

Cytoglobin

~2000



Adenosine deaminase

896



重要な残基は保存され重要性の低い部分はいろいろな残基で置き換えられてゆく

ブライスキャニオン アメリカ ユタ州



長い年月をかけ、岩の固いところを残して、侵食された

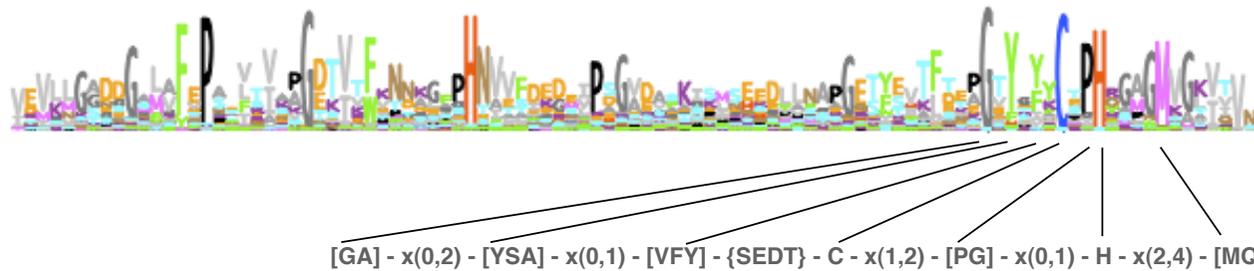


変異しにくいところ = 機能に重要 = 固い

固くない部分はランダムな配列に置き換えられてゆく

Plastocyanin

489



文字の大きい部分は一完全保存 =
PROSITE シグネチャーに対応する

マルチプルアラインメントから ロゴを作るサイト

<http://weblogo.berkeley.edu/>

WEBLOGO

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[Version 2.8.2 \(2005-09-08\)](#)

(⇒ [WebLogo 3](#))

References

[Crooks GE, Hon G, Chandonia JM, Brenner SE](#) WebLogo: A sequence logo generator, *Genome Research*, 14:1188-1190, (2004) [[Full Text](#)]

Schneider TD, Stephens RM. 1990. [Sequence Logos: A New Way to Display Consensus Sequences](#), *Nucleic Acids Res.* 18:6097-6100

Introduction

[WebLogo](#) is a web based application designed to make the [generation](#) of sequence logos as easy and painless as possible. Click [here](#) to create your own sequence logos.

[Sequence logos](#) are a graphical representation of an amino acid or nucleic acid multiple sequence alignment developed by [Tom Schneider](#) and [Mike Stephens](#). Each logo consists of stacks of symbols, one stack for each position in the sequence. The overall height of the stack indicates the sequence conservation at that position, while the height of symbols within the stack indicates the relative frequency of each amino or nucleic acid at that position. In general, a sequence logo provides a richer and more precise description of, for example, a binding site, than would a consensus sequence.

