

TAS2R38: séquence ADN et séquence en acide aminé (allèle sensible (T+))

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1 atgttgactc taactcgcat cgcactgtg tcctatgaag tcaggagtac atttctgttc
61 atttcagtc tggagtttgc agtggggttt ctgaccaatg ccttcgtttt cttgggtgaat
121 ttttgggatg tagtgaagag gcagccactg agcaacagtg attgtgtgct gctgtgtctc
181 agcatcagcc ggcttttctc gcatggactg ctgttcctga gtgctatcca gcttaccac
241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg
301 attgcaaacc aagccaacct ctggcttget gcctgcctca goctgcttta ctgctccaag
361 ctcatcogtt tctctcacac ctctctgatc tgcttggcaa gctgggtctc caggaagatc
421 tcccagatgc tcttgggtat tattctttgc tcttgcactc gcaactgtcct ctgtgtttgg
481 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca
541 aggctcaact ggcagaataa agatctcaat ttattttatt cctttctctt ctgctatctg
601 tggctctgtc ctcccttctt attgtttctg gtttctctg ggatgctgac tgtctccctg
661 ggaaggcaca tgaggacaat gaaggctat accagaaact ctctgtacc cagcctggag
721 gccacatta aagccctcaa gtctcttctc tctttttctt gcttctttgt gatatcatcc
781 tgtgctgctc tcactctctg gccctactg attctgtggc gcgacaaaat aggggtgatg
841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccgtcct gatctcaggc
901 aatgccaagt tgaggagagc tgtgatgacc attctgtctc gggctcagag cagcctgaag
961 gtaagagccg accacaaggc agattcccgg acaactgtgct ga
  
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'Translate'

MLTLTRIRTVSYEVRSTFLFISVLEFAVGFELTNAFVFLVNFWDVVKRQPLSNSDCV
LLCLSISRFLHGLLEFLSAIQQLTHFQKLSEPLNHSYQAIIMLWMIANQANLWLAAC
LSLLYCSKLIRFSHTFLICLASWVSRKISQMLLGIILCSCICTVLCVWCFFSRPHF
TVTTLVLFMNNTRLNWQIKDLNLFYSFLFCYLWSVPPFLLFLVSSGMLTVSLGRHM
RTMKVYTRNSRDPSLEAHIKALKSLVSFFCFFVISSCAAFISVPLLILWRDKIGVM
VCVGIMAACPSGHAAVLISNAKLRRVMTILLWAQSSSLKVRADHKADSR TLC

Nucleotide Position	Nucleotide Change (Taster > Nontaster)	Codon Change (Taster > Nontaster)	Amino Acid Change (Taster > Nontaster)
145	C > G	CCA > GCA	Proline > Alanine
785	C > T	GCT > GTT	Alanine > Valine
886	G > A	GTC > ATC	Valine > Isoleucine

TAS2R38: séquence ADN et séquence en acide aminé (allèle non sensible (t-))

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1 atgttgactc taactcgcat cgcactgtg tcctatgaag tcaggagtac atttctgttc
61 atttcagtc tggagtttgc agtgggggtt ctgaccaatg ccttcgttt cttggtgaat
121 ttttgggatg tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc
181 agcatcagcc ggcttttctt gcatggactg ctgttcctga gtgctatcca gcttaccac
241 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg
301 attgcaaac aagccaacct ctggcttget gcctgcctca goctgcttta ctgctccaag
361 ctcatcogtt tctctcacac ctctctgatc tgcctggcaa gctgggtctc caggaagatc
421 tcccagatgc tcttgggtat tattctttgc tcttgcactc gcaactgtcct ctgtgtttgg
481 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaataca
541 aggctcaact ggcagaataa agatctcaat ttattttatt cctttctctt ctgctatctg
601 tggctctgtc ctcttttctt attgtttctg gtttctctg ggatgctgac tgtctccctg
661 ggaaggcaca tgaggacaat gaaggctat accagaaact ctctgacct cagcctggag
721 gccacatta aagccctcaa gtctcttctc tctttttctt gcttctttgt gatatcatcc
781 tgtttgct tcatctctgt gccctactg attctgtggc gcgacaaaat aggggtgatg
841 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccatcct gatctcaggc
901 aatgccaagt tgaggagagc tgtgatgacc attctgtctc gggctcagag cagcctgaag
961 gtaagagccg accacaaggc agattcccgg acaactgtgct ga
  
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'Translate'

**MLTLTRIRTVSYEVRSTFLFISVLEFAVGFELTNAFVFLVNFWDVVKRQ^ALSNSDCV
 LLCLSISRFLFHGLLEFLSAIQ^LTHFQKLSEPLNHSYQAIIMLWMIANQANLWLAAC
 LSLLYCSKLIRFSHTFLICLASWVSRKISQMLLGIILCSCICTVLCVWCFFSRPHF
 TVTTVLFMNNTRLNWQIKDLNLFYSFLFCYLWSVPPFLLFLVSSGMLTVSLGRHM
 RTMKVYTRNSRDPSLEAHIKALKSLVSFFCFFVISSC^VAFISVPLLILWRDKIGVM
 VCVGIMAACPSGHAA^ILISGNAKLRRVMTILLWAQSSSLKVRADHKADSR^TLIC**

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