

Mrk1p	(1)	MKKLTLFIGLMALGTTSAWASCWQNS-AYEINMAMGRVVVSPDLPVGSVIATKTWTMPDNNTIYVTC	★	★
MrkDV2	(1)	MKKLTLFIGLMAMGTTSAWAYCTRLSQPTVSLDMVVGRVVVPPDLPVGSVIVSRDWTMSAPGGASYSCSS		
MrkDV3	(1)	MKKLTLFIVLMALGTTSSWAVCTRLSSPTVMLDMVVGRVVVPPDLPVGSVILTRDWTMSAPGGASYCCIF		
MrkDV4	(1)	MKKLTLFIGLMALGTTSAWAACCTRLSQPTVNLDVVGRVVVPPDLPVGSVIVSRDWTMNAAPGGASYSCTA		
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Mrk1p	(70)	NTTLKSDAKVVAAGLVQGANVYSTAIPGIGIRFSRK-GAISMIIYDPSYTTTG--SSFRLVG-STFTLDI		
MrkDV2	(71)	G-TNRFVAKIVAPGATDLGNKIYSTNVPGIGIRFSRGGATVNI IYPDTFSSYVSRTTNYSLEGSRFTLEV		
MrkDV3	(71)	G-TNRFAAKIVSPGATDLGNKIYFTNVPGIGMCFSRGGATVNIIVYFDGYSFRVYNTTNYSLK-DHVL		RGD
MrkDV4	(71)	G-TNRFAAKIVSTGSTDLEGNKIYSTNVPGIGMCFSRGGATVNI IYPDVFSSTINRTTNYSLEGSRFTLEI		
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Mrk1p	(136)	IKTSTTTGSGTLASGPYTEYGP---GFTILKTSLNADAITIVSPSCTILGGKNMNVDIGTIK		★
MrkDV2	(140)	IKTASVTGSGTLAAGKYTSYDWENGNPILLETLSANAITVWVSPSCTILSGKNMNVDVGTIKRSDLNGVG		
MrkDV3	(139)	YQTAATTRSGTLAAGKYTSYDWESGGNPILETYLSANAITVWVSPSCSVLSGKNMNVDVGAIRRTDLKGVG		
MrkDV4	(140)	IKTSSTTGSGTLAAGKYTSYDWERGNPILLETYLSANAITIVSPSCTVLSGKNMNVDVGTIKRSDLKGVG		
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Mrk1p	(203)	TWAGGTPFDIKLECSGGVSVSGYANINTSFSGTLATNTSANQGVLL-EKTGNSAAKGVGVQVIKDNTPLE	★	
MrkDV2	(210)	TTAGGKDFNIELQCCGGLSESGYANIQTSFSGTLATGTTVSRGALLNEKSGSSLAKGIGIQVLKEGVPLE		
MrkDV3	(209)	TTAGGKDFNIELQCSGALSETGYANISTSFSGTLATSTTATMGALLNEKAGSGMAKGVGIQVLKDGSPLO		
MrkDV4	(210)	TTAGGRDFNIELQCSGGLSESGYANIQTSFSGTLATSTTLKQGALLNEKTGSSAAKGVGIQVLKDGVPLE		
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Mrk1p	(272)	FNKKHNIGTLQSQETRYITLPLHARFYQYAPTTSTGEVESHLVFNLTVD		
MrkDV2	(280)	FNKKYSVGYLRTQETRYITLPLHARFYQYAPTTSTGEVESHMI FNLTVD		
MrkDV3	(279)	FNKKYTVGRLNNQETRYITLPLHARFYQYGPTTSTGEVESHMI FNLTVD		
MrkDV4	(280)	FNKKYSVGTLSRQETRYFTQPYHARFYQYLPTTSTGEVESHMI FNLTVD		

Fig. 1. Amino acid sequence comparison of MrkD_{1P}, MrkD_{V2}, MrkD_{V3}, and MrkD_{V4}: The receptor binding (→) and pilin (- ->) domains are shown. The conserved Cys residues are indicated as asterisks. The regions with varied sequences are boxed and the RGD residues are in shadow.