Supplementary Materials

Molecular Characterization of the Native (Non-Linked) CD160–HVEM Protein Complex Revealed by Initial Crystallographic Analysis

Simona Lenhartová [1], Marek Nemčovič [2], Radka Šebová [1], Mário Benko [1], Dirk M. Zajonc [3,4] and Ivana Nemčovičová [1,*]

[1] Biomedical Research Center, Slovak Academy of Sciences, Dúbravská cesta 9, Bratislava 84505, Slovakia; virusims@savba.sk (S.L.); virurama@savba.sk (R.Š.); virubenq@savba.sk (M.B.)
[2] Institute of Chemistry, Slovak Academy of Sciences, Dúbravská cesta 9, Bratislava 84538, Slovakia; chemnem@savba.sk
[3] Division of Immune Regulation, La Jolla Institute for Immunology, 9420 Athena Circle, La Jolla, CA 92037, USA; dirk.zajonc@pfizer.com
[4] Current affiliation: Cancer Immunology Discovery, Pfizer Inc., 10777 Science Center Dr., San Diego, CA 92121, USA
* Correspondence: viruivka@savba.sk

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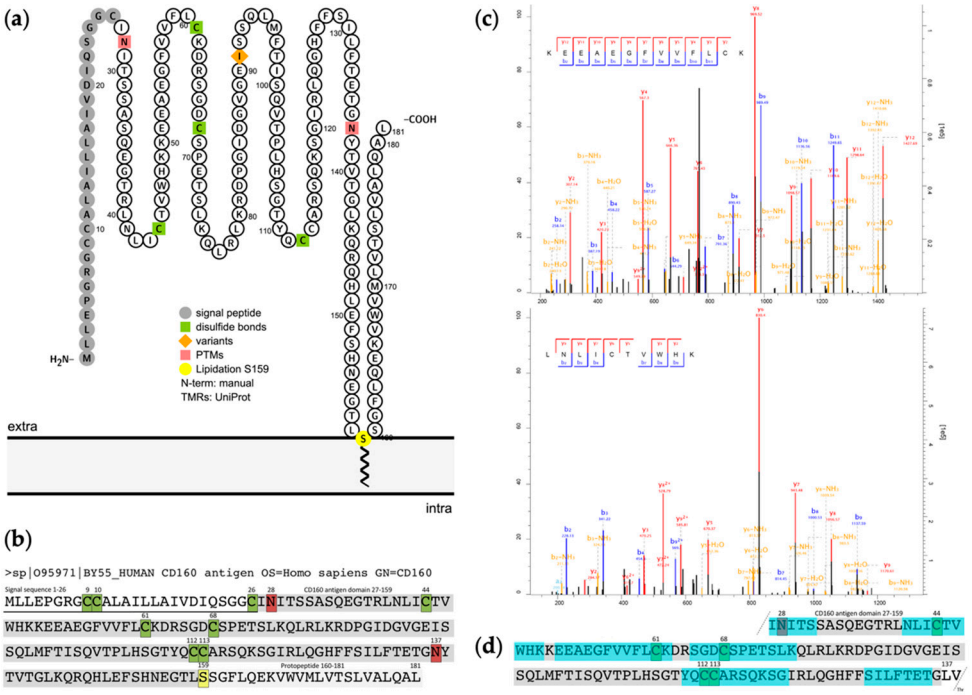

Figure S1. CD160 peptide identification by mass spectrometry. Secondary structural elements are highlighted within the amino acid sequence of CD160 (**a**) visualized by Protter [20] (an open-source tool for interactive integration and visualization of annotated and predicted protein sequence features together with experimental proteomic evidence). CD160 protein sequence generated by UniProt analysis (**b**) deduced from the cDNA sequence. The positions of the confirmed N-glycosylation sites (red), cysteine residues (green) and lipidation (yellow) are indicated with the same color code (**a,b,d**). Two representative peptides of the amino acid sequence analyses by tandem mass spectrometry of the purified CD160 trimer are shown (**c**). All identified peptides within the CD160 sequence are highlighted in cyan (**d**).