Centre for AIDS Reagents

Data Sheet

NAME: HIV-1 PTE (Env)

REPOSITORY REFERENCE: **ARP7121.1-480**

VIRUS STRAIN: HIV-1 PTE

PROVIDED: 480 vials, 1.0 mg each, lyophilized.

DESCRIPTION:

This peptide panel is designed to permit expression of the most frequent potential T cell epitopes (PTE) embedded in the sequences of circulating HIV-1 strains of HIV-1 worldwide. The peptides are 15 a.a. in length and contain naturally occurring 9 a.a. sequences that are potential T cell determinants, captured in an unbiased manner (1). Its use is intended for T cell assays (e.g., IFN-? ELISpot, intracellular cytokine staining by flow cytometry) measuring HIV-1- specific responses (2), particularly in vaccine trials.

HIV-1 M group has evolved into over ten distinct subtypes and circulating recombinant forms (CRFs) over the past two decades. Subtype A, B and C account for over 90% of the global HIV-1 prevalence, and the non-A,B,C comprise the remaining 10%. The global PTE peptides cover all PTEs with a frequency equal to or greater than 15% in any one of the subtypes A, B, C and non-A,B,C. The 9 a.a. sequences were defined first by frequency for the individual subtypes, and then the panel was assembled jointly using a forward stepwise algorithm to cover all of the subtype-specific PTE in the smallest set possible. The nature of this algorithm selects first the highly conserved PTEs, then the less conserved.

For global peptide selection, 549 full-length HIV-1 genome sequences were obtained from the Los Alamos National Laboratory (LANL) HIV sequence database as of February 2005. We further examined sequences from more contemporary clade B isolates from donors with primary HIV-1 infection, and comparative analysis with those in the more heavily weighted chronic isolates annotated in the LANL database did not indicate the need for alterations in the panel. Very similar sequences likely derived from the same subject were excluded from this sequence dataset. The four protein sequences (Gag, Pol, Nef and Env) were extracted from the collection of full-length genome sequences, and then separated into subtype A, B, C and nonABC according to their protein distances to the subtype reference sequences from LANL HIV-1 sequence database. The Gag sequences for subtype A, B, C and nonABC are 163, 89, 145 and 152 respectively. The sequence numbers for other proteins slightly vary due to the different recombinant patterns of CRFs.

SPECIAL CHARACTERISTICS: Suggested pooling protocol for T cell assays:

The peptides are used in pools of up to 160 peptides. Resuspend the peptides at 20mg/ml in 100% DMSO, then pool them into subpools of 40 peptides and add water for 400ug/ml (per peptide) in 80% DMSO/20% H2O. Four of those subpools are combined into a single pool (160 peptides) for testing, with a final concentration of 100ug/ml per peptide in 80% DMSO/20% H2O. These pools are then used at a final concentration of 1ug/ml in all assays.

Click here to view the peptides in this complete set. (Link to NIH ARRRP Datasheet)

Please Note: The peptides are listed in the order of decreasing frequency.

National Institute for Biological Standards and Control – Assuring the quality of biological medicines
Blanche Lane South Mimms Potters Bar Hertfordshire EN6 3QG United Kingdom
Tel +44 (0)1707 641000 Fax +44 (0)1707 641050 www.nibsc.ac.uk
A World Health Organization Laboratory for Biological Standards

PURITY: >80% purity (HPLC)

SOLUBLILITY: Please note: Cys and Met containing peptide sequences are highly unstable when stored in DMSO for prolonged periods of time; peptide decay is often observed within days to weeks. If DMSO is required, we recommend freshly-prepared working solutions from freeze dried aliquots of these peptides, and prepared pools.

STORAGE: -20°C

SOURCE: DAIDS, NIAID.

REFERENCES:

1. Li, F., U. Malhotra, P. B. Gilbert, N. R. Hawkins, A. C. Duerr, J. M. McElrath, L. Corey, and S. G. Self. 2006. Peptide selection for human immunodeficiency virus type 1 CTL-based vaccine evaluation. Vaccine 24:6893-6904.

2. Malhotra, U., F. Li, J. Nolin, M. Allison, H. Zhao, J. I. Mullins, S. Self, and M. J. McElrath. 2007. Enhanced detection of human immunodeficiency virus type 1 (HIV-1) Nef-specific T cells recognizing multiple variants in early HIV-1 infection. J Virol 81:5225-5237.

ACKNOWLEDGEMENTS: Publications should acknowledge the donor of the reagent and the Programme EVA Centre for AIDS Reagents. Suggested wording can be found on our website in the "Acknowledgement" section at:-

www.nibsc.ac.uk/spotlight/centre_for_aids_reagents.aspx

Please also ensure that you send us a copy of any papers resulting from work using reagents acquired through CFAR, this can be by e-mail or printed copy.