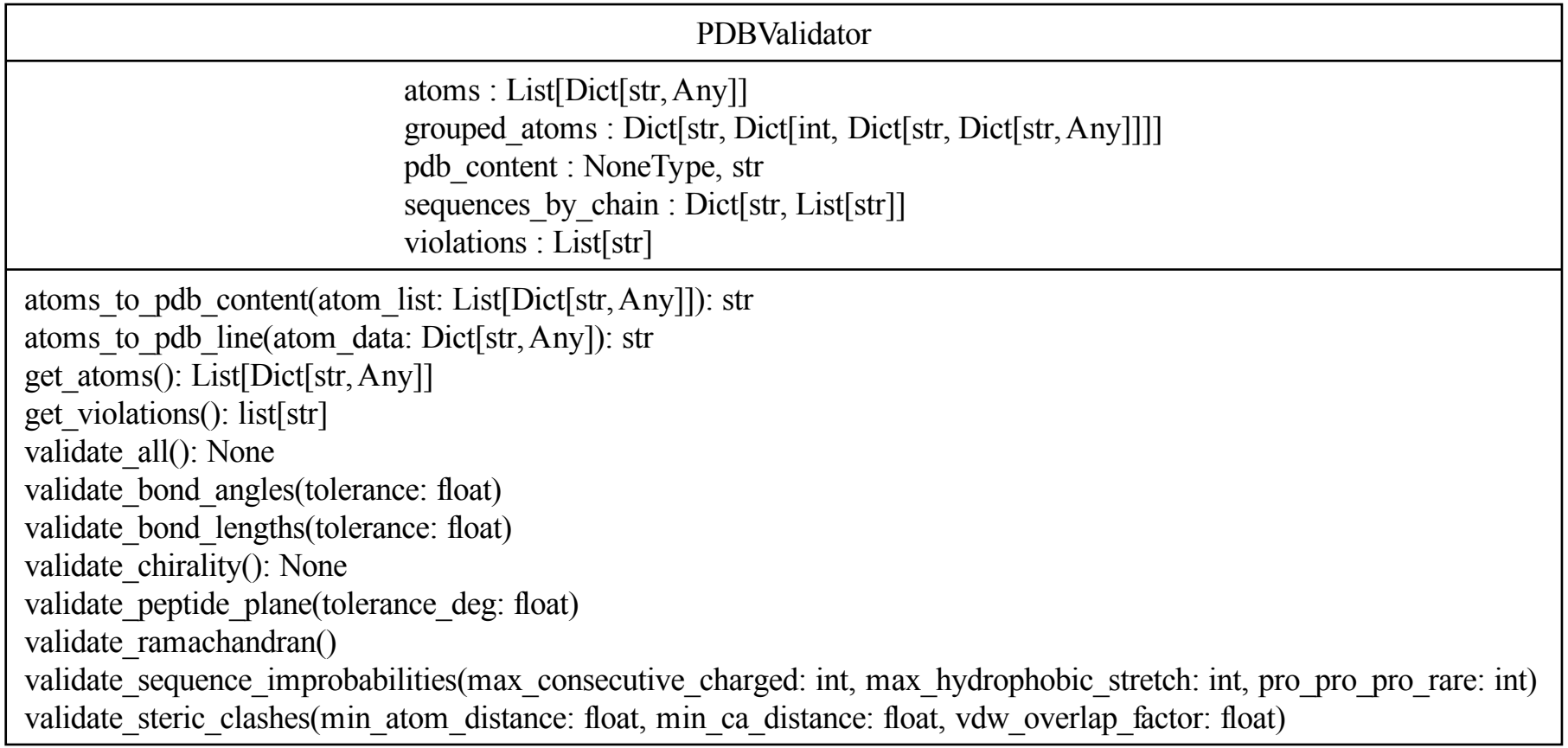
PDBValidator
atoms : List[Dict[str, Any]]
grouped_atoms : Dict[str, Dict[int, Dict[str, Dict[str, Any]]]]
pdb_content : NoneType, str
sequences_by_chain : Dict[str, List[str]]
violations : List[str]
atoms_to_pdb_content(atom_list: List[Dict[str, Any]]): str
atoms_to_pdb_line(atom_data: Dict[str, Any]): str
get_atoms(): List[Dict[str, Any]]
get_violations(): list[str]
validate_all(): None
validate_bond_angles(tolerance: float)
validate_bond_lengths(tolerance: float)
validate_chirality(): None
validate_peptide_plane(tolerance_deg: float)
validate_ramachandran()
validate_sequence_improbabilities(max_consecutive_charged: int, max_hydrophobic_stretch: int, pro_pro_pro_rare: int)
validate_steric_clashes(min_atom_distance: float, min_ca_distance: float, vdw_overlap_factor: float)