (part I) (review in Russian)	Bobkova M	HIIV Infection and Immunosuppressive Disorders	2(4)					
297	Problems of subtyping of HIV-1 on the base of pol gene and ways of their transmission (article in Russian)	Kazennova E	ВИЧИНФЕКЦИЯ И ИММУНОСУПРЕССИИ	ТОМ 2, № 3					

298	Resistance-associated mutations to etravirine (TMC-125) in antiretroviral-naïve patients infected with non-B HIV-1 subtypes	Maiga AI	Journal of Antimicrobial Agents Chemotherapy	54(2)	AAC	2010	728-33		doi: 10.1128/AAC.01335-09
299	European guidelines on the clinical management of HIV-1 tropism testing	Vandekerckhove LP	Lancet Infectious Diseases	11(5)		2011	394-407		doi: 10.1016/S1473-3099(10)70319-4
300	High prevalence of antiretroviral drug resistance among HIV-1-untreated patients in Guinea-Conakry and in Niger	Charpentier C	Antiviriral Therapy	16(3)		2011	429-33		doi: 10.3851/IMP1754
301	Impact of lopinavir/ritonavir use on antiretroviral resistance in recent clinical practice	Lambert-Niclot S	Journal of Antimicrobial Agents Chemotherapy	67(10)		2012	2487-93		
302	HIV-1 integrase variability and relationship with drug resistance in antiretroviral-naive and experienced	Reigadas S	Journal of Antimicrobial Agents Chemotherapy	68(4)		2013	969-72		doi: 10.1093/jac/dks474

	patients with different HIV-1 subtypes								
303	Prevalence of HIV-1 drug resistance in treated patients with viral load >50 copies/mL in 2009: a French nationwide study	Assoumou L	Journal of Antimicrobial Agents Chemotherapy	68(6)		2013	1400-5		doi: 10.1093/jac/dkt033
304	Prevalence of pre-existing resistance associated mutations to rilpivirine, emtricitabine and tenofovir in antiretroviral-naive patients infected with B and non-B subtype HIV-1 viruses	Lambert-Niclot S	Journal of Antimicrobial Agents Chemotherapy	68(6)		2013	1237-42		doi: 10.1093/jac/dkt003
305	Rilpivirine, emtricitabine and tenofovir resistance in HIV-1-infected rilpivirine-naive patients failing antiretroviral therapy	Lambert-Niclot S	Journal of Antimicrobial Agents Chemotherapy	69(4)		2014	1086-9		doi: 10.1093/jac/dkt463
306	Liver fibrosis progression in HIV–HCV-coinfected patients	Fernández-Montero J	Antiviral Therapy		International Medical Press	2014			doi: 10.3851/IMP2703

	treated with distinct antiretroviral drugs and impact of pegylated interferon/ribaviri n therapy								
307	Association between HLA alleles and HAM/TSP in individuals infected with HTLV-1	Trevino, A	Journal of Neurolog y	260	Springer-Verlag Berlin Heidelberg	2013	2551-55		DOI 10.1007/s00415-013-7014-z
308	International BioInformatics Workshop on Virus Evolution and Molecular Epidemiology (Editorial)	Lemey P	Infection, Genetics and Evolution	19	Elsevier	2013	335-6		http://dx.doi.org/10.1016/j.meegid.2013.08.023
309	Scaling up epidemics of acute hepatitis C and syphilis in HIV-infected men who have sex with men in Spain	Sanchez S	Liver Internatio nal	33	John Wiley & Sons Ltd	2013	1357-62		DOI:10.1111/liv.12212

TEMPLATE A2: LIST OF DISSEMINATION ACTIVITIES					
No	**Type of Activities**	**Main Leader**	**Title**	**Date/Period**	**Place**
1	Workshop	Van de Vijver D	Treatment as prevention	Apr-13	Vancouver
2	Meeting	Van de Vijver D	HIV Modelling consortium	Jun-13	Kuala Lumpur
3	Conference	Van de Vijver D, Boucher C	Symposium "Africa's Realities in a Global Perspective"	Sep-13	Rotterdam
4	Conference	Boucher C	Netherlands Conference on HIV	Nov-13	Amsterdam
5	Conference	Van de Vijver D	11th International Congress on AIDS in Asia and the Pacific	Nov-13	Bangkok
6	Meeting	Van de Vijver D, Boucher C	Annual WHO HIV-Resnet	Mar-14	Boston
7	Conference	Van de Vijver D, Boucher C, Svicher V, Perno CF, De Luca A, Calvez V, Marcelin AG, Flandre P, Descamps D, Brun-Vezinet F, Soulie C, Lambert S, Ceccherini-Silberstein F, D'Arminio Monforte A, Mussini C, Cozzi Lepri A, Balotta C, Antinori A, Andreoni A, Anne-Mieke Vandamme, Carmen de Mendoza, Vicente Soriano, Ceccherini-Silberstein Santoro MM, Castagna A, R. Schuurman, Dimitrios Paraskevis	CROI	Mar-14	Boston
8	Conference	Svicher V, De Luca A, Perno CF, Ceccherini-Silberstein F, D'Arminio Monforte A, Mussini C, Cozzi Lepri A, Balotta C, Antinori A, Andreoni A, Ceccherini-Silberstein F, Armenia D, Santoro MM, Cento V, Surdo M Castagna A	Italian Conference on AIDS and Retroviruses	May-13	Turin
9	Conference	Svicher V, De Luca A, Perno CF,Calvez V, Marcelin AG, Flandre P, Descamps D, Charpentier C, Soulie C, Lambert S, Ceccherini-Silberstein F., Cozzi Lepri A	International HIV & Hepaptitus Virus Drug Resistance Workshop	Jun-13	Toronto

10	Conference	Svicher V, De Luca A, Perno CF, Ceccherini-Silberstein F, Mussini C, Marina Bobkova, Elena Kazennova, Natalya Glushchenko, Mario Poljak, Jan Albert, Anna Mia Ekström, Anne-Mieke Vandamme, Kristel Van Laethem, Andrea Pineda-Pena, Ricardo Camacho, Mónica Eusébio, Ana Abecasis, Maurizio Zazzi, Francesco Saladini, Alejandro Pironti, Ceccherini-Silberstein F, Armenia D, Santoro MM, Cento V, Dimitrios Paraskevis Maja Lunar	12th European Workshop on HIV & Hepatitus Treatment and Antiviral Drug Resistance	Mar-14	Barcelona
11	Conference	Calvez V, Descamps D, Flandre P	International Aids Society (IAS)	Jun-13	Kuala Lumpur
12	Conference	Calvez V, Descamps D, Marina Bobkova, Elena Kazennova, Vita Laga, Anne-Mieke Vandamme, Guangdi Li, Andrea Pineda, João Sousa, Monica Eusebio, Kristof Theys, Kristel Van Laethem, Barbara Bertmeyer, Osamah Hamouda, Ricardo Camacho, Ana Abecasis, Mónica Eusébio	European AIDS Clinical Society (EACS)	Oct-13	Brussels
13	Workshop	C Soulie, Z Ait-Arkoub, DB Fofana, S Lambert-Niclot, S Fourati, S Sayon, A Simon, C Katlama,F Raffi, P Flandre, V Calvez, AG Marceli	Low Frequency of Amino Acid Changes Associated With Resistance to Attachment Inhibitor BMS-626529 in R5- and X4-tropic HIV-1 B Subtypes	Jun-13	Toronto
14	Workshop	Slim Fourati, Sidonie Lambert-Niclot, Cathia Soulie, Marc Wirden, Benjamin Descours, Isabelle Malet, Marc Antoine Valantin, Roland Tubiana, Anne simon, Christine Katlama, Guislaine Carcelain, Francois Raffi, ,Anne-Genevieve Marcelin, Vincent Calvez	Differential impact of APOBEC3- driven mutagenesis on HIV evolution in diverse anatomical compartments	Jun-13	Toronto
15	Workshop	M Wirden, E Todesco, S Sayon, S Fourati R Tubiana, I Malet, C Katlama, V Calvez, and AG Marcelin	Highly Multi-Drug Resistant HIV: Clonal Analysis and Therapeutic Strategies	Jun-13	Toronto
16	Workshop	S Fourati, R Calin, G Carcelain, P Flandre, C Soulie, S Lambert-Niclot, Z Ait-Arkoub, R Tubiana, MA Valantin, B Autran, F Raffi, C	Factors Associated With Low HIV-1 Total DNA Levels After Suppressive Antiretroviral Therapy	Jun-13	Toronto

		Katlama, V Calvez, AG Marcelin			
17	Workshop	C Charpentier, M Bertine, B Visseaux, J Leleu, LLarrouy, G Peytavin, G Collin, - ,D Descamps	Invitro Phenotypic Susceptibility of HIV-1 non-B Integrase Inhibitor Naïve Clinical Isolates to Dolutegravir and Raltegravir	Jun-13	Toronto
18	Workshop	C Charpentier, V Joly, J Ghosn, F Raffi4, D Descamps, L Morand- Joubert	HIV-1 tropism switch in PBMC despite plasma virological success in patients receiving intensification with enfuvirtide	Jun-13	Toronto
19	Conference	Wittkop L	17th International Workshop on HIV Observational Databases	Apr-14	Cavtat, Croatia
20	Conference	Bobkova M	Socially significant infectious diseases: the problems of monitoring, diagnostics, epidemiology	Oct-13	Moscow
21	Conference	Bobkova M	Neuroscence and HIV Infection	Oct-13	St Petersburg
22	Conference	Marina Bobkova, Ilyalapovok	Japan-Russia International Workshop	Oct-13	Tokyo
23	Conference	IlyaLapovok	HIV-infection and tuberculosis	Nov-13	Moscow
24	Conference	Natalya Glushchenko, Elena Kazennova	HIV epidemic monitoring	Mar-14	Suzdal, Russia
25	Conference	Elena Kazennova, Natalya Glushchenko	Molecular diagnostics 2014	Mar-14	Moscow
26	Conference	IlyaLapovok	Open World program, Molecular Diagnostics	Mar-14	Omaha USA
27	Meeting	Anders Sönnerborg,/Maurizio Zazzi, Rolf Kaiser, Thomas Lengauer, Alejandro Pironti	AREVIR	Apr-13	Cologne
28	Meeting	Anne-Mieke Vandamme, Jurgen Vercauteren	ESAR	Mar-13	Rome
29	Meeting	Anne-Mieke Vandamme	11th European Meeting on HIV and Hepatitus - Treatment Strategies and Antiviral Drug Resistance	Mar-13	Rome
30	Conference	Anne-Mieke Vandamme	2e Congresso Nacional de Medicina Tropical	Apr-13	Lisbon
31	Conference	Anne-Mieke Vandamme	23rd ECCMID, European Society of Clinical Microbiology and Infectious Diseases	Apr-13	Berlin
32	Conference	Andrea Pineda-Pena, Nuno Faria, Bram Vrancken	20th International HIV Dynamics & Evolution Conference	May-13	Utrecht
33	Meeting	Anne-Mieke Vandamme	ECDC	Oct-13	Paris
34	Congress	Daniel Schmidt, Barbara Bertmeyer, Osamah Hamouda	German-Austrian AIDS Congress	Jun-13	Innsbruck

35	Congress	Vicente Soriano	The International Liver Congress™ 2013, 48th annual meeting of the European Association for the Study of the Liver	Apr-13	Amsterdam
36	Workshop	Vicente Soriano	9th Co-infection workshop	May-13	Rome
37	Workshop	Rocío Sierra, Vicente Soriano, Alejandro Pironti, Ceccherini-Silberstein F., Santoro MM, R. Schuurman	International HIV and Hepatitis Virus Drug Resistance Workshop	Jun-13	Toronto
38	Conference	Vicente Soriano	AASLD The liver meeting 2013	Nov-13	Washington
39	Conference	Ana Treviño, Lourdes Anta	V Congreso Nacional de GESIDA	Nov-13	Barcelona
40	Meeting	Ceccherini-Silberstein F	Collaboration Italy-South Africa on HIV-Drug resistance	May-13	Johannesburg
41	Conference	Informa (?)	17th CROI	Feb-10	San Francisco
42	Workshop	Informa (?)	8th European HIV Drug Resistance Workshop	Mar-10	Sorrento
43	Conference	Svicher V, Cento V, Rozera G, Abbate I, Palamara G, Rizzardini G, Sarmati L, Ceccherini-Silberstein F, Capobianchi MR, Perno CF	18th CROI	Feb-11	
44	Workshop	Armenia D, Santoro MM, Santoro M, Fabeni L, Gori C, Forbici F, Cento V, Svicher V, Bertoli A, Dori L, Giuliani M, Palamara G, Boumis E, Zaccarelli M, Bellagamba R, Andreoni M, Antinori A, Ceccherini-Silberstein F and Perno CF, Y Feng, J Vercauteren, AP Carvalho, I Diogo, P Gomes, AM Vandamme, RJ Camacho	9th European Workshop on HIV & Hepatitis	Mar-11	Paphos
45	Conference	Santoro* MM, Armenia D, Fabeni L, Santoro M, Gori C, Forbici F, Cento V, Svicher V, Bertoli A, Dori L, Andreoni M, Narciso P, Antinori A, Ceccherini-Silberstein F, and Perno CF	3rd ICAR (Italian Conference on AIDS and Retroviruses)	Mar-11	Florence

46	Conference	Armenia D, Vandenbroucke I , Fabeni L, D'Arrigo R, VanBaelen K, VanMarck H, Micheli V, VanWesenbeeck L, Trotta MP, LoCaputo S, Bruzzone B, Capetti A, DiPerri G, Narciso P, Rizzardini G, Antinori A, Stuyver L, Perno CF, Ceccherini-Silberstein F	2nd ICAR	Jun-10	Brescia
47	Workshop	JC Silva, MF Gonçalves, KV Laethem, AM Vandamme, P Gomes, J Machado, R Abreu, N Janeiro, C Cunha, RJ Camacho	International HIV & Hepatitus Virus Drug Resistance Workshop	Jun-10	Dubrovnik
48	Congress	S Bertagnolio	11th International Congress on Drug therapy in HIV Infection	Nov-10	Glasgow
49	Conference	Icona (?) & UTV (?)	6th IAS Conference on HIV Pathogenesis, Treatment and Prevention	Jul-11	Rome
50	Workshop	Ricardo Camacho	?	?	Ljubliana
51	Conference	Anta L, Llibre JM, Poveda E, Blanco JL, García F, Pérez Elías MJ, Aguilera A, Caballero E, Soriano V, de Mendoza C, Beheydt G, Theys K, Clotet B, Schülter E, Schmit JC, Sönnerborg A, Zazzi M, Van Laethem K, Camacho R, Vandamme AM	19th CROI	Mar-12	Seattle
52	Conference	Claudia Bianco, Barbara Rossetti, Lara Ines Bellazzi, Bianca Bruzzone, Grazia Colao, Paola Corsi, Laura Monno, Gabriella Pagano, Stefania Paolucci, Grazia Punzi, Maurizio Setti, Maurizio Zazzi, Andrea De Luca	13th European Aids Conference/EACS	Oct-11	Belgrade
53	Workshop	Santoro MM, Cento V, Borghi V, Fabeni L, Armenia D, Gori C, Bertoli A, Garau M, Andreoni M, Nicastri E, Ammassari A, Loiacono L, Libertone R, Termini R, Zaccarelli M, Antinori A, Mussini C, Perno CF, Ceccherini Silberstein F., De Luca Andrea, Meini Genny, Rossetti Barbara, Bianco Claudia, Di Giambenedetto Simona, Sighinolfi Laura, Monno Laura, Castagna Antonella, Capobianchi Maria Rosaria, d'Arminio Monforte Antonella and Zazzi	10th European Workshop on HIV & Hepatitis	Mar-12	Barcelona

		Maurizio			
54	Workshop	Sangeda RZ, F Mosha, S Aboud, A Kamuhabwa, E Lyamuya, A-M Vandamme	5th International workshop on HIV Treatment, Pathogenesis and Prevention Research in Resource Limited Settings, INTEREST	May-11	Dar-el-salaam
55	Workshop	J Kjær, DK Kristensen, G Beheydt, S Imbrechts, M Rickenbach, I Fanti, F Incardona and A-M Vandamme	International Workshop on HIV 7 Hepatitis Virus Drug Resistance & Curative Strategies	Jun-11	Los Cabos
56	Meeting	Anne-Mieke Vandamme, Kristel Van Laethem, Sarah Megens, Bram Vrancken, Gertjan Beheydt, Kristof Theys, Yang Feng, Lore Vinken, Yoeri Schrooten, Andrea Pineda, Guangdi Li	1st BREACH Symposium (Belgian Research AIDS & HIV Consortium)	Sep-11	Leuven
57	Conference	?	All-Russian Conference on HIV Drug Resistance	Sep-11	?
58	Conference	Informa (?)	4th ICAR	Jun-12	Naples
59	Congress	Anne-Mieke Vandamme	21st ECCMID (European Congress of Clinical Microbiology and Infectious Diseases)	May-10	Milan
60	Conference	Anne-Mieke Vandamme	9th SIMPAIDS – Brazilian AIDS Research Conference	Sep-11	Salvador
61	Workshop	Anne-Mieke Vandamme	Segundo workshop brasileiro em banco de dados de sequências do HTLV-1 e HIV-1 para o estudo de retroviroses humanas e suporte de vacinas	Sep-11	Salvador
62	Conference	Li Guangdi	9th European Conference on Computational Biology	Sep-10	Ghent

63	Workshop	Surdo M, Di Santo F, Pollicita M, Orlandi C, Malet I, Calvez V, Marcelin A G, Casabianca A, Magnani M, Perno CF, Ceccherini-Silberstein F	8th International Workshop, HIV, Cells Macrophage/Dendritic Lineage, and other Reservoirs: Pathogenic and Therapeutic Implications	May-12	Stresa
64	Conference	Linda Wittkop, Laga V, Kazennova E, Vasilyev A, Lapovok, Kuz'mina A, Mikryukova Y, Aleksashkina A, Bobkova M	20th CROI	Mar-13	Atlanta
65	Congress	Seme K, Lunar MM, Tomažič J, Vidmar L, Karner P, Matičič M, Poljak M	6th National Congress HIV/AIDS	May-12	Sibiu
66	Meeting	Poljak M, Seme K, Lunar MM, Tomažič J	14th International Symposium on Viral Hepatitis and Liver Disease	Jun-12	Shanghai
67	Workshop	Lunar MM, Abecasis AB, Vandamme AM, Poljak M	17th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology	Aug-12	Belgrade
68	Congress	V Laga, E Kazennova, D Rukavitsyn, I Lapovok, D Neshumaev, M Bobkova	5th Annual all-Russian Congress on infectious diseases	Ma-13	Moscow
69	Conference	S Bertagnolio	International AIDS Conference	Jul-11	Washington
70	Oral	Faria NR	National Institute for Public Health Research	Apr-13	Lisbon
71	Conference	Vercauteren J, Feng Y, Carvalho AP, Diogo I, Gomes P, Vandamme AM, Camacho RJ	Leuven Statistics Days 2012	Jun-12	Leuven
72	Workshop	Faria NR	Workshop on Phylogenetics and large HIV-1 sequence databases	Aug-12	Belgrade
73	Meeting	Vercauteren J, Theys K, Carvalho AP, Valadas E, Duque LM, Teofilo E, Faria T, Faria D, Vera J, Aguas MJ, Peres S, Mansinho K, Vandamme AM, Camacho R	BREACH meeting	Sep-12	Brussels
74	Conference	Faria N., Bedford T., Ward M., Tatem A., Posada D., Peeters M., Arinaminpathy N., Suchard M., Pybus O., Rambaut A., Lemey P	The Infectious Disease Genomics and Global Health Conference	Oct-12	Cambridge
75	Conference	Vrancken, B., Rambaut, A., Baele, G., Vandamme, AM., Van Laethem, K., Van Wijngaerden, E., Drummond, A., Suchard, M., Lemey, P	International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases	Nov-12	New Orleans
76	Workshop	Vandamme AM, Camacho RJ.	7th South African HIV Drug Resistance and Treatment	Nov-12	Cape Town

			Monitoring Workshop		
77	Conference	Vrancken, B., Rambaut, A., Baele, G., Vandamme, AM., Van Laethem, K., Van Wijngaerden, E., Drummond, A., Suchard, M., Lemey, P	International Work-Conference on Bioinformatics and Biomedical Engineering	Mar-13	Granada
78	Workshop	Pantxika Bellecave1, Roger Paredes2, Lourdes Anta3, Vicente Soriano3, Anne-Geneviève Marcelin4, Anna-Maria Geretti5, Valentina Svicher6, Diane Descamps7, Ricardo Jorge Camacho8, Christophe Rodriguez9, Hervé Fleury1,11, Rolf Kaiser10, Bernard Masquelier1	International Workshop on HIV & Hepatitis Virus.	Jun-12	Sitges
79	Workshop	Ana Abecasis	Workshop on Phylogenetics and large HIV-1 sequence databases	Aug-12	?
80	Meeting	D. Paraskevis	ESAR scientific meeting	Mar-13	?

Section B (Confidential[1] or public: confidential information to be marked clearly)
Part B1

TEMPLATE B1: LIST OF APPLICATIONS FOR PATENTS, TRADEMARKS, REGISTERED DESIGNS, ETC.					
Type of IP Rights[2]:	Confidential Click on YES/NO	Foreseen embargo date dd/mm/yyyy	Application reference(s) (e.g. EP123456)	Subject or title of application	Applicant (s) (as on the application)
N.A.					

[1] Note to be confused with the "EU CONFIDENTIAL" classification for some security research projects.

[2] A drop down list allows choosing the type of IP rights: Patents, Trademarks, Registered designs, Utility models, Others.

Part B2

Please complete the table hereafter:

Type of Exploitable Foreground[3]	Description of exploitable foreground	Confidential Click on YES/NO	Foreseen embargo date dd/mm/yyyy	Exploitable product(s) or measure(s)	Sector(s) of application[4]	Timetable, commercial or any other use	Patents or other IPR exploitation (licences)	Owner & Other Beneficiary(s) involved
	Ex: New superconductive Nb-Ti alloy			*MRI equipment*	*1. Medical* *2. Industrial inspection*	*2008* *2010*	*A materials patent is planned for 2006*	*Beneficiary X (owner) Beneficiary Y, Beneficiary Z, Poss. licensing to equipment manuf. ABC*
N.A.								

In addition to the table, please provide a text to explain the exploitable foreground, in particular:

- Its purpose
- How the foreground might be exploited, when and by whom
- IPR exploitable measures taken or intended
- Further research necessary, if any
- Potential/expected impact (quantify where possible)

[19] A drop down list allows choosing the type of foreground: General advancement of knowledge, Commercial exploitation of R&D results, Exploitation of R&D results via standards, exploitation of results through EU policies, exploitation of results through (social) innovation.

[4] A drop down list allows choosing the type sector (NACE nomenclature) : http://ec.europa.eu/competition/mergers/cases/index/nace_all.html

4.3 Report on societal implications

A General Information *(completed automatically when **Grant Agreement number** is entered.*

Grant Agreement Number:	223131
Title of Project:	Collaborative HIV and Anti-HIV Drug Resistance Network
Name and Title of Coordinator:	Prof. Deenan Pillay

B Ethics

1. Did your project undergo an Ethics Review (and/or Screening)? • If Yes: have you described the progress of compliance with the relevant Ethics Review/Screening Requirements in the frame of the periodic/final project reports? Special Reminder: the progress of compliance with the Ethics Review/Screening Requirements should be described in the Period/Final Project Reports under the Section 3.2.2 *'Work Progress and Achievements'*	***Yes***
2. Please indicate whether your project involved any of the following issues (tick box) :	***YES***
RESEARCH ON HUMANS	
• Did the project involve children?	Yes
• Did the project involve patients?	Yes
• Did the project involve persons not able to give consent?	No
• Did the project involve adult healthy volunteers?	No
• Did the project involve Human genetic material?	No
• Did the project involve Human biological samples?	Yes
• Did the project involve Human data collection?	Yes
RESEARCH ON HUMAN EMBRYO/FOETUS	
• Did the project involve Human Embryos?	No
• Did the project involve Human Foetal Tissue / Cells?	No
• Did the project involve Human Embryonic Stem Cells (hESCs)?	No
• Did the project on human Embryonic Stem Cells involve cells in culture?	No
• Did the project on human Embryonic Stem Cells involve the derivation of cells from Embryos?	No
PRIVACY	
• Did the project involve processing of genetic information or personal data (eg. health, sexual lifestyle, ethnicity, political opinion, religious or philosophical conviction)?	Yes
• Did the project involve tracking the location or observation of people?	
RESEARCH ON ANIMALS	
• Did the project involve research on animals?	Yes
• Were those animals transgenic small laboratory animals?	No
• Were those animals transgenic farm animals?	No
• Were those animals cloned farm animals?	No
• Were those animals non-human primates?	Yes
RESEARCH INVOLVING DEVELOPING COUNTRIES	
• Did the project involve the use of local resources (genetic, animal, plant etc)?	Yes
• Was the project of benefit to local community (capacity building, access to healthcare, education etc)?	Yes
DUAL USE	
• Research having direct military use	No

• Research having the potential for terrorist abuse	No

C Workforce Statistics

3. Workforce statistics for the project: Please indicate in the table below the number of people who worked on the project (on a headcount basis).

Type of Position	Number of Women	Number of Men
Scientific Coordinator		
Work package leaders		
Experienced researchers (i.e. PhD holders)		
PhD Students		
Other		

4. How many additional researchers (in companies and universities) were recruited specifically for this project?	
Of which, indicate the number of men:	

D Gender Aspects

5. Did you carry out specific Gender Equality Actions under the project?

○	Yes
x	No

6. Which of the following actions did you carry out and how effective were they?

	Not at all effective				Very effective
❑ Design and implement an equal opportunity policy	○	○	○	○	○
❑ Set targets to achieve a gender balance in the workforce	○	○	○	○	○
❑ Organise conferences and workshops on gender	○	○	○	○	○
❑ Actions to improve work-life balance	○	○	○	○	○

○ Other:

7. Was there a gender dimension associated with the research content – i.e. wherever people were the focus of the research as, for example, consumers, users, patients or in trials, was the issue of gender considered and addressed?

○ Yes- please specify

○ No

E Synergies with Science Education

8. Did your project involve working with students and/or school pupils (e.g. open days, participation in science festivals and events, prizes/competitions or joint projects)?

○ Yes- please specify

x No

9. Did the project generate any science education material (e.g. kits, websites, explanatory booklets, DVDs)?

○ Yes- please specify

x No

F Interdisciplinarity

10. Which disciplines (see list below) are involved in your project?

○ Main discipline[5]:

○ Associated discipline[5]: ○ Associated discipline[5]:

G Engaging with Civil society and policy makers

11a Did your project engage with societal actors beyond the research community? *(if 'No', go to Question 14)*

○	Yes
○	No

11b If yes, did you engage with citizens (citizens' panels / juries) or organised civil society (NGOs, patients' groups etc.)?

○ No

○ Yes- in determining what research should be performed

○ Yes - in implementing the research

○ Yes, in communicating /disseminating / using the results of the project

[5] Insert number from list below (Frascati Manual).

11c In doing so, did your project involve actors whose role is mainly to organise the dialogue with citizens and organised civil society (e.g. professional mediator; communication company, science museums)?	○ ○	Yes No

12. Did you engage with government / public bodies or policy makers (including international organisations)

- ○ No
- ○ Yes- in framing the research agenda
- ○ Yes - in implementing the research agenda
- ○ Yes, in communicating /disseminating / using the results of the project

13a Will the project generate outputs (expertise or scientific advice) which could be used by policy makers?

- ○ Yes – as a **primary** objective (please indicate areas below- multiple answers possible)
- ○ Yes – as a **secondary** objective (please indicate areas below - multiple answer possible)
- ○ No

13b If Yes, in which fields?

Agriculture		Energy		Human rights	
Audiovisual and Media		Enlargement		Information Society	
Budget		Enterprise		Institutional affairs	
Competition		Environment		Internal Market	
Consumers		External Relations		Justice, freedom and security	
Culture		External Trade		Public Health	
Customs		Fisheries and Maritime Affairs		Regional Policy	
Development Economic and Monetary Affairs		Food Safety		Research and Innovation	
		Foreign and Security Policy		Space	
Education, Training, Youth		Fraud		Taxation	
Employment and Social Affairs		Humanitarian aid		Transport	

13c If Yes, at which level?

- ○ Local / regional levels
- ○ National level
- ○ European level
- ○ International level

H Use and dissemination

14. How many Articles were published/accepted for publication in peer-reviewed journals?	
To how many of these is open access[6] provided?	
How many of these are published in open access journals?	
How many of these are published in open repositories?	
To how many of these is open access not provided?	
Please check all applicable reasons for not providing open access:	
❑ publisher's licensing agreement would not permit publishing in a repository ❑ no suitable repository available ❑ no suitable open access journal available ❑ no funds available to publish in an open access journal ❑ lack of time and resources ❑ lack of information on open access ❑ other[7]: ……	

15. How many new patent applications ('priority filings') have been made? *("Technologically unique": multiple applications for the same invention in different jurisdictions should be counted as just one application of grant).*		
16. Indicate how many of the following Intellectual Property Rights were applied for (give number in each box).	Trademark	n.a.
	Registered design	n.a.
	Other	n.a.
17. How many spin-off companies were created / are planned as a direct result of the project?		
Indicate the approximate number of additional jobs in these companies:		

18. Please indicate whether your project has a potential impact on employment, in comparison with the situation before your project:

❑	Increase in employment, or	❑	In small & medium-sized enterprises
❑	Safeguard employment, or	❑	In large companies
❑	Decrease in employment,	x	None of the above / not relevant to the project
❑	Difficult to estimate / not possible to quantify		

19. For your project partnership please estimate the employment effect resulting directly from your participation in Full Time Equivalent (*FTE = one person working fulltime for a year*) jobs:	*Indicate figure:*

[6] Open Access is defined as free of charge access for anyone via Internet.
[7] For instance: classification for security project.

Difficult to estimate / not possible to quantify	x

I Media and Communication to the general public

20. As part of the project, were any of the beneficiaries professionals in communication or media relations?

○ Yes X No

21. As part of the project, have any beneficiaries received professional media / communication training / advice to improve communication with the general public?

○ Yes X No

22 Which of the following have been used to communicate information about your project to the general public, or have resulted from your project?

❑	Press Release	X	Coverage in specialist press
❑	Media briefing	❑	Coverage in general (non-specialist) press
❑	TV coverage / report	❑	Coverage in national press
❑	Radio coverage / report	❑	Coverage in international press
x	Brochures /posters / flyers	X	Website for the general public / internet
❑	DVD /Film /Multimedia	❑	Event targeting general public (festival, conference, exhibition, science café)

23 In which languages are the information products for the general public produced?

❑	Language of the coordinator	x	English
x	Other language(s)		

***Question F-10*:** Classification of Scientific Disciplines according to the Frascati Manual 2002 (Proposed Standard Practice for Surveys on Research and Experimental Development, OECD 2002):

FIELDS OF SCIENCE AND TECHNOLOGY

1. NATURAL SCIENCES

1.1 Mathematics and computer sciences [mathematics and other allied fields: computer sciences and other allied subjects (software development only; hardware development should be classified in the engineering fields)]

1.2 Physical sciences (astronomy and space sciences, physics and other allied subjects)

1.3 Chemical sciences (chemistry, other allied subjects)

1.4 Earth and related environmental sciences (geology, geophysics, mineralogy, physical geography and other geosciences, meteorology and other atmospheric sciences including climatic research, oceanography, vulcanology, palaeoecology, other allied sciences)

1.5 Biological sciences (biology, botany, bacteriology, microbiology, zoology, entomology, genetics, biochemistry, biophysics, other allied sciences, excluding clinical and veterinary sciences)

2 ENGINEERING AND TECHNOLOGY

2.1 Civil engineering (architecture engineering, building science and engineering, construction engineering, municipal and structural engineering and other allied subjects)

2.2 Electrical engineering, electronics [electrical engineering, electronics, communication engineering and systems, computer engineering (hardware only) and other allied subjects]

2.3. Other engineering sciences (such as chemical, aeronautical and space, mechanical, metallurgical and materials engineering, and their specialised subdivisions; forest products; applied sciences such as

geodesy, industrial chemistry, etc.; the science and technology of food production; specialised technologies of interdisciplinary fields, e.g. systems analysis, metallurgy, mining, textile technology and other applied subjects)

3. MEDICAL SCIENCES

3.1 Basic medicine (anatomy, cytology, physiology, genetics, pharmacy, pharmacology, toxicology, immunology and immunohaematology, clinical chemistry, clinical microbiology, pathology)

3.2 Clinical medicine (anaesthesiology, paediatrics, obstetrics and gynaecology, internal medicine, surgery, dentistry, neurology, psychiatry, radiology, therapeutics, otorhinolaryngology, ophthalmology)

3.3 Health sciences (public health services, social medicine, hygiene, nursing, epidemiology)

4. AGRICULTURAL SCIENCES

4.1 Agriculture, forestry, fisheries and allied sciences (agronomy, animal husbandry, fisheries, forestry, horticulture, other allied subjects)

4.2 Veterinary medicine

5. SOCIAL SCIENCES

5.1 Psychology

5.2 Economics

5.3 Educational sciences (education and training and other allied subjects)

5.4 Other social sciences [anthropology (social and cultural) and ethnology, demography, geography (human, economic and social), town and country planning, management, law, linguistics, political sciences, sociology, organisation and methods, miscellaneous social sciences and interdisciplinary , methodological and historical S1T activities relating to subjects in this group. Physical anthropology, physical geography and psychophysiology should normally be classified with the natural sciences].

6. HUMANITIES

6.1 History (history, prehistory and history, together with auxiliary historical disciplines such as archaeology, numismatics, palaeography, genealogy, etc.)

6.2 Languages and literature (ancient and modern)

6.3 Other humanities [philosophy (including the history of science and technology) arts, history of art, art criticism, painting, sculpture, musicology, dramatic art excluding artistic "research" of any kind, religion, theology, other fields and subjects pertaining to the humanities, methodological, historical and other S1T activities relating to the subjects in this group]