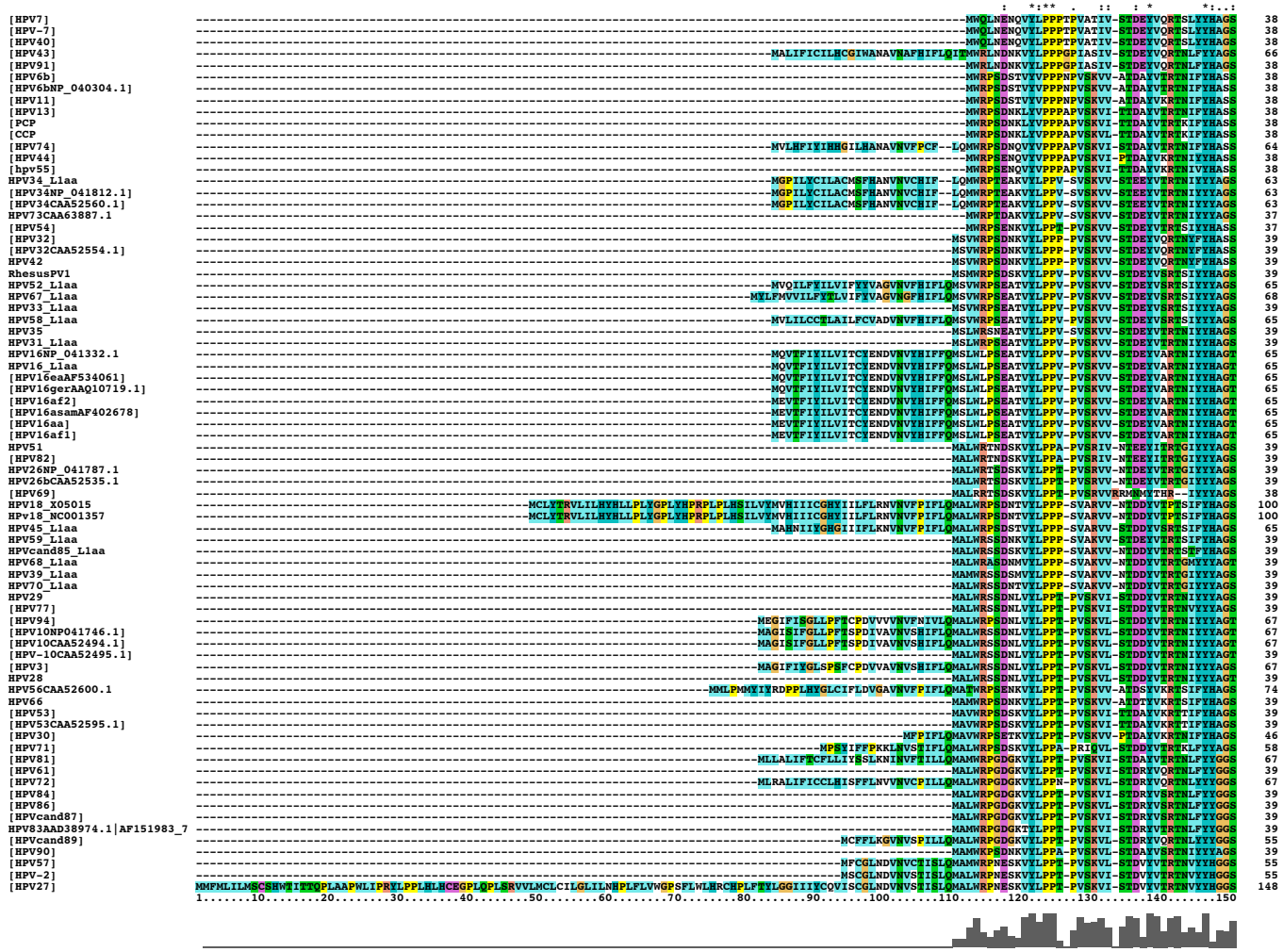
CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

File: /Users/johnlowe/Desktop/L1protein.ps **Date: Fri May 2 11:55:30 2008**



CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT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[HPV7]                       TRLLTIGHPYFELKK------PN--GDVSVPKVSGHQYRVFRVRLPDPNKFGLSDTSLFNSETQRLVWACVGVEVGRGQPLGVGISGHPYFNKDEDVENSSVY---GTVPGQDSRENVAMDYKQTQLCIVGCTPPIGEYWGMGTPCNASK   177
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[HPV91]                      SRLLAVGHPFFPIKN------NS--GKVIVPKVSGHQYRVFRVKLPDPNKFGFSETTLVTSDTQRLVWGCVGVEIGRGQPLGVGISGHPYLNKYDDIENPSGY---GTSPGQDNRENVAMDYKQTQLCIVGCTPPMGEYWGKGVPCSTSG   177
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[HPV6bNP_040304.1]           SRLLAVGHPYFSIKR-------A--NKTVVPKVSGYQYRVFKVVLPDPNKFALPDSSLFDPTTQRLVWACTGLEVGRGQPLGVGVSGHPFLNKYDDVENSGS----GGNPGQDNRVNVGMDYKQTQLCMVGCAPPLGEHWGKGKQCTNTP   175
[HPV11]                      SRLLAVGHPYYSIKK------VN---KTVVPKVSGYQYRVFKVVLPDPNKFALPDSSLFDPTTQRLVWACTGLEVGRGQPLGVGVSGHPLLNKYDDVENSGGY---GGNPGQDNRVNVGMDYKQTQLCMVGCAPPLGEHWGKGTQCSNTS   176
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[HPV74]                      SRLLAVGNPYFPIRQ-------S--NKTVVPKVSGYQFRVFKVVLPDPNKFALPDTSIFDPSSQRLVWACTGLEVGRGQPLGIGISGHPLLNKLDDVENSASY---AANPGQDNRVNVAMDYKQTQLCMVGCAPPLGEHWGKGKQCSNVN   202
[HPV44]                      SRLLAVGNPYFAIRP-------A--NKTLVPKVSGFQYRVFKMVLPDPNKFALPDTSIYDPTTQRLVWACIGLEVGRGQPLGVGISGHPLLNKLDDVENSASY---AAGPGQDNRVNVAMDYKQTQLCLVGCAPPLGEHWGKGKQCNNVS   176
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[HPV34NP_041812.1]           TRLLAVGHPYYPIKD------TNGKRKIAVPKVSGLQYRVFRIRLPDPNKFGFPDASFYNPDKERLVWACAGVEVGRGQPLGIGTSGNPFMNKLEDTENAAKY---IGGNIADSRECMSVDYKQTQLCIVGCKPPLGEHWGTGTPCGTQN   204
[HPV34CAA52560.1]            TRLLAVGHPYYPIKD------TNGKRKIAVPKVSGLQYRVFRIRLPDPNKFGFPDASFYNPDKERLVWACAGVEVGRGQPLGIGTSGNPFMNKLEDTENAAKY---IGGNIADSRECMSVDYKQTQLCIVGCKPPLGEHWGTGTPCGTQN   204
HPV73CAA63887.1              TRLLAVGHPYFPIKD-----SQK--RKTIVPKVSGLQYRVFRLRLPDPNKFGFPDASFYNPDKERLVWACSGVEVGRGQPLGIGTSGNPFMNKLDDTENAPKY---IAGQNTDGRECMSVDYKQTQLCILGCRPPLGEHWGPGTPCTSQT   177
[HPV54]                      SRLLAVGHPYFKVQK------TN--NKQSIPKVSGYQYRVFRVQLPDPNKFGLPDPSLYNPETQRLVWACTGVEVGRGQPLGLGLSGHPLLNKLDDTENAPKY----VGAGADNRENVSMDYKQTQLCILGCTPPIGEHWAKGNLCTPNT   175
[HPV32]                      SRLLAVGHPYYTIKK------TP--NRTSIPKVSGLQYRVFRVRLPDPNKFTLPETNLYNPETQRMVWACVGLEVGRGQPLGVGLSGHPLLNRLDDTENGPRY---AAGPGTDNRENVSMDCKQTQLCLVGCKPAIGEHWGKGAACSAQS   178
[HPV32CAA52554.1]            SRLLAVGHPYYTIKK------TP--NRTSIPKVSGLQYRVFRVRLPDPNKFTLPETNLYNPETQRMVWACVGLEVGRGQPLGVGLSGHPLLNRLDDTENGPRY---AAGPGTDNRENVSMDCKQTQLCLVGCKPAIGEHWGKGAACSAQS   178
HPV42                        SRLLVVGHPYYSITK------RP--NKTSIPKVSGLQYRVFRVRLPDPNKFTLPETNLYNPETQRMVWACVGLEVGRGQPLGVGISGHPLLNKLDDTENAPTY---GGGPGTDNRENVSMDYKQTQLCLVGCKPAIGEHWGKGTACTPQS   178
RhesusPV1                    SRLLAVGHPYYAVKK-------GN--NKVSVPKVSGLQYRVFRVRLPDPNKFGLPDANFYDPNTQRLVWACLGVEVGRGQPLGVGTSGHPLLNKLDDTENGPKV---AGGQGADNRECVSMDYKQTQLCMLGCKPPVGEHWGKGNPCTTGA   178
HPV52_L1aa                   SRLLTVGHPYFSIKN--TSSGNG--KKVLVPKVSGLQYRVFRIKLPDPNKFGFPDTSFYNPETQRLVWACTGLEIGRGQPLGVGISGHPLLNKFDDTETSNKY---AGKPGIDNRECLSMDYKQTQLCILGCKPPIGEHWGKGTPCNNNS   208
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HPV58_L1aa                   SRLLAVGNPYFSIKS----PNNN--KKVLVPKVSGLQYRVFRVRLPDPNKFGFPDTSFYNPDTQRLVWACVGLEIGRGQPLGVGVSGHPYLNKFDDTETSNRY---PAQPGSDNRECLSMDYKQTQLCLIGCKPPTGEHWGKGVACNNNA   206
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HPV31_L1aa                   ARLLTVGHPYYSIPK----SDNP--KKIVVPKVSGLQYRVFRVRLPDPNKFGFPDTSFYNPETQRLVWACVGLEVGRGQPLGVGISGHPLLNKFDDTENSNRY---AGGPGTDNRECISMDYKQTQLCLLGCKPPIGEHWGKGSPCSNNA   180
HPV16NP_041332.1             SRLLAVGHPYFPIKK-----PNN--NKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAY---AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVA   205
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[HPV16eaAF534061]            SRLLAVGHPYFPIKK-----PNN--NKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAY---AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVA   205
[HPV16gerAAQ10719.1]         SRLLAVGHPYFPIKK-----PNN--NKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAY---AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVA   205
[HPV16af2]                   SRLLAVGHPYFPIKK-----PNN--NKILVPKVSGLQYRVFRIYLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAY---AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCNNVA   205
[HPV16asamAF402678]          SRLLAVGHPYFPIKK-----PNN--NKILVPKVSGLQYRVFRIYLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAY---AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCNNVA   205
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HPV51                        SRLITLGHPYFPIPK------TS--TRAAIPKVSAFQYRVFRVQLPDPNKFGLPDPNLYNPDTDRLVWGCVGVEVGRGQPLGVGLSGHPLFNKYDDTENSRIA---NGNAQQDVRDNTSVDNKQTQLCIIGCAPPIGEHWGIGTTCKNTP   178
[HPV82]                      SRLITLGHPYFSIPK------TN--TRAEIPKVSAFQYRVFRVQLPDPNKFGLPDPNLFNPDTDRLVWGCVGVEVGRGQPLGVGLSGHPLFNKYDDTENSRFA---NGNDQQDVRDNISVDNKQTQLCIIGCAPPIGEHWATGTTCKNVP   178
HPV26NP_041787.1             SRLLTLGHPYFSIPK------TG--QKAEIPKVSAYQYRVFRVHLPDPNKFGLPDPQLYNPDTERLVWACVGVEVGRGQPLGIGLSGHPLFNKLDDTENSHLA---TVNADTDNRDNVSVDNKQTQLCIIGCTPPLGEHWGIGTICKNTQ   178
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[HPV69]                      SRLLTLGHPYFPIPK------SG--STAEIPKVSAYQYRVFRVHLPDPNKFGLPDPQLYNPETERLVWACVGVEVGRGQPLGVGLSGHPLFNKLDDTENSHLA---TANADTDNRDNVCVDNKQTQLCIIGCTPPLGEHWGVGTVCKNAQ   177
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HPv18_NC001357               SRLLTVGNPYFRVPA-----GGG--NKQDIPKVSAYQYRVFRVQLPDPNKFGLPDTSIYNPETQRLVWACAGVEIGRGQPLGVGLSGHPFYNKLDDTESSHAA---TSNVSEDVRDNVSVDYKQTQLCILGCAPAIGEHWAKGTACKSRP   240
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HPVcand85_L1aa               SRLLTVGHPYYKVTS-----NGG--RKQDIPKVSAYQYRVFRVTLPDPNKFGLPDTNIYNPETQRLVWACVGMEVGRGQPLGVSLSGHPFYNKLDDTENSHVA---TSVVTHDTRDNVSVDYKQTQLCIIGCVPAIGEHWAKGTACKPGA   179
HPV68_L1aa                   SRLLTVGHPYFKVPM-----SGG--RKQGIPKVSAYQYRVFRVTLPDPNKFSVPESTLYNPDTQRMVWACVGVEIGRGQPLGVGLSGHPLYNRLDDTENSPFS---SNKNPKDSRDNVAVDCKQTQLCIIGCVPAIGEHWAKGKSCKPTN   179
HPV39_L1aa                   SRLLTVGHPYFKVGM-----NGG--RKQDIPKVSAYQYRVFRVTLPDPNKFSIPDASLYNPETQRLVWACVGVEVGRGQPLGVGISGHPLYNRQDDTENSPFS----STTNKDSRDNVSVDYKQTQLCIIGCVPAIGEHWGKGKACKPNN   178
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HPV29                        SRLLTVGHPHYSIPK-----SSG--NKVDVPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPEAERLVWACTGVEVGRGQPLGVGLSGHPLYNKLNDTENSNIA---HAENGQDSRDNIAVDYKQTQLCILGCTPPMGEHWGKGTVCARTS   179
[HPV77]                      SRLLTVGHPYFAIPK-----TSG--TKVDVPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPEAERLVWACTGVEVGRGQPLGVGLSGHPLYNKLNDTENSNIA---HADNSPDSRDNISVDCKQTQLCILGCTPPMGEYWGKGTPCARTN   179
[HPV94]                      SRLLTVGHPYFPIPK-----SSN--NKVDVPKVSAYQYRVFRVRLPDPNKFGLPDARIYNPDAERLVWACTGVEIGRGLPLGVGLSGHPLYNKLDDTENSNIA---HGNVGQDSRDNISVDNKQTQLCILGCTPPMGEHWGKGTPCNRSA   207
[HPV10NP041746.1]            SRLLTVGHPYFPIPK-----SSN--NKVDVPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPDAERLVWACTGVEVGRGQPLGVGLSGHPLYNKLEDTENSNIA---HGPIGQDSRDNISVDNKQTQLCILGCTPPMGEHWGKGTPCRNPP   207
[HPV10CAA52494.1]            SRLLTVGHPYFPIPK-----SSN--NKVDVPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPDAERLVWACTGVEVGRGQPLGVGLSGHPLYNKLEDTENSNIA---HGPIGQDSRDNISVDNKQTQLCILGCTPPMGEHWGKGTPCRNPP   207
[HPV-10CAA52495.1]           SRLLTVGHPYFPIPK-----SSN--NKVDVPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPDAERLVWACTGVEVGRGQPLGVGLSGHPLYNKLEDTENSNIA---HGPIGQDSRDNISVDNKQTQLCILGCTPPMGEHWGKGTPCRNPP   179
[HPV3]                       SRLLTVGHPYFAIPK-----SSN--SKMDIPKVSAFQYRVFRVRLPDPNKFGLPDARIYNPDAERLVWACTGVEVGRGLPLGVGLSGHPLYNKLDDTENSNIA---HGDIGKDSRDNISVDNKQTQLCIVGCTPPMGEHWGKGTPCKQNA   207
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HPV66                        SRLLAVGHPYYSVSK------SG--TKTNIPKVSAYQYRVFRVRLPDPNKFGLPDPSFYNPDQERLVWACVGLEVGRGQPLGAGLSGHPLFNRLDDTEVSNLA---GNNVIEDSRDNISVDCKQTQLCIVGCAPALGEHWTKGAVCKSTP   178
[HPV53]                      SRLLTVGHPYYPISK-------S--GKADIPKVSAFQYRVFRVRLPDPNKFGLPDTNIFNPDQERLVWACVGLEIGRGQPLGVGVSGHPLFNRLDDTESSSIA---IQDTAPDSRDNVSVDPKQTQLCIIGCAPAIGEHWTKGTACRSTP   177
[HPV53CAA52595.1]            SRLLTVGHPYYPISK-------S--GKADIPKVSAFQYRVFRVRLPDPNKFGLPDTNIFNPDQERLVWACVGLEIGRGQPLGVGVSGHPLFNRLDDTESSSIA---IQDTAPDSRDNVSVDPKQTQLCIIGCAPAIGEHWTKGTACRSTP   177
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[HPV71]                      SRLLTVGHPYFPIRQ----ASGK--NRIVVPKVSGYQYRVFRVRLPDPNKFGLPDASLYNPDTQRLVWACKGLEVGRGQPLGIGVSGHPLFNKLNDTENATLF---DVNPGEDTRDNVSMDYKQTQLCIIGCKPPLGEHWAKGTPCSGAS   199
[HPV81]                      SRLLTVGHPYCTLTI----GTQG--KRSTIPKVSGYQYRVFRVKLPDPNKFALPDGTLYNPDTERMVWACRGIEVGRGQPLGVGTSGHPLYNRLDDTENTAYL----AAASEDSRDNISVDYKQTQLLIIGCKPPIGEHWARGTFCANVA   207
[HPV61]                      SRLLTVGHPYCSLQL---DGLQG--KKNTIPKVSGYQYRVFRVQLPDPNKFALPDGTLYNPDTERMVWACRGIEVGRGQPLGVGTSGHPLYNRLDDTENTTLL----VAESSDSRDNVSVDYKQTQLLIVGCKPPIGEHWTKGTACANPA   180
[HPV72]                      SRLLTVGHPYCAIPL----NGQG--KKNTIPKVSGYQYRVFRVKLPDPNKFALPDGTLYNPDTERLVWACRGIEVGRGQPLGVGTSGHPLYNRLDDTENTSLL----VADNSDSRDNVSVDYKQTQLLIIGCKPPIGEHWTKGTPCAGSN   207
[HPV84]                      SRLLTVGHPYYSVPV-STPGQNN--KKATIPKVSGYQYRVFRVHLPDPNKFGLPDAQLYNPDTERLVWACRGVEVGRGQPLGVGTSGHPLYNRLDDTENTPFL----AAGDTDSRDNVSVDYKQTQLLIIGCKPSIGEHWGKGTVCTNVQ   182
[HPV86]                      SRLLTVGHPYYPVTVSSSPGQNN--KKANIPKVSGYQYRVFRVRLPDPNKFGLPDAQLYNPDTERLVWACRGLEVGRGQPLGVGASGHPLYNRLDDTENTSFL----TTENVDSRDNVSVDYKQTQVLIVGCKPSIGEHWGKGTVCSNVQ   183
[HPVcand87]                  SRLLTVGHPYYPVTV--TTPGQN--KKSNIPKVSGYQYRVFRVRLPDPNKFGLPDAQLYNPDTERLVWACRGLEVGRGQPLGVGTSGHPLYNRLDDTENTPFL----TTENTDSRDNVSVDYKQTQLLIVGCKPSIGEHWSKGTVCANVQ   181
HPV83AAD38974.1|AF151983_7   SRLLTVGHPYYPVQV----NGQG--KKATIPKVSGYQYRVFRIRLPDPNKFSLPDTSLYNPDTERMVWACRGIEVGRGQPLGVGTSGHPLYNRLDDTENTPLL----AAADTDRRDNVSVDYKQTQLIIIGCKPPIGEHWAKGTVCSGVS   179
[HPVcand89]                  SRLITVGHPYYTVQV----NGAN--KKANIPKVSGYQYRVFRVRLPDPNKFGLPDASLYNPDTERLVWACRGVEVGRGQPLGVGTSGHPLYNRLDDTENASLL----VAADVDSRDNISVDYKQTQLLIIGCKPPIGEHWAKGTVCSSVV   195
[HPV90]                      SRLLTVGHPYFAIKK----QSGK--NPIVVPKVSGYQYRVFRVRLPDPNKFGLPDASLYNPDSQRLVWACTGVEVGRGQPLGVGVSGHPLYNRLYDTENTNLY---DVVPGDDTRDNLTMDYKQTQLFIIGCKPPLGEHWAKGTPCNMSN   180
[HPV57]                      SRLLTVGHPYYSIKK-----SGN--NKVSVPKVSGYQYRVFHVKLPDPNKFGLPDANLYDPDTQRLLWACVGVEVGRGQPLGVGISGHPYYNKQDDTENSH-----NPDAADDGREYISMDYKQTQLFILGCKPPIGEHWSKGTTCSGSS   193
[HPV-2]                      SRLLTVGHPYYSIKK------SN--NKVAVPKVSGYQYRVFHVKLPDPNKFGLPDADLYDPDTQRLLWACVGVEVGRGQPLGVGVSGHPYYNRLDDTENAH-----TPDTADDGRENISMDYKQTQLFILGCKPPIGEHWSKGTTCNGSS   192
[HPV27]                      SRLLTVGHPYYSIKK-----GSN--NRLAVPKVSGYQYRVFHVKLPDPNKFGLPDADLYDPDTQRLLWACVGVEVGRGQPLGVGVSGHPYYNRQDDTENAHTL-----DSAEDGRENISMDYKQTQLFILGCKPSIGEHWSKGTTCNGSS   286
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

File: /Users/johnlowe/Desktop/L1protein.ps **Date: Fri May 2 11:55:30 2008**


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[HPV7]                      VSP--GDCPVLELKSEVIEDGDMVDAGFGAMDFASLQANKSDVPLDLCTSISKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNRAGTTGDSVPNDLYITG---SSNRASIAGSIYYSTPSGSLVTSDSQIFNK--PLWIQKAQGHNNG 320
[HPV-7]                     VSP--GDCPVLELKSEVIEDGDMVDAGFGAMDFASLQANKSDVPLDLCTSISKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNRAGTTGDSVPNDLYITG---SSNRASIAGSIYYSTPSGSLVTSDSQIFNK--PLWIQKAQGHNNG 320
[HPV40]                     VTL--GDCPVLELKTEVIQDGDMVDTGFGAMDFASLQANKSDVPLDLCTSISKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNRAGTTGDSVPTDLYITG---TSGRTPIAGSIYYSTPSGSLVTSDSQIFNK--PLWIQKAQGHNNG 320
[HPV43]                     VTQ--GDCPVIELKSEVIQDGDMVDTGFGAMDFASLQASKSDVPLDLVNTKSKYPDYLGMAAEPYGNSLFFFLRREQMFLRHFFNKAGKTGDVVPSDMYIAG---SNTRSKIADSIYFSTPSGSLVTSDSQLFNK--PLWIQKAQGHNNG 348
[HPV91]                     ITQ--GDCPVIELKSEVIEDGDMVDTGFGALDFASLQASKSDVPLDLCNTKSKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNRAGTTGDAVPKDLYIAG---TGNRANIAGSIYYSTPSG------------------------- 295
[HPV6b]                     VQA--GDCPPLELITSVIQDGDMVDTGFGAMNFADLQTNKSDVPIDICGTTCKYPDYLQMAADPYGDRLFFFLRKEQMFARHFFNRAGEVGEPVPDTLIIKG---SGNRTSVGSSIYVNTPSGSLVSSEAQLFNK--PYWLQKAQGHNNG 318
[HPV6bNP_040304.1]          VQA--GDCPPLELITSVIQDGDMVDTGFGAMNFADLQTNKSDVPIDICGTTCKYPDYLQMAADPYGDRLFFFLRKEQMFARHFFNRAGEVGEPVPDTLIIKG---SGNRTSVGSSIYVNTPSGSLVSSEAQLFNK--PYWLQKAQGHNNG 318
[HPV11]                     VQN--GDCPPLELITSVIQDGDMVDTGFGAMNFADLQTNKSDVPLDICGTVCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEPVPDDLLVKG---GNNRSSVASSIYVHTPSGSLVSSEAQLFNK--PYWLQKAQGHNNG 319
[HPV13]                     VQP--GDCPPLELISSVIQDGDMVDTGFGAMNFAELQSNKSDVPLDICTSTCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGSVGEQIPAELYVKG---SN---TLSNSIYYNTPSGSLVSSEAQLFNK--PYWLQKAQGHNNG 316
[PCP                        VQD--GDCPPLELVTSVIQDGDMVDTGFGAMDFAQLQSNKSDVPLDICTATCKYPDYLQMAADPYGDRLFFSLRKEQMFARHFFNRAGTVGEQIPEDLLVKG---TTSRATVSSTIYFNTPSGSLVSSEAQLFNK--PYWLHKAQGHNNG 319
[CCP                        VQD--GDCPPLELVTSVIQDGDMVDTGFGAMDFAELQSNKSDVPLDICTSTCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEQIPDELFVKG---TTSRATVSSNIYFNTPSGSLVSSEAQLFNK--PYWLHKAQGHNNG 319
[HPV74]                     VKP--GDCPALELITSVIQDGDMVDTGFGAMNFADLQPIKSDVPLDICNTTCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEDIPQDLYIKG----TTRSTLANAIYFNTPSGSLVSSETQLFNK--PFWLQRAQGHNNG 344
[HPV44]                     VKD--GDCPPLELITSVIEDGDMVDTGFGAMNFAELQPNKSDVPLDICTATCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEDVSQDLVIKS----ASKNTVPNAIYFNTPSGSLVSSETQLFNK--PFWLQKAQGHNNG 318
[hpv55]                     VNS--GDCPPLELITSVIEDGDMVDTGFGAMNFAELQPNKSDVPLDICTATCKYPDYLQMAADPYGDRLFFYLRKEQMFARHFFNRAGTVGEDIPQDLVFKG----ATKSTVPNAIYFNTPSGSLVSSETQLFNK--PFWLQRAQGHNNG 318
HPV34_L1aa                  A----GECPPLELKNTTIQDGDMIDVGFGAMDFKALQANKSDVPIDISNTICKYPDYLGMAADPYGDSMWFYIRREQMFVRHLFNRAGTVGDAIPDDLMIKG---TGNTASPSSCVFYPTPSGSMVSSDAQIFNK--PYWLQKAQGQNNG 345
[HPV34NP_041812.1]          A----GECPPLELKNTTIQDGDMIDVGFGAMDFKALQANKSDVPIDISNTICKYPDYLGMAADPYGDSMWFYIRREQMFVRHLFNRAGTVGDAIPDDLMIKG---TGNTASPSSCVFYPTPSGSMVSSDAQIFNK--PYWLQKAQGQNNG 345
[HPV34CAA52560.1]           A----GECPPLELKNTTIQDGDMIDVGFGAMDFKALQANKSDVPIDISNTICKYPDYLGMAADPYGDSMWFYIRREQMFVRHLFNRAGTVGDAIPDDLMIKG---TGNTASPSSCVFYPTPSGSMVSSDAQIFNK--PYWLQKAQGQNNG 345
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[HPV54]                     LAA--GDCPPLELVNSYIQDGDMVDIGFGAMDFKTLQTSKSEVPLDVATSICKYPDYLKMAAEAYGDSLFFYLRREQMFVRHMLNRAGTMGEPVPNDLYIKK---SSG--NLDSSIYAATPSGSMVTSEYQIFNK--PYWLQRAQGQNNG 316
[HPV32]                     N----GDCPPLELQNSVIQDGDMADVGFGAMDFSALQTSKAEVPLDIMNSISKYPDYLKMSAEAYGDNMFFFLRREQMFVRHLFNRAGTLGEPVPEDMYIKASNGASGRNNLASSIYYPTPSGSMVTSDAQIFNK--PYWLQQAQGHNNG 322
[HPV32CAA52554.1]           N----GDCPPLELQNSVIQDGDMADVGFGAMDFSALQTSKAEVPLDIMNSISKYPDYLKMSAEAYGDNMFFFLRREQMFVRHLFNRAGTLGEPVPEDMYIKASNGASGRNNLASSIYYPTPSGSMVTSDAQIFNK--PYWLQQAQGHNNG 322
HPV42                       N----GDCPPLELKNSFIQDGDMVDVGFGALDFGALQSSKAEVPLDIVNSITKYPDYLKMSAEAYGDSMFFFLRREQMFVRHLFNRAGAIGEPVPDELYTKAANNASGRHNLGSSIYYPTPSGSMVTSDAQLFNK--PYWLQQAQGHNNG 322
RhesusPV1                   A----GDCPALELVNSVIQDGDMVDTGYGAMDFNALQANKSDVPIDICTSVCKYPDYLKMASDPYGDSLFFYLRREQMFVRHLFNRAGTMGDSVPDDLYIKG---SGSNVKLASHVFYPTPSGSMVTSDAQLFNK--PYWLQKAQGHNNG 319
HPV52_L1aa                  GNP--GDCPPLQLINSVIQDGDMVDTGFGCMDFNTLQASKSDVPIDICSSVCKYPDYLQMASEPYGDSLFFFLRREQMFVRHFFNRAGTLGDPVPGDLYIQG-SNSGNTATVQSSAFFPTPSGSMVTSESQLFNK--PYWLQRAQGHNNG 353
HPV67_L1aa                  NGP--GACPPLELMNTVIEDGDMIDTGFGCMDFKSLQANKSDVPLDICTSICKYPDYLGMASEAYGDSLFFFLRREQMFVRHLFNRAGKLGEDVPTDLYFKG---SANTSALQTSAFFPTPSGSMVSSESQLFNK--PYWLQRAQGHNNG 352
HPV33_L1aa                  PA---NDCPPLELINTIIEDGDMVDTGFGCMDFKTLQANKSDVPIDICGSTCKYPDYLKMTSEPYGDSLFFFLRREQMFVRHFFNRAGTLGEAVPDDLYIKG---SGTTASIQSSAFFPTPSGSMVTSESQLFNK--PYWLQRAQGHNNG 322
HPV58_L1aa                  AA---TDCPPLELFNSIIEDGDMVDTGFGCMDFGTLQANKSDVPIDICNSTCKYPDYLKMASEPYGDSLFFFLRREQMFVRHFFNRAGKLGEAVPDDLYIKG---SGNTAVIQSSAFFPTPSGSIVTSESQLFNK--PYWLQRAQGHNNG 348
HPV35                       VKA--GECPPLELLNTVLQDGDMVDTGFGAMDFTTLQANKSDVPLDICSSICKYPDYLKMVSEPYGDMLFFYLRREQMFVRHLFNRAGTVGETVPADLYIKG---TTG--TLPSTSYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 323
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HPV16NP_041332.1            VNP--GDCPPLELINTVIQDGDMVHTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGTVGENVPDDLYIKG---SGSTANLASSNYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 348
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[HPV16gerAAQ10719.1]        VNP--GDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKG---SGSTANLASSNYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 348
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[HPV16asamAF402678]         VTP--GDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKG---SGSTANLASSNYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 348
[HPV16aa]                   VNP--GDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKG---SGSTANLASSNYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 348
[HPV16af1]                  VNP--GDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKG---SGSTANLASSNYFPTPSGSMVTSDAQIFNK--PYWLQRAQGHNNG 348
HPV51                       VPP--GDCPPLELVSSVIQDGDMIDTGFGAMDFAALQATKSDVPLDISQSVCKYPDYLKMSADTYGNSMFFHLRREQIFARHYYNKLVGVGEDIPNDYYIKG--SGNGRDPIESYIYSATPSGSMITSDSQIFNK--PYWLHRAQGHNNG 322
[HPV82]                     VPQ--GDCPPLELVSTVIEDGDMVDTGFGAMDFANLQATKSDVPLDIAQSVCKYPDYLKMSADTYGNSMFFHLRREQIFARHYYNKAGVVGDAIPDKAYIKG--TGAGRDPISSYIYSATPSGSMITSDSQIFNK--PYWLHRAQGHNNG 322
HPV26NP_041787.1            TQR--GDCPPLELISSIIEDGDMIDTGFGAMDFTALQATKSDVPIDISQSTCKYPDYLKMSADTYGNSMFFFLRREQLFARHFYNKAGAVGDAIPTTLYIKG--AESGREPPTSSIYSATPSGSMVTSDAQLFNK--PYWLQRAQGHNNG 322
HPV26bCAA52535.1            TQR--GDCPPLELISSIIEDGDMIDTGFGAMDFTALQATKSDVPIDISQSTCKYPDYLKMSADTYGNSMFFFLRREQLFARHFYNKAGAVGDAIPTTLYIKG--AESGREPPTSSIYSATPSGSMVTSDAQLFNK--PYWLQRAQGHNNG 322
[HPV69]                     SQVQRGDCPPLELISSVIEDGDMIDTGFGAMDFTALQATKCDVPLDINQSICKYPDYLKMSADTYGNSMFFFLRREQLFARHFFNKAGTIGDSVPVSMYIKG--AGQGREPPTTSIYSRTPSGSMVTSDAQLFNK--PYWLQRAQGHNNG 323
HPV18_X05015                LSQ--GDCPPLELKNTVLEDGDMVDTGYGAMDFSTLQDTKCEVPLDICQSICKYPDYLQMSADPYGDSMFFCLRREQLFARHFWNRAGTMGDTVPQSLYIKG---TGMPASPGSCVYSPSPSGSIVTSDSQLFNK--PYWLHKAQGHNNG 383
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HPV59_L1aa                  VVQ--GDCPPLELINTPIEDGDMVDTGYGAMDFKLLQDNKSEVPLDICQSICKYPDYLQMSADAYGDSMFFCLRREQVFARHFWNRSGTMGDQLPESLYIKG---TDIRANPGSYLYSPSPSGSVVTSDSQLFNK--PYWLHKAQGLNNG 322
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HPV39_L1aa                  VST--GDCPPLELVNTPIEDGDMIDTGYGAMDFGALQETKSEVPLDICQSICKYPDYLQMSADVYGDSMFFCLRREQLFARHFWNRGGMVGDAIPAQLYIKG---TDIRANPGSSVYCPSPSGSMVTSDSQLFNK--PYWLHKAQGHNNG 321
HPV70_L1aa                  Q----GDCPPLELVNTAIEDGDMIDTGYGAMDFRTLQETKSEVPLDICQSVCKYPDYLQMSADVYGDSMFFCLRKEQLFARHFWNRGGMVGDTIPSELYIKG---TDIRERPGTHVYSPSPSGSMVSSDSQLFNK--PYWLHKAQGHNNG 320
HPV29                       SAA--GDCPPLELMTTHIEDGDMVDTGYGAMDFAALQVNKSDVPLDICQSTCKYPDYLGMAADPYGDSMFFFLRREQLFARHFFNRAGVVGDKIPDSLYLKG---NNGRETPGSAIYSPTPSGSMVTSEAQIFNK--PYWLQQAQGHNNG 322
[HPV77]                     TTP--GDCPPLELMTSYIQDGDMVDTGYGAMDFTALQFNKSDVPLDICQSICKYPDYLGMAADPYGDSMFFFLRREQLFARHFFNRAGDVGDKIPESLYLKG---SSGRETPGSAIYSPTPSGSMVTSEAQIFNK--PYWLQQAQGHNNG 322
[HPV94]                     PAP--GDCPPLELVTSVIQDGDMVDTGYGAMDFTALQLNKSDVPIDICQSTCKYPDYLGMAAEPYGDSMFFYLRREQLFARHFFNRASAVGDTIPDTLILKS---AGGDQNVGSAVYSPTPSGSMVTSEAQLFNK--PYWLKRAQGHNNG 350
[HPV10NP041746.1]           AQ---GDCPPLELITSPIQDGDMVDTGYGAMDFTALQLNKSDVPIDICQSTCKYPDYLGMAAEPYGDSMFFYLRREQLFARHFFNRASAVGDAIPDTFILKS---NGGGRDVGSAVYSPTPSGSMVTSEAQLFNK--PYWLRRAQGHNNG 349
[HPV10CAA52494.1]           AQ---GDCPPLELITSPIQDGDMVDTGYGAMDFTALQLNKSDVPIDICQSTCKYPDYLGMAAEPYGDSMFFYLRREQLFARHFFNRASAVGDAIPDTFILKS---NGGGRDVGSAVYSPTPSGSMVTSEAQLFNK--PYWLRRAQGHNNG 349
[HPV-10CAA52495.1]          AQ---GDCPPLELITSPIQDGDMVDTGYGAMDFTALQLNKSDVPIDICQSTCKYPDYLGMAAEPYGDSMFFYLRREQLFARHFFNRASAVGDAIPDTFILKS---NGGGRDVGSAVYSPTPSGSMVTSEAQLFNK--PYWLRRAQGHNNG 321
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HPV28                       QQ---GDCPPLELITAPIQDGDMVDTGFGAMDFAVLQANKSDVPLDICQSTCKYPDYLGMAAEPYGDSMFFYLRKEQLFARHFFNRAGVAGDTIPETLYIKG--QGNGRDVIGSAVYSPTPSGSMISSEAQLFNK--PYWLRRAQGHNNG 322
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HPV66                       GNT--GDCPPLALVNTPIEDGDMVDTGFGAMDFKLLQESKAEVPLDIVQSTCKYPDYLKMSADAYGDSMWFYLRREQLFARHYFNRAGNVGEAIPTDLYWKG---GNGRDPPPSSVYVATPSGSMITSEAQLFNK--PYWLQRAQGHNNG 321
[HPV53]                     TTA--GDCPPLELINSPIEDGDMVDTGFGALNFKALQESKSDVPLDIVQSTCKYPDYLKMSADAYGDSMWFYLRREQLFTRHFFNRAGVIGEEIPNDLYIKG---SNGRDPPPSSVYVATPSGSMITSEAQLFNK--PYWLQRAQGHNNG 320
[HPV53CAA52595.1]           TTA--GDCPPLELINSPIEDGDMVDTGFGALNFKALQESKSDVPLDIVQSTCKYPDYLKMSADAYGDSMWFYLRREQLFTRHFFNRAGVIGEEIPNDLYIKG---SNGRDPPPSSVYVATPSGSMITSEAQLFNK--PYWLQRAQGHNNG 320
[HPV30]                     PAQ--GDCPPLELVNSPIQDGDMVDIGFGAMDFKTLQESKSDVPLDISQSTCKYPDYLKMSADAYGDSMWFYLRREQLFARHYFNRAGAIGEQLPSTLYIKG---TNNRDPPPSSVYVATPSGSMVTSEAQLFNK--PYWLQRAQGHNNG 329
[HPV71]                     AAA--GSCPPLELASTVIQDGDMVDTGFGAMDFAALQTNRSDVPLDIVTTTCKY-QIISNGCRAIGDRMFF-LRREQCF-KTFYNRQAHLG-RVPDDYYLKV-HLLPFVLPLQALFMHPHLVGPWLPQSHSCLTSLTGYNVHRAQTMA-- 340
[HPV81]                     PAQ--NECPPLEFKNTTIQDGDMVETGYGAIDFKALQENKSEVPLDICNTTCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRHGTMGEALPADLYMKG-AAGSDRITPGSYIYAPTPSGSMVSSDSQLFNK--PYWLQRAQGHNNG 352
[HPV61]                     PRP--TDCPPLEFTNTTIQDGDMVETGYGAIDFAALQENKSEVPLDICTTICKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGVMGEALPDSYYLKG---ANDKAAPGSYIYSPTPSGSMVSSDSQLFNK--PYWLQRAQGHNNG 323
[HPV72]                     SQP--TDCPPLEFTNSTIQDGDMVETGYGAIDFATLQENKSEVPLDICTTTCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGTMGEALPASLYLKG-ASGSDRVTPGSYIYSPTPSGSMVSSDAQLFNK--PYWLQRAQGHNNG 352
[HPV84]                     YRA--GDCPPLQFTNSTIEDGDMVEAGYGAIDFATLQESKSEVPLDLCTTTCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGTMGEEVPQSFYLKG---TSSRATLSSSVYAPTPSGSMVSSDSQLFNK--PYWLQKAQGHNNG 325
[HPV86]                     PKP--GDCPPLQFTNSTIQDGDMVEAGYGAMDFDKLQENKSEVPLDICATVCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGVMGEPVPETYYLKG--SSGPRGSLSSYVYAPTPSGSMVSSDSQLFNK--PYWLQKAQGHNNS 327
[HPVcand87]                 PKT--GDCPPLQFTNSTIQDGDMVEAGYGAIDFEKLQENKSEVPLDICTTVCKYPDYLQMAAEPYGDCMFFCLRREQMFARHYFNRQGTMGEEVPDTYFLKG-ASSGPRASLSSYVYAPTPSGSMVSSDSQLFNK--PYWLQRAQGHNNG 326
HPV83AAD38974.1|AF151983_7  PQR--GDCPPLQFVNSTIQDGDMVETGYGAMDFATLQESKSEVPIDICTATCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRHGTMGEVLPTSYYIPG-TSANSRNTLTSYIYAPTPSGSLVSSDSQLFNK--PYWLHRAQGHNNG 324
[HPVcand89]                 PQQ--GDCPPLQLLNTTIEDGDMVETGYGAMDFSKLQESKSEVPIDICDSTCKYPDYLQMAAEPYGDCMFFCLRREQMFARHFFNRQGVMGEDLPKTLYMPG-SAANNRNTLTSYVYAPTPSGSMVTSDSQLFNK--PYWLHRAQGHNNG 340
[HPV90]                     VQA--GDCPPIELKSSTIQDGDMIDTGFGALDFAALQTNKSDVPLDIVTTTCKYPDFLQMAAEPYGDLMFFCLRREQMFIRHFYNRAGTMGDAIPDGFVLKG-TSSTSRGTPTSSVYGSTPSGSMVTSESQLFNK--PYWLQRAQGPNNG 325
[HPV57]                     AV---GDCPPLQFTNTTIEDGDMVETGFGALDFAALQSNKSDVPLDICTNICKYPDYLKMAADPYGDSMFFSLRREQMFTRHFFNRGGSMGDALPDELYVKS----STVQTPGSYVYTSTPSGSMVSSEQQLFNK--PYWLRRAQGHNNG 334
[HPV-2]                     AA---GDCPPLQFTNTTIEDGDMVETGFGALDFATLQSNKSDVPLDICTNTCKYPDYLKMAAEPYGDSMFFSLRREQMFTRHFFNLGGKMGDTIPDELYIKS----TSVPTPGSHVYTSTPSGSMVSSEQQLFNK--PYWLRRAQGHNNG 333
[HPV27]                     AA---GDCPPLQFTNSTIEDGDMVETGFGALDFATLQSNRSDVPLDICTNVCKYPDYLKMAAEPYGDSMFFSLRREQMFTRHFFNRAGKMGDTIPDELYIKS----TTISDPGSHVYTSTPSGSMVSSEQQLFNK--PYWLRRAQGHNNG 427
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

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[HPV7]                          ICFGNQLFVTVVDTTRSTNLTLCAATQ-SPTPTPYDNSKFKEYLRHGEEFDLQFIFQLCVITLNAEVMTYIHAMDSSLLDDWNFKIGPPASATLEDTYRFLTNKAIACQRDAP-PKEKE-DPYKKYKFWEVNLTEKFSSQLDQFPLGRKF  467
[HPV-7]                         ICFGNQLFVTVVDTTRSTNLTLCAATQ-SPTPTPYDNSKFKEYLRHGEEFDLQFIFQLCVITLNAEVMTYIHAMDSSLLDDWNFKIGPPASATLEDTYRFLTNKAIACQRDAP-PKEKE-DPYKKYKFWEVNLTEKFSSQLDQFPLGRKF  467
[HPV40]                         ICFGNQLFVTVVDTTRSTNLTLCAATQ-SPTPTPYNNSNFKEYLRHGEEFDLQFIFQLCVITLNAEVMTYIHAMDPTLLEDWNFKIAPPASASLEDTYRFLTNKAIACQRDAP-PKVRE-DPYKKYKFWDVNLTERFSSQLDQFPLGRKF  467
[HPV43]                         ICFGNQLFVTVVDTTRSTNLTLCASTD-PTVPSTYDNAKFKEYLRHVEEYDLQFIFQLCIITLNPEVMTYIHTMDPTLLEDWNFGVSPPASASLEDTYRFLSNKAIACQKNAP-PKERE-DPYKKYTFWDINLTEKFSAQLTQFPLGRKF  495
[HPV91]                         --------VTVVDTTRSTNLTLCASTE-SVLPTTYDNTKFKEYLRHAEEFDLQFIFQLCIITLNPEVMTYIHTMDASLLEDWNFGVSPPATASLEDTYRFLANKAIACQKNVP-PKAKE-DPYKNYTFWDVDLTERFSAQLTQFPLGRKF  434
[HPV6b]                         ICWGNQLFVTVVDTTRSTNMTLCASVT-TS--STYTNSDYKEYMRHVEEYDLQFIFQLCSITLSAEVMAYIHTMNPSVLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-EKEKP-DPYKNLSFWEVNLKEKFSSELDQYPLGRKF  463
[HPV6bNP_040304.1]              ICWGNQLFVTVVDTTRSTNMTLCASVT-TS--STYTNSDYKEYMRHVEEYDLQFIFQLCSITLSAEVMAYIHTMNPSVLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-EKEKP-DPYKNLSFWEVNLKEKFSSELDQYPLGRKF  463
[HPV11]                         ICWGNHLFVTVVDTTRSTNMTLCASVS-KS--ATYTNSDYKEYMRHVEEFDLQFIFQLCSITLSAEVMAYIHTMNPSVLEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-EKEKQ-DPYKDMSFWEVNLKEKFSSELDQFPLGRKF  464
[HPV13]                         ICWGNHLFVTVVDTTRSTNMTVCAATT-SSLSDTYKATEYKQYMRHVEEFDLQFIFQLCTIKLTAEVMSYIHTMNPTILEDWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-DKEKQ-DPYAGLSFWEVNLKEKFSSELDQYPLGRKF  463
[PCP                            ICWGNTLFVTVVDTTRSTNMTVCASTT-SSPSATYTASEYKQYMRHVEEFDLQFIFQLCSIKLTAEVMAYIHTMNPTVLEEWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-DKEKQ-DPYAGLSFWEVNLKEKFSSELDQYPLGRKF  466
[CCP                            ICWGNTLFVTVVDTTRSTNMTVCASTT-SSPSATYTASEYKQYMRHVEEFDLQFIFQLCTIKLTAELMAYIHTMNPTVLEEWNFGLSPPPNGTLEDTYRYVQSQAITCQKPTP-DKEKQ-DPYAGLSFWEVNLKEKFSSELEQYPLGRKF  466
[HPV74]                         ICWGNQLFVTVVDTTRSTNMTVCAPTS-QSPSATYNSSDYKQYMRHVEEFDLQFIFQLCSIKLTAEVMAYIHTMNPTVLEEWNFGLTPPPNGTLEDTYRYVQSQAITCQKPTP-DKAKP-NPYANLSFWEVNLKEKFSSELDQYPLGRKF  491
[HPV44]                         ICWGNQLFVTVVDTTRSTNMTICAATT-QSPPSTYTSEQYKQYMRHVEEFDLQFMFQLCSITLTAEVMAYLHTMNAGILEQWNFGLSPPPNGTLEDKYRYVQSQAITCQKPPP-EKAKQ-DPYAKLSFWEVDLREKFSSELDQYPLGRKF  465
[hpv55]                         ICWGNQLFVTVVDTTRSTNMTICAATT-QSPSTTYNSTEYKQYMRHVEEFDLQFMFQLCSITLTAEVMAYLHTMNPGILEQWNFGLSPPPNGTLEDKYRYVQSQAITCQKPPP-EKAKQ-DPYAKLSFWEVDLREKFSSELDQYPLGRKF  465
HPV34_L1aa                      ICWHNQLFLTVVDTTRSTNFSVCVGTQSTSTTAPYANSNFKEYLRHAEEYDLQFVFQLCKINLTTDVMTYIHSMSSSILEQWNFGLTPPPSGTLEETYRYVTSQAITCQRPQP-PKETE-DPYGKMTFWEVDLKEKFSAELDQFALGRKF  493
[HPV34NP_041812.1]              ICWHNQLFLTVVDTTRSTNFSVCVGTQSTSTTAPYANSNFKEYLRHAEEYDLQFVFQLCKINLTTDVMTYIHSMSSSILEQWNFGLTPPPSGTLEETYRYVTSQAITCQRPQP-PKETE-DPYGKMTFWEVDLKEKFSAELDQFALGRKF  493
[HPV34CAA52560.1]               ICWHNQLFLTVVDTTRSTNFSVCVGTQSTSTTAPYANSNFKEYLRHAEEYDLQFVFQLCKINLTTDVMTYIHSMSSSILEQWNFGLTPPPSGTLEETYRYVTSQAITCQRPQP-PKETE-DPYGKMTFWEVDLKEKFSAELDQFALGRKF  493
HPV73CAA63887.1                 ICWHNQLFLTVVDTTRSTNFSVCVGTQASSSTTTYANSNFKEYLRHAEEFDLQFVFQLCKISLTTEVMTYIHSMNSTILEEWNFGLTPPPSGTLEETYRYVTSQAISCQRPQP-PKETE-DPYAKLSFWDVDLKEKFSAELDQFPLGRKF  468
[HPV54]                         ICWGNQVFLTVVDTTRSTNLTLCATAS-TQ--DSFNNSDFREYIRHVEEYDLQFIFQLCTITLTADVMAYIHGMNPTILEDWNFGITPPATSSLEDTYRFVQSQAIACQKNNA-PAKEKEDPYSKFNFWTVDLKERFSSDLDQFPLGRKF  462
[HPV32]                         ICWGNQVFLTVVDTTRSTNMTVCATVT-TE--DTYKSTNFKEYLRHAEEYDIQFIFQLCKITLSVEVMSYIHTMNPDILDDWNVGVAPPPSGTLEDSYRFVQSQAIRCQAKVT-APEKK-DPFSDYSFWEVNLSEKFSSDLDQFPLGRKF  467
[HPV32CAA52554.1]               ICWGNQVFLTVVDTTRSTNMTVCATVT-TE--DTYKSTNFKEYLRHAEEYDIQFIFQLCKITLSVEVMSYIHTMNPDILDDWNVGVAPPPSGTLEDSYRFVQSQAIRCQAKVT-APEKK-DPFSDYSFWEVNLSEKFSSDLDQFPLGRKF  467
HPV42                           ICWGNQLFLTVVDTTRSTNMTLCATAT-SG--DTYTAANFKEYLRHAEEYDVQFIFQLCKITLTVEVMSYIHNMNPNILEEWNVGVAPPPSGTLEDSYRYVQSEAIRCQAKVT-TPEKK-DPYSDFWFWEVNLSEKFSTDLDQFPLGRKF  467
RhesusPV1                       ICWGNQVFLTVVDTTRSTNMTLCASTA-STVTTPYNNESFKEYLRHVEEFDLQFIFQLCKVTLNTEVMAYIHSMDASILEDWNFGLQPPPSGSLQDTYRFVTSAAITCQKPAP-PKEKE-DPLAKYTFWEVDLKEKFSADLDQFPLGRKF  466
HPV52_L1aa                      ICWGNQLFVTVVDTTRSTNMTLCAEVK-KE--STYKNENFKEYLRHGEEFDLQFIFQLCKITLTADVMTYIHKMDATILEDWQFGLTPPPSASLEDTYRFVTSTAITCQKNTP-PKGKE-DPLKDYMFWEVDLKEKFSADLDQFPLGRKF  498
HPV67_L1aa                      ICWGNQIFVTVVDTTRSTNMTLCSEEK-SE--ATYKNENFKEYLRHVEEYDLQFIFQLCKISLTANVMQYIHTMNPDILEDWQFGLTPPPSGNLQDTYRFVTSQAITCQKTSP-PTAKE-DPLKKYSFWEINLKEKFSADLDQFPLGRKF  497
HPV33_L1aa                      ICWGNQVFVTVVDTTRSTNMTLCTQVT-SD--STYKNENFKEYIRHVEEYDLQFVFQLCKVTLTAEVMTYIHAMNPDILEDWQFGLTPPPSASLQDTYRFVTSQAITCQKTVP-PKEKE-DPLGKYTFWEVDLKEKFSADLDQFPLGRKF  467
HPV58_L1aa                      ICWGNQLFVTVVDTTRSTNMTLCTEVT-KE--GTYKNDNFKEYVRHVEEYDLQFVFQLCKITLTAEIMTYIHTMDSNILEDWQFGLTPPPSASLQDTYRFVTSQAITCQKTAP-PKEKE-DPLNKYTFWEVNLKEKFSADLDQFPLGRKF  493
HPV35                           ICWSNQLFVTVVDTTRSTNMSVCSAVS-SSD-STYKNDNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNPSILEDWNFGLTPPPSGTLEDTYRYVTSQAVTCQKPSA-PKPKD-DPLKNYTFWEVDLKEKFSADLDQFPLGRKF  469
HPV31_L1aa                      ICWGNQLFVTVVDTTRSTNMSVCAAIA-NSD-TTFKSSNFKEYLRHGEEFDLQFIFQLCKITLSADIMTYIHSMNPAILEDWNFGLTTPPSGSLEDTYRFVTSQAITCQKTAP-QKPKE-DPFKDYVFWEVNLKEKFSADLDQFPLGRKF  469
HPV16NP_041332.1                ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVT-QAIACQKHTP-PAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
HPV16_L1aa                      ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVT-QAIACQKHTP-PAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16eaAF534061]               ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTP-PAPKE-DPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16gerAAQ10719.1]            ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTP-PAPKE-DPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16af2]                      ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-PTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTP-PAPKE-DPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16asamAF402678]             ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-PTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMSYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTP-PAPKE-DPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16aa]                       ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-PTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVT-QAIACQKHTP-PAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
[HPV16af1]                      ICWGNQLFVTVVDTTRSTNMSLCAAIS-TSE-TTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTP-PAPKE-DPLKKYTFWEVNLKEKFSADLDQFPLGRKF  494
HPV51                           ICWNNQLFITCVDTTRSTNLTISTAT--AAVSPTFTPSNFKQYIRHGEEYELQFIFQLCKITLTTEVMAYLHTMDPTILEQWNFGLTLPPSASLEDAYRFVRNAATSCQKDTP-PQAKP-DPLAKYKFWDVDLKERFSLDLDQFALGRKF  468
[HPV82]                         ICWNNQLFITCVDTTKSTNLTISTAVT-PSVAQTFTPANFKQYIRHGEEYELQFIFQLCKITLTTEIMAYLHTMDSTILEQWNFGLTLPPSASLEDAYRFVKNAATSCHKDSP-PQAKE-DPLAKYKFWNVDLKERFSLDLDQFALGRKF  469
HPV26NP_041787.1                ICWGNQLFVTCVDTTRSTNLTISTLSA-ASASTPFKPSDYKQFIRHGEEYELQFIFQLCKITLTTDVMAYIHLMNASILEDWNFGLTLPPTASLEDAYRFIKNSATTCQRNAP-PVPKE-DPFQKFKFWDVDLKEKFSIDLDQFPLGRKF  469
HPV26bCAA52535.1                ICWGNQLFVTCVDTTRSTNLTISTLSA-ASASTPFKPSDYKQFIRHGEEYELQFIFQLCKITLTTDVMAYIHLMNASILEDWNFGLTLPPTASLEDAYRFIKNSATTCQRNAP-PVPKE-DPFQKFKFWDVDLKEKFSIDLDQFPLGRKF  469
[HPV69]                         ICWGNQLFVTCVDTTRSTNLTISTVSA-QSASATFKPSDYKQFIRHGEEYELQFIFQLCKITLTTDVMAYIHTMNSTILENWNFGLTLPPTASLEDAYRFIKNSATTCQRDAP-AQPKE-DPFSKLKFWDVDLKEKFSIDLDQFPLGRKF  470
HPV18_X05015                    VCWHNQLFVTVVDTTPSTNLTICASTQ-SPVPGQYDATKFKQYSRHVEEYDLQFIFQLCTITLTADVMSYIHSMNSSILEDWNFGVPPPPTTSLVDTYRFVQSVAITCQKDAA-PAENK-DPYDKLKFWNVDLKEKFSLDLDQYPLGRKF  530
HPv18_NC001357                  VCWHNQLFVTVVDTTPSTNLTICASTQ-SPVPGQYDATKFKQYSRHVEEYDLQFIFQLCTITLTADVMSYIHSMNSSILEDWNFGVPPPPTTSLVDTYRFVQSVAITCQKDAA-PAENK-DPYDKLKFWNVDLKEKFSLDLDQYPLGRKF  530
HPV45_L1aa                      ICWHNQLFVTVVDTTRSTNLTLCASTQ-NPVPSTYDPTKFKQYSRHVEEYDLQFIFQLCTITLTAEVMSYIHSMNSSILENWNFGVPPPPTTSLVDTYRFVQSVAVTCQKDTT-PPEKQ-DPYDKLKFWTVDLKEKFSSDLDQYPLGRKF  498
HPV59_L1aa                      ICWHNQLFLTVVDTTRSTNLSVCASTT-SSIPNVYTPTSFKEYARHVEEFDLQFIFQLCKITLTTEVMSYIHNMNTTILEDWNFGVTPPPTASLVDTYRFVQSAAVTCQKDTA-PPVKQ-DPYDKLKFWPVDLKERFSADLDQFPLGRKF  469
HPVcand85_L1aa                  ICWHNQLFITVVDTTRSTNLTLSTATT-NPVPSIYEPSKFKEYTRHVEEYDLQFIFQLCKITLTTDVMSYIHNMDPTILDSWNFGVSPPPSASLVDTYRFLQSSAITCQKDVV-VPQKK-DPYEKLKFWNVDLKEHFSSDLDQFPLGRKF  469
HPV68_L1aa                      ICWHNQLFLTVVDTTRSTNFTLSTTTD-STVPAVYDSNKFKEYVRHVEEYDLQFIFQLCTITLSTDVMSYIHTMNPAILDDWNFGVAPPPSASLVDTYRYLQSAAITCQKDAP-APVKK-DPYDGLNFWNVDLKEKFSSELDQFPLGRKF  469
HPV39_L1aa                      ICWHNQLFLTVVDTTRSTNFTLSTSIE-SSIPSTYDPSKFKEYTRHVEEYDLQFIFQLCTVTLTTDVMSYIHTMNSSILDNWNFAVAPPPSASLVDTYRYLQSAAITCQKDAP-APEKK-DPYDGLKFWNVDLREKFSLELDQFPLGRKF  468
HPV70_L1aa                      ICWHNQLFITVVDTTRSTNFTLSACTE-TAIPAVYSPTKFKEYTRHVEEYDLQFIFQLCTITLTADVMAYIHTMNPAILDNWNIGVTPPPSASLVDTYRYLQSAAIACQKDAP-TPEKK-DPYDDLKFWNVDLKEKFSTELDQFPLGRKF  467
HPV29                           ICWANQVFLTVVDTTRSTNMSLCATTE-SQPLTTYDATKIKEYLRHGEEYDLQFIFQLCKVTLTPEIMAYLHTMNSALLEDWNFGLTLPPSTSLEDTYRFVTSSAITCQKDLA-PTEKQ-DPYAKLNFWDVDLKDRFTLDLSQFPLGRKF  469
[HPV77]                         ICWGNQVFLTVVDTTRSTNMSLSASTE-SQTPSTYDATKIKEYLRHGEEYDLQFIFQLCKVTLTPEIMAYIHTMNTALLEDWNFGLTLPPSTSLEDTYRFVTSSAITCQKDVA-PTEKQ-DPYAKLNFWDVDLKDRFTLDLSQFPLGRKF  469
[HPV94]                         ICWGNQMFVTVVDTTRSTNLSLCVPSD-ASTATTYDATKFKEFLRHGEEYDLQFIFQLCKVTLTPEIMAYLHTMNSSLLEDWNFGLTLPPSTSLEDTYRFLSSSAITCQKEAP-PTEKQ-DPYAKLNFWDVDLKDRFTLDLSQFPLGRKF  497
[HPV10NP041746.1]               ICWANQLFVTVVDTTRSTNMCLCVPSE-ASPATTYDATKFKEYLRHGEEYDLQFIFQLCKVTLTPDIMAYLHTMNSSLLEDWNFGLTLPPSTSLEDTYRFLSSSAITCQKDTP-PTEKQ-DPYAKLNFWDVDLKDRFSLDLSQFPLGRKF  496
[HPV10CAA52494.1]               ICWANQLFVTVVDTTRSTNMCLCVPSE-ASPATTYDATKFKEYLRHGEEYDLQFIFQLCKVTLTPDIMAYLHTMNSSLLEDWNFGLTLPPSTSLEDTYRFLSSSAITCQKDTP-PTEKQ-DPYAKLNFWDVDLKDRFSLDLSQFPLGRKF  496
[HPV-10CAA52495.1]              ICWANQLFVTVVDTTRSTNMCLCVPSE-ASPATTYDATKFKEYLRHGEEYDLQFIFQLCKVTLTPDIMAYLHTMNSSLLEDWNFGLTLPPSTSLEDTYRFLSSSAITCQKDTP-PTEKQ-DPYAKLNFWDVDLKDRFSLDLSQFPLGRKF  468
[HPV3]                          ICWANQLFVTVVDTTRSTNMTLCVSTE-TS--ATYDATKFKEYLRHGEEYDLQFIFQLCKVTLTPEIMAYLHTMNSTLLEDWNFGLTLPPSTSLEDTYRFLTSSAITCQKDAP-PTEKQ-DPYAKLNFWDVDLKDRFSLDLSQFPLGRKF  497
HPV28                           ICWANQLFVTVVDTTRSTNMTLCVSTD-SS--ATYDASKFKEYLRHGEEYDLQFIFQLCKVTLTPDIMAYLHTMNNSLLEDWNFGLTLPPSTSLEDTYRFISSSAITCQKDAS-PTTKE-DPYAKLNFWEVDLKDRFSLDLSQFPLGRKF  467
HPV56CAA52600.1                 ICWGNQLFVTVVDTTRSTNMTISTATE-QL--SKYDARKINQYLRHVEEYELQFVFQLCKITLSAEVMAYLHNMNANLLEDWNIGLSPPVATSLEDKYRYVRSTAITCQREQP-PTEKQ-DPLAKYKFWDVNLQDSFSTDLDQFPLGRKF  501
HPV66                           ICWGNQVFVTVVDTTRSTNMTINAAKS-TL--TKYDAREINQYLRHVEEYELQFVFQLCKITLTAEVMAYLHNMNNTLLDDWNIGLSPPVATSLEDKYRYIKSTAITCQREQP-PAEKQ-DPLAKYKFWEVNLQDSFSADLDQFPLGRKF  466
[HPV53]                         ICWNNQLFVTVVDTTRNTNMTLSATTQ-SM--STYNSKQIKQYVRHAEEYELQFVFQLCKISLSAEVMAYLHTMNSTLLEDWNIGLSPPVATSLEDKYRYVKSAAITCQKDQP-PPEKQ-DPLSKYKFWEVNLQNSFSADLDQFPLGRKF  465
[HPV53CAA52595.1]               ICWNNQLFVTVVDTTRNTNMTLSATTQ-SM--STYNSKQIKQYVRHAEEYELQFVFQLCKISLSAEVMAYLHTMNSTLLEDWNIGLSPPVATSLEDKYRYVKSAAITCQKDQP-PPEKQ-DPLSKYKFWEVNLQNSFSADLDQFPLGRKF  465
[HPV30]                         ICWGNQVFVTVVDTTRNTNMTISATTQ-TL--STYNSSQIKQYVRHVEEYELQFVFQLCKISLSAETMAYLHTMNSTLLEGWNIGLSPPAATSLEDKYRYVKSLAITCQKDQP-PAEKE-DPLAKYKFWDVNLQDSFSADLDQFPLGRKF  474
[HPV71]                         -FVGQSAFCNSCDTSRSTNMSICATKT-VE--STYKASSFMEYLRHGEEFDLQFIFQLCVINLTAEIMAYLHGMDATLLEDWNFGSLPPPTASLGDTYRFLQSQAITCQKNSPPPAEKK-DPYADLTFWEVDLKERFSLELDQFPLGRKF  485
[HPV81]                         ICWFNEMFVTVVDTTRSTNFTICTATS-AA--AEYKASNFKEFLRHTEEYDLQFIFQLCKIQLTPEIMAYLHNMNKALLDDWNFGVLPPPSTSLDDTYRFLQSRAITCQKGAAAPAPKE-DPYADMSFWTVDLKDKLSTDLDQFPLGRKF  498
[HPV61]                         ICWFNELFVTVVDTTRSTNLTICTATS-PPV-SEYKATSFREYLRHTEEFDLQFIFQLCKIHLTPEIMAYLHNMNKALLDDWNFGVVPPPSTSLEDTYRFLQSRAITCQKGAAAPPPKE-DRYAKLSFWTVDLRDKFSTDLDQFPLGRKF  470
[HPV72]                         ICWFNELFVTVVDTTRSTNVTICTATA-SSV-SEYTASNFREYLRHTEEFDLQFIFQLCKIHLTPEIMAYLHNMNKALLDDWNFGVVPPPSTSLDDTYRFLQSRAITCQKGAATPPPKE-DPYANLSFWTVDLKDKFSTDLDQFPLGRKF  499
[HPV84]                         ICWFNQLFVTVVDTTRSTNFTISAATN-TE--SEYKPTNFKEYLRHVEEYDLQFIFQLCKVRLTPEVMSYLHTMNDSLLDEWNFGVVPPPSTSLDDTYRYLQSRAITCQKGAAAAKPKD-DPYAGMSFWDVDLKDKFSTDLDQYPLGRKF  471
[HPV86]                         ICWFNQLFVTVVDTTRSTNFTISAATQ-KA--SEYDPSKFNEYLRHAEEYDLQFIFQLCKVRLTPEIMSYLHSMNESLLDEWNFGVVPPPSTSLEDTYRFLQSRAITCQKGATAPQPKE-DPYAGMVFWEVDLKDKLSTDLDQFPLGRKF  473
[HPVcand87]                     ICWFNQLFVTVVDTTRSTNFTISAATQ-TT--TEYDPTKFKEYLRHVEEYDLQFIFQLCKVRLTPEVMAYLHTMNESLLDEWNFGVVPPPSTSLDDTYRYLQSRAITCQKGSAATKPKE-DPYTGMLFWEVDLKDKLSTDLDQFPLGRKF  472
HPV83AAD38974.1|AF151983_7      ICWFNELFVTVVDTTRSTNITISAAAT-QA--NEYTASNFKEYLRHTEEYDLQVILQLCKIHLTPEIMAYLHSMNEHLLDEWNFGVLPPPSTSLDDTYRYLQSRAITCQKGPSAPAPKK-DPYDGLVFWEVDLKDKLSTDLDQFPLGRKF  470
[HPVcand89]                     ICWFNELFVTVVDTTRSTNLTICAASQ-SG--TEYSSTRFKEYLRHTEEYDLQFIFQLCKIHLTPEIMSYLHNMNDTLLDEWNFGVIPPPSTSLDDTYRFLTSRAITCQKGTAAPEPKK-DPYDKLSFWDVDLKERLSTDLDQFPLGRKF  486
[HPV90]                         ICWGNQLFVTVVDTTRSTNMTICATQT-PS--DTYKASNFKEYMRHGEEFDLQFIFQLCVINLTTEVMAYLHGMNATLLEDWNFGSLPPPTASLGDTYRFLQSQAISCQKPSAVPTENK-DPYAGLTFWEVDLSERFSLELDQFPLGRKF  471
[HPV57]                         MCWGNRIFLTVVDTTRSTNVSLCATVT-TE--TNYKASNYKEYLRHMEEYDLQFIFQLCKITLTPEIMAYIHNMDARLLEDWNFGVPPPPSASLQDTYRYLQSQAITCQKPTP-PKTPT-DPYATMTFWDVDLSESFSMDLDQFPLGRKF  479
[HPV-2]                         MCWGNRVFLTVVDTTRSTNVSLCATEA-SD--TNYKATNFKEYLRHMEEYDLQFIFQLCKITLTPEIMAYIHNMDPQLLEDWNFGVPPPPSASLQDTYRYLQSQAITCQKPTP-PKTPT-DPYASLTFWDVDLSESFSMDLDQFPLGRKF  478
[HPV27]                         MCWGNRIFLTVVDTTRSTNVSLCAAEV-SDN-TNYKATNFKEYLRHMEEYDLQFIFQLCKITLTPEIMAYIHNMDPQLLEDWNFGVPPPPSASLQDTYRYLQSQAITCQKPTP-PKTPT-DPYANMTFWDVDLRESFSMDLDQFPLGRKF  573
                                .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT


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                                  ::*             :
[HPV7]                            LMQAG---LRTGPKFKSRKRPAPTSSSSSGSVTPKRK---KTKR--   505
[HPV-7]                           LMQAG---LRTGPKFKSRKRPAPTSSSSSGSVTPKRK---KTKR--   505
[HPV40]                           LMQAG---VRAGPRFKSRKRPAPSSSSSKPVTPKRK---KTKR--   505
[HPV43]                           VMQAG---LRPKPKLKTVKRSAPSSSTSAPA--SKRK---KTKR--   531
[HPV91]                           VMQAG---LRPRPKLKSGKRAAPSSSSAPAS---KRK---KTKR--   469
[HPV6b]                           LLQSG---YRGRSSIRTGVKRPAVSKASAAP-KRKRA---KTKR--   500
[HPV6bNP_040304.1]                LLQSG---YRGRSSIRTGVKRPAVSKASAAP-KRKRA---KTKR--   500
[HPV11]                           LLQSG---YRGRTSARTGIKRPAVSKPSTAP-KRKRT---KTKK--   501
[HPV13]                           LLQTG---VQSRSPIRVGRKRAASTSTAPTPT---TRK---KAKRK-   499
[PCP]                             LLQTG---VQTTSPARAGTKRAASTSSSPPT---TRK---RVKRK-   502
[CCP                              LLQTG---VQSTSLARAGTKRAASTSTAPP---TRK---KVKRK-   501
[HPV74]                           LLQTG---VQARSSVRVSKKRSAPTAPSQAT---KQK---RSRKR-   527
[HPV44]                           LLQTG---VQARSSVRVGRKRPASAATSSS---KQK---RSRKK-   500
[hpv55]                           LLQTG---VQARSSVRVGRKRPASAATSSSS-KPKRS---RKK---   501
HPV34_L1aa                        LLQLG---MRARPRLQASKRSAPSSSSTAP----KKK---RAKRI-   528
[HPV34NP_041812.1]                LLQLG---MRARPRLQASKRSAPSSSSTAP----KKK---RAKRI-   528
[HPV34CAA52560.1]                 LLQLG---MRARPRLQASKRSAPSSSSTAP----KKK---RAKRI-   528
HPV73CAA63887.1                   LLQLG---MRARPKLQASKRSASAPTSAPP----KKK---RAKRI-   503
[HPV54]                           LLQAG---LRARPRLRPVKRAAPSSSKGSAR---KRA---KTKR--   497
[HPV32]                           LLQAG---LRARPKLTAVKRTASSSQKSSSP--AKRR---KTRK--   503
[HPV32CAA52554.1]                 LLQAG---LRARPKLTAVKRTASSSQKSSSP--AKRR---KTRK--   503
HPV42                             LLQAG---LRARPKLSVGKRKASTAKSVSSA---KRK---KTHK--   502
RhesusPV1                         LLQAG---MRARPTLRAPKRTASSTSSSSPR---KRK---RTKR--   501
HPV52_L1aa                        LLQAG---LQARPKL---KRPASSAPRTST----KKK---KVKR--   529
HPV67_L1aa                        LLQAG---FTAKPKL---KRSSPSSSSSSSA---KRK---KVKR--   529
HPV33_L1aa                        LLQAG---LKAKPKL---KRAAPTSTPTSSA---KRK---KVKK--   499
HPV58_L1aa                        LLQSG---LKAKPRL---KRSAPTTRAPPT----KRK---KVKK--   524
HPV35                             LLQAG---LKARPNFRLGRRAAPASTSKKSS--TKRR---KVKS--   505
HPV31_L1aa                        LLQAG---YRARPKFKAGKRSAPSASTTTPA---KRK---KTKK--   504
HPV16NP_041332.1                  LLQAG---LKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
HPV16_L1aa                        LLQAG---LKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16eaAF534061]                 LLQAG---LKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16gerAAQ10719.1]              LLQAG---LKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16af2]                        LLQAG---FKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16asamAF402678]               LLQAG---FKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16aa]                         LLQAG---FKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
[HPV16af1]                        LLQAG---FKAKPKFTLGKRKATPTTSSTST-TAKRK---KRKL--   531
HPV51                             LLQVG---VQRKPRPGL-KRPASSASSSSSS-SAKRK---RVKK--   504
[HPV82]                           LLQIG---AQRKPRPGL-KRPAPSSSASSSA---KRK---RVKK--   503
HPV26NP_041787.1                  MLQAG---IQRRPKLGT-KRPLSSTSSST-----KRK---KRKLTK   503
HPV26bCAA52535.1                  MLQAG---IQRRPKLGT-KRPLSSTSSSTKR---KRK---KLTK--   503
[HPV69]                           MLQAG---IQRRPKLGT-KRPASSLSASSSSTTRKKR---KLTK--   507
HPV18_X05015                      LVQAG---LRRKPTIGPRKRSAPSATTSSKPAKRVRV---RARK--   568
Hpv18_NC001357                    LVQAG---LRRKPTIGPRKRSAPSATTSSKPAKRVRV---RARK--   568
HPV45_L1aa                        LVQAG---LRRRPTIGPRKRPAASTSTASTASRPAKRVRIRSKK--   539
HPV59_L1aa                        LLQLG---ARPKPTIGPRKRAAPAPTSTPSPKRVKRR---KSSRK-   508
HPVcand85_L1aa                    LLQAG---LRPKPTIGPRKRVASTSTATRPS---KRK---RTAK--   504
HPV68_L1aa                        LLQAG---VRRRPTIGPRKRTATATTTSTSK--HKRK---RVSK--   505
HPV39_L1aa                        LLQAR---VRRRPTIGPRKRPAASTSSSSAT-KHKRK---RVSK--   505
HPV70_L1aa                        LLQVG---ARRRPTIGPRKRPASAKSSSSAS-KHKRK---RVSK--   504
HPV29                             LLQIG---ARRRSVVPSRKRRTTTTAPTPA----KRK---RSKK--   503
[HPV77]                           LLQIG---ARRRSVVPSRKRRAPTPSPATT----KRK---RSKK--   503
[HPV94]                           LLQLG---VRSRSAISVRKRSATAASGSTAA---KRK---RTKK--   532
[HPV10NP041746.1]                 LLQLG---VRSRSAVSVRKRPATSATGSTAA---KRK---RTKK--   531
[HPV10CAA52494.1]                 LLQLG---VRSRSAVSVRKRPATSATGSTAA---KRK---RTKK--   531
[HPV-10CAA52495.1]                LLQLG---VRSRSAVSVRKRPATSATGSTAA---KRK---RTKK--   503
[HPV3]                            LMQLG---VGTRSSISVRKRSATTTSRTAAA---KRK---RTKK--   532
HPV28                             LMQLG---VGARSSVSVRKRPASTTRGSSAA---KRK---RAKK--   502
HPV56CAA52600.1                   LMQLG---TRSKPAVASKKRSAPTSSSTPA---KRK---KR----   534
HPV66                             LMQLGPRPRPKASVSASKRRAAPTSSSSSP---AKR---KKR---   503
[HPV53]                           LMQVG---VRTKPPVSSKKRSASTTSTSAPS---SKR---KRK---   499
[HPV53CAA52595.1]                 LMQVG---VRTKPPVSSKKRSASTTSTSAPS---SKR---KRK---   499
[HPV30]                           LMQLG---VRTKPSTTTKKRSAPSSSTSTPS---AKR---KRR---   508
[HPV71]                           LLQSG---TRSRPTALSRKRVAASTTSTAP----KRK---RVKRSR   521
[HPV81]                           LLQSG---SRTRSFAVSRKRPASARTPTTSA---KRK---RKK---   532
[HPV61]                           LLQAG-----PRSVSVSRKRAAPSSTPTSSP-ATKRK---KRKQ--   505
[HPV72]                           LLQVG-----SRAVSVSRKRAAPPSTSTPA-PTKRK---KRKK--   534
[HPV84]                           LLQSA-----PRSTLVSRKRTASASTTPAS---KRR---KAKK--   503
[HPV86]                           LLQSA-----PRVSHVSRKRPASTSTASS---KRR---KTKK--   505
[HPVcand87]                       LLQSA-----PRVSRVSRKRPASTSTASTS---KRR---KAKK--   504
HPV83AAD38974.1|AF151983_7        LLQLG-----PRSVSVSRKRPASTAPSAPSK---KKV---KRRK--   503
[HPVcand89]                       LLQLG-----GRPSSVPRKRAAPVSTSKAP----KRK---KAKR--   518
[HPV90]                           LLQRG---TRVRSSPVSRKRPAPSTAPSA-----KRK---RSKRS-   505
[HPV57]                           LLQRG-------ATPTVSRKRAAAPAAAPTA---KRK---KVRR--   510
[HPV-2]                           LLQRG-----AMPTV-SRKRAAVSCTPPTS---KRK---RVRR--   510
[HPV27]                           LLQRG---P---TPTVSRKRTAVGRGH-----------------   594
                                  .......610.......620.......630.......640......
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

File: /Users/johnlowe/Desktop/L2muscle.ps **Date: Fri May 2 13:22:30 2008**


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                                                   ::            ****.*::* :** :** * *:: *::  * *:.:*:: .   ::* ****:.:*:***:** *:        .          :*.         .:.. :.*:: ::*:: .:  .
[HPVcand89]                                        -MTHPVR--RR------------KRASVTDLYRTCKATGTCPSDVIPKVEGNTLADKILKWASLGVFFGGLGIGTSSGTGGRTGYVPL--G-TR--PPTVVDVGPTARPPVVI-----EPVGAGEPSIVNLVEDSSIVESGAVLPN---F   122
[HPV81]                                            -MPKVLH--RR------------KRASVTDLYRSCKVSGTCPSDVVPKVEGNTLADKILKWASLGVFFGGLGIGTASGSGGRTGYIPI--G-GR--PPSVVDIGPVSRPPVVI-----DPVGAADPSIVTLVEESSVIEAGATHPN---F   122
[HPV61]                                            ---MALK--RR------------KRASATDLYRTCKQSGTCPPDVVPKVEGDTLADRILKWASLGVFFGGLGIGTGSGTGGRTGYVPI--G-TR--PPTVVDIGPVSRPPVVI-----DPVGAADPSIVTLVEESSVIEAGATVPT---F   120
[HPV72]                                            -MTQAVR--RR------------KRASATDLYRTCKQAGTCPPDVIPKVEGDTLADRFLKWASLGVFFGGLGIGTGSGTGGRTGYVPI--G-TR--PPTVVDIGPTTRPPVVI-----EPVGAADPSIVTLVEESSVVEAGATVPT---F   122
[HPV83]                                            -MSHVHR--RR------------KRASATDLYRTCKAGTCPPDIVPKIEGDTWADRFLKWASLGLFFGRLGIGTSSGTGGRTGYVPL--G-TR--PPTVVDVGPTARPPVVI-----EPVGATEPSIVNLVEDSSVIESGATIPT---F   122
[HPV84]                                            -MPKVLK--RR------------KRASATDLYRTCKATGTRPADVIPKVEGDTWADRFLKWASLGVFFGGLGIGTSSGTGGRTGYIPL--G-TR--PPTVVDVGPTARPPVVI-----EPVGAADPSIVTLVEDSSVINAGAPFPN---F   122
[HPV86]                                            -MPKVKS--RR------------KRASATDLYRTCKASGTCPADVVPKVEGDTLADRILKWASLGVFFGGLGIGTSSGSGGRTGYVPL--G-TR--PPTVVDVGPTARPPVVI-----EPVGATDPSIVTLVEDSSVINAGAPLPN---F   122
[HPVcand87]                                        MPKS-----RR------------KRASATDLYRTCKVTGTCPADVVPKVEGDTLADRILKWASLGVFFGGLGIGTSSGTGGRTGYIPL--G-TR--PPTVVDVGPTARPPVVI-----EPVGAADPSIVTLVEDSSVINSGAPFPN---F   120
[HPV71]                                            --MPRAR--RR------------KRASVTQLYQSCKLTGTCPPDVINKVEHNTLADKILRWGSLGIFLGGLGIGTGSGTGGRTGYIPI--G-TR--PPTVVDVGPPARPPVVI-----ETVGASDPSIVTLVEDSSIIEAGAPYPN---F   121
[HPV90]                                            --MHRSK--RR------------KRASATQLYQTCKLAGTCPSDVINKVEHTTLADKILQWGSLGVFFGGLGIGTGSGTGGRTGYIPI--G-TR--PPTVVDVGPPARPPVVI-----EPVGASDPSIVTLVEDSSIIASGSPHPT---F   121
[HPV10]gi|196272621|ref|NP_041745.1|               MVAQRAR--RR------------KRASATQLYRTCKASGTCPPDVIPKVEGTTLADRILQWGSLGVYLGGLGIGTGSGTGGRTGYVPI--S-TR--PGTVVDVSVPARPPVVI-----EPVGPSDPSIVNLLEDSSIINSGSTIPT---F   123
[Hpv10]gi|396907|emb|CAA52493.1|                   MVAQRAR--RR------------KRASATQLYRTCKASGTCPPDVIPKVEGTTLADRILQWGSLGVYLGGLGIGTGSGTGGRTGYVPI--S-TR--PGTVVDVSVPARPPVVI-----EPVGPSDPSIVNLLEDSSIINSGSTIPT---F   123
[Hpv94]                                            MVAHRAR--RR------------KRASATQLYRTCKASGTCPPDVIPKVEGTTLADKILQWGSLGIFLGGLGIGTGSGTGGRTGYVPV--S-TR--PGTVVDVSVPVKPPVVI-----DPVGPSDPSIVNLLEDSSIVNAGSTIPT---F   123
[Hpv3]                                             MVAHRAR--RR------------KRASATQLYRTCKAAGTCPPDVIPKVEGTTLADRILQWGSLGVYLGGLGIGTGSGTGGRTGYAPI--S-TR--PGTVVDVSVPAKPPVVI-----EPVGPSDPSIVNLLEDSSIINSGSTIPT---F   123
hpv28                                              MVAHRAR--RR------------KRASATQLYRTCKAAGTCPPDVIPKVEGTTLADRILQWGGLGIYLGGLGIGTGSGTGGRTGYVPL--S-TR--PGTVVDVSVPARPPVVI-----EPVGPSDPSIVNLLEDSSIINSGSTVPT---F   123
hpv29                                              MVAHRAR--RR------------KRASATELYKTCKVAGTCPPDVIPKVEGTTLADRILQWGSLGVYLGGLGIGTGSGTGGRTGYVPV--G-TR--PGTVVDVSIPTRPPVVI-----EPVGPSDPSIVTLLEESSVINSGATIPT---F   123
[Hpv77]                                            MVAHRAR--RR------------KRASATELYKTCKAAGTCPPDVIPKVEGTTLADRILQWGSLGVYLGGLGIGTGTGTGGRTGYVPI--G-TR--PGTVVDVSVPTRPPVVV-----EPVGPTDPSIVTLLEESSVIDSGASIPT---F   123
[HPV56]                                            MVAHRAT--RR------------KRASATQLYKTCKLSGTCPEDVVNKIEQKTWADKILQWGSLFTYFGGLGIGTGTGSGGRAGYVPL--G-SR--PSTIVDVT-PARPPIVV-----ESVGPTDPSIVTLVEESSVIESGAGIPN---F   122
[hpv66]gi|1020296|gb|AAA79504.1|                   MVAHRAT--RR------------KRASATQLYKTCKLSGTCPEDVINKVEQKTWADRILQWGSLFTYFGGLGIGTGSGSGGRAGYVPL--G-SR--PSTIVDVT-PARPPIVV-----ESVGPTDPSIVTLVEESSVINSGAGVPN---F   122
[HPV53]gi|9627381|ref|NP_041847.1|                 MVAHRAR--RR------------KRASATQLYQTCKQSGTCPEDVINKIEHKTWADKILQWGSLFTFFGGLGIGTGSGTGGRTGYIPL--G-TR--PSTVVDVT-PARPPIVV-----ESVGPTDPSIVTLVEESSVIESGASFPN---F   122
[HPV53]gi|397051|emb|CAA52594.1|                   MVAHRAR--RR------------KRASATQLYQTCKQSGTCPEDVINKIEHKTWADKILQWGSLFTFFGGLGIGTGSGTGGRTGYIPL--G-TR--PSTVVDVT-PARPPIVV-----ESVGPTDPSIVTLVEESSVIESGASFPN---F   122
[HPV30]                                            MVAHRAR--RR------------KRASATQLYQTCKQAGTCPSDVINKIEHTTLADKILQWGSLFTFFGNLGIGTGAGSGGRAGYVPL--G-TR--PTTVVDAS-PARPPIVV-----ESVGPTDPSIVTLVEESSVVNAGASFPN---F   122
HPVcand85_L2aa                                     MVSHRAA--RR------------KRASATDLYKTCKQSGTCPPDVINKVEGTTLADKILLQWTSLGIFLGGLGIGTGSGTGGRTGYIPL--G-GR--PNTVVDVS-PARPPVVI-----ESVGPSDPSIVTLVEESSIVTSGAPVPT---F   122
HPV39_L2aa                                         MVSHRAA--RR------------KRASATDLYRTCKQSGTCPPDVVDKVEGTTLADKILQWTSLGIFLGGLGIGTGTGTGGRTGYIPL--G-GR--PNTVVDVS-PARPPVVI-----EPVGPSEPSIVQLVEDSSVITSGTPVPT---F   122
HPV70_L2aa                                         MVSSRAS--RR------------KRASATDIYKTCKQSGTCPPDVVNKVEGTTLADRFLQWASLGIFLGGLGIGTGTGTGGRTGYIPL--G-GR--PSTVVDVT-PARPPVVI-----EPVGPTEPSIVQLVEESSVVSGCTPIPI---F   122
HPV59_L2aa                                         MVSHRAA--RR------------KRASATDLYKTCKQAGTCPSDVINKVEGTTLADKILQWTSLGIFLGGLGIGTGSGTGGRTGYIPL--G-GR--TNTIVDVS-PAKPPVVI-----EPVGPTDPSIVTLVEDSSVITSGAPAPT---F   122
HPV18_NP_040316.1                                  MVSHRAA--RR------------KRASVTDLYKTCKQSGTCPPDVVPKVEGTTLADKILQWSSLGIFLGGLGIGTGSGTGGRTGYIPL--G-GR--SNTVVDVG-PTRPPVVI-----EPVGPTDPSIVTLIEDSSVVTSGAPRPI---F   122
HPV18_CAA28670.1                                   MVSHRAA--RR------------KRASVTDLYKTCKQSGTCPPDVVPKVEGTTLADKILQWSSLGIFLGGLGIGTGSGTGGRTGYIPL--G-GR--SNTVVDVG-PTRPPVVI-----EPVGPTDPSIVTLIEDSSVVTSGAPRPI---F   122
HPV45_L2aa                                         MVSHRAA--RR------------KRASATDLYRTCKQSGTCPPDVINKVEGTTLADKILQWSSLGIFLGGLGIGTGSGSGGRTGYVPL--G-GR--SNTVVDVG-PTRPPVVI-----EPVGPTDPSIVTLVEDSSVVASGAPVPT---F   122
[HPV82]                                            MVAARAR--RR------------KRASVTQLYSTCKAAGTCPPDVIPKVKGTTLADKILQWSGLGIFLGGLGIGTGGTGGRTGYIPLGGG-GR--PG-VVDIA-PARPPIII-----EPVAPTEPSIVNLVEDSSIINSGSTIPT---F   123
[HPV69]                                            MVAVRAS--RR------------KRASATDLYKTCKAAGTCPPDVIPKIEGSTLADKILQWSGLGIFLGGLGIGTGTGTGGRTGYIPLGGG-GR--PS-VVDIG-PTRPPIII-----EPVGPTEPSIVTLVEESSIIQSGSPFPN---F   123
[HPV26]                                            MVAVRAP--RR------------KRASATDLYKTCKAAGTCPPDVIPKIEGSTLADKILQWSGLGIFLGGLGIGTGSGGRTGYIPLGGG-GR--PS-VVDIG-PTRPPIII-----EPVGTEPSIVTLVEESSIIQSGAPIPT---F   123
[HPV26b_CAA52534.1]                                MVAVRAP--RR------------KRASATDLYKTCKAAGTCPPDVIPKIEGSTLADKILQWSGLGIFLGGLGIGTGTGSGGRTGYIPLGGG-GR--PS-VVDIG-PTRPPIII-----EPVGPTEPSIVTLVEESSIIQSGAPIPT---F   123
Pcpv1_L2aa                                         MAHSRPR--RR------------KRASATQLYQTCKASGTCPPDIIAKVEQNTLADKILKWGSLGVFFGGLGIGTGSGTGGRTGYVPV--Q-TA--PRPAIPFGPTARPPIIV-----DTVGPSDSSIVSLVEDSTIINSAASDFV---P   123
[ccpv1]                                            MAHSRPR--RR------------KRASATQLYQTCKASGTCP-DIIPKVEQNTLADKILKWGSLGVFFGGLGIGTGSGTGGRTGYVPL--E-SA--PRPAIPFGPTARPPIVV-----DTVGPTDSSIVSLVEDSAIINSGASDLV---P   122
[HPV6b]gi|196260611|ref|NP_040303.1|               MAHSRAR--RR------------KRASATQLYQTCKLTGTCPPDVIPKVEHNTIADQILKWGSLGVFFGGLGIGTGSGTGGRTGYVPL--Q-TS--AKPSITSGPMARPPVVV-----EPVAPSDPSIVSLIEESSVINAGAPEIV---P   123
[HPV74]gi|27462490|gb|AAO15461.1|AF436130_7        MAHSRAR--RR------------KRASATQLYQTCKVSGTCPSDIIPKIEHNTIADQILKWGSLGVFFGGLGIGTGSGTGGRTGYIPLQSA-PR--PDI--PSGPAARPPIIV-----DTVGPGDPSIVSLVEESAIINSGAPEVV---P   123
HPV7gi|196273941|ref|NP_041858.1|                  MVSSRPR--RR------------KRASATQLYQTCKAAGTCPPDVVNKVEQTTVADQILKWGSMGVFFGGLGIGSGSGSGGRAGYVPLSTG-SRAIPPKSLAPDVIARPPVVV-----DTVAPTDPSIVSLIEESSIIQSGAPSPV---I   127
Hpv7gi|397066|emb|CAA52480.1|                      MVSSRPR--RR------------KRASATQLYQTCKAAGTCPPDVVNKVEQTTVADQILKWGSMGVFFGGLGIGSGSGSGGRAGYVPLSTG-SRAIPPKSLAPDVIARPPVVV-----DTVAPTDPSIVSLIEESSIIQSGAPSPV---I   127
[HPV40]                                            MVSSRPR--RR------------KRASATQLYQTCKAAGTCPPDVVHKVEQTTVADQILKWGSMGVFFGGLGIGSGSGTGGRAGYVPLSTG-SRAVPPKSLVPDVVARPPVVV-----DTVAPSDPSIVSLIEESSIIQSGAPSLT---I   127
[HPV43]                                            MVSHTHK--RR------------KRASATQLYQTCKAAGTCPSDVINKVEHTTIADQILKWASMGVYFGGLGIGTGSGTGGRTGYVPLTTGRTGIVPKVTAEPGVVSRPPIVV-----ESVAPTDPSIVSLIEESSIIQSGAPITN---I   128
[Hpv91]                                            MVSYTLK--RR------------KRASATQLYQTCKAAGTCPSDVINKVEHTTIADQILKWASMGVYFGGLGIGTGSGSGGRTGYVPIPTGRTGTVPKVSAEPGVVSRPPVVI-----EPVAPTDPSIVSLIEESSIIESGAPITT---I   128
[HPV54]                                            MAKARAP--RR------------KRASATQLYQTCKASGTCPSDVIPKVEGTTIADQILRWGSMGVFFGGLGIGTGSGTGGRTGYIPL--G--R--PSTTLEPGPPVRPAGAV-----ETVAPSDPSIVSLVEESSVVDVGAPTPT---I   122
[HPV32]gi|9627332|ref|NP_041805.1|                 MPPHRSR--RR------------KRASATQLYQTCKASGTCPPDVIPKIEGRTWADQILKWGSTGVFFGGLGIGTGAGSGGRTGYVPI--G-TR--PPVVAEPGPAIRPPVVV-----DTIGPTDPSVISLLEESAVIDSSIPVPT---D   123
[HPV32]gi|396987|emb|CAA52553.1|                   MPPHRSR--RR------------KRASATQLYQTCKASGTCPPDVIPKIEGRTWADQILKWGSTGVFFGGLGIGTGAGSGGRTGYVPI--G-TR--PPVVAEPGPAIRPPVVV-----DTIGPTDPSVISLLEESAVIDSSIPVPT---D   123
[HPV4]2gi|333218|gb|AAA47047.1|                    MPPQRSR--RR------------KRASATQLYQTCKASGTCPPDVIPKVEGTTLADKILQWGSLGVFFGGLGIGTGAGTGGRTGYVPL--G-TR--PPVIAEPGPAVRPPIAV-----DTVGPSDPSIVSLLEESSVIDAGITVPD---I   123
HPV34_L2aa                                         MRRKRDTHIRR------------KRASATQLYKTCKQSGTCPPDIIPKVEGNTLADQILKYGSIGVFFGGLGIGSGSGTGGRTGYVPLPTT-TP--SRPVEIPLQPTRPPVIT------SVGASDSSIVSLVEESSFIEAGVPGPT-SIV   128
HPV34gi|9627339|ref|NP_041811.1|                   MRRKRDTHIRR------------KRASATQLYKTCKQSGTCPPDIIPKVEGNTLADQILKYGSIGVFFGGLGIGSGSGTGGRTGYVPLPTT-TP--SRPVEIPLQPTRPPVIT------SVGASDSSIVSLVEESSFIEAGVPGPT-SIV   128
HPV34gi|396995|emb|CAA52559.1|                     MRRKRDTHIRR------------KRASATQLYKTCKQSGTCPPDIIPKVEGNTLADQILKYGSIGVFFGGLGIGSGSGTGGRTGYVPLPTT-TP--SRPVEIPLQPTRPPVIT------SVGASDSSIVSLVEESSFIEAGVPGPT-SIV   128
[HPV73]                                            MRRKRDTHIRK------------KRASATQLYKTCKQAGTCPPDVIPKVEGSTIADNILKYGSIGVFFGGLGIGSGSGSGGRTGYVPLSTG-TP--SKPVEIPLQPIRPSVVT------SVGPSDSSIVSLVEESSFIESGIPGPT-SIV   128
RMPV_L2aa                                          MKHAHLS--RRKRAAPRPPGGRQKRASATQLYQTCKAAGTCPPDVIPKVEGTTVADQILKYGSMGVYFGGLGIGSGAGTGGRSGYVPL--G-SR--PASIPEPLP--RPPVTI-----EPVGPSDPSIVSLLEESRLIEAGVPAPT---F   133
HPV52_L2aa                                         MRYRRST--RH------------KRASATQLYQTCKASGTCPPDVIPKVEGTTIADQILKYGSLGVFFGGLGIGTGAGSGGRAGYVPL--S-TR--PPTSSITTSTIRPPVTV-----EPIGPLEPSIVSMIEETTFIESGAPAPS---I   123
HPV67_L2aa                                         MRHKRST--RR------------KRASATQLYQTCKAAGTCPPDVIPKVERTTIADQILKFGSLGVFFGGLGIGTGSGTGGRTGYVPL--S-TR--PPTASAPTSTIRPPVSV-----DTVGPLDSSIVSMIEETSFIESGAPAPS---I   123
HPV33_L2aa                                         MRHKRST--RR------------KRASATQLYQTCKATGTCPPDVIPKVEGSTIADQILKYGSLGVFFGGLGIGTGSGSGGRTGYVPI--G-TD--PPTAAIPLQPIRPPVTV-----DTVGPLDSSIVSLIEETSFIEAGAPAPS---I   123
HPV58_L2aa                                         MRHKRST--RR------------KRASATQLYQTCKASGTCPPDVIPKVEGTTIADQILRYGSLGVFFGGLGIGTGGTGGRTGYVPL--G-ST--PPSEAIPLQPIRPPVTV-----DTVGPLDSSIVSLIEETSFIDAGAPAPS---I   123
[HPV35]                                            MRHKRST--KR-----------VKRASATQLYRTCKAAGTCPPDVIPKVEGNTVADQILKYGSMAVFFGGLGIGSGSGTGGRSGYVPL--G-TT--PPTAA-TNIPIRPPVTVESIPLDTIGPLDSSIVSLVEETSFIESGAPVVTPRVP   131
HPV31_L2aa                                         MRSKRST--KR-----------TKRASATQLYQTCKAAGTCPSDVIPKIEHTTIADQILRYGSMGVFFGGLGIGSGSGTGGRTGYVPL--S-TR--PSTVSEASIPIRPPVSI-----DPVGPLDPSIVSLIEESGIVDVGAPAPIPH-P   126
[HPV16EAvar]                                       MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIADQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSFVEETSFIDAGAPTSVPSIP   127
HPV16_L2aa                                         MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIAEQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDAGAPTSVPSIP   127
[Hpv16NP_041331.1]                                 MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIAEQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDAGAPTSVPSIP   127
[HPV16EGvar]                                       MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIADQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDAGAPTSVPSIP   127
[HPV16AAvar]                                       MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIADQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDAGAPTPVPSIP   127
[HPV16Af2]                                         MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIADQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDAGAPTPVPSIP   127
[HPV16Af1]                                         MRHKRSA--KR-----------TKRASATQLYKTCKQAGTCPPDIIPKVEGKTIADQILQYGSMGVFFGGLGIGTGSGTGGRTGYIPL--G-TR--PPTATDTLAPVRPPLTV-----DPVGPSDPSIVSLVEETSFIDVGAPTPVPSIP   127
                                                   1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

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[HPVcand89]                                TGTDGFEITTSS---TTTPAVLDITPSGATVQVSSTSYSNPAFTEPSIIEPPQHGSVSGHVFTS--TPTSGSHTFEEIPMSTFATSGDVDAGPISSTPVPGVRRIAGPRLNLYSKATQQVPVSDSAFVSRPASFVTYDNPVYDP---EET   264
[HPV81]                                    TGTSGFEITTSS---TTTPAVLDITPTGTTVQVSSTNFLNPLYTEPSIIDPPQTGEITGHVFTS--TPTAGSHSYEEIPMVTFASNTGTGGEPISSTPMPGVRRLAGPRLRLYTKATQQVPVRDPAFVSHPASFATFDNPVYDP---EET   264
[HPV61]                                    SGSGGFNVTSSS---TTTPAVLDITPSGGSVQVSSTSFINPLFTEPSIIEPPQAGDLAGHVISS--TPTAGSHSFEEIPMHTFATS----EGPGSSTPLPGIRRLARPRLNLYSKANQQIKVANPTFMSDPASLITYDNPIFDP---EET   258
[HPV72]                                    TGSGGFEVTTSS---TTTPAVLDITPSGASVQVSSSSFTNPLFTEPSIIEPPQAGDLSGHVFTS--TPTSGSHSFEEIPMHTFATHSSTSTDPFSSTPLPGVRRLAQPRLGLYSKANQQVRVTNPAFLSRPQSLVTYDNPVYDP---EET   264
[HPV83]                                    TGTHGFEVTSSS---TTTPAVLDITPSSATVQVSSSSFTNPLFTEPSIIEPPQHGDITGHVFTS--TATSGTHGFEEIPMQTFATSGGTGQEPISSTPIPGVRRVAGPRLGLYSRATSQVKVPDSAFMSRPASFVTYDNPVFDP---DET   264
[HPV84]                                    TGTGGFEVTTSS---ITTPAVLDITPSGSSVQVSSTSYVNPLFTEPSIIEPPQAGDITGHVLSS--TATSGSHTYEEIPMQTFAVQGGTGLEPISSTPTPGVRRLAGPRLNLYSRATQQVPVADTAFLSRPESFVTFDNPVFDP---EET   264
[HPV86]                                    TGTGGFEITTSS---TTTPAVLDITPSGSSVQVSSTSYINPLFTEPSIIEVPQAGDITGHVLSS--TATSGTHTYEEIPMQTFAVQGGTGHEPISSTPIPGVRRLAGPRLNLYSRATQQVPVADSAFLSRPDSFVTFDNPVYDP---DET   264
[HPVcand87]                                TGTGGFEVTTSS---TTTPAVLDITPSGSSVQVSSTSYINPLFTEPSIIEVPQAGDIAGHVLSG--TATSGTHTFEEIPMQTFAVQGGTGQEPISSTPIPGVRRLAGPRLNLYSRVTQQVPVTDSAFLSRPESFVTFHNPMYDP---EET   262
[HPV71]                                    TGTGGFEVTTAS---TTTPAVLDITP-GNTVQVSSSSFTNPSFTEPALVEPPQTGEVSGHILVS--TSTSGTHGYEEIPMQTFASE-GTGNEPISSTPIPGVRRLAGPR--LYSRAYQQVRVDESTFLRHPASMVTYDNPVYDP---EET   259
[HPV90]                                    TGTGGFEVTTAS---TTTPAVLDITPSGGNVQVSSSSFINPLFTEPAIVEPPQAGEVTGHVLVS--TPTAGSHGYEEIPMQTFAVR-GTGDEPIISTPLPGVRRVAGPR--LYSRAYQQVHVQDPRFLSQPETLVTYDNPVFDT---EET   260
[HPV10]gi|9627262|ref|NP_041745.1|         SGTSGFEVTSSA---TTTPAVLDITPASENVVISSTNFTNPAFTEPSLVEVPQSGEVSGHILIS--TPTAGTHGYEEIPMDTFASS-GTGTEPISSTPVPGVSRIAGPR--LYSRANTQVKVSDPAFLSRPSSLLTFDNPVFEPE--DET   263
[Hpv10]gi|396907|emb|CAA52493.1|           SGTSGFEVTSSA---TTTPAVLDITPASENVVISSTNFTNPAFTEPSLVEVPQSGEVSGHILIS--TPTAGTHGYEEIPMDTFASS-GTGTEPISSTPVPGVSRIAGPR--LYSRANTQVKVSDPAFLSRPSSLLTFDNPVFEPE--DET   263
[Hpv94]                                    SGTGGFEVTSSA---TTTPAVLDITPAGDNVVISSTSFTNPAYTEPSLVEVPQSGEVSGHILIS--TPTAGTHGYEEIPMDTFASS-GTGTEPISSTPVPGVSRIAGPR--LYGKATTQVKVSDPAFLSRPSTFLTFDNPAFEPE--DET   263
[Hpv3]                                     TGTDGFEVISSA---TTTPAVLDITPASDNVVVSSTNFSNPAFTEPSLLEVPQNGEVSGHILIS--TPTSGTHGYEEIPMETFASP-GTGTEPISSTPVPGVSRIAGPR--LYSKAVTQVKVTDPAFLTRPRSLMTFDNPVFEPE--DET   263
hpv28                                      SGTGGFEVTSSA---TTTPAVLDITPATDNVVISSSNFTNPAFTEPSLLEVPQNGEVSGHILVS--TPTAGTHSYEEIPMETFASP-GTGNEPISSTPVPGVSRIAGPR--LYAKAVTQVKVTDPAFLSRPTSLVTFDNPAFEPG--DET   263
hpv29                                      TGTSGFEITSSA---TTTPAVLDITPAGDNVVITSTNFNNPLFTEPSLLEIPQTGETSGRVLVG--TPTSGVHGYEEIPMDTFATS-GTGLEPISSTPVPGVSRVAGPR--LYGKALTQVRVSDPAFLTQPSSFVTFDNPVYDPE--DET   263
[Hpv77]                                    TGTSGFEITSSA---TTTPAVLDITPAGDTVVVTSTNFTNPLYTEPSLVEVPQTGEISGHLLVS--TATSGTHGYEEIPMDTFATS-GTGSEPISSTPVPGVSRVAGPR--LYGKAMTQVRVPDPAFLSRPSSFVTFDNPVYDPG--DET   263
[HPV56]                                    TGSGGFEITSSS---TTTPAVLDITPTSSTVHVSSTHITNPLFIDPPVIEAPQTGEVSGNILIS--TPTSGIHSYEEIPMQTFAVH-GSGTEPISSTPIPGFRRIAAPR--LYRKAFQQVKVTDPAFLDRPATLVSADNPLFEGT--DTS   262
[hpv66]gi|1020296|gb|AAA79504.1|           TGSGGFEVTSSS---TTTPAVLDITPTSSTVHVSSTTITNPLYIDPPVIEAPQTGEVSGNILIS--TPTSGIHSYEEIPMQTFAIH-GTGNEPISSTPIPGFRRLAAPR--LYSRAFQQVRVTDPAFLDNPTTLISADNPVFEGA--DTT   262
[HPV53]gi|9627381|ref|NP_041847.1|         TGTAGFEVTSSS---TTTPAVLDITPTSTSVHVSSTTYTNPTFVDPPVIEVPQTGEVSGNILIS--TPTSGVHSYEEIPMQTFAVQ-GTGNEPISSTPIPGLRRIAAPR--LYKKAFQQVKVTDPAFLHKPETLINVDNPIFQNA--DTT   262
[HPV53]gi|397051|emb|CAA52594.1|           TGTAGFEVTSSS---TTTPAVLDITPTSTSVHVSSTTYTNPTFVDPPVIEVPQTGEVSGNILIS--TPTSGVHSYEEIPMQTFAVQ-GTGNEPISSTPIPGLRRIAAPR--LYKKAFQQVKVTDPAFLHKPETLINVDNPIFQNA--DTT   262
[HPV30]                                    TGTAGFEVTSSS---TTTPAVLDITPTTGSVHVSSTHFTNPSFVEPPVIEVPQTGEVSGHILVS--TPTSGVHSYEEIPMQTFAVH-GTGTEPISSTPIPGLRRIAAPR--LYQRAFQQVKVTDPTFLTKPETLITVDNPVFEDA--DTT   262
HPVcand85_L2aa                             TGTSGFEITSSA---TTTPAVLDITPASGSVQLSSTSFTNPAFTDPSVIEVPQTGEVSGDIFIT--TPTSGTHGYEEIPMHTFATQ-GRGTEPISSTPIPGVRRVAGPR--LYSQAYQQVKITNSDFISRPSTLVTFTNPAYEPI--DTT   262
HPV39_L2aa                                 TGTSGFEITSSS---TTTPAVLDITPSSGSVQITSTSYTNPAFTDPSLIEVPQTGETSGNIFVS--TPTSGTHGYEEIPMEVFATH-GTGTEPISSTPTPGISRVAGPR--LYSRAHQQVRVSNFDFVTHPSSFVTFDNPAFEPV--DTT   262
HPV70_L2aa                                 TGTSGFEITSSA---TTTPAVLDITPASGSVQISTTSYTNPAFADPSLIEVPQTGEVSGNIFVT--TPTSGTHGYEEIPMQVFASH-GTGTEPISSTPVPGVSRVAGPR--LYSRAYHQVRVNNFDFVTRPSSFVTFDNPAFEPG--DTS   262
HPV59_L2aa                                 TGTSGFEISTSS---TTTPAVLDITPTS-SVQISSSSFINPAFTDPSVIEVPQTGEISGNILIS--TPTSGAHGYEEIPMQTFATE-GTGLEPISSTPNPTVRRVAGPR--LYSRANQQVRVSNADFLTRPSTFVTYDNPAYDPI--DTT   261
HPV18_NP_040316.1                          TGTSGFDITSAG---TTTPAVLDITPSSTSVSISTTNFTNPAFSDPSIIEVPQTGEVAGNVFVG--TPTSGTHGYEEIPLQTFASS-GTGEEPISSTPLPTVRRVAGPR--LYSRAYQQVSVANPEFLTRPSSLITYDNPAFEPV--DTT   262
HPV18_CAA28670.1                           TGTSGFDITSAG---TTTPAVLDITPSSTSVSISTTNFTNPAFSDPSIIEVPQTGEVAGNVFVG--TPTSGTHGYEEIPLQTFASS-GTGEEPISSTPLPTVRRVAGPR--LYSRAYQQVSVANPEFLTRPSSLITYDNPAFEPV--DTT   262
HPV45_L2aa                                 TGTSGFEITSSG---TTTPAVLDITPTVDSVSISSTSFTNPAFSDPSIIEVPQTGEVSGNIFVG--TPTSGSHGYEEIPLQTFASS-GSGTEPISSTPLPTVRRVRGPR--LYSRANQQVRVSTSQFLTHPSSLVTFDNPAYEPL--DTT   262
[HPV82]                                    TGTDGFEITSSS---TTTPAVLDITPSAGTVHVTSTNIENPLYIEPPFIEAPQSGEVSGHIFTS--TPTSGTHGYEEIPMEVFASNVTTGKEPISSTPTPGVRRIAAPR--LYSRAFSQVKVTNPDFISKPSTFVTFDNPAFEPA--DTS   264
[HPV69]                                    SGGDGFEVTTSS---TTTPAVLDITPSPGTVHVTSTNIQNPLYIEPP-VDIPQSGEALGHIFTS--TSTAGTHSYEEIPMEVFASNTSSGSKPISSTPIPGIRRVAAPR--LYSKAYQQVKVTDPNFISKPSTFITFDNPAYEPM--DTT   263
[HPV26]                                    SGGNGFELTTSS---ATTPAVLDITPSAGTVHVTSTNIQNPLYIEPP-IDIPQAGEASGHIFTT--TSTAGTHSYEEIPMEVFASTNGTGLEPISSTPIPGIQRVSAPR--LYSKAYQQVKVTDPNFIGNPSTFVTFDNPAYEPI--DET   263
[HPV26b_CAA52534.1]                        SGGNGFELTTSS---ATTPAVLDITPSAGTVHVTSTNIQNPLYIEPP-IDIPQAGEASGHIFTT--TSTAGTHSYEEIPMEVFASTNGTGLEPISSTPIPGIQRVSAPR--LYSKAYQQVKVTDPNFIGNPSTFVTFDNPAYEPI--DET   263
Pcpv1_L2aa                                 PIREGFEISTSE---TTTPAILDVSVTTHNT-TSTSIFKNPAFAEPSIVQSQPSVEASGHVLTSTYTSTISSHSVEDIPLDTFIVS-SSDSNPASSTPVP--TPVARPRLGLYSKALQQVQVTNPAFLSSPQRLITFDNPAYEGE--DIS   264
[ccpv1]                                    SIHGGFEISTSE---STTPAILDVSITTHNT-TSTSIFRNPAFAEPSIVQSQPSVEAGGHLLTSTFTSTISPHSVEEIPLDTFIVS-SSNSNPASSTPVPTT--VARPRLGLYSKALHQVQVTDPAFLSSPQRLITFDNPVYEGE--DIS   263
[HPV6b]gi|9626061|ref|NP_040303.1|         PAHGGFTITSSE---TTTPAILDVSVTS---HTTTSIFRNPVFTEPSVTQPQPPVEANGHILIS--APTVTSHPIEEIPLDTFVVS-SSDSGPTSSTPVPGTAP--RPRVGLYSRALHQVQVTDPAFLSTPQRLITYDNPVYEGE--DVS   260
[HPV74]gi|27462490|gb|AAO15461.1|AF436130_7 PSHGGFEITTSE---STTPAILDVSVTTHNT-TSTSVFRNPSFTDPSVIQSQPPVEAGGHVLIS--SSTVSSHPVEEIPLDTFIVS-SSDSNPASSTPIPTAA--TRPRIGLYSRALHQVQVTDPAFLSSPQRLITFDNPVYEGE--DVS   262
HPV7gi|9627394|ref|NP_041858.1|            PTEGGFSITSSG---TDVPAILDIS-STNTVHVTSTTHHNPIFTDPSVVQPIPPVEASGRIIVS--HSSITTGAAEEIPMDTFVVH----SDPLSSTPVPGVS--ARPKVGLYSKALQQVEIVDPTFMSTPQRLITYDNPVFDNI--EDT   263
Hpv7gi|397066|emb|CAA52480.1|              PTEGGFSITSSG---TDVPAILDIS-STNTVHVTSTTHHNPIFTDPSVVQPIPPVEASGRIIVS--HSSITTGAAEEIPMDTFVVH----SDPLSSTPVPGVS--ARPKVGLYSKALQQVEIVDPTFMSTPQRLITYDNPVFDNI--EDT   263
[HPV40]                                    PTEGGFSVTSSG---TDVPAILDVS-STNTVHVTATTHHNPVFTDPSVVQPIPPVEAGGRLIVS--HSTITTSAAEEIPLDTFVVH----SDPLSSTPVPGTS--GRPRLGLYSKALQQVEIVDPAFLSTPQRLITYDNPVFENV--DDT   263
[HPV43]                                    PSHGGFEVTSSG---SEVPAILDVSPST-SVHITTSTHLNPAFTDPTIVQPTPPVEAGGRIIIS--HSTVTADSAEQIPMDTFVIH----SDPTTSTPIPGTAP--RPRLGLYSKALQQVEIVDPTFLSSPQRLITYDNPVFEDP--NAT   264
[Hpv91]                                    PSHGGFEVTSSG---SDVPAILDVSPTT-SVHVTTTTHLNPAFTDPAIVQPTPPLEAGGRIIIS--QSTITAHSAEDIPMDTFVVH----SDPLTSTPIPGNA--SRPRLGLYSKALQQIEIVDPAFLSSPQRLITYDNPVFEDP--DAT   264
[HPV54]                                    PSQGGFEIATSS---DATPAILDVTSTTTPIRVSITSHDNPIYTEPSLLDPPPPVQMDGRVLVS--TSTLQSSTAENIPMDTFIIM-QDHIGTTTSTPIP--RPPARPRLGLYSRALQQVPVQDPAFLQQPSSLITYDNPVYEGN-PDVT   263
[HPV32]gi|9627332|ref|NP_041805.1|         TSHGGFNITSSASGPSSTPAVLDISPPTNTIRVASTTSHNPVYSDPFTLRPSLPVEGNGRLLTS--HPTIAPHSYEEIPMDTFVVS-TDTSNTVTSTPIPGPRPTM--RLGLYTRVTQQRPVATTTFLTSPERLVTYDNPAYEGP-AEGT   267
[HPV32]gi|396987|emb|CAA52553.1|           TSHGGFNITSSASGPSSTPAVLDISPPTNTIRVASTTSHNPVYSDPFTLRPSLPVEGNGRLLTS--HPTIAPHSYEEIPMDTFVVS-TDTSNTVTSTPIPGPRPTM--RLGLYTRVTQQRPVATTTFLTSPERLVTYDNPAYEGP-AEGT   267
[HPV4]2gi|333218|gb|AAA47047.1|            TSHGGFNITTSTGGPASTPAILDISPPTNTIRVTTTTSTNPLYIDPFTLQPPLPAEVNGRLLIS--TPTITPHSYEEIPMDTFVVS-TDTTNTFTSTPIPGPRSSA--RLGLYSRATQQRPVTTSAFLTSPARLVTYDNPAYEGL-TEDT   267
HPV34_L2aa                                 PSSSGFNVTTSV---DSTPAIIDVATISDTTQVSVSTFNNPTFTDPSVLQPPPPLEASGRLLFS--NDTVTTHSYENIPLDTFVVT-TDNNSIVSSTPIPGRHPPA--RLGLYGRAIQQVKVVDPAFVTTPTRLVTYDNPAFEGL-QDTT   269
HPV34gi|9627339|ref|NP_041811.1|           PSSSGFNVTTSV---DSTPAIIDVATISDTTQVSVSTFNNPTFTDPSVLQPPPPLEASGRLLFS--NDTVTTHSYENIPLDTFVVT-TDNNSIVSSTPIPGRHPPA--RLGLYGRAIQQVKVVDPAFVTTPTRLVTYDNPAFEGL-QDTT   269
HPV34gi|396995|emb|CAA52559.1|             PSSSGFNVTTSV---DSTPAIIDVATISDTTQVSVSTFNNPTFTDPSVLQPPPPLEASGRLLFS--NDTVTTHSYENIPLDTFVVT-TDNNSIVSSTPIPGRHPPA--RLGLYGRAIQQVKVVDPAFVTTPTRLVTYDNPAFEGL-QDTT   269
[HPV73]                                    PSTSGFDITTSV---NSTPAIIDVSAISDTTQISVTTFKNPTFTDPSVLQPPPPLEASGRLLFS--NDTVTTHSYENIPLDTFVVT-TDHNSIVSSTPIPGRQPAA--RLGLYGRAIQQVKVVDPAFLTTPTRLVTYDNPAFEGL-QDTT   269
RMPV_L2aa                                  PTHGGFEISTSE---VSTPAVLDVSSGGSDVHVSVTSFTNPTFTEPSVLRPPPPVEASGRLVIS--ASSVSTHSYEEIPMDTFVIT-GDHNYNTTSTPIPGSRAPA--RLGLYGRATQQVRVVDPAFITTPARLVTYDNPAYEGV-DDAT   274
HPV52_L2aa                                 PSATGFDVTTSA---NNTPAIINVTSIGESSVQSVSTHLNPTFTEPSIIQPPAPAEASGHVLFS--SPTISTHTYEEIPMDTFVTS-TDSSSVTSSTPIPGSRPTT--RLGLYSRATQQVKVVDPAFMSSPQKLVTYNNPVFEGVDTDET   265
HPV67_L2aa                                 PTASGFDVATSA---DNTPAIINVSSIGESSVQSVTTHLNPTFTEPSVLRPFSSSEASGHLIFS--TPTISTHSYEDIPMDTFIVS-TTSDNVTSSTPIPRPRPTA--RLGLYSKGTQQVKVVDPAFLTSPRRLITFDNPAFQPTEPDET   265
HPV33_L2aa                                 PTPSGFDVTTSA---DTTPAIINVSSVGESSIQTISTHLNPTFTEPSVLHPPAPAEASGHFIFS--SPTVSTQSYENIPMDTFVVS-TDSSNVTSSTPIPGSRPVA--RLGLYSRNTQQVKVVDPAFLTSPHKLITYDNPAFESFDPEDT   265
HPV58_L2aa                                 PTPSGFDITTSA---DTTPAILNVSSIGESSIQTVSTHLNPSFTEPSVLRPPAPAEASGHLIFS--SPTVSTHSYENIPMDTFVIS-TDSGNVTSSTPIPGSRPVA--RLGLYSRNTQQVKVVDPAFLTSPHRLVTYDNPAFEGFNPEDT   265
[HPV35]                                    PTT-GFTITTST---DTTPAILDVT--------SISTHDNPTFTDPSVLHPPTPAETSGHFVLS--SSSISTHNYEEIPMDTFIVS-TDSNNITNSTPIPGSRPTT--RLGLYSKGTQQVKVVDPAFMTSPAKLITYDNPAYEGLNPDTT   264
HPV31_L2aa                                 PTTSGFDIATTA---DTTPAILDVT--------SVSTHENPTFTDPSVLQPPTPAETSGHLLLS--SSSISTHNYEEIPMDTFIVS-TNNENITSSTPIPGVRRPA--RLGLYSKATQQVKVIDPTFLSAPKQLITYENPAYETVNAEES   260
[HPV16EAvar]                               PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
HPV16_L2aa                                 PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
[Hpv16NP_041331.1]                         PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
[HPV16EGvar]                               PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
[HPV16AAvar]                               PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTAPTKLITYDNPAYEGIDVDNT   265
[HPV16Af2]                                 PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
[HPV16Af1]                                 PDVSGFSITTST---DTTPAILDI----NNTVTTVTTHNNPTFTDPSVLQPPTPAETGGHFTLS--SSTISTHNYEEIPMDTFIVS-TNPNTVTSSTPIPGSRPVA--RLGLYSRTTQQVKVVDPAFVTTPTKLITYDNPAYEGIDVDNT   265
                                           .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT

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[HPVcand89]                              IIFEHPDL--HAPPDPDFLDVVALHRPALTSRKGTVRFSRVGQRATLKTRSGKQIGARVHFYHDVSPI----SAA-----ESIEMQPL---LPS--------------PDLTQPVY----DIYADTTHL--DSVLAERPFPAYSSANTTF   380
[HPV81]                                  IIFEHPSI--YQPPDPDFLDIVQLHRPALTARQGTVRVSRIGQRASLRTRSGKHIGARVHFYHDISPI----PTE-----ADIELQPL---LPPSS------------VSSADALY----DVYADDQHL--DAVLQ----SVPSLSSRSS   378
[HPV61]                                  IIFEHPSI--YTPPDPDFLDIVSLHRPALTSRQGTVRFSRLGQRATLRTRSGRRIGARVHFYHDISPI-----PS-----DAVELQPL---VP---------------SSSPSITY----DIYADPEVL--DLPAQ--------HTQPTL   364
[HPV72]                                  IIFEHPSI--YTPPDPDFLDIISLHRPALTARQGTVRVSRLGQRATLRTRSGKRIGARVHFYQDISPI-----SS-----DTIEMQSL---AS---------------STQPDITY----DIYADPDLG--EPPPR------ASVSSTSL   372
[HPV83]                                  IIFEHPSL--HNPPDPDFLDIVSLHRPALTARQGTVRVSRVGQRATLRTRSGKQIGARVHFYHDISPI----PPT-----ESIELQPL---EP---------------SVANTSLY----DIYADDVFL--ESSVP--LRPSPSSTSVSL   377
[HPV84]                                  IIFEHPSL--HAPPDPDFLDIVTLHRPALTARRSGVRFSRIGQRASMRTRSGKHIGARVHFYHDLSPI----PHL-----EDIELQPL---VSSS-------------AVPTDSLY----DIYADDAHL--SSVLR---PPSVSALRPAS   378
[HPV86]                                  IIFEHPSL--HAPPDPDFLDIVTLHRPALTARRSGVRYSRIGQRASMRTRSGKHIGARVHFYHDLSPI----AQA-----EDIELQPL---GATTS---------SGQASGQDTLY----DIYADDTHL--SSILQ-----EPSVPSLHS   380
[HPVcand87]                              IIFEHPSL--HAPPDPDFLDIVTLHRPALTARRSGVRYSRIGQRASMRTRSGKHIGARVHFYHDISPI----APA-----DSIELQPL---VSST-------------APSDDTLY----DIYADDTHL--SSVLR---GPSLPSLHSST   376
[HPV71]                                  IIFEHPSI--HQAPDPAFMDIVALHRPALTARKGTVRFSRLGQKSTLRTRSGKQIGARVHFYHDISPI----QPT-----EHLELQPLGRALQ---------------QEPIDTLY----DIYLTQIIP--MILSFNLLLCPAGLHLLLY   377
[HPV90]                                  ILFEHPSI--HQVPDPDFLDIVALHRPALTARRGTVRYSRLGQRATLKTRSGKRIGATVHFYQDLSPIA---PVA-----DELEMQPL---VSDT-------------PDYLDSLY----DIYADTASVSRHRTLT----PTRPSTPLQA   376
[HPV10]gil9627262lreflNP_041745.1l       IIFERPYSP-SRVPDPDFLDIVRLHRPALTSRRGTVRFSRLGQKFSMRTRSGKGIGARVHYYQDLSPI----API-----EDIEMEPL---LA---------------PAASDTIY----DIFADVDDG--DVAFT---EGYRSTTQSRG   376
[Hpv10]gil396907lemblCAA52493.1l         IIFERPYSP-SRVPDPDFLDIVRLHRPALTSRRGTVRFSRLGQKFSMRTRSGKGIGARVHYYQDLSPI----API-----EDIEMEPL---LA---------------PAASDTIY----DIFADVDDG--DVAFT---EGYRSTTQSRG   376
[Hpv94]                                  IIFERPYSP-SRVPDPDFLDIVRLHRPALTSRRGAVRFSRLGQKFSMRTRSGKNIGARVHYYHDLSPI----AAT-----EEIEMEPL---LA---------------PADPDTLY----DIFADVDDG--DVAFT---NGTRSVTPARS   376
[Hpv3]                                   IIFERPYSP-SQVPDSDFLDILRLHRPALTSRRGTVRYSRVGQKLSMRTRSGKGLGARVHYYQDLSPI----GPT-----EDIEMEPL---IAPAS------------ASAYDSLY----DVYADVDDA--DIGFT---SGGRSDTLSRG   379
hpv28                                    IIFERPYPP-SQVPDPDFMDIIRLHRPALTSRRGTVRFSRLGTKLSMHTRSGKGIGARVHYYQDLSPI----GPT-----EDIEMEPL---LAPAE------------NAAGDSIY----DVFADVEDA--DIAFT---GRSRSATSSRG   379
hpv29                                    IIFERPSPG-TRVPDPDFMDIVKLHRPALTSRRGTVRFSRVGQKFSMRTRSGTNIGARVHYYHDLSPI----LPT-----EDIELEPL---LPPAD------------PTAEESLY----DIYADVDEA--DMAFT---GGGRGATTYGG   379
[Hpv77]                                  IIFERPSPG-TRVPDPDFLDIVRLHRPALTSRRGTVRFSRVGQKFSMRTRSGTQIGARVHYYHDLSPI----THT-----EDIELEPL---LPPAD------------SAAEDSLY----DVYADVDDA--DVAFT---NSGRNLTSFGG   379
[HPV56]                                  LAF-SPS---GVAPDPDFMNIVALHRPAFTTRRGGVRFSRLGRKATIQTRRGTQIGARVHYYYDISPI----AQA-----EEIEMQPL---LSA--------------NNSFDGLY----DIYANIDDE--APGLSSQSVATPSAHLPIK   376
[hpv66]gi|1020296|gb|AAA79504.1|         LTF-SPS---GVAPDPDFMDIVALHRPAFTTRRTGVRFSRLGKKATMQTRRGTQIGARVHYYYDISPI----AQA-----DEIEMQPL---LST--------------DNSFDGLY----DIYANIDDE--APISFRQSGATPSAQLPIK   376
[HPV53]gi|9627381|ref|NP_041847.1|       LTF-SPS---GVAPDPDFLDIVALHRPAFTTRRGGVRFSRLGTKATMRTRSGKQIGARVHYYYDVSPI----TQT-----EEIEMQPL---LST--------------DNTFDGLY----DIYANIDDE--APVSS----RFSIATPSRL   372
[HPV53]gi|397051|emb|CAA52594.1|         LTF-SPS---GVAPDPDFLDIVALHRPAFTTRRGGVRFSRLGTKATMRTRSGKQIGARVHYYYDVSPI----TQT-----EEIEMQPL---LST--------------DNTFDGLY----DIYANIDDE--APVSS----RFSIATPSRL   372
[HPV30]                                  LTF-SPS---GVAPDPDFLDIVALHRPAFTTRRGGVRFSRLGTKATMRTRSGKQIGARVHYYYDVSPI----AHT-----EEIEMQPL---LSA--------------NNSFDGLY----DIYANLDDE--APVSS----HLSIATPSRL   372
HPVcand85_L2aa                           LTF-SPQ---DVVPDPDFMDIVRLHRPALTSRRGTVRFSRLGKKLTMSTRSGKQIGAQVHYYHDISPIS---HIG-----ESIEMQPL---LPDAA-----------VTADTNGLF----DIYADTDID--NNAML----YDRNISDVTQ   376
HPV39_L2aa                               LTYEAAD----IAPDPDFLDIVRLHRPALTSRKGTVRFSRLGKKATMVTRRGTQIGAQVHYYHDISSI----APA-----ESIELQPL---VHAEP------------SDASDALF----DIYADVDNN--TYLDT-----AFNNTRDSG   373
HPV70_L2aa                               LTFEPAD----TAPDPDFLDIVRLHRPALTSRRGTVRFSRLGKKATMFTRRGTQIGAQVHYYHDISNI----TAT-----EDIEMQPL---LT---------------SESTDGLY----DIYADADID--NAMLH-----TTSHTGSTG   370
HPV59_L2aa                               LTF-DPS---SEVPDPDFMDIVRLHRPALTSRRSTVRFSRLGQRATMFTRSGKQIGARVHFYHDISPI----PHA-----EDIELQPL---VSS--------------QAATDDIY----DIYADITDE--APTST----ANTAFTIPKS   371
HPV18_NP_040316.1                        LTF-DPR---SDVPDSDFMDIIRLHRPALTSRRGTVRFSRLGQRATMFTRSGTQIGARVHFYHDISPI----APSP----EYIELQPL---VS---------------ATEDNDLF----DIYADDMDP--AVPVP-----SRSTTSFAF   371
HPV18_CAA28670.1                         LTF-DPR---SDVPDSDFMDIIRLHRPALTSRRGTVRFSRLGQRATMFTRSGTQIGARVHFYHDISPI----APSP----EYIELQPL---VS---------------ATEDNDLF----DIYADDMDP--AVPVP-----SRSTTSFAF   371
HPV45_L2aa                               LSF-EPT---SNVPDSDFMDIIRLHRPALSSRRGTVRFSRLGQRATMFTRSGKQIGGRVHFYHDISPI----AAT-----EEIELQPL---IS---------------ATNDSDLF----DVYADFPPP--ASTTP-----STIHKSFTY   370
[HPV82]                                  LSFEEPT---DVAPDPDFLDIIKLHRPALTSRRGTVRFSRLGQKATIRTRSGKQIGARGHYYHDISSI----APA-----EELEMQPL---LS---------------PSTNNYSY----DIYADLNEA--ETGFM---QPTQTTPMLRS   375
[HPV69]                                  LTFSADS---HVAPDPDFLDIIALHRPALTSRRGTVRFSRLGQKATLKTRSGKQIGAKVHYYHDISPIH---ATE-----EAIELQPL---ITS--------------EQHSTPLF----DVYADADPA---PTFT-----FPSTTPTTI   373
[HPV26]                                  LTYASSS---TVAPDPDFLDIIALHRPALTSRKGTVRYSRLGQKATMKTRSGKQIGATVHYYHDISPIQSF-AEH-----EEIELQPL---HTS--------------THSSAPLF----DIYADPDTV--PSIHT--PRMSYSPTTLPV   379
[HPV26b_CAA52534.1]                      LTYASSS---TVAPDPDFLDI-ALHRPALTSRKGTVRYSRLGQKATMKTRSGKQIGATVHYYHDISPIQSF-AEH-----EEIELQPL---HTS--------------THSSAPLF----DIYADPDTV--PSIHT--PRMSYSPTTLPV   378
Pcpv1_L2aa                               LQFQHNTI--HNPPDDAFMDIVRLHRPAITSRRGIVRFSRIGQRGSMYTRSGKHIGGRVHFYTDISPIS---AAA-----EELEMQPL---VAA--------------AQDDSGLF----DVYVDPTPG--PVAVQ----------NMSY   371
[ccpv1]                                  LHFEHNSI--HEPPNEAFMDIIRLHRPAITSRRGVVRFSRIGQRGSMYTRSGKHIGGRVHFFTDISPIS---ADA-----QDIELQPL---VAA--------------AQDDSDLF----DIYVDPDTT--PVAVD---------NIPSA   371
[HPV6b]gil9626061lreflNP_040303.1l       VQFSHDSI--HNAPDEAFMDIIRLHRPAIASRRGLVRYSRIGQRGSMHTRSGKHIGARIHYFYDISPIA---QAA-----EEIEMHPL--------------------VAAQDDTF----DIYAESFEPGINPTQH---------PVTNI   367
[HPV74]gil27462490lgblAAO15461.1lAF436130_7 LQFQHNTI--HNPPDDAFMDIIRLHRPAITSRRGLVRFSRIGQRGSMHTRSGKHIGGRVHFFQDISPISAAESAA-----EEIELHPL---VAH--------------AQDSSGLF----DIYAEPDLE------------VMEEPVPLS   372
HPV7gil9627394lreflNP_041858.1l         LHFEQPSI--HNAPDPAFMDIITLHRPALTSRRGVVRFSRVGQRGTMYTRRGTRIGGRVHFFKDISPI----ASS-----EEIELHPL---VA---------------SPNNSDLF----DVYADIDDI--DENIL------YSTIDNNT   372
Hpv7gi|397066|emb|CAA52480.1|            LHFEQPSI--HNAPDPAFMDIITLHRPALTSRRGVVRFSRVGQRGTMYTRRGTRIGGRVHFFKDISPI----ASS-----EEIELHPL---VA---------------SPNNSDLF----DVYADIDDI--DENIL------YSTIDNNT   372
[HPV40]                                  LQFEQPSI--HDAPDPAFMDIITLHRPALTSRRGVIRFSRVGQRGTMYTRRGTRIGGRVHFFRDISPI----GAA-----DDIELHPL---VASAPHTLETPHTLETPLDTTDALF----DVYADMDTIDDDAAYA--------------   381
[HPV43]                                  LTFEQPTV--HEAPDSRFMDIVTLHRPALTSRRGIVRFSRVGARGTMYTRSGIRIGGRVHFFTDISSI----PTE-----ESIELQPL---GRSQSFP---------TVSDTSDLY----DIYADENLLNNDISFT--------------   373
[Hpv91]                                  LAFEQPTV--HEAPDSNFMDIVTLHRPALTSRRGLVRFSRVGARGTMYTRSGIRIGGRVHFFKDISPI----ATQ-----ESIELQPL---GHSTV-----------NVPDATDLY----DIYADDSIL--DVPHT--------------   369
[HPV54]                                  LHFEQPTI--HNAPDPAFMDIFALHRPALTTRRGVVRYSRVGDRATLHTRSGLQLKPRVHFFQDLSPIA---HVP-----EEIELHPL---ISANN------------TSINNGLYSDIYDVYADTDFA--DTGGF-------SSSTVSH   379
[HPV32]gi|9627332|ref|NP_041805.1|       LEFEHPTI--HEAPDSDFMDIIALHRPVLSARQGTVRVSRIGQRASLQTRSGARIGSRVHFFHDISPIT---RPS-----EAIELQPL---GSSST-----AVSTTASSAINDGLF----DVYVDPDIP------------PSHALPPLRS   384
[HPV32]gi|396987|emb|CAA52553.1|         LEFEHPTI--HEAPDSDFMDIIALHRPVLSARQGTVRVSRIGQRASLQTRSGARIGSRVHFFHDISPIT---RPS-----EAIELQPL---GSSST-----AVSTTASSAINDGLF----DVYVDPDIP------------PSHALPPLRS   384
[HPV4]2gi|333218|gb|AAA47047.1|          LVFEHPSI--HTAPDPDFMDIVALHRPMLSSKQGSVRVSRIGQRLSMQTRRGTRFGSRVHFFHDLSPIT---HSS-----ETIELQPL---SASSV---------SAASNINDGLF----DIYVDTSDV--NVTNTTSSIPMHGFATPRL   389
HPV34_L2aa                               LEFQHSDL--HNAPDSDFLDIVKLHRPALTARKTGIRVSRLGQRATMFTRSGKRIGGRVHFYHDLSPI-----PT-----ENIELQPL---LPSAS------ATVTDANGINDGLY----DVLLDNNVD------------ITEVETPTG   382
HPV34gi|9627339|ref|NP_041811.1|         LEFQHSDL--HNAPDSDFLDIVKLHRPALTARKTGIRVSRLGQRATMFTRSGKRIGGRVHFYHDLSPI-----PT-----ENIELQPL---LPSAS------ATVTDANGINDGLY----DVLLDNNVD------------ITEVETPTG   382
HPV34gi|396995|emb|CAA52559.1|           LEFQHSDL--HNAPDSDFLDIVKLHRPALTARKTGIRVSRLGQRATMFTRSGKRIGGRVHFYHDLSPI-----PT-----ENIELQPL---LPSAS------ATVTDANGINDGLY----DVLLDNNVD------------ITEVETPTG   382
[HPV73]                                  LEFQHSDL--HNAPDSDFLDIVKLHRPALTSRKTGIRVSRLGQRATLSTRSGKRIGAKVHFYHDISPI-----PT-----NDIEMQPL---VTPQT------PSIVTGSSINDGLY----DVFLDNDVE--ETVLQ------QTYTPTSI   386
RMPV_L2aa                                LQFSHSDI--HQPPDPDFLDIVALHRPALTSRKGTVRFSRLGQRATLTTRSGKRIGAKVHFYHDLSPI----APA-----ESIELQPL--------------------SSQGELY----DIYADVDGQEDAAAVA--------------   374
HPV52_L2aa                               IIFDRSQL--LPAPDPDFLDIIALHRPALTSRRGTVRFSRLGNKATLRTRSGKQIGARVHYYHDISPI----QPAEVQ--EDIELQPL---LPQSV----------SPYTINDGLY----DVYADSLQQ----------------PTFHL   374
HPV67_L2aa                               LYFQHQDI--SPAPDPDFLDIVALHRPALTSRKGTIRFSRLGSKATMKTRSGKQIGARVHYYQDLSPI----VPA-----DSIELQPLSRPVSSAS------------HSINDGLY----DVYMDPD------------------TPFPQ   370
HPV33_L2aa                               LQFQHSDI--SPAPDPDFLDIIALHRPAITSRRHTVRFSRVGQKATLKTRSGKQIGARIHYYQDLSPIV---PLDHTVPNEQYELQPL---HDTST----------SSYSINDGLY----DVYADDVDN--------------VHTPMQH   379
HPV58_L2aa                               LQFQHSDI--SPAPDPDFLDIVALHRPALTSRRGTVRYSRVGQKATLRTRSGKQIGAKVHYYQDLSPIQPVQEQVQQQ--QQFELQSLNTSVSP--------------YSINDGLY----DIYADDADT-----------------IHDF   376
[HPV35]                                  LQFEHEDI--SLAPDPDFMDIIALHRPALTSRKGTIRYSRVGNKRTMHTRSGKAIGARVHYYQDLSSIT-----------EDIELQPL-QHVPSSL------PHTTVSTSLNDGMF----DIYAPIDTE--EDIIF------SASSNNTL   382
HPV31_L2aa                               LYFSNTSH--NIAPDPDFLDIIALHRPALTSRRNTVRYSRLGNKQTLRTRSGATIGARVHYYYDISSI----NPAG----ESIEMQPL---GASAT----------TTSTLNDGLY----DIYADTDFTVDTPATH-----------NVS   372
[HPV16EAvar]                             LYFPNNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVRYYYDLSTI----DPA-----EEIELQTI---TPSTY---TTTSHAASPTSINNGLY----DIYADDFIT-----------DTFTTPVPSV   385
HPV16_L2aa                               LYFSSNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----DPA-----EEIELQTI---TPSTY---TTTSHAASPTSINNGLY----DIYADDFIT--DTSTT---------PVPSV   385
[Hpv16NP_041331.1]                       LYFSSNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----DPA-----EEIELQTI---TPSTY---TTTSHAASPTSINNGLY----DIYADDFIT--DTSTT---------PVPSV   385
[HPV16EGvar]                             LYFPSNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----DPA-----EEIELQTI---TPSTY---TTTLHAASPTSINNGLY----DIYADDFIT--DTSTT---------PVPSV   385
[HPV16AAvar]                             FYFPSNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----NPA-----EEIELQTI---TPSTY---TTTSHAASPTSINNGLY----DIYADDFIT--DTVTT---------PVPAI   385
[HPV16Af2]                               LYFASNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----NPA-----EEIELQTI---TPSTY---TTPSHAASPTSINNGLY----DIYADDFIT-----------DTFTTPVPSI   385
[HPV16Af1]                               LYFPSNDNSINIAPDPDFLDIVALHRPALTSRRTGIRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTI----NPA-----EEIELQTI---TPSTY---TTASHAASPTSINNGLY----DIYADDFIT--DTSTT---------PVPSI   385
                                         .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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CLUSTAL 2.0.5 MULTIPLE SEQUENCE ALIGNMENT


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                                                                    . : *:                    .                                  : .
[HPVcand89]                                  SGP----TVTAT-SAVSSQ--YTNVTVPLSQGFD------VPAVT---GPDIAFPTAPSVPPIFP---------------SYTLGPSTGYI-----YSRYGFLFSTQLCVFS   456
[HPV81]                                      VSG----SATLSATSVASS---YNTTVPLSSGFT------IPAST---GPDVELPYAPLAPSIVPSFPATTPYAIYVVGTDFYLFPSYIFFPKK--HKRIHYSFTDGYVAAW   472
[HPV61]                                      TVQ----GPSLSAASASTK--VHNVTVPLATGLD------TPVTS---GPDVDFAHAPAPVPAVPYVPATHPHSIYIQGSDFYLLPAYVFFPKR--RKRVPYSFSDGFVAAW   459
[HPV72]                                      HSP----SLSAA-SAVSAK--YDNVTVPLSLGPH------IPASS---GPDIDLSFAPAPVPTMPLVPSTHPHSIYVEGFDFYLLPAYIFFPKR--RKRVPYSFADGFVAAW   466
[HPV83]                                      QST----NVSAT-SAVTAQ--YDNVTVPLSPGLD------VPALS---GPDIHGAAHMPADPSVPVPSNIPIQSVFIDGTDYYLLPNYIFFPKK--RKRVHYSFADGYVAAW   471
[HPV84]                                      PFA----SADLSATSITAST-YDNVTVPLFSGTD------VPVYT---GPDIDHSAAPSAPPFVPVIPSTTPYAIYILGSDYYLLPNYIFFPKK--RKRVPYSFSDGFVAAW   474
[HPV86]                                      TTPVSSATVSAT-SMVSST--YDNVTVPLSSATE------VPLYT---GPDIDHAIAPSPTPLPPVVPSTTPYAIYIQGSDYYLLPNYIFFPRK--RKRVHYSFSDGFVAAW   478
[HPVcand87]                                  PTA----STKVSATSILSSSHYDNVTVPL-SATD------VPLYT---GPDIDHSMAPSPTPFVPVVPSTAPYSVYIQGSDYYLLPNYIFFPKR--RKRVPYSFSDGFVAAW   472
[HPV71]                                      PSV------TAT-SAVSASR-TQNVTAPLSAGAD------VPVFD---GPDIDFSTSHATTPTPVVPSIAPPSSFIVYGTEVLFNA--------------------------   446
[HPV90]                                      PSV------TAS-SALSSA--ASNTTVPLSTGLD------IPVFS---GPDSALPDSHAVWPVPPAPPGVVPGSVLVNGSTYYLLPPLGLLPKK--RKRFPYFFADGNVEA-   467
[HPV10]gil9627262lreflNP_041745.1l           YNT----TSPLS-STLSTK--YGNVTIPFVSPVD------VTLHT---GPDIVLPTS-AQWPYVPLSPADTTHYVYIDGGDFYLWPVTFHFSRHRRRKRVSYFFADGTLAL-   470
[Hpv10]gil396907lemblCAA52493.1l             YNT----TSPLS-STLSTK--YGNVTIPFVSPVD------VTLHT---GPDIVLPTS-AQWPYVPLSPADTTHYVYIDGGDFYLWPVTFHFSRHRRRKRVSYFFADGTLAL-   470
[Hpv94]                                      YST----ASPLS-STLSTK--FGNVTIPFVSPVD------VTLHT---GPDIILPTS-AQWPYVPLTPADTTHYVYIDGGDFYLWPVTFYLSRRRRRKRV-----------   459
[Hpv3]                                       RAT----VSPLS-STLSTK--YGNVTIPFVSPVD------VPLQP---GPDILLPAS-AQWPFVPLSPVDTTHYVYIDGGDFYLWPVTFFLPRRRRRKRVSYFLADGTVAL-   473
hpv28                                        YTT----VSPLS-STLTTK--YGNVTIPFVSPVD------VHLHP---GPDIITPAS-TQWPFVPLVPADTTHYVYIDGGDFYLWPVTLFVPRRRRRKRLSYFLADGTVAL-   473
hpv29                                        RIT----PSVFS-STLSTR--YGNVTIPFVSPVD------VPLHT---GPDIILPSS-AQWPFVPVAPADTTHYVYIDGGDYFLWPVTFPVSRKRRRKRLSYFLADGFVAL-   473
[Hpv77]                                      RGA----SSSLP-SALSTK--IGNVTIPFISPVD------VHLHT---GPDIVLPSS-AQWPFVPVLPADTTHYVYIDGGNFYLWPVTFSVSRKRRRKRLSYFFADGTVAL-   473
[HPV56]                                      PST----------LSFASN--TTNVTAPLGNVWE------TPFYS---GPDIVLPTGPSTWPFVPQSPYDVTHDVYIQGSSFALWPVYFFRRRR--RKRIPYFFADGDVAA-   464
[hpv66]gi|1020296|gb|AAA79504.1|             PST----------LSFASN--TANVTAPLGNVWE------TPFYS---GPDIVLPTGPSTWPFVPQSPSDVTHDVYIQGATFALWPVYFFKRRR--RKRIPYFFADGDVAA-   464
[HPV53]gi|9627381|ref|NP_041847.1|           PTN----TVPLS---FSGS--TSNVTIPFGTSWD------VPIYS---GPDVVLPTGPPTWPYAPQSPFDTTHDVVIQGSTFALWPVYFLKRRR--RKRIPYFLADGGVAA-   463
[HPV53]gi|397051|emb|CAA52594.1|             PTN----TVPLS---FSGS--TSNVTIPFGTSWD------VPIYS---GPDVVLPTGPPTWPYAPQSPFDTTHDVVIQGSTFALWPVYFLKRRR--RKRIPYFLADGGVAA-   463
[HPV30]                                      PTN----TVPLS---FSSQ--TTNVTIPLGKYWD------VPIYS---GPDIVLPTGPTTWPYAPQAPFDTTHDVVIHGSTFALWPVYFLRRRR--RKHVPYFLADGGVAA-   463
HPVcand85_L2aa                               PTT------STI-SSVSSR--YSNTTIPLATSWD------VPVHT---GPDMTLPTTIPQWPNIVPLLPNNTHSVVLQGTNYYLWPNYYFIFKK--RKRVPYFLTDGFVAF-   467
HPV39_L2aa                                   TTYNTGSLPSVA-SSASTK--YANTTIPFSTSWN------MPVNT---GPDIALPSTTPQLPLVPSGPIDTTYAITIQGSNYYLLPLLYFFLKK--RKRIPYFFSDGYVAV-   470
HPV70_L2aa                                   PRSHL-SFPSIP-STVSTK--YSNTTIPFTTSWD------IPVTT---GPDIVLPTASPNLPFVPPTSIDTTVAIAIQGSNYYLLPLLYYFLKK--RKRIPYFFTDGFVAV-   466
HPV59_L2aa                                   SFQ----SLSLT-RSASST--FSNVTVPLATAWD------VPVNT---GPDIVLPNTNIVEPTYSTTPFTTIQSINIEGTNYFLWPIYYFLPRK--RKRVPYFFTDGSMAF-   464
HPV18_NP_040316.1                            FKY----SPTIS-SASS----YSNVTVPLTSSWD------VPVYT---GPDITLPSTTSVWPIVSPTAPASTQYIGIHGTHYYLWPLYYFIPKK--RKRVPYFFADGFVAA-   462
HPV18_CAA28670.1                             FKY----SPTIS-SASS----YSNVTVPLTSSWD------VPVYT---GPDITLPSTTSVWPIVSPTAPASTQYIGIHGTHYYLWPLYYFIPKK--RKRVPYFFADGFVAA-   462
HPV45_L2aa                                   PKY----SLTMP-STAASS--YSNVTVPLTSAWD------VPIYT---GPDIILPSHTPMWPSTSPTNASTTTYIGIHGTQYYLWPWYYYFPKK--RKRIPYFFADGFVAA-   463
[HPV82]                                      PFSPLSTQLPSLSSSVSSS--YANVTIPFSTTYN------VPIHT---GPDVVLPTSPTVWPFIPHTSIDTQHAIVIQGGDYYFVAVYIFVTQT------P-----------   459
[HPV69]                                      PRF----SSTIF-STTSSA--PLNVTIPLSTSFD------IPIYN---GPDIYAPVPSSTWPYIPPPPTTMSHSVVAQGGNYYLWPYIYLIHKR-RRKRVPCFFSDGLAAY-   467
[HPV26]                                      PRY----ASNVF-SSINTS--TTNVTVPLSTSFE------LPVYS---GSDIYTPTSSPTWPSLPPPPTTNLPAIVVHGDNYYLWPYIYLIHKR--RKRMPYFFSDGFVAY-   472
[HPV26b_CAA52534.1]                          PRY----ASNVF-SSINTS--TTNVTVPLSTSFE------LPVYS---GSDIYTPTSSPTWPSLPPPPTTNLPAIVVHGDNYYLWPYIYLIHKR--RKRMPYFFSDGFVAY-   471
Pcpv1_L2aa                                   PSS----TSFVRSSMFTTK--WGNTTVPLSLPSN------IFAQP---GPDIIFPAAPGVPPYNPVIPSLPITPIFISGSQFYLHPSLYLARKR--RKRVSLFFAD--VAA-   463
[ccpv1]                                      NST----LFIKS-SIFDTS--WGNTTIPLSLPNN------IFVQP---GPDILFPTTPAVPPYGPVISPLPVGPVFISGSEFYLHPSLYFARKR--RKRVSLFFSD--VAA-   462
[HPV6b]gil9626061lreflNP_040303.1l           SDT----YLTSTPNTVTQP--WGNTTVPLSLPND------LFLQS---GPDITFPTAPMGTPFSPVTPALPTGPVFITGSGFYLHPAWYFARKR--RKRIPLFFSD--VAA-   459
[HPV74]gil27462490lgblAAO15461.1lAF436130_7  FST----STPFQRSAVSAT--WGNTTVPLSLPGD------MFIQP---GPDIMFPTASSTTPYSPVTPALPTGPVFINGSTFYLYPSWYFARKR--RKHVPLFFTD--VAA-   464
HPV7gil9627394lreflNP_041858.1l              PTS----TYSLY-PGNSTR--IANTSIPLATIPD------TFLTS---GPDIVFPSVPAGTPYLPVSPSIPAISVLIRGTDYYLNPAYYFRKRR--KRILAY----------   456
Hpv7gi|397066|emb|CAA52480.1|                PTS----TYSLY-PGNSTR--IANTSIPLATIPD------TFLTS---GPDIVFPSVPAGTPYLPVSPSIPAISVLIRGTDYYLNPAYYFRKRR--KRILAY----------   456
[HPV40]                                      -------TFSLH-PADSTR--ISNTSIPLATVSD------TLLTS---GPDIVFPSIPAGTPYLPVSPSIPAISVLIHGTDYYLHPAYY-LRKR--RKRI---LAHQYVAT-   467
[HPV43]                                      -------DTHVS-LQNSTK--VVNTAVPLATVPD------IYAQT---GPDISFPTIPIHIPYIPVSPSISPQSVSIHGTDFYLHPSLWHLGKR--RKRFSYFFTDNYVAA-   463
[Hpv91]                                      -------NTNVSTLPNTTK--IVNTTVPLATVPD------IYTQA---GPDITFPTVPLSVPYVPLSPSVTPSAVSIYGTDFYLHPSLLHFGKR--RKRISYFFADNYVAA-   460
[HPV54]                                      SSV----QTALQTTSIPSQ--YGNTTVPLTAS--------SPYTP---IPTSFRPSS-GHTPFVPARPIFPQTPIAVNGGDFYLHPSYTYVRKR--RKRFPYFLADGYVAA-   470
[HPV32]gi|9627332|ref|NP_041805.1|           PTHVSTVSLTSL-GSVPAQ--TANTTVPLSLPTN------INV-----GPDLSPPESPPFISTRPVSP--SFDSVMVLGWDFILHPSY-MWRKR--RKPVPYFFADVRVAA-   476
[HPV32]gi|396987|emb|CAA52553.1|             PTHVSTVSLTSL-GSVPAQ--TANTTVPLSLPTN------INV-----GPDLSPPESPPFISTRPVSP--SFDSVMVLGWDFILHPSY-MWRKR--RKPVPYFFADVRVAA-   476
[HPV4]2gi|333218|gb|AAA47047.1|              STT----SFPTL-PSMSTH--SANTTIPFSFPAT------VHV-----GPDLSVVDHPWDSTPTSVMP--QGNFVMVSGWDFILHPSYF-WRRR--RKPVPYFFADVRVAA-   477
HPV34_L2aa                                   TNT----QSVFA-SEISTT--TANTTIPLNAGLD--------THP---GPDIALPVPTAETIFTPTVPVQPSGPIYIYGSDFILHPSLYVIPRK--RKRLSYFFAD--VATY   472
HPV34gi|9627339|ref|NP_041811.1|             TNT----QSVFA-SEISTT--TANTTIPLNAGLD--------THP---GPDIALPVPTAETIFTPTVPVQPSGPIYIYGSDFILHPSLYVIPRK--RKRLSYFFAD--VATY   472
HPV34gi|396995|emb|CAA52559.1|               TNT----QSVFA-SEISTT--TANTTIPLNAGLD--------THP---GPDIALPVPTAETIFTPTVPVQPSGPIYIYGSDFILHPSLYVIPRK--RKRLSYFFAD--VATY   472
[HPV73]                                      HSN------SLVSSDISTA--TANTTIPFSTGLD--------THP---GPDIALPLPSTETIFTPIVPLQPAGPIYIYGSGFILHPSYYLLKRK--RKRLSYSFTD--VATY   475
RMPV_L2aa                                    -------NTPLN-SNSSGIASPWNTTVPLSAGAD------VTLQS---GPDVSLDAPVAESPVHPGVPLRPSAHIILYGGDFYLHPSYLGIRRK--RKRMHNFFSDVYVAA-   466
HPV52_L2aa                                   PST------------LSTH--NNTFTVPINSGIDFVYQPTMSIES---GPDIPLPSLPTHTPFVPIAPTAPSTSIIVDGTDFILHPSYFLLRRR--RKRFPYFFTDVRVAA-   466
HPV67_L2aa                                   PSI----SYSLH-SPQT-----TNVTVPLSSGFDFPFSSTVPLQP---GPDIVSPVAPTYTPFVPVIPTSPFNNVLVYGSDFILHPSYF-LRRR--RKRFPYFFADVRVAA-   465
HPV33_L2aa                                   SYS----------TFATTR--TSNVSIPLNTGFD------TPVMS---GPDIPSPLFPTSSPFVPISPFFPFDTIVVDGADFVLHPSYFILRRR--RKRFPYFFTDVRVAA-   467
HPV58_L2aa                                   QSP----LHSHT-SFATTR--TSNVSIPLNTGFD------TPLVSLEPGPDIASSVTSMSSPFIPISPLTPFNTIIVDGADFMLHPSYFILRRR--RKRFPYFFADVRVAA-   472
[HPV35]                                      YTT----------SNTAYV--PSNTTIPLSSGYD------IPITA---GPDIVFNSNTITNSVLPV-PTGPIYSIIADGGDFYLHPSYYLLKRR--RKAIPYFFADVSVAV-   469
HPV31_L2aa                                   PST----AVQST-SAVSAYV-PTNTTVPLSTGFD------IPIFS---GPDVPIEHAPTQVFPFPLAPTTPQVSIFVDGGDFYLHPSYYMLKRR--RKRVSYFFTDVSVAA-   466
[HPV16EAvar]                                 PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINITDQAPSLLPIVPGSPQYTIIADAGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
HPV16_L2aa                                   PST------SLS-GYI-----PANTTIPFGGAYN------IPLVS---GPDIPINITDQAPSLIPIVPGSPQYTIIADAGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
[Hpv16NP_041331.1]                           PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINITDQAPSLIPIVPGSPQYTIIADAGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
[HPV16EGvar]                                 PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINITDQAPSLIPIVPGSPQYTIIADAGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
[HPV16AAvar]                                 PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINTTDQTPSLIPIVPGSPQYTIIADGGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
[HPV16Af2]                                   PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINTTDQTPSLIPIVPGSPQYTIIADGGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
[HPV16Af1]                                   PST------SLS-GYIP-----ANTTIPFGGAYN------IPLVS---GPDIPINTTDQTPSLIPIVPGSPQYTIIADGGDFYLHPSYYMLRKR--RKRLPYFFSDVSLAA-   473
                                             .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560..
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HPV16              1 MRHKRSAKRTKRASATQLYKTCKQAGTCPPDIIPKVEGKTIAEQILQYGS     50
                                          .....||.:|...|
bpv1               1                      PAIVTPDAVPADSG------------     14

HPV16             51 MGVFFGGLGIGTGSGTGGRTGYIPLGTRPPTATDTLAPVRPPLTVDPVGP    100
                         ...|.|||.|                 :|:||..:     ::|.||
bpv1              15 ----LDALSIGTDS----------------STETLITL-----LEPEGP     38

HPV16            101 SDPSIVSLVEETSFIDAGAPTSVPSIPPDVSGFSITTSTDTTPAILDINN    150
                     .|.:::.|          .|...|:                    ..::|
bpv1              39 EDIAVLEL----------QPLDRPT-------------------WQVSN     58

HPV16            151 TVTTVTTHNNPTFTDPSVLQPPTPAETGG--HFTLSSSTISTHNYEEIPM    198
                     .|     |.:..:..|..|| .:.|||.|  :..:..|.:.....|.|.:
bpv1              59 AV-----HQSSAYHAPLQLQ-SSIAETSGLENIFVGGSGLGDTGGENIEL    102

HPV16            199 DTFIVSTNPNTVTSSTPIPGSRPVARLGLYSRTTQQVKVVDPAFVTTPTK    248
                     ..|   .:|.|   |||
bpv1             103 TYF---GSPRT---STP                                    113
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