

Search Antibody Database

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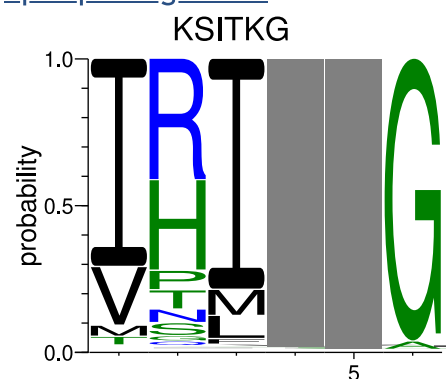
Displaying record number 945

[MAb ID](#) 1006-15D (1006)
[HXB2](#) gp160(307-312)
[Location](#) DNA(7143..7160)
[Author](#)
[Location](#) gp120(RF)
[Research](#) Susan Zolla-Pazner
[Contact](#) (Zollas01@mccrcr6.med.nyu) (NYU Med. Center)

[gp160 Epitope Map](#)

[Epitope](#) KSITKG

[Epitope Alignment](#)



[Subtype](#) B
[Ab Type](#) gp120 V3 // V3 glycan (V3g)
[Neutralizing](#)
[Species](#)
[\(Isotype\)](#) human(IgG1λ)
[Patient](#)
[Immunogen](#) HIV-1 infection
[Keywords](#) antibody binding site, antibody generation, antibody lineage, antibody sequence, binding affinity, mimotopes, neutralization, review,

structure, subtype comparisons, vaccine
antigen design, variant cross-reactivity

Notes

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- 1006-15D: This study analyzed the neutralization sensitivity of sequential HIV-1 primary isolates during their natural evolution in 5 subtype B and CRF02_AG HIV-1 infected drug naive individuals to 13 anti-HIV-1 MAbs (including this MAb) directed at epitopes in the V2, V3, CD4bd and carbohydrates. Patient viruses evolved to become more sensitive to neutralization by MAbs directed at epitopes at V2, V3 and CD4bd, indicating that cross sectional studies are inadequate to define the neutralization spectrum of MAb neutralization with primary HIV-1 isolates. [Haldar2011](#) (**neutralization**)
- 1006-15: VH5-51 gene segment was used by 18 of 51 (35%) anti-V3 MAbs. This study analyzed the crystal structure of 5 Fabs encoded by VH5-51/VL lambda genes. Each Fab interacted with key residues at the same 7 positions in the crown of the V3 loop, although the amino acids could vary, suggesting that while V3 is variable in sequence and structurally flexible, a common structure is retained across strains. MAb 1006 interacted with amino acids R304, K305, I307, H308, I309, F317, Y318 of MN V3 peptide. Most MAb 1006 contact residues were also present at the corresponding positions of the germline VH5-51 gene. [Gorny2011](#) (**mimotopes, antibody sequence, structure, antibody lineage**)
- 1006-15D: Two V3-scaffold immunogen constructs were designed and expressed using 3D structures of cholera toxin B (CTB), V3 in the gp120 context, and V3 bound to 447-52D MAb. The construct (V3-CTB) presenting the complete V3 was recognized by 1006-15D MAb and by the large majority of other MAbs (18/24), indicating correctly folded and exposed MAb epitopes. V3-CTB induced V3-binding Abs and Abs displaying cross-clade neutralizing activity in immunized rabbits. Short V3-CTB construct, presenting a V3 fragment in conformation observed in complex with 447-52D, was recognized by 1006-15D but only at the highest MAb concentrations. [Totrov2010](#) (**vaccine antigen design, binding affinity, structure**)
- 1006-15D: Crystal structures of 1006-15D Fab in complex with different V3 peptides revealed that its interactions with V3 are highly similar to those of MAbs 2557 and 2219, indicating that 2219, 2557 and 1006-15D recognize V3 using similar modes of binding. It is shown that broadly-reactive Abs can bind to conserved elements in four regions of the V3: the arch, the circlet, the band, and the V3 peptide main chain backbone. These conserved elements are either unaffected by or are subjected to minimal sequence variation. A mimotope that preserved the key structural elements in the circlet and band regions, but with GPG of the arch replaced by a disulfide bond, interacted with broadly reactive MAbs 2557, 1006-15D and 2219. It did not react with 447-52D nor 268-D, which are dependent on the Arg in the arch. Thus, mimotopes can be constructed that may focus the immune response on structurally conserved elements. [Jiang2010](#) (**antibody binding site, mimotopes, structure**)

- 1006-15D: The Ig usage for variable heavy chain of this Ab was as follows:IGHV:5-51*03,IGHD:3-22, D-RF:2, IGHJ:3. There was a preferential usage of the VH5-51 gene segment for V3 Abs. The usage of the VH4 family for the V3 Abs was restricted to only one gene segment, VH4-59, and the VH3 gene family was used at a significantly lower level by these Abs. The V3 Abs preferentially used the JH3 and D2-15 gene segments. [Gorny2009](#) (antibody sequence)
- 1006-15D: The neutralization potency of this Ab against 7 HIV-1 primary isolates was compared to the neutralization potency of the Ab KD-247. The same Ab concentrations were needed for neutralization of the N-NIID and 92TH022 isolates, while higher concentrations of 1006-15D were needed for the neutralization of the rest of the HIV-1 isolates suggesting 1006-15D has lower neutralization potency. [Eda2006a](#) (variant cross-reactivity)
- 1006-15D: Called 1006-15: V3 MAb neutralization is influenced by retaining the epitope, exposure on the intact virion, mobility during CD4-induced conformational change, and affinity. Anti-V3 MAbs selected using V3 peptides neutralize less effectively than V3 MAbs selected using fusion proteins or gp120, suggesting antigenic conformation is important. This MAb was selected using V3 peptides. [Gorny2004](#) (antibody binding site)
- 1006-15D: This review provides summaries of Abs that bind to HIV-1 Env. There are many V3 MAbs, many neutralize some TCLA strains, and a subset can also neutralize some primary isolates. [Gorny2003](#) (review)
- 1006-15D: Called 1006 -- Transgenic mice carrying human genes allowing production of fully human MAbs were used to rapidly create a panel of anti-HIV gp120 MAb producing hybridomas by immunization with HIV SF162 gp120 -- the previously described human MAbs 5145A(CD4BS) , 4117C (plus others, V3) and 697D (and SC258, V2) were used as controls. [He2002](#)
- 1006-15D: A panel of 47 human MAbs was tested against 26 HIV-1 group M primary isolates from clades A through H -- 19 V3 MAbs were tested, and of 494 combinations, 44% displayed some viral binding -- V3 MAbs tended to have the most cross-reactive binding to clade A, B, C, and D isolates, less to E, F, G, and H -- 1006-15D showed strong cross-reactivity. [Nyambi2000](#) (subtype comparisons)
- 1006-15D: MAb peptide-reactivity pattern clustered with immunological related MAbs: 838, 782, 1027, 908, and 1006, all selected with RF V3 peptide -- the core amino acids KSITK tended to be critical for reactivity in this group. [Zolla-Pazner1999a](#) (antibody binding site)
- 1006-15D: Review of clade specificity and anti-V3 HIV-1-Abs -- this Ab showed strong binding to several B and F peptides, one C peptide, and some reactivity with A peptides -- no binding was observed with D and E peptides. [Zolla-Pazner1999b](#) (review, subtype comparisons)
- 1006-15D: Five human MAbs against were derived from HIV-infected North American subjects after selection by the V3 RF peptide -- was somewhat cross-reactive with V3 peptides from clade A, C and other B clade V3 peptides, but not E clade. [Gorny1997](#) (antibody generation, subtype comparisons)

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