



Report generated by: CLCuser

Sequence name: Q6WN29

Length: 147 aa

Organism: Alouatta belzebul (black-and-red howler monkey)

Description: Hemoglobin beta subunit (Hemoglobin beta chain) (Beta-globin).

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# 1. Protein statistics

## 1.1 Sequence information

Sequence type	Protein
Length	147 aa
Organism	Alouatta belzebul (black-and-red howler monkey)
Locus	Q6WN29
Description	Hemoglobin beta subunit (Hemoglobin beta chain) (Beta-globin).
Modification Date	24-JAN-2006
Weight	16,057 kDa
Isoelectric point	7,11
Aliphatic index	94,15

## 1.2 Half-life

N-terminal aa	Half-life mammals	Half-life yeast	Half-life E.Coli
Methionine	30 hours	>20 hours	>10 hours

## 1.3 Extinction coefficient

Conditions	Extinction coefficient at 280nm	Absorption at 280nm 0.1% (=1 g/l)
Non-reduced cysteines	15.340	0,955
Reduced cysteines	15.220	0,948

## 1.4 Atomic composition

Atom	Count	Frequency
sulphur (S)	4	0,002

Atom	Count	Frequency
oxygen (O)	203	0,090
hydrogen (H)	1.129	0,499
carbon (C)	729	0,322
nitrogen (N)	199	0,088

## 1.5 Count of hydrophobic and hydrophilic residues

Hydrophobicity	Count	Frequency
Hydrophobic (A,F,G,I,L,M,P,V,W)	82	0,558
Hydrophil (C,N,Q,S,T,Y)	27	0,184
Other	38	0,259

## 1.6 Count of charged residues

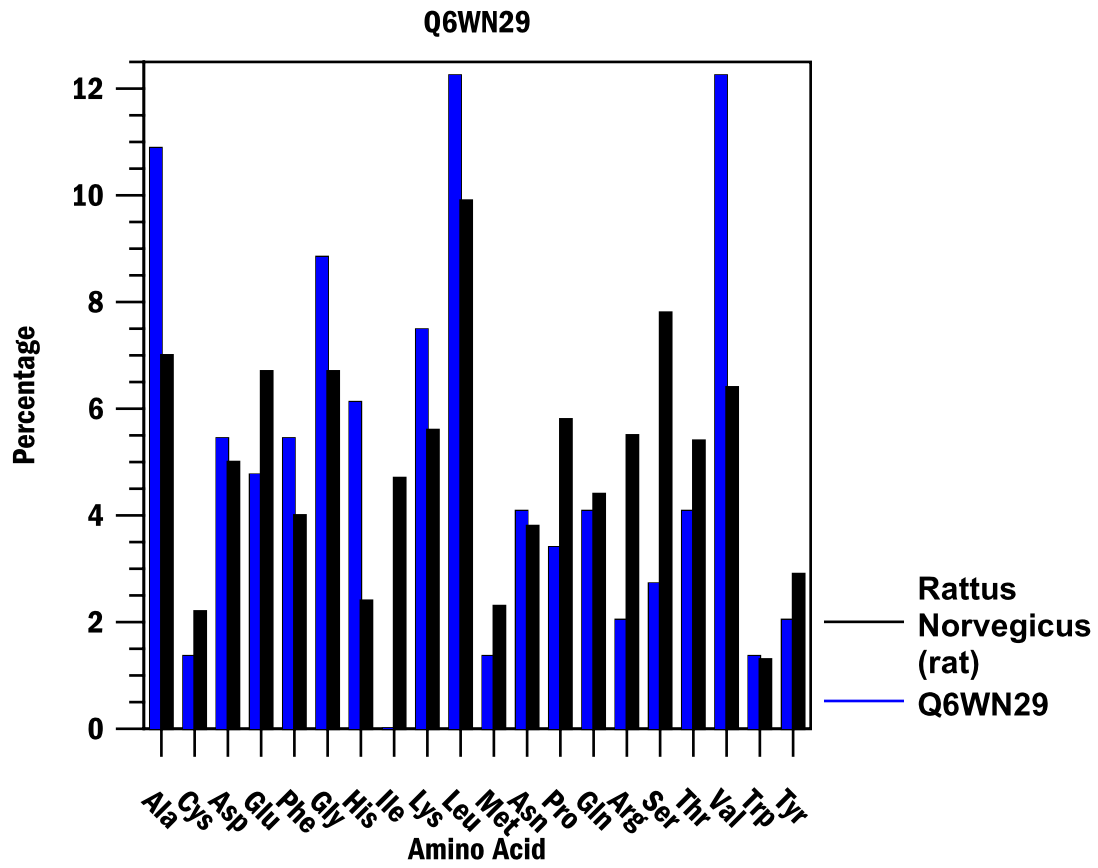
Charge Type	Count	Frequency
Negatively Charged (D & E)	15	0,102
Positively Charged (R & K)	14	0,095
Other	118	0,803

## 1.7 Amino acid distribution table

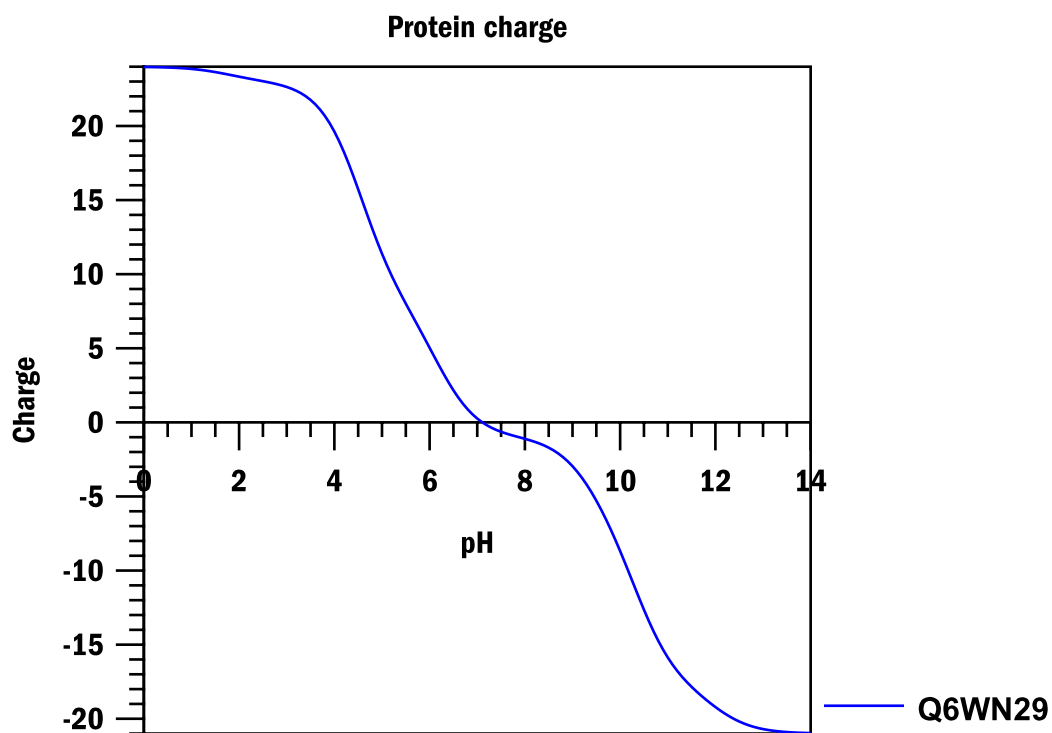
Amino acid	Count	Frequency	Freq. in Rattus Norvegicus (rat)
Alanine (A)	16	0,109	0,070
Cysteine (C)	2	0,014	0,022
Aspartic Acid (D)	8	0,054	0,050
Glutamic Acid (E)	7	0,048	0,067
Phenylalanine (F)	8	0,054	0,040
Glycine (G)	13	0,088	0,067
Histidine (H)	9	0,061	0,024
Isoleucine (I)	0	0,000	0,047

Amino acid	Count	Frequency	Freq. in Rattus Norvegicus (rat)
Lysine (K)	11	0,075	0,056
Leucine (L)	18	0,122	0,099
Methionine (M)	2	0,014	0,023
Asparagine (N)	6	0,041	0,038
Proline (P)	5	0,034	0,058
Glutamine (Q)	6	0,041	0,044
Arginine (R)	3	0,020	0,055
Serine (S)	4	0,027	0,078
Threonine (T)	6	0,041	0,054
Valine (V)	18	0,122	0,064
Tryptophan (W)	2	0,014	0,013
Tyrosine (Y)	3	0,020	0,029

## 1.8 Amino acid distribution histogram

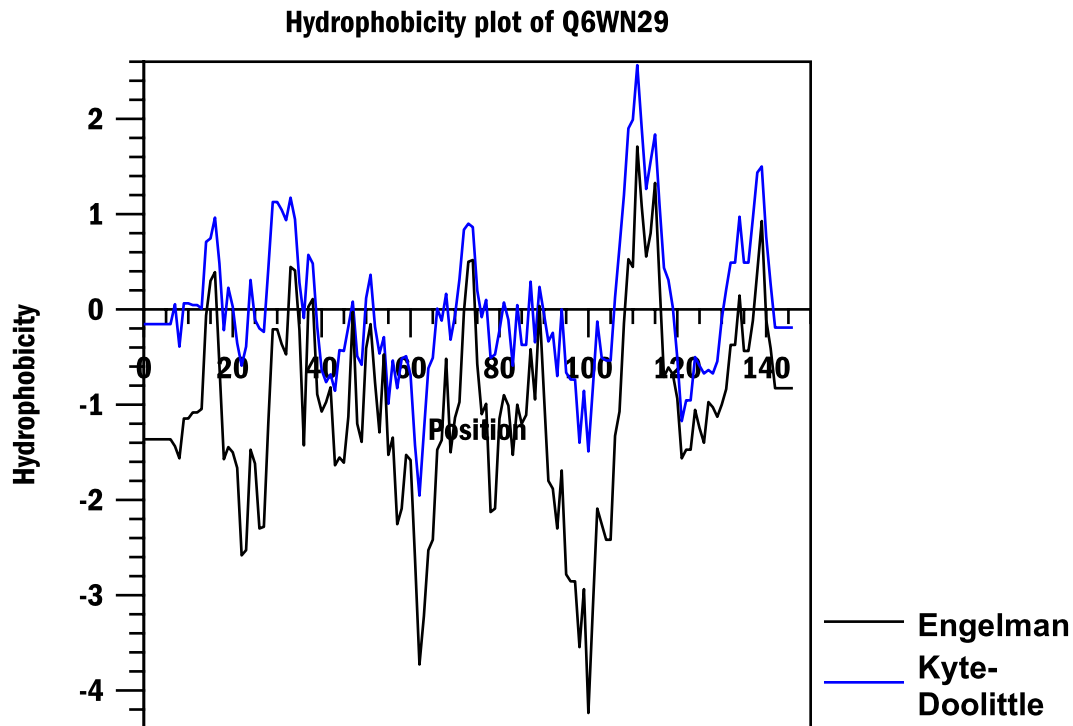


## 2. Electrical charge as a function of pH



Parameters: Selected sequences: = Q6WN29

### 3. Plot of local Hydrophathy



Parameters: Selected sequence: = Q6WN29 Window size: = 11 Applied scale = Kyte-Doolittle Applied scale = Engelman

Kyte-Doolittle scale:

Kyte-Doolittle hydrophathy plots provide information about the possible structure of a protein, and can identify features such as transmembrane or surface regions. For surface region discovery in a globular protein, a window size of 9 is considered optimal, marked negative dips in the graph indicate possible surface regions. A region size of 19 is considered optimal for the discovery of transmembrane regions which can be identified by peaks above a value of 1.8.

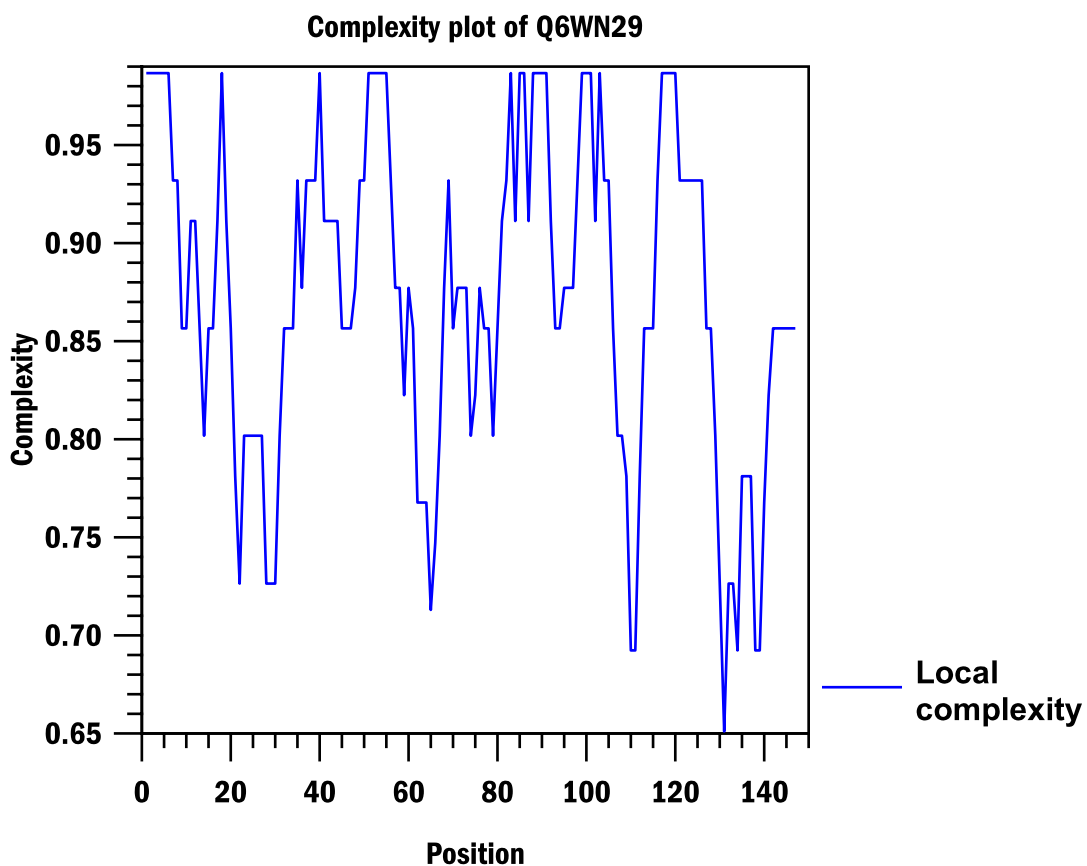
Kyte, J. and Doolittle, R. (1982). A simple method for displaying the hydrophobic character of a protein. *J. Mol. Biol.* 157: 105-132.

Engelman scale:

The Engelman hydrophobicity scale, also known as the GES-scale, is another scale which can be used for prediction of protein hydrophobicity. As the Kyte-Doolittle scale, this scale is useful for prediction transmembrane regions in proteins.

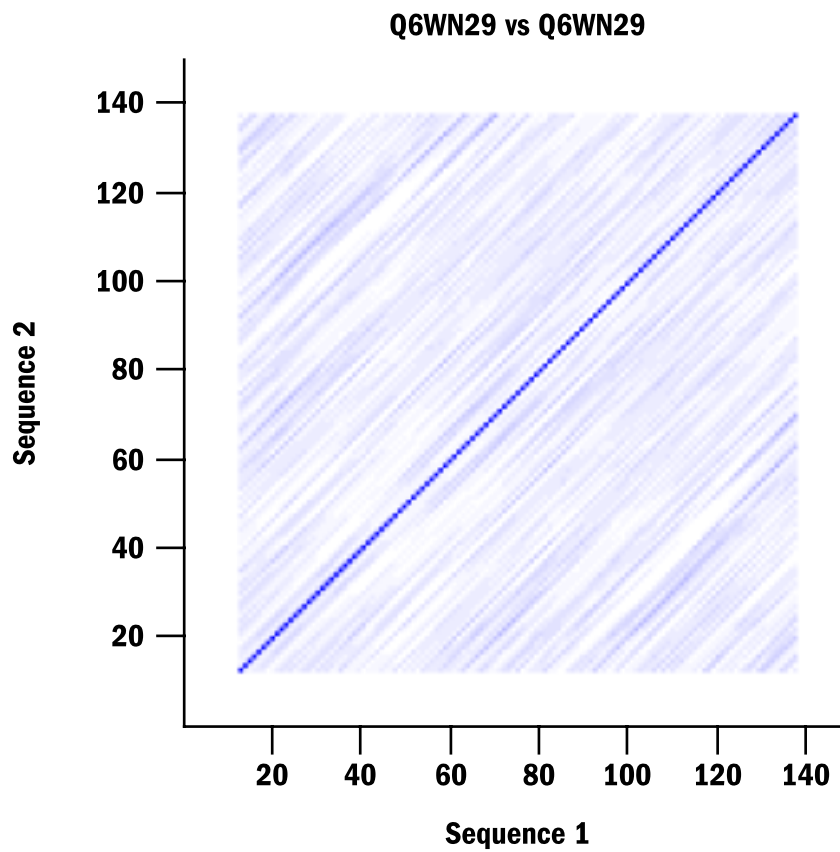
Engelman, D.M., Steitz, T.A., and Goldman, A. (1986). Identifying nonpolar transbilayer helices in amino acid sequences of membrane proteins. *Annu. Rev. Biophys. Chem.* 15: 321-353.

## 4. Plot of local sequence complexity



Parameters: Selected sequence: = Q6WN29 Window size: = 11  
Y-axis shows the K2 measure of local sequence complexity, as defined in (Wootton and Federhen, 1993, *Computers Chem.*, Vol. 17, pp. 149-163)

## 5. Dot-plot of the sequence against itself



Parameters: Selected sequences: = Q6WN29 Window length: = 25 Correction model: = None