CEDRIC-HIV Checklist of items that should be included in reports of HIV drug resistance incidence or prevalence.

CEDRIC-HIV
ChEcklist for studies of Drug ResIstanCe in HIV

	Item No.	Recommendation	Pg. No.
Title	1	Identify the report as a study of HIV drug resistance incidence or prevalence, include where possible the type of drug resistance i.e., pre-treatment, transmitted or acquired, population i.e., paediatric, pregnant women, and location (city or country)	
Introduction			
Contextual information	2	Provide information on the antiretroviral therapy used in the setting of the study, and any other information that may influence drug resistance patterns. This may include local or country-level access to Antiretroviral Therapy (ART), HIV prevalence/incidence and information on any specific groups under study.	
Methods			
Study design	3	**(a)** Present key elements of study design early in the paper (e.g., survey, cross-sectional or cohort design)	
		(b) Provide details on ethics approvals or waivers, including consent for use of data beyond current study.	
Setting	4	Describe the setting (e.g., hospital or community based), locations, and relevant dates (e.g., periods of recruitment, exposure, follow-up, and data collection)	
Participants	5	**(a)** Give the eligibility criteria, and the sources and methods of selection of participants	
		(b) Describe the target population (e.g., sex workers, incarcerated people, men who have sex with men etc.) and how it was defined (e.g., based on registries, self-report etc.)	
Type of HIV drug resistance	6	Clearly define the type of HIV drug resistance that is of interest e.g., pre-treatment, transmitted or acquired drug resistance. For transmitted drug resistance, describe how recent infection is defined, e.g., lab assay.	
Laboratory methods	7	**(a)** Describe the type of specimen used (e.g., plasma, dried blood spots)	
		(b) Describe the methods of viral load testing including the assay used, the lower limit of detection etc.	
		(c) Describe the method for HIV subtype characterization or phylogenetic analysis i.e., subtyping tool used and version (e.g., Stanford, Rega, EuResist)	
		(d) Describe any approaches used for quality assurance (e.g., annual proficiency testing)	
		(e) Provide definitions and thresholds for predicted resistance mutations	
		(f) Provide the mutation list, version, and year (e.g., IAS-USA 2022, Stanford)	
		(g) Provide the algorithm used to interpret the data, version, and year (e.g., ANRS 2022 v33)	
Sampling issues	8	Explain how the study sample size was arrived at, i.e., the assumptions used to calculate the sample size, the sampling strategy used and the data source where applicable (e.g., population-based survey, random sample, registry, convenience). This may also include incidental identification of drug resistance.	
Statistical methods	9	If applicable, describe analytical methods taking account of sampling strategy (including weighting), any adjusted analyses and the variables used for weighting or adjusted analyses.	

Results			
Participants	10	**(a)** Report numbers of individuals at each stage of study—e.g., numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, and number of successful genotypes.	
		(**b)** Give reasons for non-participation at each stage, and missing data for each variable of interest	
		(c) Consider use of a flow diagram	
Descriptive data	11	Give characteristics of study participants (e.g., demographic, clinical, social) and information on exposures and potential confounders. Where applicable consider: **(a)** Age	
		(b) Sex/Gender	
		(c) Risk factors and transmission risk group	
		(d) Recent or late-stage infection	
		(e) Viral load at time of specimen collection	
		(f) CD4 cell count levels	
		(g) For children, HIV status of the mother, maternal breastfeeding, maternal and infant treatment history	
		(h) For participants with any exposure to antiretroviral drugs, provide treatment or prophylaxis history (e.g., current, and past regimens, lines of ART, if applicable, time on ART, number of regimens/switches), level of adherence to ART (with a description of the tools used to measure adherence); other exposures to ART including PrEP, PEP, PMTCT	
Main results	12	Give estimates of prevalence (or incidence) and their precision (e.g., 95% confidence interval). Where applicable report: **(a)** Report numbers and proportions with any drug resistance mutations, for each class (NNRTI, NRTI, PI, INSTI) and for each drug	
		(b) Report numbers and proportions with more than one drug resistance mutation	
		(c) Distinguish major/clinically relevant mutations from minor/accessory mutations, where applicable	
		(d) Report for each subgroup of interest (See Item 11)	
		(e) Report a mutations frequency table	
Other analyses	13	Report other analyses done—e.g., adjusted analyses, phylogenetic analysis, and phylogenetic tree	
Discussion			
Discussion	14	Discuss the generalizability of the findings with due consideration of the study sample and sampling approaches used.	
Additional information	15	Nucleotide sequences: Specify if the nucleotide sequence data are publicly available, available upon request or not, and the reason for not making them publicly available Report the repository where they are stored, the DOI (if available) and the procedures for access, where applicable. Report the Genbank Accession Numbers for the nucleotide sequences used.	

Abbreviations: ANRS: Agence Nationale de Recherches sur le SIDA et les hépatites virales; ART: Antiretroviral therapy; DOI: Digital Object Identifier; IAS: International AIDS Society; INSTI: Integrase strand transfer inhibitor; NNRTI: Non-nucleoside reverse transcriptase inhibitor; NRTI: Nucleoside reverse transcriptase inhibitor; PEP: Post Exposure Prophylaxis; PI: Protease inhibitor; PMTCT: Prevention of mother to child transmission; PrEP: Pre Exposure Prophylaxis; USA: United States of America.