

STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN S AND AGGREGATION

Created with Jmol; Jmol: an open-source Java
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SICKLE CELL ANAEMIA
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SICKLE CELL ANAEMIA AND THALASSEMIA

STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN S

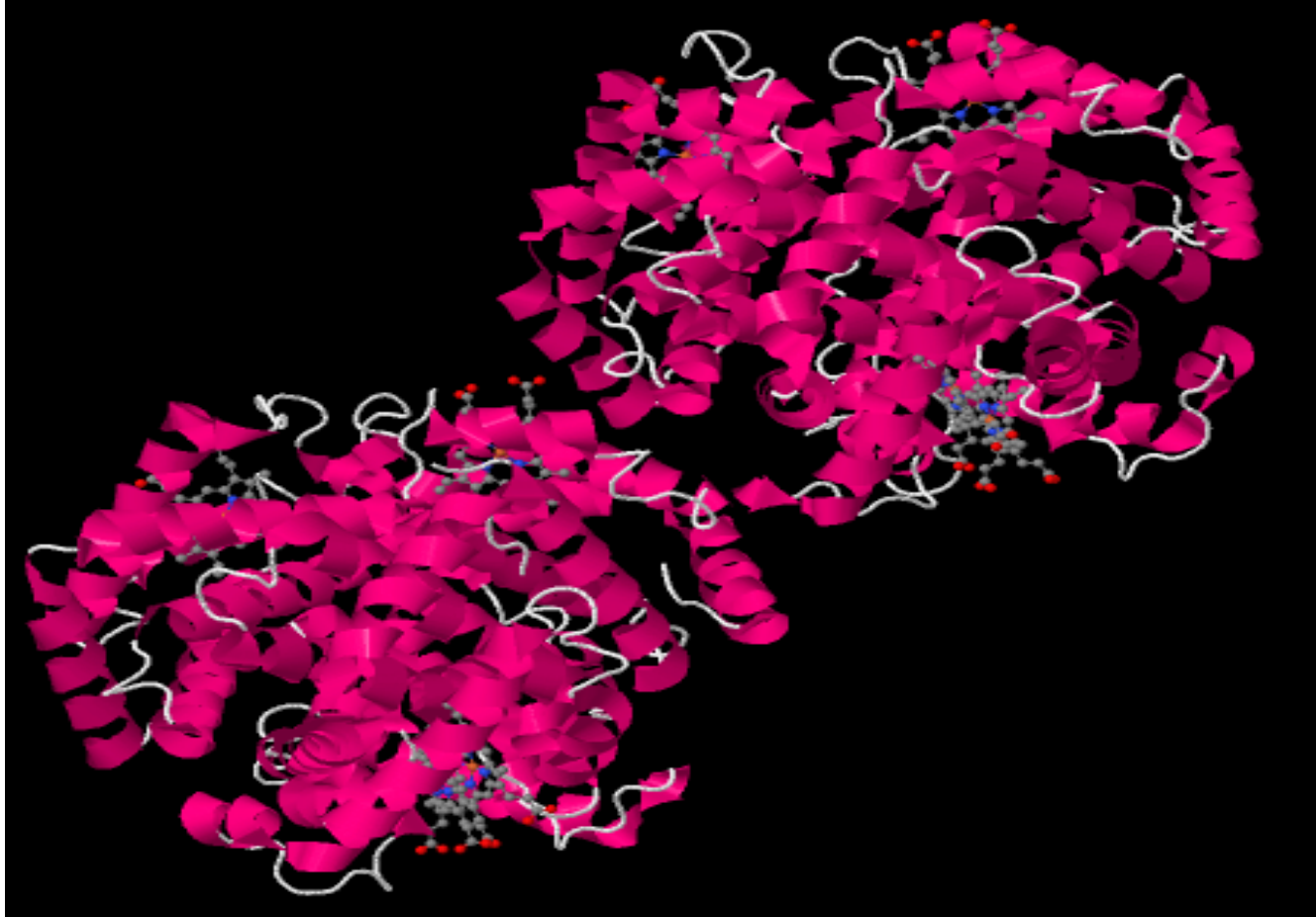


Image of 2HBS (The high resolution crystal structure of deoxyhemoglobin S.

Harrington DJ, Adachi K, Royer WE Jr. J Mol Biol. 1997 Sep 26;272(3):398-407)

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The structure of human deoxyhaemoglobin S. The structure of the asymmetric unit is shown representing the interaction of two deoxyhaemoglobin tetramers as would occur in sickle cell disorder.

Jmol settings:

Display style: cartoon

Colour: secondary structure

STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN S

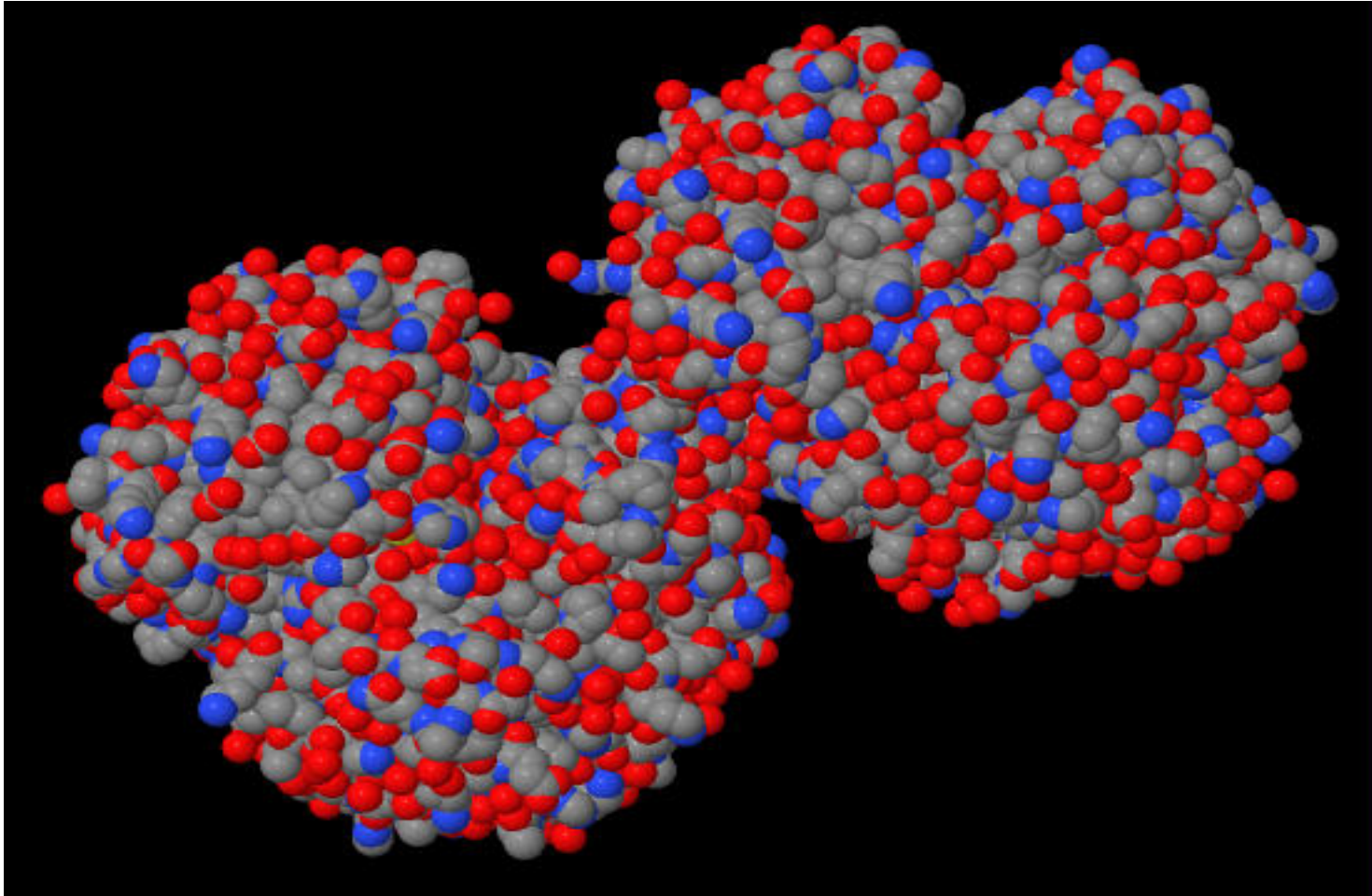
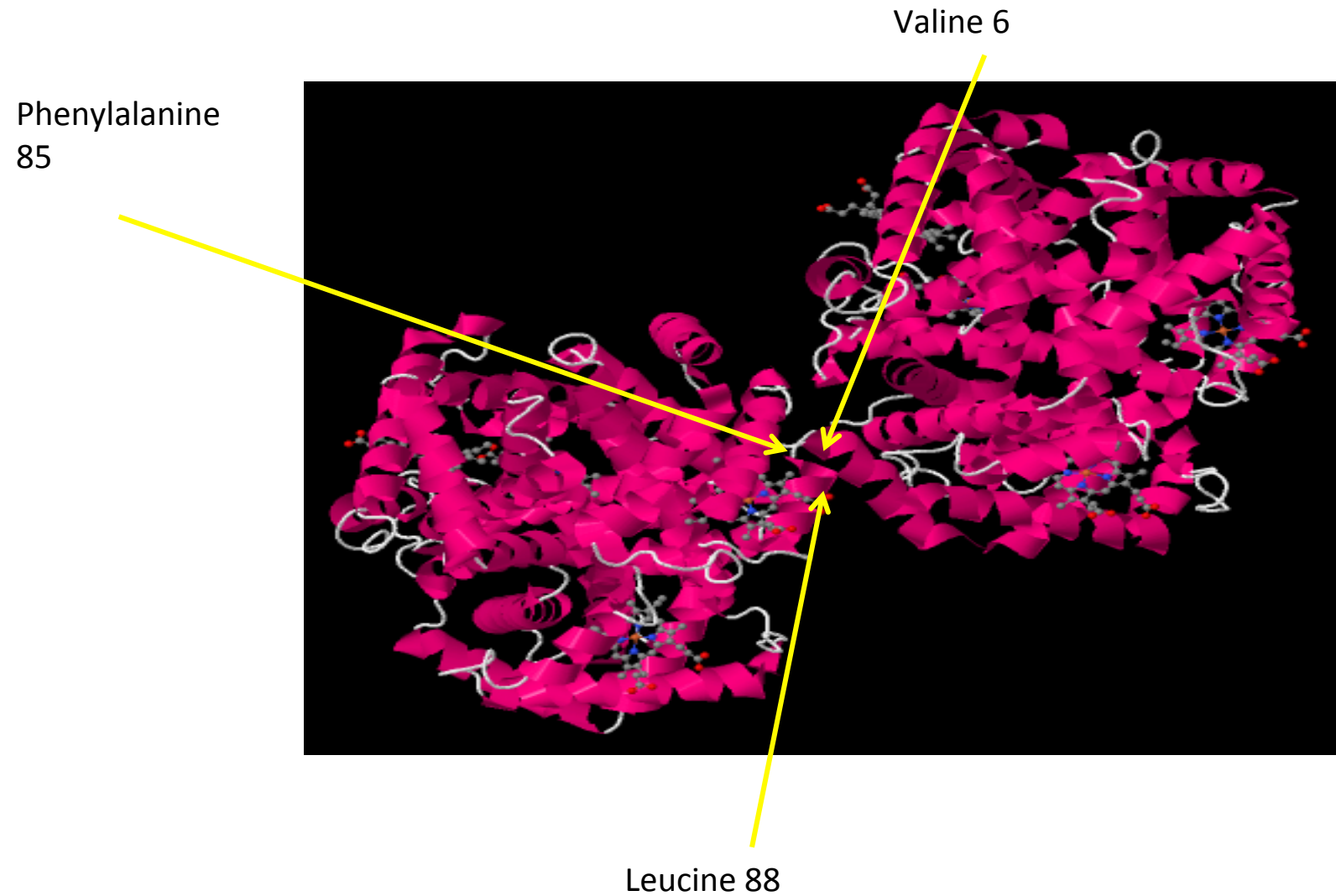


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Space fill (Jmol CPK) model of human deoxyhaemoglobin S.

STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN S - AGGREGATION



In both haemoglobin A and haemoglobin S the β -chains contain a hydrophobic pocket formed by phenylalanine (phe) 85 and leucine (leu) 88. In oxyhaemoglobin A and oxyhaemoglobin S the hydrophobic pocket is “closed”, but in deoxyhaemoglobin A and deoxyhaemoglobin S this hydrophobic pocket opens. In deoxyhaemoglobin A this presents no problems because the residues at the surface of the globin subunits (specifically glutamic acid 6) are hydrophilic or polar and do not interact with the hydrophobic pocket. However, in haemoglobin S the glutamic acid at position 6 is replaced by a valine residue which is itself hydrophobic and can interact with the hydrophobic pocket formed by phe85 and leu88.

Normally it is hydrophilic, so don't get an interaction. But with valine it is phobic, causing the Hb S to clump together...low o₂ tensions causes this to happen.