Crystal structures of HIV-1 RT, either unliganded or complexed with different nonnucleoside RT inhibitors (NNRTI) or a double-stranded DNA, have been reported. There are significant differences between different HIV-1 RT structures; this serves to illustrate the high flexibility of this enzyme.

Comparison of various RT structures with or without bound ligand or substrate reveals that the p66 thumb subdomain can occupy at least three different positions that depend on whether RT interacts with or without substrate or various ligands. In contrast to the "thumb down" position found in the unliganded form, when HIV-1 RT binds a DNA substrate the p66 thumb is rotated open at the thumb's "knuckle", which is near residues Trp239 and Val317.

This thumb movement of the p66 thumb affects only the position of the p66 thumb, not other subdomains. The binding of an NNRTI, however, induces a hinge-like movement at the base of the p66 thumb subdomain, between the β6-β10-β9 and β12-β13-β14 ("primer grip") sheets. Associated with this hinge-like movement, the p66 thumb subdomain is further extended to a wide open position. The p66 connection subdomain, RNase H domain, and the subdomains in the p51 subunit are displaced by this hinge-like movement as well.

The polymerase active site is composed of structural elements from both protein and nucleic acid. NNRTI binding to HIV-1 RT leads to altered positions of both the p66 thumb and the primer grip, which consequently would alter the position of template-primer relative to both the polymerase and the RNase H active site. These conformational changes could account for the inhibition activity of NNRTIs, and explain the alteration of cleavage specificity of RNase H by NNRTI binding.

Bar-headed goose (Anser indicus) live and hatch their young at the west China’s Qinhtai lake, but at the end of autumn they migrate to the plains of northwest India. Flocks has been observed flying over the Himalayan Mountains at altitudes of about 9000 m where ambient pO₂ only have about 50 mmHg which accounts to 20% of pO₂ at sea level (Swan, L. A. 1970, Nat. Hist., 79, 68).

The Hbs from bar-headed goose shows more high oxygen affinity compared to closely related lowland species of goose, such as greylag goose. There are only four amino acid differences between the major Hb types of these two species, only one of which appears likely to effect oxygen affinity, the e119 Pro matures to Ala at c191 interface (Oberhür, W., et al 1982, Hoppe-seyer’s Z. Physiol. Chem.,363, 581)

We have determined the X-ray crystallographic structure of bar-headed goose haemoglobin in the Oxy form to a resolution of 0.2 nm. Now we have got the crystals of deoxyHb and done the preliminary crystallographic studies in order to elucidate high oxygen affinity mechanism. DeoxyHb of bar-headed goose was prepared with Na₂SO₄ as reducing agent. The single crystals suitable for X-ray analysis have been grown from PEG 6000 at pH 7.2, protein 20 mg/ml with the hanging drop vappor diffusion method. DeoxyHb crystalizes in a PI space group with lattice constants a=7.09 nm, b=9.54 nm, c=8.87 nm, the asymunitic cell has two molecules, Vm=0.256 nm³/Dal. The crystals diffract to about 0.23 nm resolution and 60% of X-ray diffraction data has been collected to 0.28 nm on X-200B Area Detector. A total of reflections is 30654, Rm=5.14%. The determination of deoxyHb structure using the molecular replacement method is in progress.