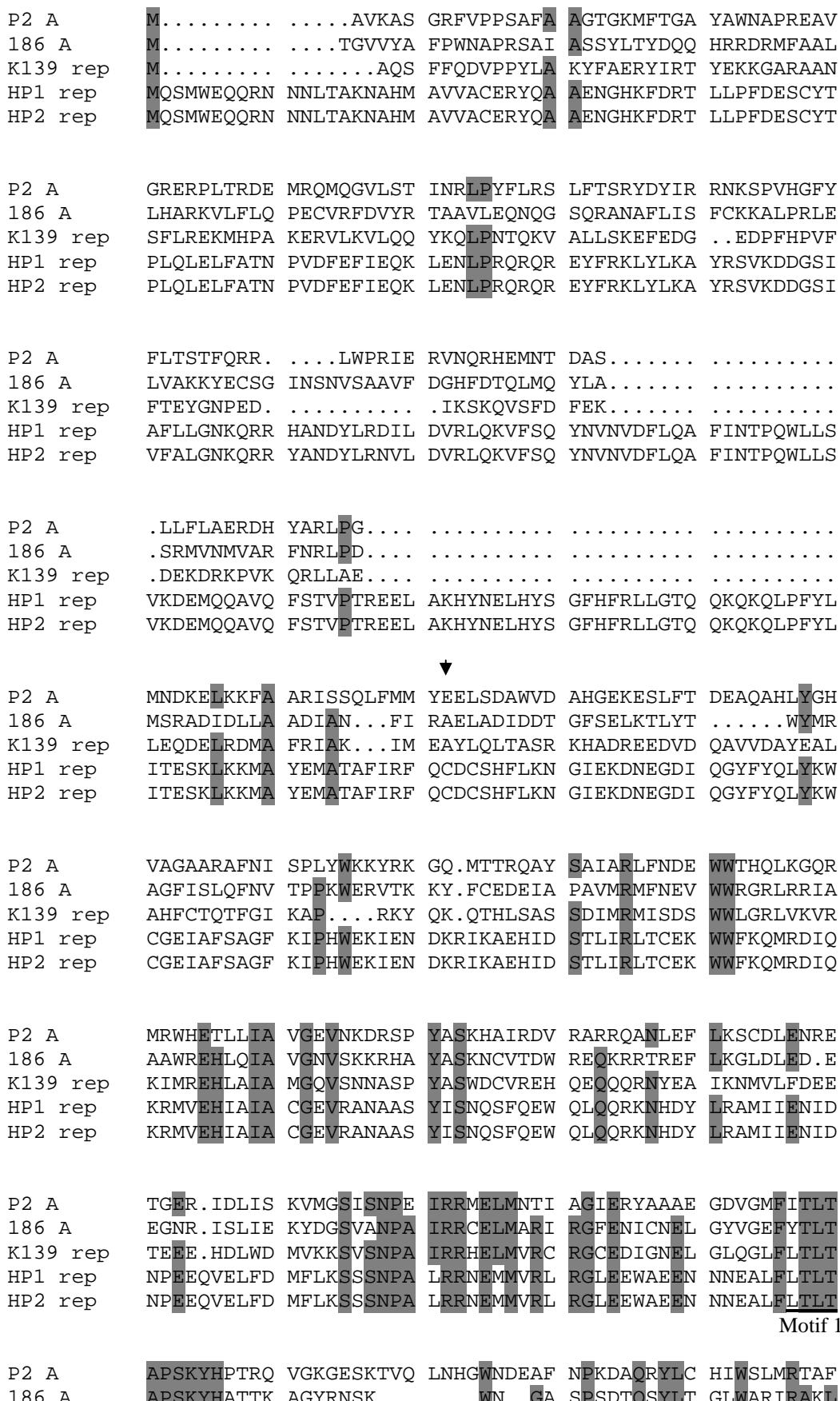


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Fig. 25-3. Alignment of the initiation proteins of P2 and some P2-like phages. The amino acids were aligned using the CLUSTAL X program (58). Amino acids identical in at least 4 proteins are indicated by dark gray shadings. The common motifs for proteins initiating rolling-circle replication are boxed (61, 74). The location of P2 *ori* (in the corresponding DNA sequence), and the amino acid in phage 186 believed to interact with the REP protein, are indicated by arrowheads.



K139 rep	TPSKYHNSYK KGGFIDH...	WN..GA SPRDAQAYLN KKWLQLIRAKL
HP1 rep	APSSFHAGNG NKK.....	WL..GV NPRETQNYLN KVWQQFRALL
HP2 rep	APSSFHAGNG NKK.....	WL..GV NPRETQNYLN KVWQQFRALL

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P2 A	KDNDLQVYGL	RVVEPHHDGT	PHWHMMILFCN	PRQRNQIIEI	MRRYALKEDG
186 A	HREEIRIFGI	RVAEPPHHDT	PHWHMLMFML	PEDVERVRLI	IRDYAWEEDH
K139 rep	NRDEIRWFGV	RVAEPPHHDT	PHWHLLIWVR	KEDISAVRDT	FITYATEEEDR
HP1 rep	SKRNIKFYGM	RVAEPKDGT	PHWHALAYVP	AEHKEEVIRL	FKQKALELDG
HP2 rep	SKRNIKFYGM	RVAEPKDGT	PHWHALAYVP	AEHKEEVIRL	FKQKALELDG
Motif 2					
P2 A	DERG.....	AARNRF	QAKHLN..QG	GAAGYIAKYI
186 A	YELRSOK	AKKARF	HAAEADPEKG	SATGYVAKYI
K139 rep	GELHPEFEKE	KQKPFRKGVY	VGPLDYRPRC	DFGYIDPTKG	TATGYIAKYI
HP1 rep	NEKG.....	AAEHRC	KVEKCDKTKG	SATAYIAKYI
HP2 rep	NEKG.....	AAEHRC	KVEKCDKTKG	SATAYIAKYI
Motif 3					
P2 A	SKNIDGYALD	GQLDND.TGR	PLKDTAAAVT	AWASTWRIPQ	FKTVGLPTMG
186 A	SKNIDGYALD	GETDDE.SGE	LLKETAPAVS	AWAARWHIRO	FQFIGGAPVT
K139 rep	SKNIDGYAMD	GDISDE.TGK	PVKDMARNVS	AWKSRWSIRO	FQFFGGAPVT
HP1 rep	AKNIDGFALA	GEVSDEDPTL	SLHDNALRVR	AWASRWGIRQ	FQFYGGASIC
HP2 rep	AKNIDGFALA	GEVSDEDPTL	SLHDNALRVR	AWASRWGIRQ	FQFYGGASIC
P2 A	AYRELRLKLP	R G.....
186 A	VYRELRRMAD
K139 rep	TYRELRRRLAN	QNKKAFMEYI	FMQERADLIS	MYELLHYQLI	GAFKPARVMT
HP1 rep	VWRELRRRLIS	G.....
HP2 rep	VWRELRRRLIS	G.....
P2 AVSIADefd	ERVEAARAAA	DSGDFALYIS	AQGGANVPRD
186 APETARALS	VEFAAVHDAA	HYGRWADYVN	AQGGPFVRRD
K139 rep	NQELVEVIAQ	SYEARAKTEI	PHVAAVLRSA	DEGRWHGYIM	NQGGPFVKRK
HP1 repQADDEII	NKAQAAAGIA	N..DYAAYME	IQGGALAKRA
HP2 repQADDEII	NKAQAAAGIA	N..DYAAYME	IQGGALAKRA
P2 A	CQTVRVARSP	SDEVNEYEEE	VERVVGIYAP	HLGARHIHIT	RTTDWR....
186 A	DLQVRTLYEP	RTEFNQYGEE	TVCIKGVYDA	SIGAGSPILT	RLTQWK....
K139 rep	ELLVTNVYQE	LPFASPYAEA	IRKLEGIATP	EVIKTRKEV	WTIKRKGKET
HP1 rep	DQPIKLDYET	KP.ANKYGEQ	RKAIIGLANR	FSLKQVISRT	KKWQIKKRQ
HP2 rep	DQPIKLDYET	KP.ANKYGEQ	RKAIIGLANR	FSLKQVISRT	KKWQIKKRQ
ori ↓					
P2 A	.IVPKVPVVE	PLTLKS...G	IAAPRSPVNN	CGKLTGGDTS	LPAPTPSEHA
186 A	.IVPKRAVDL	AVDVKG...A	SAPSRSSVNN	C.....TGSESD
K139 rep	TEGEAVFGS	EATAFG...G	SAASRSSVNN	CTDP.....FTGQVST
HP1 rep	DFAQRTESMV	ERSSTANNSA	RSAPWTCVSN	CN.....RSILE
HP2 rep	DFAQRTESMV	ERSSTANNSA	RSAPWTCVSN	CN.....RSNLE
P2 A	AAVLNLVDDG	VIEWNEPEVV	RALRGALKYD	MRTPNRQQRN	GSPLKPHEIA
186 A	PPILDLTKP.LSRRER	RELTNRLRKK	KPTTRRKFIH	GTDKQNVAIT
K139 rep	QLTRLLQPDR	LKGSQLNDQIV	DEVAISALFK	GSTLRLDDET	ELKIRPAEVD
HP1 rep	QKIKLLTQP.	...ICAPLSA	QKLDYLFKYK	RLTIDKYTAL	ELTENDVQLV
HP2 rep	QKIKLLTQP.	...ICTPLSA	QKLDYLFKYK	RLTIDKYTAL	ELTENDVQLV
P2 A	PSARLTRSER	LQITRIRVDL	AQNGIRPQRW	ELEALARGAT	VNYDGKKFTY
186 A	KTIDEIHSDN	RHHNQPGRSP	APDGRW		
K139 rep	EHGKIRPARL	VEVKREVDS	IWCRFEGWEK	FEQQMEKLNQ	KPQEHSQPDL
HP1 rep	KRNQNMMMTSL	SPVSRNFQKL	KDFHKNQRIQ		
HP2 rep	KRNQNMMMTSL	SPVPRNLQKL	KNFHKKQRIQ		

P2 A PVADEWPGFS TVMEWT
K139 rep SFFQELEGDW PLA...

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