**Acetylation sites in MnSOD**

**K53: QLHHSKHHAAY**

**K68: NVTEEKYQEAL**

**K89: LQPALKFNGGG**

**K122: LLEAIKRDFGS**

H MLSRAVCGTSRQLAPVLGYLGSRQKHSLPDLPYDYGALEPHINAQIM**QLHHSKHHAAY**VN

M MLCRAACSTGRRLGPVAGAAGSRHKHSLPDLPYDYGALEPHINAQIM**QLHHSKHHAAY**VN

Rattus MLCRAACSAGRRLGPAASTAGSRHKHSLPDLPYDYGALEPHINAQIM**QLHHSKHHATY**VN

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H NL**NVTEEKYQEAL**AKGDVTAQIA**LQPALKFNGGG**HINHSIFWTNLSPNGGGEPKGE**LLEA**

M NLNATEEKYHEALAKGDVTTQVA**LQPALKFNGGG**HINHTIFWTNLSPKGGGEPKGE**LLEA**

Rattus NLNVTEEKYHEALAKGDVTTQVA**LQPALKFNGGG**HINHSIFWTNLSPKGGGEPKGE**LLEA**

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H **IKRDFGS**FDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPLL

M **IKRDFGS**FEKFKEKLTAVSVGVQGSGWGWLGFNKEQGRLQIAACSNQDPLQGTTGLIPLL

Rattus **IKRDFGS**FEKFKEKLTAVSVGVQGSGWGWLGFNKEQGRLQIAACSNQDPLQGTTGLIPLL

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H GIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK

M GIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYTACKK

Rattus GIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVSQRYIVCKK

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The p53 sequence I have in the lab is 18 amino acids long.

Pep1: NH2-KKGQSTSRHK(KAc)LMFKTEG-COOH

Pep1c: NH2-KKGQSTSRHKKLMFKTEG-COOH

Since I am detecting the peptide at 214 nm (peptide bond) and p53 detectability is OK, we should have at-least 18 amino acids peptide or more.

We can add couple of extra W, Y, or F to increase the detectability at 280 nm. While looking at the alignment, choosing peptide length which will encompass W will be impractical (too far from acetylated sites, see yellow highlighted W in alignment. Or we can just add 2Ws at the end of 18 aa long peptide but I am not sure if the detectability of this peptide at 280 will be better than peptide without W at 214 nm.

In case of Y: K53, K68 peptide already have one Y in each, if we get 18 aa of these peptides, the detectability may be similar to p53 as p53 has one F within the sequence.

K89, K122 has one F in each and if we decide to get 18 mer peptide, the detectability again will be similar to p53, at 214 nm.