```
##NOTE: all calls to Atom in this code will need:
## ", missing=True" as a final argument, omitted for clarity
seq = []
curres = '---'
res = []
first = True
atomnum = 5
resnum = 0
for line in pdb.lines:
    # Decode from byte array
    line = line.decode()
    # Grab only ATOM lines
    if line[:6] == 'ATOM  ':
        # Get the atomname (N,CA,C,O)
        atomname = line[12:16]

        # First make sure you're only storing N, CA, C and O
        if atomname not in (' N  ',' CA ',' C  ',' O  ') or line[16] not in ('
','A'):
            continue

        # Check to see if residue changed
        if line[17:20] != curres or atomnum > 4:
            if self.debug:
                print("%8s%8s%8s%8s" % ('CURRES','NEWRES','RESNUM','ATONUM'))
                print("%8s%8s%8d%8d" % (curres,line[17:20],resnum,atomnum))
                print(line)
            # Check to make sure the last residue was complete
            if atomnum < 5:
                # Add on the missing atoms to the end of the residue
                if atomnum == 1:
                    atom = Atom(atomName=' N  ',resName=curres,elemSym=' N')
                    res.append(atom)
                    atomnum += 1
                if atomnum == 2:
                    atom = Atom(atomName=' CA ',resName=curres,elemSym=' C')
                    res.append(atom)
                    atomnum += 1
                if atomnum == 3:
                    atom = Atom(atomName=' C  ',resName=curres,elemSym=' C')
                    res.append(atom)
                    atomnum += 1
                if atomnum == 4:
                    atom = Atom(atomName=' O  ',resName=curres,elemSym=' O')
                    res.append(atom)
                    atomnum += 1
            # Append the residue to the sequence
            if res: seq.append((amino3to1[curres],res))

            # If this is the first atom fill in the blanks from the PDB
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    if first:
        first = False
        if self.debug:
            print("Starting resnum:",int(line[22:26]))
        # Residue number of first residue in PDB
        for k in range(1,int(line[22:26])):
            resname = '---'
            res = []
            res.append(Atom(atomName=' N  ',resName=resname,elemSym=' N'))
            res.append(Atom(atomName=' CA ',resName=resname,elemSym=' C'))
            res.append(Atom(atomName=' C  ',resName=resname,elemSym=' C'))
            res.append(Atom(atomName=' O  ',resName=resname,elemSym=' O'))
            seq.append((amino3to1[resname],res))
        # Decrement resnum by one to mimic the last res not in the PDB
        resnum = int(line[22:26])-1

    # Check for resnum increment so we don't miss residues
    resinc = int(line[22:26])-resnum
    if resinc != 1:
        if self.debug:
            print("Resiude skip:",resnum,"->",int(line[22:26]))
        for k in range(1,resinc):
            resname = '---'
            res = []
            res.append(Atom(atomName=' N  ',resName=resname,elemSym=' N'))
            res.append(Atom(atomName=' CA ',resName=resname,elemSym=' C'))
            res.append(Atom(atomName=' C  ',resName=resname,elemSym=' C'))
            res.append(Atom(atomName=' O  ',resName=resname,elemSym=' O'))
            seq.append((amino3to1[resname],res))

    # Reset the residue
    res = []
    # Store residue numbers
    resnum = int(line[22:26])
    # Store the atom number
    atomnum = 1

# Make sure current residue name is set
curres = line[17:20]

'''
if self.debug:
    print("Line:",line)
'''

# Check to make sure the right atom is being stored
if atomnum == 1:
    if atomname != ' N  ':
        atom = Atom(atomName=' N  ',resName=curres,elemSym=' N')
        res.append(atom)
        atomnum += 1
```

```
        if atomnum == 2:
            if atomname != ' CA ':
                atom = Atom(atomName=' CA ',resName=curres,elemSym=' C')
                res.append(atom)
                atomnum += 1
        if atomnum == 3:
            if atomname != ' C  ':
                atom = Atom(atomName=' C  ',resName=curres,elemSym=' C')
                res.append(atom)
                atomnum += 1
        if atomnum == 4:
            if atomname != ' O  ':
                atom = Atom(atomName=' O  ',resName=curres,elemSym=' O')
                res.append(atom)
                atomnum += 1
                continue
        if atomnum > 4:
            continue
        # Store off the atom information if valid
        atom = Atom(
            atomName=atomname,
            altLoc=line[16],
            resName=line[17:20],
            chainId=line[21],
            codeForInsertion=line[26],
            xcoord=float(line[30:38]),
            ycoord=float(line[38:46]),
            zcoord=float(line[46:54]),
            occ=float(line[54:60]),
            temp=float(line[60:66]),
            elemSym=line[76:78],
            charge=line[78:80]
        )
        # And add it to the residue (in the proper order)
        res.append(atom)
        atomnum += 1

# Add the final residue to the sequence
seq.append((amino3to1[curres],res))
```