C13 Arg – A (29.50%)

>tr|Q4JM47|Q4JM47_HUMAN AGR2 OS=Homo sapiens GN=AGR2 PE=2 SV=1
MSNYTDAESSFSKQEIIRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL
PQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQK**L**
AEQFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNR**LYAYEPADTALL**
LDNMKKALKLLKTEL

C13 Arg – B (23.90%)

>tr|Q4JM47|Q4JM47_HUMAN AGR2 OS=Homo sapiens GN=AGR2 PE=2 SV=1
MSNYTDAESSFSKQEIIRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL
PQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQK**L**
AEQFVLLNLVYETTDKHLSPDGQYVPR**IMFVDPSLTVR**ADITGRYSNR**LYAYEPADTALL**
LDNMKKALKLLKTEL

C13 Lys – A (8.70%)

>tr|Q4JM47|Q4JM47_HUMAN AGR2 OS=Homo sapiens GN=AGR2 PE=2 SV=1
MSNYTDAESSFSKQEIIRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL
PQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKL
AEQFVLLNLVYETTDKHLSPDGQYVPRIMFVDPSLTVRADITGRYSNR**LYAYEPADTALL**
LDNMKKALKLLKTEL

C13 Lys – B (14.40%)

>tr|Q4JM47|Q4JM47_HUMAN AGR2 OS=Homo sapiens GN=AGR2 PE=2 SV=1
MSNYTDAESSFSKQEIIRVAMEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKL
PQTLSRGWGDQLIWTQTYEEALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKL
AEQFVLLNLVYETTDKHLSPDGQYVPR**IMFVDPSLTVR**ADITGRYSNR**LYAYEPADTALL**
LDNMKKALKLLKTEL

Supplementary Figure 6e: Amino acid sequence of AGR2 and its identified peptides.

Figure to show the percentage coverage of the full amino acid sequence of AGR2 that is represented by the peptide sequences identified in all four SILAC experiments. (The amino acids highlighted in red bold represent identified peptides).