C13 Arg – A (31.30%)

>sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

MSK**GPAVGIDLGTTYSCVGVFQHGK**VEIIANDQGNR**TTPSYVAFTDTER**LIGDAAK**NQVA**
MNPTNTVFDAKRLIGR**RFDDAVVQSDMKHWPFMVVNDAGRPK**VQVEYKGETK**SFYPEEVS**
SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATK**DAGTIAGLNVLR**I**INEPTAAA**
IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVK**STAGDTHLGGEDFDNRMVNH**
FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITR**A**
RFEELNADLFRGTLDPVEKALRDAKLDK**SQIHDIVLVGGSTR**IPKIQK**LLQDFFNGK**ELN
KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSK**N**
SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIINWLDKNQTAEKEEFEHQQKELE
KVCNPIITKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD

C13 Arg – B (25.90%)

>sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

MSK**GPAVGIDLGTTYSCVGVFQHGK**VEIIANDQGNR**TTPSYVAFTDTER**LIGDAAK**NQVA**
MNPTNTVFDAKRLIGRRFDDAVVQSDMK**HWPFMVVNDAGRPK**VQVEYKGETK**SFYPEEVS**
SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATK**DAGTIAGLNVLR**I**INEPTAAA**
IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH
FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITR**A**
RFEELNADLFRGTLDPVEKALRDAKLDK**SQIHDIVLVGGSTR**IPKIQK**LLQDFFNGK**ELN
KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSK**N**
SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIINWLDKNQTAEKEEFEHQQKELE
KVCNPIITKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD

C13 Lys – A (21.60%)

>sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNR**TTPSYVAFTDTER**LIGDAAK**NQVA**
MNPTNTVFDAKRLIGRRFDDAVVQSDMK**HWPFMVVNDAGRPK**VQVEYKGETK**SFYPEEVS**
SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRI**INEPTAAA**
IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNR**MVNH**
FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITR**A**
RFEELNADLFRGTLDPVEKALRDAKLDK**SQIHDIVLVGGSTR**IPKIQK**LLQDFFNGK**ELN
KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSK**N**
SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIINWLDKNQTAEKEEFEHQQKELE
KVCNPIITKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD

C13 Lys – B (24.70%)

>sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

MSKGPAVGIDLGTTYSCVGVFQHGKVEIIANDQGNR**TTPSYVAFTDTER**LIGDAAK**NQVA**
MNPTNTVFDAKRLIGRRFDDAVVQSDMK**HWPFMVVNDAGRPK**VQVEYKGETK**SFYPEEVS**
SMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRI**INEPTAAA**
IAYGLDKKVGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNH
FIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITR**A**
RFEELNADLFRGTLDPVEKALRDAKLDK**SQIHDIVLVGGSTR**IPKIQK**LLQDFFNGK**ELN
KSINPDEAVAYGAAVQAAILSGDKSENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTI
PTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDI
DANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSK**N**
SLESYAFNMKATVEDEKLQGKINDEDKQKILDKCNEIINWLDKNQTAEKEEFEHQQKELE
KVCNPIITKLYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD

Supplementary Figure 6a: Amino acid sequence of HSC70 and its identified peptides.

Figure to show the percentage coverage of the full amino acid sequence of HSC70 that is represented by the peptide sequences identified in all four SILAC experiments. (The amino acids highlighted in red bold represent identified peptides).