

The nucleotide sequence of a pseudorabies virus gene similar to ICP18.5 of herpes simplex virus type 1

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A 2524 bp region from the Sall-3 fragment of pseudorabies (PRV, strain Becker) was determined by double-stranded sequencing. This region is 75% G+C and encodes an 80kd protein 56% identical to the herpes simplex virus type 1 (HSV-1, strain Angelotti) ICP18.5 protein (1). HSV-1 ICP18.5 is an essential gene reported to affect glycoprotein localization (2). This protein is also 49% identical to Varicella-Zoster virus (VZV) gene 30 (3) and 47% identical to the Bovine herpes virus (BHV-2) 72kd gene (4). A previously unreported open reading frame lies 5' to this gene and the 3' end overlaps with gII by 44 codons (5). The overall gene arrangement is similar to ICP8, ICP18.5, and gB of HSV-1 (1, 6, 7, 8) and their counterparts in VZV and BHV-2. We retain the nomenclature for ICP8 and ICP18.5 in PRV. The presumed polyadenylation signal for ICP8 is underlined. The intergenic region upstream of ICP18.5 is 147bp in PRV, 306bp in HSV-1, and without significant homology after the polyadenylation signal. Initiation and termination codons for ICP18.5 are in bold type. ICP18.5 encodes 724 amino acids which are predominantly hydrophilic and acidic.

1 CTCGAGGGCCAGACGGGCGCGGACGGCGCGGAGGAGACCGCCTTCGACTTTGGGGCTCGCCGCGGGCGGGGACGTCGCGGGGCTCGCCCGCCCTCGC
101 TGGTGCCTCCGCGAGCTGGGGGCAAGCGCCCGCCCGGAGGACGACTGTTTGACATGGCGCCCGCCGAGAGCGGCTGACTTCGACATGCTGTG
201 AGGGGAGGAGGAGGGGAGGGGACGGCGCGGCTGCCCGCTGTATCAATBAAGACGACCGGTTTGACAGACACACCGCGCTCCCGTGCCTCTCTC
301 CGCGCGGACGGGCGGGGAGGGGGGAGCGAGCGGGCCGACCTGGCCATGGCGGAGCGGGCGCTCGTGGCGGCTCTGGGCGAGGTGACAGCTACGTTG
401 TTCAGCTGGAGATGCTGAACCGCTGCGACCCCGGCTGGTGGCGGACGCTGGCCCAACCGTCAAGCTGAACCGCTGATGTGCCCTACCTCGCGGGG
501 GCTCCGCTGAGGGGCGAGACGACGCGCTCAGCTGCGCGCTGGCGCTGGCGCTCGCTACGCGCGGGGCGAGGGGGACCGCTGCTGGGGCGCTGGCC
601 CGCGCGGCGGACGACGCGGAGGCTACTTTGAGCGCACCAATGGGCGCGCGTTCGCTTCCACGCGGGCTGCGGCTCGACAGCTACGGCGGGCGGCTGG
701 AGACGGAGCTGCACTTCCACGACGCGGAGAACCTGCTCAAGCAGCTCAAACTACTGCCACTGATCAGCGCCACCGCGGTGGACCTGTTCGGCCGTGA
801 CGAGTTCTCGCGCGACGATGGCGGGCGGGCTCGTGGTGGCGCGGAGCTGTACGACCGGGCGAGCCGCTGGCGGTGCTGTTGAGGAGCTGTGGCTG
901 ACGGCAACACAGGGCGAGGCCACGACGCGGCTGCTCGGCTGGCTGTGGCGACCACTCAGCGGGCTGGCGGTGCGCTGGACCCCGAGGACGCTGG
1001 CCAAGAACTCGCGCAGCTGCACGGGCTGACGAGGGCGCGCGCGGGCGCGCGCTGGCGGCTGGCGGCTGGACCGCCGAGCCCGGAGGGCGGA
1101 GCGCGGCTCCACGGCGCGCGCGCGCGGAGCGGGGACGCGGGCGAGACGCGCGCGCGCGCGGGAGCGGCTCTGAGCGCGCACGACGCTGTTCGG
1201 CCGCGCTCGCGGCGCTGTACCGCTGAGGAGCTGCAAGTTTGGCTGGCGTCCACGAAACAGGGCGTGGCGGCTCGACTGTTCCAGCAAACTGG
1301 ACAGCTGGAGCGCGGCGGACGCGCGCGCGGAGTGGCGCGCGCGCGCTGAGACTCGGCTCTTCGGGCGGCGCGCGGACACTTTGACGCGCGCGCG
1401 GCGCGCGAGCTCGACATCATCGACGGGCTGCTCGTGGCGGGCTCGCGCGCTCGCGGACGAGCGGCTCGCGGCGGCTCGAGGCGCTATCCGCGGCTGACTCGACAC
1501 CACATGTCACGCCATGCTGCGCATGCTGGACCGGACCGGGCCAAACCGGACGCGCTCGAGCGGCTCTCGAGGCGGCGGACGACCGGACCGCGGACG
1601 CGCGCGCGCGGGGCGCGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
1701 CGCGCGCGCGGCTGCGCGACGCGGAGCGCGGCGGCGGCGGCTGACGCGGACCGGCTCGCGGCGGCTCGGCGGCGGAGCTGGCGGAGTGGCTGGCGGAG
1801 CAGGGCGCGGAGCTGGAGAAGACCTGCGCGTGAACGCTGACGGGACCGGCTGCTGACACAGCTAGCTGGCGGTTGCGCCCGGGTTCCGCGACGGCGG
1901 CGTTCTGGAGCGCGGCTCTTCGCGCGTCAACGGCAAGTCTTCGAGCTGTTCAACGGCGGCTCTTCGCGACGACGACGCTTCATGAGGCCACGGTTCGCGGCGCA
2001 CCGCGTGGAGCGCGGCTCTTCGCGCGTCAACGGCAAGTCTTCGAGCTGTTCAACGGCGGCTCTTCGCGACGACGACGCTTCGCGGCGGCGGCGG
2101 CCGCGTGGAGCGCGGCTCTTCGCGCGTCAACGGCAAGTCTTCGAGCTGTTCAACGGCGGCTCTTCGCGACGACGACGCTTCGCGGCGGCGGCGG
2201 CGAGTTCGCGGCTTCACTCCGCTTCCAGCGCGGCGGCTAACCCACCGCGGCGGCGGCTGGCGATATATCCGCGGAGCTGGTGTGGCTGTGCACT
2301 CTCAGGTCGCTTCCACTCGGGGAGCTCGAGGCTCTCGCGCGGATCGCTTCGCGGACCGGCGGCGGCTGACTGACGAGGGCGTCAAGCGGCTG
2401 CTGGTGGCGGCTTTTGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
2501 TCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

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