**PyMol script to identify missing residues**

**Without comments**

load 5BRZ\_cleaned.pdb

for chain in cmd.get\_chains():

seq = cmd.get\_fastastr('chain ' + chain)

residues = []

cmd.iterate('chain ' + chain, 'residues.append(resi)')

residues = [int(res) for res in residues]

missing\_residues = []

for i in range(min(residues), max(residues) + 1):

if i not in residues:

missing\_residues.append(i)

if missing\_residues:

print(f"Chain {chain} - Missing Residues: {', '.join(map(str, missing\_residues))}")

else:

print(f"Chain {chain} - No missing residues")

**With comments**

# Load the cleaned PDB file

load 5BRZ\_cleaned.pdb

# Iterate over each chain and identify missing residues

for chain in cmd.get\_chains():

# Get the sequence of the chain

seq = cmd.get\_fastastr('chain ' + chain)

# Get the residue numbers present in the chain

residues = []

cmd.iterate('chain ' + chain, 'residues.append(resi)')

# Convert residue numbers to integers

residues = [int(res) for res in residues]

# Find missing residues

missing\_residues = []

for i in range(min(residues), max(residues) + 1):

if i not in residues:

missing\_residues.append(i)

# Print missing residues for the chain

if missing\_residues:

print(f"Chain {chain} - Missing Residues: {', '.join(map(str, missing\_residues))}")

else:

print(f"Chain {chain} - No missing residues")