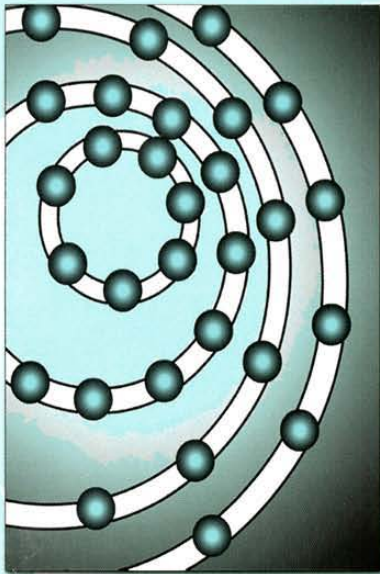


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Peptide Mapping of C-terminal Region of the ORF K8.1 Encoded Protein of *Human Herpes Virus type 8*

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Background: The strong antigenic domain of the HHV-8 ORF K8.1 protein was previously mapped to the N-terminal region, but several epitopes located on C-terminal were predicted to be highly immunogenic. The purpose of this study was to identify predicted antigenic regions within the C-terminal part of HHV-8 ORF K8.1 - encoded protein by peptide mapping.

Methods: At least three potential antigenic epitopes of C-terminal region of K8.1 protein have been predicted by hydrophilicity - based algorithm of Hoop and Woods. A set of 21 overlapping 25mer peptides spanning the C-terminal region (101-213 aa) of the ORF K8.1 - encoded protein of the HHV-8 was synthesized and tested by enzyme immunoassay against a panel of 24 well defined anti HHV-8 positive sera and 24 anti HHV-8 negative sera obtained from normal blood donors. HHV-8 peptides were considered to be specifically immunoreactive when P/N ratio was greater than 1.5, where P represents the signal of anti HHV-8 positive specimens and N represents the signal of anti HHV-8 negative specimens. Each serum specimen in every experiment was also tested with an irrelevant peptide.

Results: Only two peptides showed immunoreactivity with in >30% of anti HHV-8 positive sera. The most immunoreactive peptide (comprising aa 145 to 169) detected anti HHV 8 IgG in 33.3% of positive samples, but also immunoreacted with 12.5% of normal serum samples. In general, the seroreactivity patterns of positive and negative serum specimens were almost identical and none of synthetic peptides was found to be immunoreactive with P/N ratio greater than 1.5.

Conclusions: No antigenic epitopes within C-terminal region (101-213 aa) of the envelope protein encoded by HHV-8 open reading frame K8.1 could be modeled with 25 mer synthetic peptides.