

# Comparative analysis of carbon distribution and hydropathy plot

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## Abstract

The hydrophobic interactions are the dominant force that determines the biomolecular association. Carbon is the only element that contributes towards the hydrophobic interactions. The carbon distribution along protein is studied and compared with hydropathy plot. The study is carried out for human erythrocyte glucose transporter protein. Carbon distribution profile clearly explain the where there is maximum hydrophilicity or hydrophobicity. The carbon distribution profile can be an alternative method to hydropathy plot.

**Keywords:** Carbon distribution; sequence analysis; hydropathy plot; transporter protein.

## Introduction

Proteins are large organic compounds made of amino acid arranged in a linear fashion. The side chain of these amino acids are chemically different from one another in some respect can be classified broadly in two ways hydrophobic and hydrophilic. Carbon content in these side chains makes the amino acid different. All Proteins are constructed from linear sequences of smaller molecules called amino acids. Proteins also fold up to form particular three dimensional shapes, which give them their specific chemical functionality. It is easily demonstrable that the linear amino acid sequence completely specifies the three dimensional structure of most proteins. In addition a protein's three-dimensional structure is not fixed; many proteins move and flex in constrained ways and that can have a significant role in their biochemical function. Also some proteins bind to other groups of atoms that are required for them to function (P.Baudouin-Cornu *et al.*, 2001). A widely accepted principle is that protein evolution is mainly determined by constraints on activity, specificity, folding and stability. The lowest level of biological organization is that of atoms in biological macromolecules. Specifically, individual amino acids and whole proteins can vary greatly in their content of carbon (J.G.Bragg and A.Wagner, 2007). Hydrophobic and hydrophilic residues play a major role in protein folding and function (R.Schwartz *et al.*, 2001). The distribution hydrophobic and hydrophilic residue along polypeptide chain is critical feature of the ability of biologically evolved amino acid sequence to direct the folding of proteins (D.J.Brooks *et al.*, 2002). Carbon is the only element contributes towards this, which is dominated by large hydrophobic residues. Protein prefers to have 27% of large hydrophobic residues (and 31.44% of carbon) in its structure for stability. This paper analyzes of carbon content in Human (Hs) Erythrocyte Glucose Transporter and compare with hydropathy plot.

## Materials and Methods

To understand carbon distribution in proteins, the Erythrocyte Glucose Transporter protein of Homo sapiens is selected here. It's a facilitative glucose transporter and this isoform may be responsible for constitutive or basal glucose uptake. It has very broad substrate specificity and can transport a wide range of aldoses including both pentoses and hexoses. The protein sequence is downloaded from the protein sequence database (SWISS PROT). The home made ATOMSCAN program written in C is used for scanning the carbon distribution along the protein sequences. The outer and inner window lengths are taken as 777 and 77 atoms respectively. The carbon distribution are shown in the figure [1] and discussed. The hydropathy plot is obtained from online using PROTSSCALE program online ([www.expasy.ch/tools/protscale.html](http://www.expasy.ch/tools/protscale.html)).

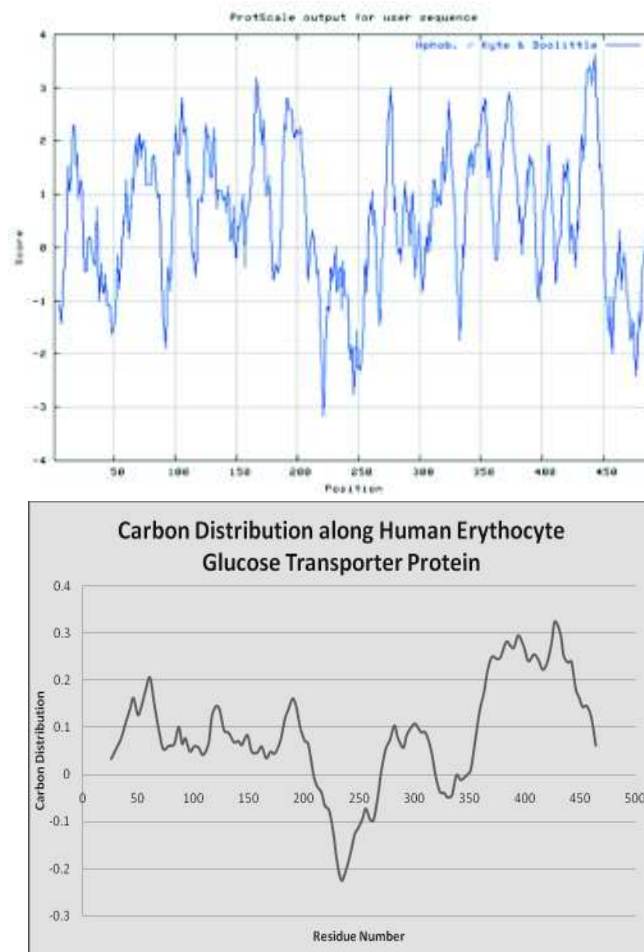


Fig 1: Hydropathy plot and carbon distribution profile are compared

## Result and discussion

Distribution of Carbon usage in human erythrocyte glucose transporter protein the averaged number of carbon atoms found in residue side chains for each protein was calculated, and the totality of all these frequencies was described by X Y scatter with smooth lines. The study is carried out for human erythrocyte glucose transporter .and it's expressed at variable levels in many human tissues and defects in SLC2A1 (solute carrier family 2 (facilitated glucose transporter), member 1) are the cause of autosomal dominant GLUT1 (glucose transporter type 1) deficiency syndrome (David M. Blodgett et al., 2008) .This disease causes a defect in glucose transport across the blood-brain barrier. It is characterized by infantile seizures, delayed development, and acquired microcephaly .This method is able to identify the active sites (carbon rich portion) occurs between 350 and 464. This is not revealed by hydropathy plot as seen in the figure. So carbon distribution plot reveal the hydrophobicity very well. So this can be an alternative plot for hydropathy plot.

The carbon distribution profile of protein in human erythrocyte glucose transporter is studied. The protein maintains a fair amount of carbon content all along the sequence to be a membrane protein. Between 209 and 267 week hydrophilicity is observed Fig. [1].

## Conclusion

This paper analyzes the carbon content in human Erythrocyte Glucose Transporter Protein and compare with hydropathy plot. The carbon distribution profile of the protein is presented here. Carbon distribution profile clearly locates the hydrophobic, hydrophilic and active sites. Here in human transporter protein the active site occurs between 350 and 464. Between 209 and 270 week hydrophilicity is observed. This method predicts the location of hydrophobic and hydrophilic region better over the hydropathy plot. Carbon distribution profile can be an alternative method for hydropathy plot.

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[www.expasy.ch/tools/protscale.html](http://www.expasy.ch/tools/protscale.html)

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Hi (2.5 - 25 kb),	PCR marker, Customized
Restriction digests of	ladders
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