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 knuckle 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 sites. Those conformational changes could account for the inhibition activity of NNRTIs, and explain the alteration of cleavage specificity of RNase H by NNRTI binding.

Crystallographic and crystallographic studies of bar-headed goose deoxyhaemoglobin Ziqian Hu*, Yiling Fang, Xiaoxi Zhou, Qian Xu, Bao Kuang, Xincheng Wei, Guangying Lu, Xiaocheng Gu, College of Life Sciences, Peking University, Beijing 100871 China

Bar-headed goose (Anser indicus) live and hatch their young at the west China's Qinhai 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, which appears likely to effect oxygen affinity, the "thumb down" form, when Hbs from bar-headed goose 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).

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### References


### Preliminary Crystallization of Plastocyanin from Silene Expresssed in E. Coli (PCSIL)

Preliminary crystallization of Plastocyanin from Silene expressed in E. Coli (PCSIL). PCSIL has been crystallized in a form suitable for X-ray diffraction analysis by macroseeding method using ammonium sulfate as a precipitant in acetate buffer (pH=5.5). These crystals belong to space group P3_2_1 with lattice parameters a=b=76.6 Å and c=65.5 Å, indicating an asymmetric unit containing two plastocyanin molecules. The crystals diffract up to at least 2.0 Å resolution. 44196 diffraction data were observed, from which 11515 were unique, in the resolution range 15.0-2.0 Å, with an Rmerge of 6.0%. Molecular replacement method was applied to solve the crystal structure with AMoRe in CCP4. Rigid-body refinement of the model and subsequent refinement using molecular dynamics were carried out with XPLOR, leading to a current R factor of 17.6%, for the diffraction intensities up to 2.5 Å resolution.

### References


### Preliminary Crystallization of a Cyclin-Dependent Kinase Inhibitor: P18

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Eukaryotic cell-cycle progression is regulated by a family of serine/threonine protein kinases, cyclin-dependent kinases (CDK's). CDK activity is regulated by subunit phosphorylation, activation via cyclin binding, and inhibition via binding of small regulatory proteins. Currently, these small inhibitor proteins can be classified into two families: the universal inhibitors of the p21/p53 family and the more specific inhibitors p16INK4 (p16)/p14INK4 (p14) family. A member of the p16/p14 family, p18 binds and inhibits CDK6 and CDK4, halting cell cycle progression.

Recombinant human p18 has been purified to homogeneity and diffusion quality crystals have been obtained by dialysis. Crystals have a typical size of 0.1 x 0.1 x 0.2 mm and can diffract to 2.4 Å resolution. The space group has been determined to be P1 with unit cell dimensions of: a=60.3, b=40.2, c=28.4 Å, α=90.6°, β=92.1°, γ=95.8°. Diffraction data have been collected on a RIGAKU R-Axis image plate system. A data set of 16,785 measurements has been reduced to 11,595 independent reflections with an Rmerge of 0.089. This data set is 70.5% complete to 2.06 Å resolution. Heavy atom derivative preparation and structural analysis is in progress.