

- Getting structures from the PDB (<https://www.rcsb.org/>) is pretty straightforward.
- For a particular crystal structure, you can just click on “Download Files” and select “PDB format”
- We will use the PDB files for 1HVY and 6NNR, which has superceded 2G8O.
- Next, let’s go through getting a model for W.g.b. thymidylate synthase.

The screenshot shows the RCSB PDB website interface. At the top, there's a search bar and navigation links. The main content area displays the entry 1HVY, which is Human thymidylate synthase complexed with dUMP and dUMP in the closed conformation. The page includes a 3D ribbon diagram of the protein structure, a search bar, and a 'Download Files' dropdown menu with options like PDB Format, PDB Format (gz), PDBx/mmCIF Format, PDBx/mmCIF Format (gz), PDBML/XML Format (gz), Biological Assembly 1, Biological Assembly 2, Structure Factors (CIF), Structure Factors (CIF - gz), 2fo-fc Map (DSN6), fo-fc Map (DSN6), and Map Coefficients (MTZ format). The page also displays experimental data snapshot, wwPDB Validation metrics, and standalone viewers.

Structure Prediction