Welcome to the PDB, the single international repository for the processing and distribution of 3-D macromolecular structure data primarily determined experimentally by X-ray crystallography and NMR.

DEPOSIT  Contribute structure data
STATUS   Find entries awaiting release
DOWNLOAD Retrieve structure files (FTP)
LINKS    Browse related information
PREVIEW  Beta-test new features
Search 3-D macromolecular structure data primarily determined experimentally by X-ray crystallography and NMR.

Enter keywords known to relate to the biological macromolecules of interest and select the "Search" button or "Enter" on your keyboard.

HIV-1 Reverse Transcriptase

Search strings are case insensitive.

A more advanced, customizable search can be performed using the SearchFields interface.
Other PDB search interfaces and related databases are found here.

Examples:

4hhb
Find all structures containing the term 4hhb. This will include the structure with the PDB code and any other structures that reference that code.

idcode: 4hhb
Find the single structure with the PDB code 4hhb. IDCODE is an example of an attribute.
Your query found 47 structures in the current PDB release and you have selected 0 structures so far. (There are currently 4 structures being processed or "on hold" matching your query!) You can select specific structures by clicking on the checkbox next to their id. If you do not select any structures, certain options will default to all structures. To examine an individual structure select the Explore link!

<table>
<thead>
<tr>
<th>Structure</th>
<th>Deposited:</th>
<th>Exp. Method:</th>
<th>Resolution:</th>
</tr>
</thead>
<tbody>
<tr>
<td>1BQM</td>
<td>17-Aug-1998</td>
<td>X-ray Diffraction</td>
<td>3.10 Å</td>
</tr>
<tr>
<td>1BQN</td>
<td>17-Aug-1998</td>
<td>X-ray Diffraction</td>
<td>3.30 Å</td>
</tr>
<tr>
<td>1COT</td>
<td>19-Jul-1999</td>
<td>X-ray Diffraction</td>
<td>2.70 Å</td>
</tr>
<tr>
<td>1COU</td>
<td>19-Jul-1999</td>
<td>X-ray Diffraction</td>
<td>2.52 Å</td>
</tr>
</tbody>
</table>

Classification: Nucleotidyltransferase
Compound: Mol_Id: 1; Molecule: Reverse Transcriptase; Chain: A, B; Synonym: Hiv-1 Rt; Ec: 2.7.7.49; Engineered: Yes; Mutation: C280S

CLICK HERE
**Summary Information**

**Compound:** Mol_Id: 1; Molecule: Hiv-1 Reverse Transcriptase (A-Chain); Chain: A; Fragment: P66; Ec: 2.7.7.49; Engineered: Yes
Mol_Id: 2; Molecule: Hiv-1 Reverse Transcriptase (B-Chain); Chain: B; Fragment: P51; Ec: 2.7.7.49; Engineered: Yes

**Authors:** J. Ren, R. M. Esnouf, A. L. Hopkins, D. I. Stuart, D. K. Stammers

**Exp. Method:** X-ray Diffraction

**Classification:** Transferase

**EC Number:** 2.7.7.49

**Source:** Human Immunodeficiency Virus Type 1; Human Immunodeficiency Virus Type 1


**Deposition Date:** 19-Jul-1999

**Release Date:** 19-Jul-2000

**Resolution:** 2.50 Å

**R-Value:** 0.234
Structure Explorer - 1C0T

Classification
Transerase

Compound
Mol_Id: 1; Molecule: Hiv-1 Reverse Transcriptase (A-Chain); Chain: A; Fragment: P66; Ec: 2.7.7.49; Engineered: Yes
Mol_Id: 2; Molecule: Hiv-1 Reverse Transcriptase (B-Chain); Chain: B; Fragment: P51; Ec: 2.7.7.49; Engineered: Yes

X-ray Diffraction

View Structure

Interactive 3D Display:

Choose from the following display options:

- VRML (default options): Interactive immersive ribbon diagram
- VRML (custom options, full screen display): Interactive immersive ribbon or cylinder diagram with ligands
- PDB file
- FirstGlance (needs Chime)
- Protein Explorer (needs Chime)
- Java (simple interactive sequence/structure/property backbone diagram):

Still Images:

- Ribbons (250x250)
- Ribbons (500x500)
- Cylinders (250x250)
- Cylinders (500x500)