

A

Kpn5N: 1 MAYTVSIAPLAASAVIGATTNFTATTSGAAAEGTEAFVWTVNGVKQSSVTAAMNYVAAGP 60
MAY+VSIAPLAASAVIGATTNFTATTSGAAAEGTE FVWTVNGVKQSSVTAAMNYVAAGP

Kpn6N: 1 MAYSVSIAPLAASAVIGATTNFTATTSGAAAEGTETVWTVNGVKQSSVTAAMNYVAAGP 60

Kpn5N: 61 AGSKTVKVVATVTPAEGEAETAEAEETTLTVQNKTMPAITLTLSPSTSVSKEIGSQVVTAD 120
AGSKTVKVVATVTPAEGEAETAEAEETTLTV+NKTMPAITLTLSPSTSVSKEIGSQVVTAD

Kpn6N: 61 AGSKTVKVVATVTPAEGEAETAEAEETTLTVKNKTMPAITLTLSPSTSVSKEIGSQVVTAD 120

Kpn5N: 121 VTGAPSGASIAVWVWKRGSVISGQTGKTITLTPAEANYTLNCEVTVSAADYNPATATKG 180
VTGAPSGASIAVWVWKRGSVISGQTGKTITLTPAE +YTLNCEVTVSA DYN TATKG

Kpn6N: 121 VTGAPSGASIAVWVWKRGSVISGQTGKTITLTPESAETSYTLNCEVTVSAPDYNNGTATKG 180

Kpn5N: 181 VEVVFTKKTMSGVSVTLTPESITVEQGSDFKADVIGAPGASGTYSWTKDGSFVEGST 240
+ V F KKTMSGVSVTL+P S++ E G A+V+GAPEGAS Y W + +EG T

Kpn6N: 181 IAVAFIKKTMSGVSVTLSPSTSVSKEIGSQVVTANVVGAPGASIAVWVWKRGTVVIEGQT 240

Kpn5N: 241 S-TLVIDTSDIGSQVIGVSVEVSAEDYNSVTVTGNTITKR 282 (of 373)
+ T+ I S + + VSA DYN VTV+ +VTITK+

Kpn6N: 241 AKTITITESAEANYTLNCEATVSAPDYNPVTVSKGASVTITKK 283 (of 468)

B

Kpn5N: 2 AYTVSIAPLAASAVIGATTNFTATTSGAAAEGTEAFVWTVNGVKQSSVTAAMNYVAAGPA 61
A T++++P + S IG + TA +GA + + A+VW S T +

Kpn6N: 97 AITLTLSPSTSVSKEIGSQVVTADVTGAPSGASIAVWVWKRGSVISGQTGKTITLTESAE 156

Kpn5N: 62 GSKTVKVVATVTPAEGEAETAEAEETTLTVQNKTMPAITLTLSPSTSVSKEIGSQVVTADV 121
S T+ TV+ + TA + KTM +++TLSPSTSVSKEIGSQVVTAV

Kpn6N: 157 TSYTLNCEVTVSAPDYNNGTATKGI AVAFIKKTMSGVSVTLSPSTSVSKEIGSQVVTANV 216

Kpn5N: 122 TGAPSGASIAVWVWKRGSVISGQTGKTITLTPAEANYTLNCEVTVSAADYNPATATKGV 181
GAP GASIAVWVWKR+ VI GQT KTIT+TE AEANYTLNCE TVSA DYNP T +KG

Kpn6N: 217 VGAPEGASIAVWVWKRGTVVIEGQTAKTITITESAEANYTLNCEATVSAPDYNPVTVSKGA 276

Kpn5N: 182 EVVFTKKTMSGVSVTLTPESITVEQGSDFKADVIGAPGASGTYSWTKDGSFVEGSTS 241
V TKKTMSGVSVTLTPESITVEQGSDFKADVIGAPGASGTYSWTKDGSFVEGSTS

Kpn6N: 277 SVTITKKTMSGVSVTLTPESITVEQGSDFKADVIGAPGATGVYSWTKDGSFVEGSTS 336

Kpn5N: 242 TLVIDTSDIGSQVIGVSVEVSAEDYNSVTVTGNTITKRVAAPDGELPYIHPLPFRG 301
TLVIDTSDIGSQVIGVSVEVSA+DY VTVT TGNVTITKRVA PDGELPYIHPLPFRG

Kpn6N: 337 TLVIDTSDIGSQVIGVSVEVSADYTPVTVTGNTITKRVAPEPDGELPYIHPLPFRG 396

Kpn5N: 302 TAYIWCWWVMDEIQRMTVEGKDWKLDLDPDSYLLHRYTLAKMLDDYPEVDVQESRNGYI 361
TAYIWCWWVMDEIQRMTVEGKDWKLDLDPDSYLLHRYTLAKMLDDYPEVDVQESRNGYI

Kpn6N: 397 TAYIWCWWVMDEIQRMTVEGKDWKLDLDPDSYLLHRYTLAKMLDDYPEVDVQESRNGYI 456

Kpn5N: 362 VHRTALEAGIIY 373 (of 373)
VHRTALEAGIIY

Kpn6N: 457 VHRTALEAGIIY 468 (of 468)

Figure S4: Alignment of amino acid sequences of N-terminal (A) and C-terminal (B) regions of phage Kpn5N and Kpn6N gp17 proteins, counterparts of bacteriophage T4 Hoc.