```
#
# Hydrogen bond distances were specified for charge-charge and charge-neutral
# hydrogen bonding pairs according to the following:
#
# (+) charge H-bond donor of protein[4]: NR3, NC2, NP, NH3
# neutral H-bond donor of protein [7]: NR1, NH1, NH2, NY, OH1, S, OT [water]
# neutral H-bond acceptor of protein [8]: OH1, S, O, OB, OS, NR2, OT [water], OX
# (-) charge H-bond acceptor of protein [1]: OC
# (+) charge H-bond donor of ligand [5]: NG2P1, NG2R52, NG3P1, NG3P2, NG3P3
# neutral H-bond donor of ligand [13]: NG2S1, NG2S2, NG2S3, NG2R43, NG2R51, NG2R53,
# NG2R61, NG311, NG321, NG331, NG3C51, OG311, SG311
# neutral H-bond acceptor of ligand [29]: NG1T1, NG2D1, NG2S0, NG2R50, NG2R57,
# NG2R60, NG2R62, NG2R67, NG2RC0,  NG301, NG3N1, OG2D1, OG2D3, OG2D4, OG2D5, OG2R50,
# OG3R60, OG301, OG302, OG303, OG304, OG311, OG3C31, OG3C51, OG3C61, SG2D1, SG2R50,
# SG311, SG301
# (-) charge H-bond acceptor of ligand [5]: OG2D2, OG2N1, OG2P1, OG312, SG302
# Polar atoms, none of above categories NG3P0, NG2O1, SG3O2, SG3O1, SG3O3
#
#     Atom  element  van der Waals
#     type  number  radius energy_min (absolute value)
#   -----------------------------------
p29
225
1      H      1     0.22450 0.046000  # polar H
2      HC     1     0.22450 0.046000  # N-ter H
3      HA     1     1.32000 0.022000  # nonpolar H
4      HP     1     1.35820 0.030000  # aromatic H
5      HB1    1     1.32000 0.022000  # backbone H
6      HR1    1     0.90000 0.046000  # his he1, (+) his HG,HD2
7      HR2    1     0.70000 0.046000  # (+) his HE1
8      HR3    1     1.46800 0.007800  # neutral his HG, HD2
9      HS     1     0.45000 0.100000  # thiol hydrogen
10     HE1    1     1.25000 0.031000  # for alkene; RHC=CR
...

...
220    ZN     30    1.0900  0.2500    # zinc (II) cation
221    CAD    48    1.3570  0.1200    # cadmium (II) cation
222    CLA    17    2.27    0.150     # Chloride Ion
223    CT     6     2.275   0.020     # TIP3P
224    OT     8     1.7682  0.1521    # TIP3P
225    HT     1     0.2245  0.0460    # TIP3P
#
# Hydrogen bond distances between donor and acceptor
#
# The table cannot be separated
#
# First  line: Default distance for all atom and element types
#
# First block:
# element  donor
# number   acceptor
# i  j     distance
# ------------------
#
# Second block:
# atom     donor
# type     acceptor
# i  j     distance
# ------------------
#
#
#
p30
2.9
9
7    7    3.1
7    8    2.9
7   16    2.9
8    8    2.7
8   16    2.9
16  16    2.9
```