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ERRATUM

Autoacetylation of Purified Calreticulin Transacetylase Utilizing Acetoxycoumarin as the Acetyl Group Donor

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In the original paper, the figures were incorrectly labeled. The figures and their corresponding legends should appear as follows.

Figures 1, 2, 3, 4, 5 and 6

The online version of the original article can be found at http://dx.doi.org/10.1007/s12010-008-8357-2

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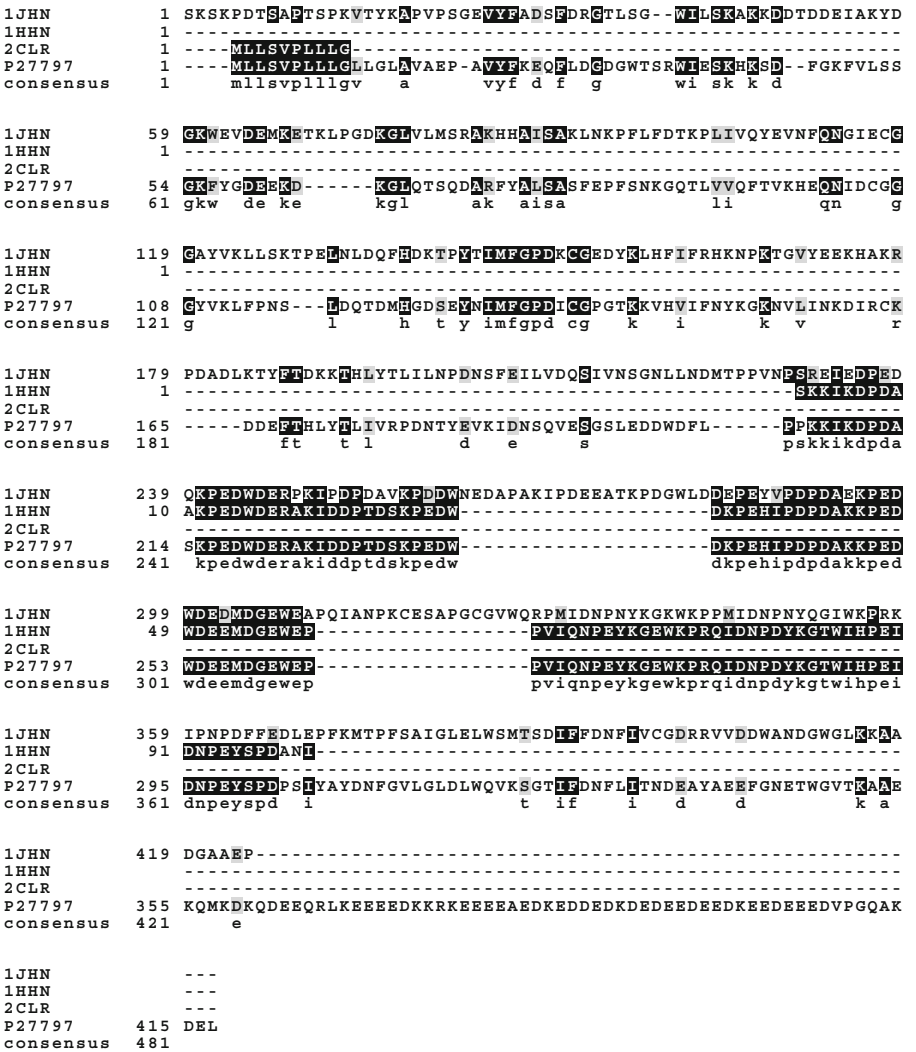

Fig. 1 Sequences of calnexin (PDB ID 1JHN), CR P-domain (PDB ID 1HHN), CR signal peptide sequence (PDB ID 2CLR) and human CR sequence swissprot accession no. P27797 are aligned using InsightII/ Homology and displayed by BOXSHADE program (http://www.ch.embnet.org/software/BOX_form.html). Shaded residues denote identity (*Black*) or close similarity (*Gray*) between sequences

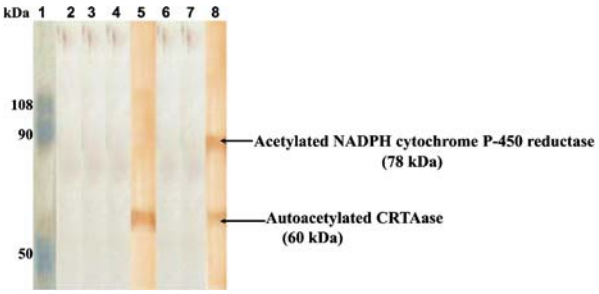

Fig. 2 Effect of Ca^{2+} on CRTAase catalyzed acetylation of NADPH cytochrome P-450 reductase by DAMC. Lane *1* Prestained molecular weight markers; lane *2* CRTAase +DMSO; lane *3* NADPH cytochrome P-450 reductase + DAMC; lane *4* CRTAase + DMSO + $CaCl_2$ (5 μM) +NADPH cytochrome P-450 reductase; lane *5* CRTAase + DAMC; lane *6* CRTAase + $CaCl_2$ (5 μM) + DAMC; lane *7* CRTAase + $CaCl_2$ (5 μM) + DAMC+ NADPH cytochrome P-450 reductase; lane *8* CRTAase + DAMC + NADPH cytochrome P-450 reductase

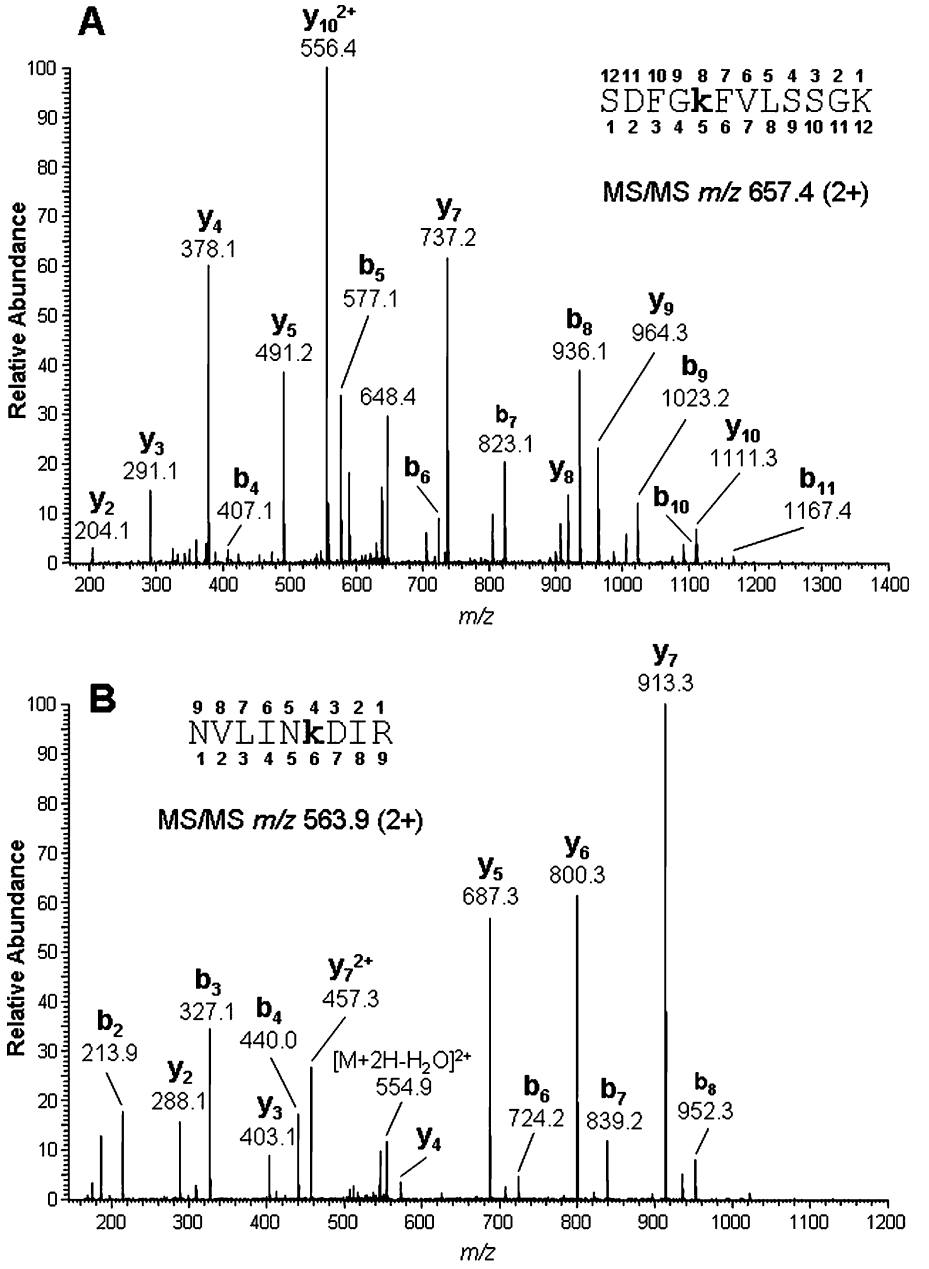

Fig. 3 Tandem mass spectra of selected CR tryptic peptides containing acetyl-lysine. residue numbers shown in *boldface* type above and below the peptide sequences indicate detected collision-induced dissociation fragments for y-series (C-terminal) and b-series (N-terminal) ions, respectively. (**a**) Sequence SDFGkFVLSSGK (Corresponding to residues 45–55 of CR) observed in the tryptic digest of CR, the ion at m/z 648.4 was generated by loss of water from doubly charged precursor; (**b**) sequence NVLINkDIR. (Corresponding to residues 154–162 of CR) peak at m/z 554.9 represents the ion due to loss of water in the doubly charged precursor; (**c**) sequence kIKDPDASKPEDWDER (Corresponding to residues 207–222 of CR) observed in the tryptic digest of CR. MS/MS m/z 657.9 (3+). *Asterisk* corresponds to internal fragments

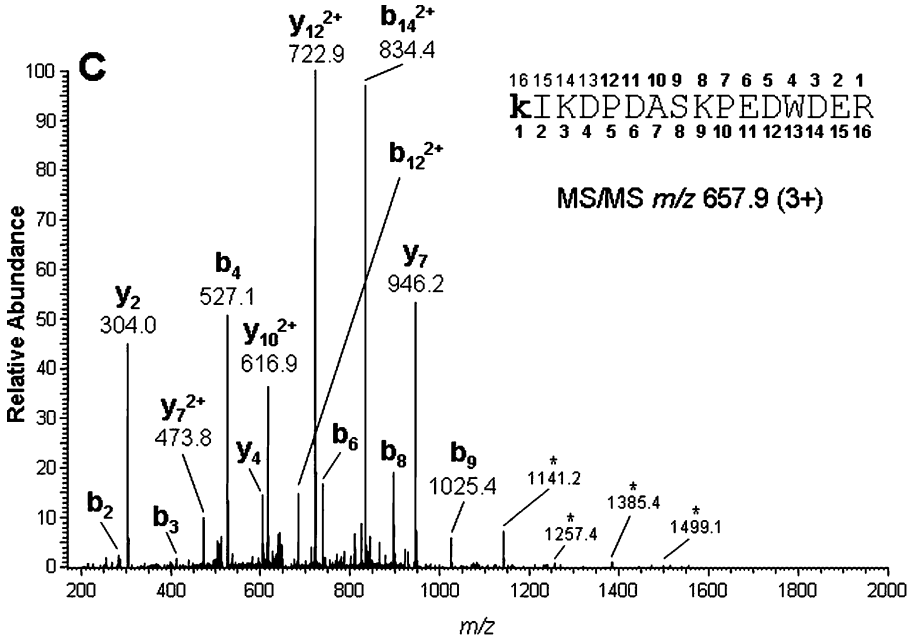

Fig. 3 (continued)

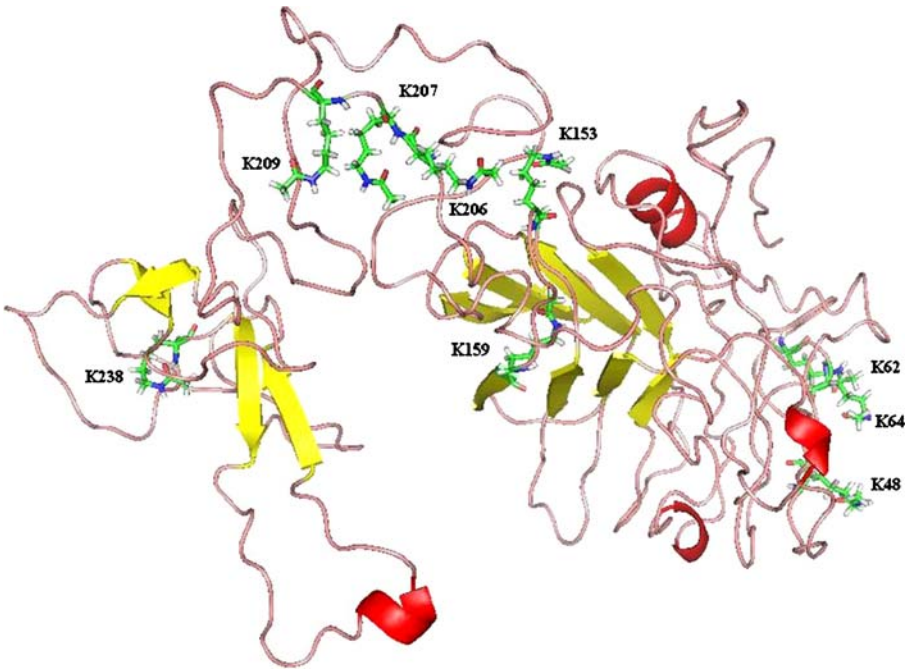

Fig. 4 The predicted structure of CR is represented in Kabsch–Sander secondary structure with α-helices in *red* and β-sheets in *yellow*. The modified lysine residues are in stick representation with standard atom colors. The figure was prepared using Pymol software [43]

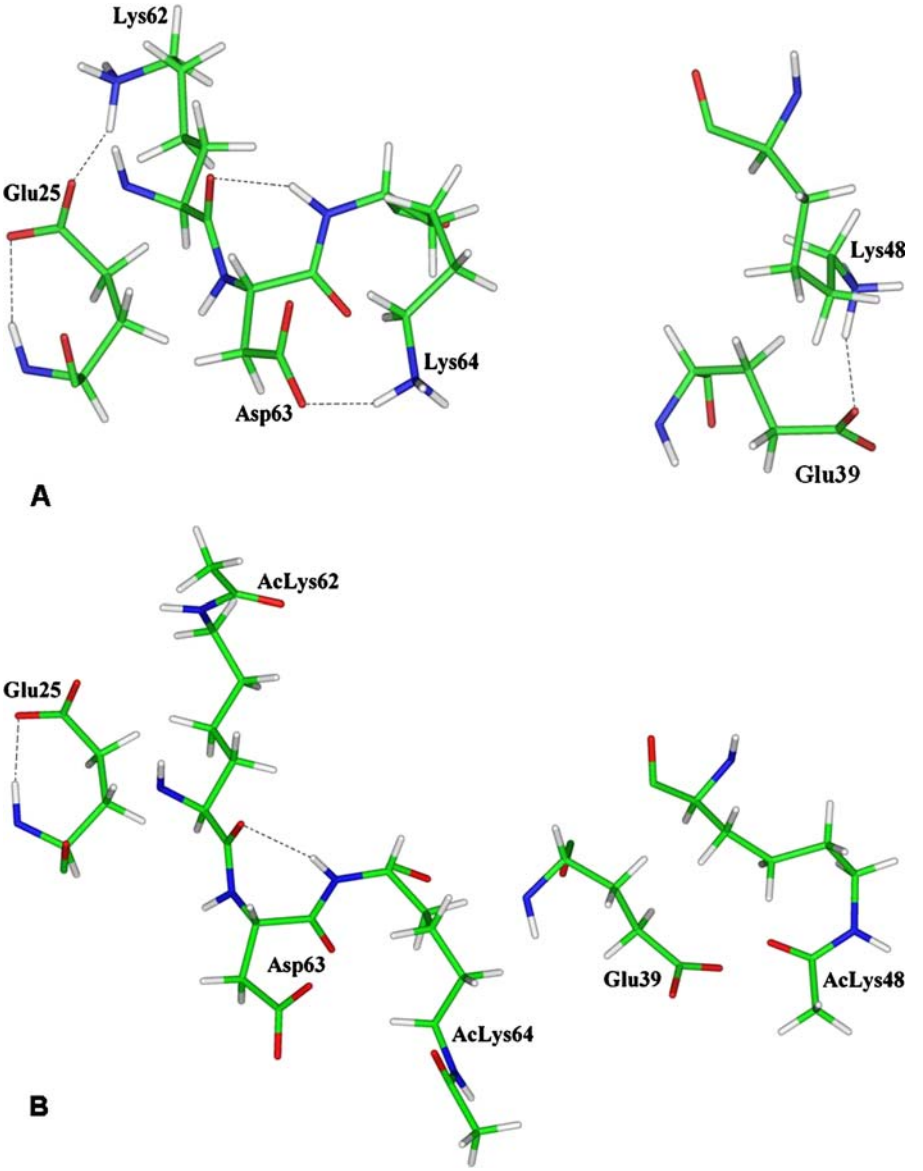

Fig. 5 Comparison of intermolecular H-bonds (*dotted lines*) of lysines with glutamate and aspartate residues in non-acetylated (**a**) and acetylated (**b**) CR, after energy minimization. The amino acid residues are rendered in *sticks with standard atom colors*. Loss of H-bonds between Lys-62 and Glu-25, Lys-64 and Asp-63 also in Lys-48 and Glu-39 was observed due to neutralization of the positively charged lysine residue by acetylation. The acetylated lysine residues of N-domain are *highlighted* here. The figure was generated using InsightII program [26]

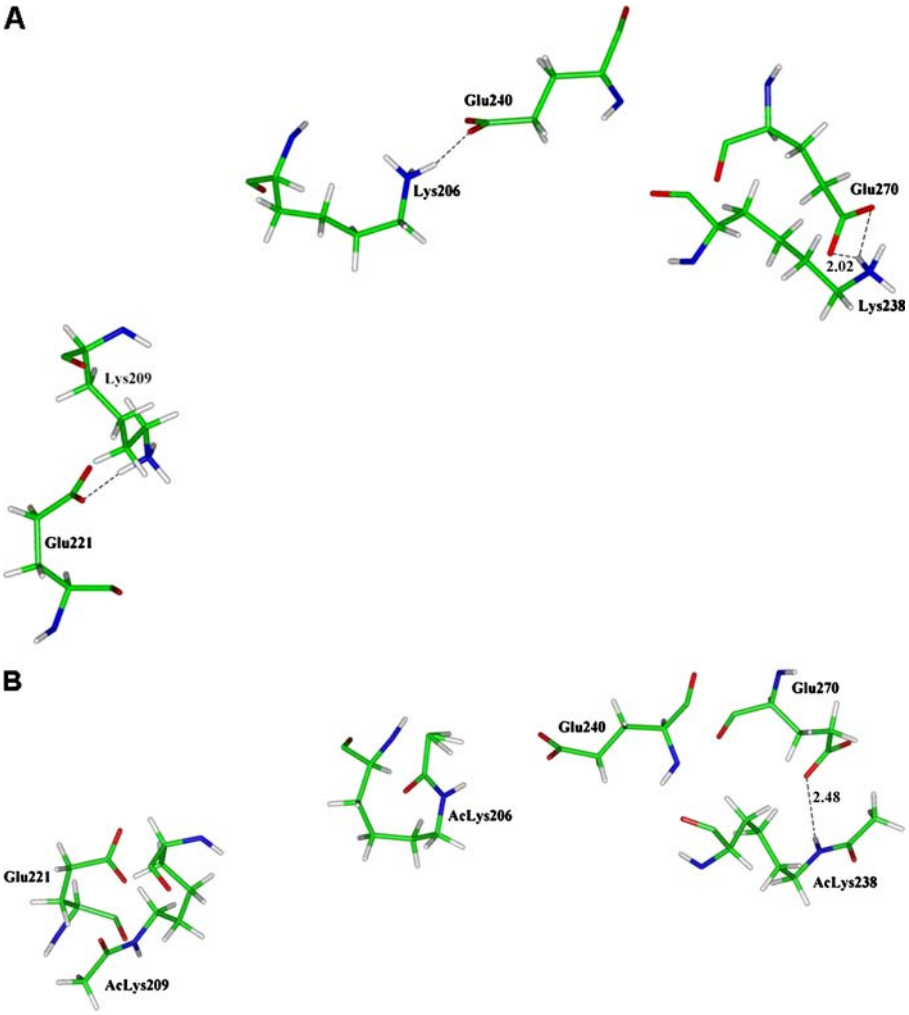

Fig. 6 Comparison of non-acetylated (**a**) and acetylated (**b**) CR P-domain lysines. Loss of H-bonds between Lys-206 and Glu-240, Lys-238 and Glu-270 as well as Lys-209 and Glu-221 was observed due to *N*-ε-acetylation of lysine residues. Also, increase in the intermolecular distances between acetyl-lysine (AcLys-238) and glutamate (Glu-270) is observed. The amino acid residues are rendered in *sticks with standard atom colors*. The amino acid residues rendered in sticks with standard atom colors and figure is realized using InsightII program [26]