

4A

Det7 Tsp	PKVVPAGSTPASTGGVGLGAWVSVGDAAFRQEAN-----KKFKYSVKLSDYS	176
SETP12 Tsp	PKVIPAASTPLTAGGGISDSAWVAFGDITFRAEAD-----KKFKYSVKLSDFT	153
Phil9 Tsp3	PKTVDAGSTPETSGGVGLGAWLSVGDAAFRQEAN-----KKFKYSVKLSDYS	176
k1H Tsp63D sialidase	PKTIPASSSPQSTGGVSEGAWQRAGSVVLRQQISNANGAILYPDLHVARWKDEYDPRAWG	166
K1G Tsp63D sialidase	PKIIPASSSPQSTGGVADGAWQPVGSVILRQQISDVNGAILYPDLHVARWKDEYDPRAWG	166
K1F tail fibre	PKNVPAGSTPETSGGIGLGAWVSVGDAAALRSQISNPEGAILYPELHRRARWLDEKDARGWG	245
Vi01 Tsp3	PKVVAAGSTPDNSGGVGTGAWIPVGINSLSGDGGWSRIGSEFGKSLKEHIQSLPLSAVK	189
Phil9 Tsp1	PKTVAPGSTPATTGGVGLGAWVSVGDVSLRSELS-----KEDGFKYIGYS	172
SboM-AG3 orf00207	PKSVNAGGTIANTGGLSSSNWVKLDPDALRDELY-----SGFYRLT	169
EcoDS1 gp17	PKEVPAGSTPSTTGGVGLGAWVSVGDASLRSNLIS-----DNSINGDALI	230
EPECa14 tail fibre	PKDVPENSTPESTGGVSLGAWVSVGDASLRSDLIS-----QETDKGS	293
SboM-AG3 orf 00210	PKTVNKNSTPQSTGGVSSSAWVSVESKTLGSELLTG-----EKASLVG	111
K. pneumoniae prophage tail	PKTVPIASSPATTGGVRAGGWAYTSDAAIRQNLAADSGAKLVGGLNYVTPEMSGFVTGAG	152
ViII-E1 maturation/adhesion	PKTVPPGSTPYSSGGTGNGKWMAVDVADVLRKDLAKPTGANLIGIHDTTVGEVLRQKVYI	173
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4B

ST64T Tsp	GESGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWGGFDLGAD	400
ST104 Tsp	GESGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWGGFDLGAD	400
P22 Tsp	GESGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWGGFDLGAD	400
SETP13 Tsp	GESGVKTWQGTVGSTTSRNYNLQFRDSAVLYPVWGGFDLGAD	421
SETP12 Tsp	GESGVKTWQGTVGSTTSRNYNLQFRDSAVLYPVWGGFDLGAD	421
SP6 Tsp	GESGFKTWQGSVAGTSRNYNLQFRDSVALSPVWGGFDLGSD	287
Det7 Tsp	GESGFKTYQGSVGGGTARNYNLQFRDSVALSPVWGGFDLGSD	444
19 Tsp3	GESGTKTYQNEIGGRSARNYRLVFDNITTIQCYYGIDVNAD	440

4C

ST64T Tsp	KLSKTLDSGALYSHINVGPGSGSAWTQLTAISGNTPDAYS	606
ST104 Tsp	KLSKTLDSGALYSHINGGPGSGSAWTQLTAISGNTPDAYS	606
P22 Tsp	KLSKTLDSGALYSHINVGPGSGSAWTQLTAISGNTPDAYS	606
SETP13 Tsp	KLSKTLDSGSVYSHINGGPGSGSAWTEITAISGSSPDAYS	627
SETP12 Tsp	KLSKTLDSGSVYSRINVGPGSGSAWTEITAIAIGSLPDAYS	627
SP6 Tsp	KLTKTLDSGAIRSTLNGGPGTGSAWTEMTAISGSAPNAVS	493
Det7 Tsp	KLSATLDSGALRSHLNGYAGSGSAWTELTALSGSTPNAVS	650
φSH19 Tsp3	MGGTTNPSSLMTADCQVATPGGEASIVKLSAIQEGVRVGE	641

ST64T Tsp	LKVNHKDCRGAIEIPFVPDIASDDFIKDSSCFLPYWENNSTSLKALVKKPENGELVR	661
ST104 Tsp	LKVNHKDCRGAIEIPFVPDIASDDFIKDSSCFLPYWENNSTSLKALVKKPENGELVR	661
P22 Tsp	LKVNHKDCRGAIEIPFVPDIASDDFIKDSSCFLPYWENNSTSLKALVKKPENGELVR	661
SETP13 Tsp	LKINRGDYRAVEIPVAMSALPDNAVRDIGSISMYLEGD--SLKALVRRADGSYTR	680
SETP12 Tsp	LKINRGDYRAVEIPVAMTVLPDNAVDRNGSISLYLEGD--SLKALVKRADGSYTR	680
SP6 Tsp	LKINRGDFKATEIPVAPTVPDPDEAVRDHSSIALYFDQE--ALWALVKKPNGSLTR	546
Det7 Tsp	LKVNRGDYKTTEIPISGTVLPDEGVLDINTMSLYLDAG--ALWALIRLPDGSKTR	703
φSH19 Tsp3	FQLNR LGFKHMSIPAAPLQLPESALEHNSSIGFFFGSDG-ALRLIAKKPDGSYVT	695

ST64T Tsp	LTLATL---	667
ST104 Tsp	LTLATL---	667
P22 Tsp	LTLATL---	667
SETP13 Tsp	LTLA----	684
SETP12 Tsp	LTLA----	684
SP6 Tsp	MKLA----	550
Det7 Tsp	MKLSV----	708
φSH19 Tsp3	YTL-----	698