**Sequence alignment of L1SHORT proteins of MnPV and HPV6, 16 & 18**

CLUSTAL O(1.2.4) multiple sequence alignments

**BC loop**

MnPV-L1 MAYWLPNNQKLYLP-PAPVQRILSTDEFTTRTDIYYYASSDRLLTVGNPYYPILDG--DT 57

HPV18-L1 MALWRPSDNTVYLPPP-SVARVVNTDDYVTRTSIFYHAGSSRLLTVGNPYFRVPAGGGNK 59

HPV16-L1 MSLWLPSEATVYLP-PVPVSKVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNK 59

HPV6-L1 M--WRPSDSTVYVPPPNPVSKVVATDAYVTRTNIFYHASSSRLLAVGHPYFSIKRA--NK 56

\* \*.: .:\*:\* \* \* ::: \*\* :.:\*\*.\*:\*:\*.:.\*\*\*:\*\*:\*\*: : :.

**BC loop** **DE loop**

MnPV-L1 VTVPKVSPNQYRVFRCKLPDPNRFAFGEKSVYDPEKQRLAWCIRGVEIARGQPLGIGITG 117

HPV18-L1 QDIPKVSAYQYRVFRVQLPDPNKFGLPDTSIYNPETQRLVWACAGVEIGRGQPLGVGLSG 119

HPV16-L1 ILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISG 119

HPV6-L1 TVVPKVSGYQYRVFKVVLPDPNKFALPDSSLFDPTTQRLVWACTGLEVGRGQPLGVGVSG 116

:\*\*\*\* \*\*\*\*\*: \*\*\*\*\*:\*.: :.\*.::\* .\*\*\*.\*. \*:\*:.\*\*\*\*\*\*:\*::\*

**DE loop EF loop**

MnPV-L1 HPLYNRLEDVENPGKYPSAPGTDNRQNVGLDPKQTQMFIVGCVPAQGEHWSRALTCSNQV 177

HPV18-L1 HPFYNKLDDTESSHAATSNVSEDVRDNVSVDYKQTQLCILGCAPAIGEHWAKGTACKSRP 179

HPV16-L1 HPLLNKLDDTENASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVA 179

HPV6-L1 HPFLNKYDDVENSG-SGGNPGQDNRVNVGMDYKQTQLCMVGCAPPLGEHWGKGKQCTNTP 175

\*\*: \*: :\*.\*. . . \* \* :.:\* \*\*\*\*: ::\*\* \* \*\*\*\*.:. \*..

**EF loop**

MnPV-L1 VKKGDCPPIQRMSGMIEDGDMGDIGYGNLDFRVLQENKSEVPLEVVDSICKYPDYLGMSK 237

HPV18-L1 LSQGDCPPLELKNTVLEDGDMVDTGYGAMDFSTLQDTKCEVPLDICQSICKYPDYLQMSA 239

HPV16-L1 VNPGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVS 239

HPV6-L1 VQAGDCPPLELITSVIQDGDMVDTGFGAMNFADLQTNKSDVPIDICGTTCKYPDYLQMAA 235

:. \*\*\*\*\*:: . :::\*\*\*\* \* \*:\* ::\* \*\* .\*.:\*\*::: : \*\*\*\*\*\*: \*

**FG loop**

MnPV-L1 ETHGNSCFFYARQARLYSRHFFNRAGVQGETVPESLYKKGKDGQAQSTLALATYSGTPSG 297

HPV18-L1 DPYGDSMFFCLRREQLFARHFWNRAGTMGDTVPQSLYIKGTGMRA--SPGSCVYSPSPSG 297

HPV16-L1 EPYGDSLFFYLRREQMFVRHLFNRAGTVGENVPDDLYIKGSGSTA--NLASSNYFPTPSG 297

HPV6-L1 DPYGDRLFFFLRKEQMFARHFFNRAGEVGEPVPDTLIIKGSGNRT--SVGSSIYVNTPSG 293

: :\*: \*\* \*: ::: \*\*::\*\*\*\* \*: \*\*: \* \*\*.. : . . . \* :\*\*\*

**HI loop**

MnPV-L1 SLVSSDAVLFNRPYWLERAQGQNNGILWNNDLFVTVLDNTRGTHFSISIATQ--DENDYT 355

HPV18-L1 SIVTSDSQLFNKPYWLHKAQGHNNGVCWHNQLFVTVVDTTRSTNLTICASTQSPVPGQYD 357

HPV16-L1 SMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAIST-SETTYK 356

HPV6-L1 SLVSSEAQLFNKPYWLQKAQGHNNGICWGNQLFVTVVDTTRSTNMTLCASVTT-S-STYT 351

\*:\*:\*:: :\*\*:\*\*\*\*.:\*\*\*:\*\*\*: \* \*:\*\*\*\*\*:\*.\*\*.\*::::. : \*

**HI loop**

MnPV-L1 ASNYKQYTRHVEEFELEFIFQLVKINLSTEVLAYLHGMDPSILDNWNLTLGPPNDGSLAD 415

HPV18-L1 ATKFKQYSRHVEEYDLQFIFQLCTITLTADVMSYIHSMNSSILEDWNFGVPPPPTTSLVD 417

HPV16-L1 NTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLED 416

HPV6-L1 NSDYKEYMRHVEEYDLQFIFQLCSITLSAEVMAYIHTMNPSVLEDWNFGLSPPPNGTLED 411

:.:\*:\* \*\* \*\*::\*:\*\*\*\*\* .\*.\*:::\*::\*:\* \*: ::\*::\*\*: : \*\* :\* \*

MnPV-L1 KYRFIESLATKCPDN-VEVTKPDPYKGRIFWNIDLTERLTADLDQFSLGRKFLYQHARIS 474

HPV18-L1 TYRFVQSVAITCQKDAAPAENKDPYDKLKFWNVDLKEKFSLDLDQYPLGRKFLVQAGLRR 477

HPV16-L1 TYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQAGLKA 476

HPV6-L1 TYRYVQSQAITCQKPTPEKEKPDPYKNLSFWEVNLKEKFSSELDQYPLGRKFLLQSGYRG 471

.\*\*:: \* \* \* . : \*\* . \*\*:::\*.\*::: :\*\*\*: \*\*\*\*\*\* \* .

MnPV-L1 NRKRSLPASRNGGGTSSSSTKRRK-K---- 499

HPV18-L1 KPTIGPRKRSAPSATTSSKPAKRVRVRARK 507

HPV16-L1 KPKFTLGKRKATPTTSSTSTTAKRKKRKL- 505

HPV6-L1 RSSIRTGVKRPAVSKASAAPKRKRAKTKR- 500

. . .:\*: :

Marked areas based on: Zhang, X., Li, S., Modis, Y., Li, Z., Zhang, J., Xia, N., and Zhao, Q. (2016). Functional assessment and structural basis of antibody binding to human papillomavirus capsid. Reviews in medical virology *26*, 115-128.