

# SLC1A3 variant M128R

## Overview of the raw variants

Raw variant 1: substitution at 859

GGAATGCGAGCTGTAGTCTATTATA T GACTACCACCATCATTGCTGTGGTG  
GGAATGCGAGCTGTAGTCTATTATA G GACTACCACCATCATTGCTGTGGTG

[NM\\_004172.4:n.859T>G](#)

## Affected transcripts - 1

[NM\\_004172.4\(SLC1A3\\_v001\):c.383T>G](#)

## Affected proteins - 1

NM\_004172.4(SLC1A3\_i001):p.(Met128Arg)

## Reference protein

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTIV	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Protein predicted from variant coding sequence

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYRTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTIV	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Effects on Restriction sites

### Raw variant Created Deleted

1

Experimental services Genomic description: 859T>G

# SLC1A3 variant C186S

## Overview of the raw variants

Raw variant 1: substitution at 1032

GTTCCCTCCAAATCTGGTAGAAGCC T GCTTTAAACAGTTTAAACCAACTA  
GTTCCCTCCAAATCTGGTAGAAGCC A GCTTTAAACAGTTTAAACCAACTA

[NM\\_004172.4:n.1032T>A](#)

## Affected transcripts - 1

[NM\\_004172.4\(SLC1A3\\_v001\):c.556T>A](#)

## Affected proteins - 1

NM\_004172.4(SLC1A3\_i001):p.(Cys186Ser)

## Reference protein

1	MTKSNGE	EPK	MGGRMER	FQQ	GVRKR	TLLAK	KKVQN	ITKED	VKSYL	FRNAF	VLLTV	TAVIV
61	GTILGF	TLRP	YRMSY	REVKY	FSFPG	ELLMR	MLQML	VLPLI	ISSLV	TGMAA	LDSKAS	GKMG
121	MRAVV	YYMTT	TIIAV	VIGII	IVIII	IHPGK	G	TKENM	HREGK	IVRVTA	ADAF	LDLIRN
181	NLVEA	FKQF	KTNYE	KRSFK	VPIQA	NETLV	GAVINN	VSEA	METL	TRITEE	LVPVP	GSVNG
241	VNALGL	VVFS	MCFGF	VIGNM	KEQGQ	ALREF	FDSLNE	AIMR	LVAVI	MWYAP	VGILF	LIAGK
301	IVEMED	MGVI	GGQLA	MYTVT	VIVGL	LIHAV	IVLPL	LYFLV	TRKNP	WVFIG	GLLQA	LITAL
361	GTSSSS	SATLP	ITFKC	LEENN	GVDKR	VTRFV	LPVGAT	INMD	GTALY	EALAA	IFIAQ	VNNFE
421	LNFGQ	IITIS	ITATA	AASIG	AGIPQ	AGLVT	MVIVL	TSVGL	PTDDI	TLIIA	VDWFL	DRLRT
481	TTNVL	GDSL	G	AGIVE	HLSRH	ELKNR	DVEMG	NSVIE	ENEMK	KPYQL	IAQDN	ETEKPI
541	KM	*										

## Protein predicted from variant coding sequence

1	MTKSNGE	EPK	MGGRMER	FQQ	GVRKR	TLLAK	KKVQN	ITKED	VKSYL	FRNAF	VLLTV	TAVIV
61	GTILGF	TLRP	YRMSY	REVKY	FSFPG	ELLMR	MLQML	VLPLI	ISSLV	TGMAA	LDSKAS	GKMG
121	MRAVV	YYMTT	TIIAV	VIGII	IVIII	IHPGK	G	TKENM	HREGK	IVRVTA	ADAF	LDLIRN
181	NLVEA	FKQF	KTNYE	KRSFK	VPIQA	NETLV	GAVINN	VSEA	METL	TRITEE	LVPVP	GSVNG
241	VNALGL	VVFS	MCFGF	VIGNM	KEQGQ	ALREF	FDSLNE	AIMR	LVAVI	MWYAP	VGILF	LIAGK
301	IVEMED	MGVI	GGQLA	MYTVT	VIVGL	LIHAV	IVLPL	LYFLV	TRKNP	WVFIG	GLLQA	LITAL
361	GTSSSS	SATLP	ITFKC	LEENN	GVDKR	VTRFV	LPVGAT	INMD	GTALY	EALAA	IFIAQ	VNNFE
421	LNFGQ	IITIS	ITATA	AASIG	AGIPQ	AGLVT	MVIVL	TSVGL	PTDDI	TLIIA	VDWFL	DRLRT
481	TTNVL	GDSL	G	AGIVE	HLSRH	ELKNR	DVEMG	NSVIE	ENEMK	KPYQL	IAQDN	ETEKPI
541	KM	*										

## Effects on Restriction sites

Raw variant	Created	Deleted
1	AluI	

Experimental services Genomic description: 1032T>A

# SLC1A3 variant T318A

## Overview of the raw variants

Raw variant 1: substitution at 1428

GATTGGGGGGCAGCTTGCCATGTAC A CCGTGACTGTCATTGTTGGCTTACT  
GATTGGGGGGCAGCTTGCCATGTAC G CCGTGACTGTCATTGTTGGCTTACT

[NM\\_004172.4:n.1428A>G](#)

## Affected transcripts - 1

[NM\\_004172.4\(SLC1A3\\_v001\):c.952A>G](#)

## Affected proteins - 1

NM\_004172.4(SLC1A3\_i001):p.(Thr318Ala)

## Reference protein

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTVT	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Protein predicted from variant coding sequence

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYAVT	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Effects on Restriction sites

Raw variant	Created	Deleted
1	BceAI, MwoI BsrGI,	Hpy166II

Experimental services Genomic description: 1428A>G

# SLC1A3 variant A329T

## Overview of the raw variants

Raw variant 1: substitution at 1461

TGTCATTGTTGGCTTACTCATTCAC G CAGTCATCGTCTTGCCACTCCTCTA  
TGTCATTGTTGGCTTACTCATTCAC A CAGTCATCGTCTTGCCACTCCTCTA

[NM\\_004172.4:n.1461G>A](#)

## Affected transcripts - 1

[NM\\_004172.4\(SLC1A3\\_v001\):c.985G>A](#)

## Affected proteins - 1

NM\_004172.4(SLC1A3\_i001):p.(Ala329Thr)

## Reference protein

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTVT	VIVGLLIH <b>AV</b>	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Protein predicted from variant coding sequence

1	MTKSNGEETPK	MGGRMERFQQ	GVKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTVTAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPLI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTVT	VIVGLLIH <b>TV</b>	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIS	ITATAASIGA	AGIPQAGLVT	MVIVLTSVGL	PTDDITLIIA	VDWFLDRLRT
481	TTNVLGDSL	AGIVEHLRSH	ELKNRDVEMG	NSVIEENEMK	KPYQLIAQDN	ETEKPIDSET
541	KM*					

## Effects on Restriction sites

Raw variant	Created	Deleted
1	HpyCH4III	

Experimental services Genomic description: 1461G>A

# SLC1A3 variant V393I

## Overview of the raw variants

Raw variant 1: substitution at 1653

GCGCGTCACCAGATTCGTGCTCCCC G TAGGAGCCACCATTAAACATGGATGG  
GCGCGTCACCAGATTCGTGCTCCCC A TAGGAGCCACCATTAAACATGGATGG

[NM\\_004172.4:n.1653G>A](#)

## Affected transcripts - 1

[NM\\_004172.4\(SLC1A3\\_v001\):c.1177G>A](#)

## Affected proteins - 1

NM\_004172.4(SLC1A3\_i001):p.(Val393Ile)

## Reference protein

```
1  MTKSNGEEPK MGGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV
61  GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI ISSLVTGMAA LDSKASGKMG
121 MRVVVYMTT TIIAVVIGII IVIIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP
181 NLVEACFKQF KTNYEKRSFK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG
241 VNALGLVVFS MCFGFVIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK
301 IVEMEDMGVI GGQLAMYTVT VIVGLLIHAV IVLPLLYFLV TRKNPWVFIG GLLQALITAL
361 GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNNFE
421 LNFGQIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT
481 TTNVLGDSL GAGIVEHL SRH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET
541 KM*
```

## Protein predicted from variant coding sequence

```
1  MTKSNGEEPK MGGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV
61  GTILGFTLRP YRMSYREVKY FSFPGELLMR MLQMLVLPLI ISSLVTGMAA LDSKASGKMG
121 MRVVVYMTT TIIAVVIGII IVIIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP
181 NLVEACFKQF KTNYEKRSFK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG
241 VNALGLVVFS MCFGFVIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK
301 IVEMEDMGVI GGQLAMYTVT VIVGLLIHAV IVLPLLYFLV TRKNPWVFIG GLLQALITAL
361 GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNNFE
421 LNFGQIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLDRLRT
481 TTNVLGDSL GAGIVEHL SRH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET
541 KM*
```

## Effects on Restriction sites

### Raw variant Created Deleted

1

Experimental services Genomic description: 1653G>A

# SLC1A3 variant R454Q alias R499Q

## Overview of the raw variants

Raw variant 1: substitution at 1467

GCTGGGATTGTGGAGCACTTGTAC G ACATGAACTGAAGAACAGAGATGTT  
GCTGGGATTGTGGAGCACTTGTAC A ACATGAACTGAAGAACAGAGATGTT

## Affected transcripts - 1

[XM\\_024446182.1\(SLC1A3\\_v001\):c.1361G>A](#)

## Affected proteins - 1

XM\_024446182.1 (SLC1A3\_i001):p.(Arg454Gln)

## Reference protein

1	MTKSNGEETPK	MGGRMERFQQ	GVRKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTDTVAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPPI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTVT	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIR	DRLRTTTNVL	GDSLGAGIVE	HLS <b>R</b> HELKNR	DVEMGNSVIE	ENEMKKPYQL
481	IAQDNETEKP	IDSETKM*				

## Protein predicted from variant coding sequence

1	MTKSNGEETPK	MGGRMERFQQ	GVRKRTLLAK	KKVQNITKED	VKSYLFRNAF	VLLTDTVAVIV
61	GTILGFTLRP	YRMSYREVKY	FSFPGELLMR	MLQMLVLPPI	ISSLVTGMAA	LDSKASGKMG
121	MRAVVYYMTT	TIIAVVIGII	IVIIIHPGKG	TKENMHREGK	IVRVTAADAF	LDLIRNMFPP
181	NLVEACFKQF	KTNYEKRSFK	VPIQANETLV	GAVINNVSEA	METLTRITEE	LVPVPGSVNG
241	VNALGLVVFS	MCFGFVIGNM	KEQGQALREF	FDSLNEAIMR	LVAVIMWYAP	VGILFLIAGK
301	IVEMEDMGVI	GGQLAMYTVT	VIVGLLIHAV	IVLPLLYFLV	TRKNPWVFIG	GLLQALITAL
361	GTSSSSATLP	ITFKCLEENN	GVDKRVTRFV	LPVGATINMD	GTALYEALAA	IFIAQVNNFE
421	LNFGQIITIR	DRLRTTTNVL	GDSLGAGIVE	HLS <b>Q</b> HELKNR	DVEMGNSVIE	ENEMKKPYQL
481	IAQDNETEKP	IDSETKM*				

## Effects on Restriction sites

Raw variant	Created	Deleted
1		Hpy188III

Experimental services Genomic description: 1467G>A

# CLCN4 variant E281Q (not confirmed in humans)

## Overview of the raw variants

Raw variant 1: substitution at 1241

TGGAGGCGTGCTTTTCAGTCTAGAA G AGGTCAGTTACTACTTTCCCCTGAA  
TGGAGGCGTGCTTTTCAGTCTAGAA C AGGTCAGTTACTACTTTCCCCTGAA

## Affected transcripts - 1

[NM\\_001830.4\(CLCN4\\_v001\):c.841G>C](#)

## Affected proteins - 1

NM\_001830.4(CLCN4\_i001):p.(Glu281Gln)

## Reference protein

1	MVNAGAMSGS	GNLMDFLDEP	FPDVGTYEDF	HTIDWLREKS	RDTDRHRKIT	SKSKESIWEF
61	IKSLDDAWSG	WVVMLLIGLL	AGTLAGVIDL	AVDWMTDLKE	GVCLSAFWYS	HEQCCWTSNE
121	TFEDRDKCP	LWQKSELLV	NQSEGASAYI	LNLYMYILWA	LLFAFLAVSL	VRVFAPYACG
181	SGIPEIKTIL	SGFIIRGYLG	KWTLLIKTVT	LVLVVSSGLS	LGKEGPLVHV	ACCCGNFFSS
241	LFSKYSKNEG	KRREVLASAA	AAGVSVAFGA	PIGGVLFSLE	VSYFFPLKT	LWRSFFAALV
301	AAFTLRSINP	FGNSRLVLFY	VEYHTPWYMA	ELFPFILLGV	FGGLWGTLFI	RCNIAWCRRR
361	KTTRLGKYPV	LEVIVVTAIT	AIIAYPNPYT	RQSTSELISE	LFNDCGALES	SQLCDYINDP
421	NMTRPVDDIP	DRPAGVGvyT	AMWQLALALI	FKIVVTIFTF	GMKIPSGLFI	PSMAVGAIAG
481	RMVGIGVEQL	AYHHHDWIIF	RNWCPRGADC	VTPGLYAMVG	AAACLGGVTR	MTVSLVVIMF
541	ELTGGLYIV	PLMAAAVTSK	WVADAFGKEG	IYEAHIHLNG	YPFLDVKDEF	THRTLATDVM
601	RPRRGEPPLS	VLTQDSMTVE	DVETLIKETD	YNGFPVVVSR	DSERLIGFAQ	RRELILAIKN
661	ARQRQEGIVS	NSIMYFTEEP	PELPANSPHP	LKLRRILNLS	PFTVTDHTPM	ETVVDIFRKL
721	GLRQCLVTRS	GRLGIIITKK	DVLRHMAQMA	NQDPESIMFN	*	

## Protein predicted from variant coding sequence

1	MVNAGAMSGS	GNLMDFLDEP	FPDVGTYEDF	HTIDWLREKS	RDTDRHRKIT	SKSKESIWEF
61	IKSLDDAWSG	WVVMLLIGLL	AGTLAGVIDL	AVDWMTDLKE	GVCLSAFWYS	HEQCCWTSNE
121	TFEDRDKCP	LWQKSELLV	NQSEGASAYI	LNLYMYILWA	LLFAFLAVSL	VRVFAPYACG
181	SGIPEIKTIL	SGFIIRGYLG	KWTLLIKTVT	LVLVVSSGLS	LGKEGPLVHV	ACCCGNFFSS
241	LFSKYSKNEG	KRREVLASAA	AAGVSVAFGA	PIGGVLFSLE	VSYFFPLKT	LWRSFFAALV
301	AAFTLRSINP	FGNSRLVLFY	VEYHTPWYMA	ELFPFILLGV	FGGLWGTLFI	RCNIAWCRRR
361	KTTRLGKYPV	LEVIVVTAIT	AIIAYPNPYT	RQSTSELISE	LFNDCGALES	SQLCDYINDP
421	NMTRPVDDIP	DRPAGVGvyT	AMWQLALALI	FKIVVTIFTF	GMKIPSGLFI	PSMAVGAIAG
481	RMVGIGVEQL	AYHHHDWIIF	RNWCPRGADC	VTPGLYAMVG	AAACLGGVTR	MTVSLVVIMF
541	ELTGGLYIV	PLMAAAVTSK	WVADAFGKEG	IYEAHIHLNG	YPFLDVKDEF	THRTLATDVM
601	RPRRGEPPLS	VLTQDSMTVE	DVETLIKETD	YNGFPVVVSR	DSERLIGFAQ	RRELILAIKN
661	ARQRQEGIVS	NSIMYFTEEP	PELPANSPHP	LKLRRILNLS	PFTVTDHTPM	ETVVDIFRKL
721	GLRQCLVTRS	GRLGIIITKK	DVLRHMAQMA	NQDPESIMFN	*	

## Effects on Restriction sites

Raw variant	Created	Deleted
1	LpnPI	EarI, MboII, MnlI

Experimental services Genomic description: 1241G>C