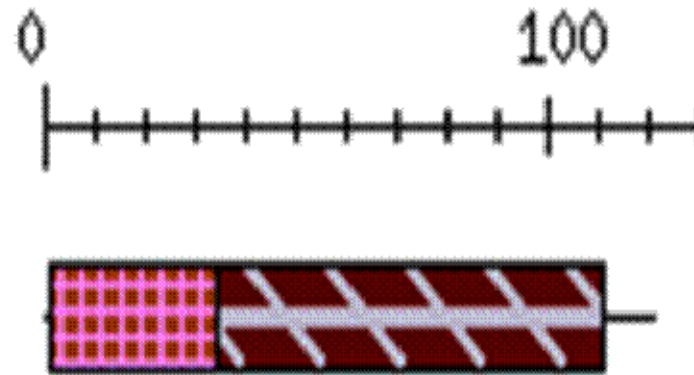


# VirB2



	<u>Domain ID</u>	<u>BEGIN</u>	<u>END</u>	<u>Total ID</u>
1.	PD009344	34	110	39
2.	PD015823	1	33	4
3.	PD570722	29	89	1

	1	10	20	30	40	50	60	70	80	90	101	
066170_AGRTU(5-100)	IRIAIALAAFAA	VSFIGLADPA	FASS-GGSL	PWESPLQQ	IQQSITGP	VAGFIALA	AAVAIAGG	MLIFGGEL	NDFARRLC	YVALVGG	VLLGATQ	IIALF
Q8U693_AGRT5(9-104)	IRIAIALAAFAA	VSFIGLADPA	FASS-GGSL	PWESPLQQ	IQQSITGP	VAGFIALA	AAVAIAGG	MLIFGGEL	NDFARRLC	YVALVGG	VLLGATQ	IIALF
Q9R489_AGRT5(5-100)	IRIAIALAAFAA	VSFIGLADPA	FASS-GGSL	PWESPLQQ	IQQSITGP	VAGFIALA	AAVAIAGG	MLIFGGEL	NDFARRLC	YVALVGG	VLLGATQ	IIALF
TRBC_RHISN(13-96)	LASPLILASV	APALASS-GG	SLPMEGPLE	IQESITGP	VAGYIALA	AAVAIAGG	MLIFGGEL	NDFARRLC	YVALVGG	VLLGATQ	IIALF	
TRBC_AGRTU(25-100)	ALASSG-GG	SLPMEESPL	QQIQQSIT	GPVAGFIALA	AAVAIAGG	MLIFGGEL	NDFARRLC	YVALVGG	VLLGATQ	IIVALF		
P71178_ENTAE(18-110)	MGLFALLAFF	LAPQHAFSE	GTGGSL	PYESML	TNLRNSVT	GPVAFAL	SIIGIVVAG	GILIFGGEL	NGFLRTL	IFIVLVM	GLLVGAQ	NMMSTF
Q9AHH6_COMTE(18-111)	MGLFALLAFF	LAPQHAFSE	GTGGSL	PYESML	TNLRNSVT	GPVAFAL	SIIGIVVAG	GILIFGGEL	NGFFRTL	IFIVLVM	GLLVGAQ	NMMSTF
Q8RSJ5_PRBO2(21-111)	FALLAFFLLA	PQHAFSEGT	GGSLPYE	GMLTNLRNS	VTGPVAFAL	SIIGIVVAG	GILIFGGEL	NGFFRTL	IFIVLVM	GLLVGAQ	NMMSTF	
Q60210_ECOLI(23-111)	FVLALALSA	HPAMASEGT	GGSLPYE	SMLTNLRNS	VTGPVAFAL	SIIGIVVAG	GVLIFFGGEL	NAFFRTL	IFIVLVM	GLLVGAQ	NMMSTF	
Q9PBT4_XYLFA(45-122)	AFASNTAGG	GLPSDEMFT	RIRESVT	GPFAFTVA	IVGIVAAG	AGLIFGGDM	NGFLRTL	IFIVLVS	FLVAQMS	LSAIT		
Q84EN2_BBBBB(35-107)	LAALLFLAG	TAAAGSSM	PMEGPLE	QSILES	IQGVPARIV	AVIIIIAT	GLALAFGD	TSGGF-R	KLIIQIV	FGLSI		
Q8XM92_RAL50(44-110)	FIAGTAQA	AGSSM	PMEGPLE	QSILES	IQGVPARIV	AVIIIIAT	GLALAFGD	TSGGF-R	KLIIQIV	FGLSI		
Q89B78_BRAJA(19-106)	AAIAYISIA	IAPAYASG	SSMPWETPL	NQILES	VQGPVAKIM	SVIIITV	GLTLAFGD	S	GGF-RRL	IIQIV	FGLSIA	F
Q98P50_RHILO(19-90)	IAYNLMV	APYAHASG	SSMPWEQ	PLEKIL	QSV	EGPVSKIM	AVIIIIY	TGLTLAF	GD	S	GGF-RRL	IIQIV
Q989J3_RHILO(10-82)	FAALAFLL	TPAHAAG	SSMPWEQ	PLQQI	LESVQ	GPVAKI	AVIIIIIT	TGLTLAF	GD	T	AGGF-RRL	IIQIV
066282_AGRTU(34-110)	AMGWSIF	SSGPARAQ	SAGGTD	DPATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L
VIB2_AGRT5(34-110)	AMGWSIF	SSGPARAQ	SAGGTD	DPATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L
Q8KJL4_RHILO(32-110)	AAAGAANT	VFSIGP	ASQVTT	GG-TDPA	KMYNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L
Q8YTA1_AGRTU(44-109)	PARAAQA	AGG-TDPA	TMYNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L	VAGV	VGGI
Q9F5A1_AGRRH(40-109)	FFCEPAA	QAAGG-TD	PATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L	VAGV
VIB2_AGRT9(45-110)	AAAQSAG	GGTD	DPATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L	VAGV
VIB2_AGRTU(45-110)	AAAQSAG	GGTD	DPATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L	VAGV
VirB2(34-110)	AMAWSIS	SCGPARAQ	SAGGTD	DPATM	VNNICT	FILGPF	GQSLAVL	GIVAIG	IS	MMFGR	ASLG---	L
Q8GJ66_BBBBB(20-99)	AVFISDF	SYAAPA	ANGG	GLNLDG	VLGNI	VYTM	GGTAR	LIAIC	VA	AVIG	WMYGF	IDLR---
Q9R3F2_BARHE(29-106)	AAARTGS	ASGLGN	VDVLS	QSVY	TM	GTAK	LIAIC	VA	AVIG	WMYGF	IDLR---	K
Q8KQC3_BARQU(34-99)	SSLGNV	DVSLQ	NIY	TM	GTAK	LIAIC	VA	AVIG	WMYGF	IDLR---	K	A
Q9A5N0_CAUCR(25-98)	VQSDPA	GS	PLLA	LQ	MM	QTLL	GNL	ATTA	VA	VA	IVGL	MLT
Q83U07_PSEPU(57-144)	KLATLGS	ILSLAL	IPEFANA	ALDF	SGLK	MAKDF	YSFL	IFD	VGYL	GI	AAIA	FCG
Q8VME7_PSEPU(57-144)	KFAVLGS	FIS	FAILPE	IANA	AMDF	SGLK	NLAKD	VYS	FLIF	D	IGYYL	GI
Q9R2I1_PSEPU(57-144)	KIAYLGS	LSF	FAILPE	IANA	AMDF	SGLK	NLAKD	VYS	FLIF	D	IGYYL	GI
Q8PRI5_XANAC(37-114)	VFLPQLA	YAQDV	GGTF	GGIT	AF	LK	SIT	QLLI	YEW	GGY	IGIIT	LA
Q8KN75_BBBBB(121-194)	AAFATPAL	AQ--DL---	SP	IQT	M	L	T	V	E	A	A	L
Q981S7_RHILO(14-100)	VAMPLML	LATQ	MAGG	GML---	QP	V	Q	S	T	L	Q	T
Q9PHK0_XYLFA(2-85)	KYSALL	CLTAV	FLTPE	IAMA---	AA	W	N	V	A	Q	V	L
Q8KIM6_RHIET(27-76)	PAFAQA	AGI	ETV	LQ	NI	VD	ML	T	GN	I	A	K
Q92YZ4_RHINE(27-76)	PAFAQA	AGI	ETV	LQ	NI	VD	ML	T	GN	I	A	K
Q93DC3_AGRTU(14-76)	SYMAYAI	IVTM	VEPA	FA	Q	S	A	G	I	E	T	V
Q84G59_RHILY(22-48)	VAAPIV	LASVAP	ALASS	GGSL	PMEG	PLQ	IQ	E	S	I	T	GP
Q93UM7_AGRTU(13-49)	VAAPIV	LASVAP	ALASS	GGSL	PMEG	PLQ	IQ	E	S	I	T	GP
Q84HS2_RHIET(13-49)	LAAPIV	LASVAP	ALASS	GGSL	PMEG	PLQ	IQ	E	S	I	T	GP
Consensus	.....	g	g	g	p	l	q	i	t	g	p	a
	.....	g	g	g	p	l	q	i	t	g	p	a

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1      10      20      30 33
|-----+-----+-----+-----|
066282_AGRTU(1-33) MRHFEKYHVMNRLSLSNAVMRMVSGYAPSLGG
VIB2_AGRT5(1-33)  MRCFERYRVHLNRLSLSNAVMRMVSGYAPSVVG
VIB2_AGRT9(1-33) MRCFERYRLHLNRLSLSNAMMRVISSCAPSLGG
VirB2(1-33)      MRCFERYRLHLNRLSLSNAMMRVISSCAPSLGG
VIB2_AGRTU(1-33) MRCFERYRLHLNRLSLSNAMMRVISSCAPSLGG
Consensus        MRcFErYrvH$NRLSLSNAvMRn!SgyAPSLgG

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1      10      20      30      40      50      60      70      80      90      100     110     120     130
|-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
Q9F5K8_RHOSH(214-674) QASFDALGRITTYTLGSAPGGPLLLLEGTAARSTLGYAEAGGLVLEYTRAGATLQSRQITGGSLQGYASALSAYDNAAEELDALARQLVAEMNTVHAQGIDQSGARGGDLFALEGHQAADAGNRGTGGASVY
VirB2(29-89)
Consensus .....

131     140     150     160     170     180     190     200     210     220     230     240     250     260
|-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
Q9F5K8_RHOSH(214-674) AFDTATAPGPLTLLHDAAGLWHAYDAGGTLGSGAETLAL TGLTLQMTGAAMDGDRLTVSPRQGRALDMRFLLDTRQIAAAAPYIVSARSGNAGSAQASVFPVSTLTPATGSLGGLLTDAGGADAATL
VirB2(29-89)
Consensus .....

261     270     280     290     300     310     320     330     340     350     360     370     380     390
|-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----|
Q9F5K8_RHOSH(214-674) IRAGVVGHIPAGTGSYTLASLGSQSQQEFLLSDPAAAGATTLSFSIGGTVHSFDLSALGATDPATLAAALNAGAVSTGGQTLAELGVTASGSTGRFTLMLGQGF DAGASVYTGAGTVAGSLTAEPPAGG
VirB2(29-89)
Consensus .....PaaAGaaLSiSicGpaaa..qSAGGaTDPAT$aaainagalpggGQsLaeLG!tAiGisgrF.....

391     400     410     420     430     440     450     461
|-----+-----+-----+-----+-----+-----+-----|
Q9F5K8_RHOSH(214-674) TIQITRDGRHIAGAALTAEEAALLL TEANGFLPGAYYDASTLNGAGGTGFRGTGIAGAILPGERVLSLHP
VirB2(29-89)
Consensus .....

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