

Histidine (protonated, neutral, deprotonated) Extended description of residue

Overall residue properties section:

3-letters residue name

	Residue type (0=Amino Acid, 1=Sugar, 2=Nucleic Acid, 3=Heme, 4=Phosphate, 5=Co-factor, 6=Ion, 7=Detergent, 8=Other)	Residue anhydrous molecular volume (Å ³)	Maximum accessible surface area (Å ²)	Number of atoms in residue	Number of beads for residue	Residue partial specific volume (cm ³ /g)	Partial specific volume (repeated for potential pH-dependence, not implemented)	Selected atom pK1 (order is automatically sorted, lowest-->highest)	Additional partial specific volume (repeated again, as above), needed if a second pK is present	Selected atom pK2 (order is automatically sorted, lowest-->highest)
HIS	0	160	193	10	2	0.668	0.668	6.54	0.668	11.5

Residue atoms properties section:

Atom identifier as in PDB

	Hybridization (at pH=0, if it applies)	Atom molecular weight (hybridization-linked, pH=0, if it applies)	Atom van der Waals radius (hybridization-linked; at pH=0, if it applies)	Atom assignment to bead #	Atom determines bead position (0=no, 1=yes)	Atom progressive number	Number of atom-associated water molecules (at pH=0, if it applies)	Order of pK application in the computations with multiple pKs (automatically sorted)	Hybridization at pH=14	Atom molecular weight (hybridization-linked, at pH=14)	Atom van der Waals radius (hybridization-linked; at pH=14)	Atom assignment to bead #	Atom determines bead position (0=no, 1=yes)	Atom progressive number	N. of atom-associated water molecules at pH=14
N	N3H1	15.02	1.64	0	0	0	1								
CA	C4H1	13.02	1.88	0	0	1	0								
C	C3H0	12.01	1.61	0	1	2	0								
O	O1H0	16	1.42	0	1	3	0								
CB	C4H2	14.03	1.88	1	0	4	0								
CG	C3H0	12.01	1.61	1	0	5	0								
ND1	N3H1	15.02	1.64	1	1	6	1	2	N2H0-	14.01	1.64	1	1	6	4
CD2	C3H1	13.02	1.76	1	0	7	0								
CE1	C3H1	13.02	1.76	1	0	8	0								
NE2	N3H1+	15.02	1.64	1	1	9	2	1	N2H0	14.01	1.64	1	1	9	0

Beads properties section:

Number of bead-associated water molecules at pH=7, used in the generation of the hydrated bead volume (it is overridden if pH-dependence applies)

	Bead "color" (from 0 to 15; 0, 6, 7, 8 are reserved and thus never used in this file)	Bead positioning method (0=CM of included atoms, 1=farthest atom from CM, 2=no positioning)	Bead belongs to 0=main chain, 1=side chain	Bead anhydrous volume
1	1	0	0	64.9
3	4	0	1	95.1