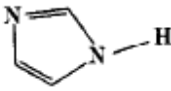
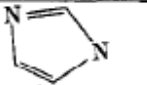


Table 1
Hydrogen bond donors and acceptors from amino acid residues

Nsp^2	>NH peptide, Trp 1.90 Å (1)	-NH ₂ Asn, Gln 1.90 Å (2)	-NH ₂ ⁺ Arg 1.90 Å (2)	>NH ⁺ Arg 1.90 Å (1)	 His 1.90 Å (1)
Nsp^3	-NH ₃ ⁺ Lys 2.10 Å (3)	Donors			
Osp^3	-OH Ser, Thr 1.70 Å (1)				
Osp^2	-OH Tyr 1.70 Å (1)				
Nsp^2	 His 1.60 Å (1/N)	Acceptors			
Osp^3	-OH Ser, Thr 1.70 Å (2)				
Osp^2	=O peptide, Asn, Gln 1.60 Å (2)	-COO- Asp, Glu 1.60 Å (2/O)	-OH Tyr 1.70 Å (1)		
Ssp^3	-S- Met 1.95 Å (2)	-SH Cys 2.10 Å (2)			

All main-chain and side-chain polar groups from the 20 natural amino acid residues. Groups are classified by atom type (N or O) and hybridization (sp^2 or sp^3). Each Table entry contains (1) either a donor or acceptor, (2) residues in which the group is found, (3) the assigned hydrogen bond radius, and (4) the maximum number of hydrogen bonds expected for the group, in parenthesis.