

Peptide Hydrogen-bonded Organic Frameworks

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Table S1. Summary of properties and functionality in peptide-based hydrogen-bonded porous frameworks (P-HPFs)

P-HPFs name	No of hydrophobic residues	No of hydrophilic residues	Percentage of hydrophobic
VA	2	0	100
AV	2	0	100
AI	2	0	100
IA	2	0	10
VV	2	0	100
VI	2	0	100
IV	2	0	100
LS	1	1	50
FF	2	0	100
FG	2	0	100
FL	2	0	100
FW	2	0	100
LL	2	0	100
LF	2	0	100
IL	2	0	100
WG	2	0	100
Abu-Abu	2	0	100
Abu-Nva	2	0	100
Abu-Val	2	0	100
Abu-Leu	2	0	100
Abu-Ile	2	0	100
Nva-Abu	2	0	100

Nva-Nva	2	0	100
Nva-Val	2	0	100
Nva-Leu	2	0	100
Nva-Ile	2	0	100
HYF	2	0	100
DYF	2	1	75
YFD	2	1	75
F- ^D Nva-F	3	0	100
SP1	8	1	88.89
SP2	4	0	100
SP3	14	13	51.85
SP4	12	14	46.15
SP5	14	12	53.85
SP6	13	13	50
SP7	11	15	42.31
SP8	10	6	62.5
F1	7	4	63.63
F2	5	5	50
F3	8	4	66.67
F4	15	0	100

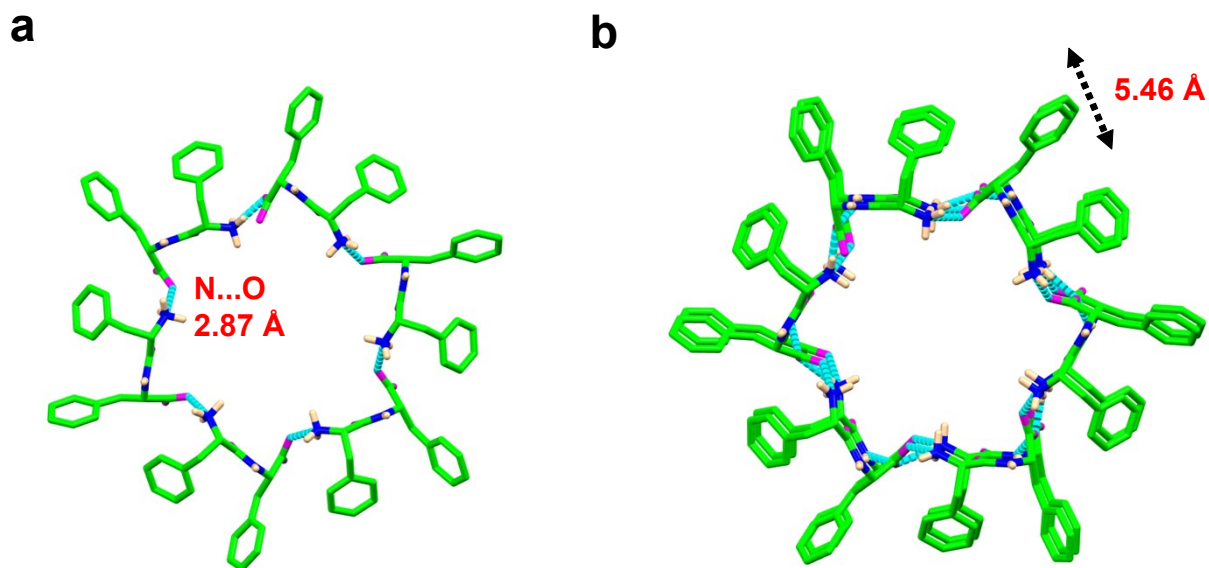


Figure S1. Unit-cell packing diagram of FF showing the formation of molecular rings by six FF molecules and its donor-acceptor interactions (a) and its pi-pi stacking modes (b). The hydrophilic channels formed by six FF molecules are shown and the solvent water molecules are removed for structural clarity.

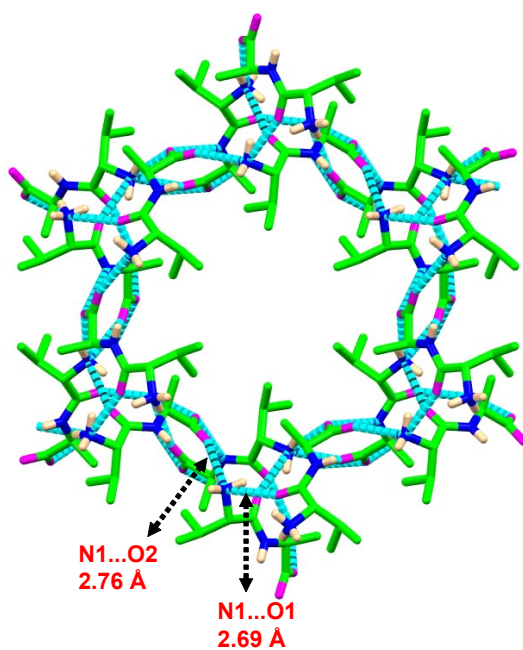


Figure S2. Unit-cell packing diagram of AV displaying a porous framework mediated via head-to-tail hydrogen-bonded interactions between ammonium (NH₃⁺) and carboxylate (COO⁻) residues.

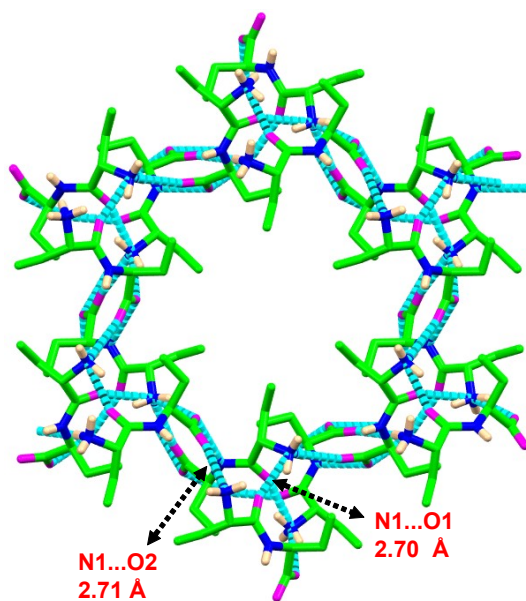


Figure S3. Unit-cell packing diagram of Abu-Abu displaying a porous framework mediated via head-to-tail hydrogen-bonded interactions between ammonium (NH_3^+) and carboxylate (COO^-) residues.

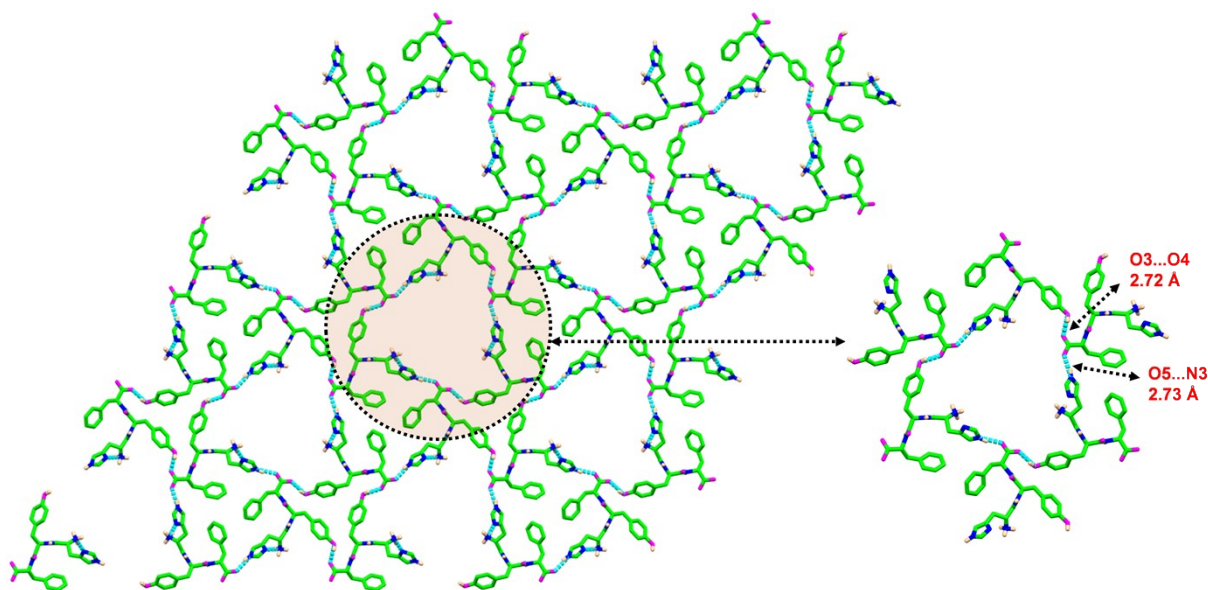


Figure S4. Higher-order crystal packing structure of HYF displaying hydrogen-bonded porous assemblies. The highlighted part shows the hydrogen-bonded porous framework channels formed by six HYF molecules and the solvent water molecules are removed for structural clarity.

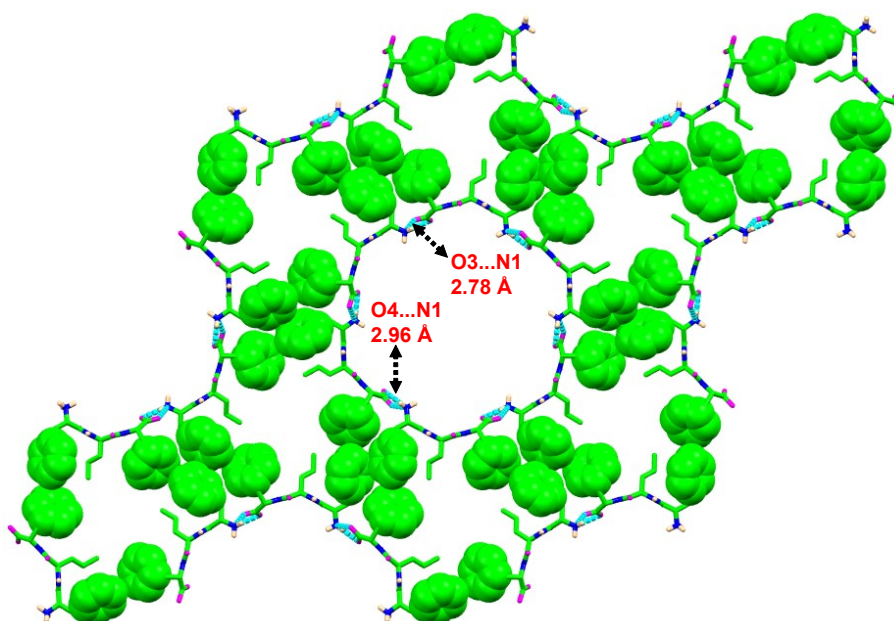


Figure S5. Higher-order crystal structure of F-PNva-F displaying a porous framework mediated via head-to-tail hydrogen-bonded interactions between ammonium (NH_3^+) and carboxylate (COO^-) residues. The aromatic phenyl rings are highlighted in the space-filling model.

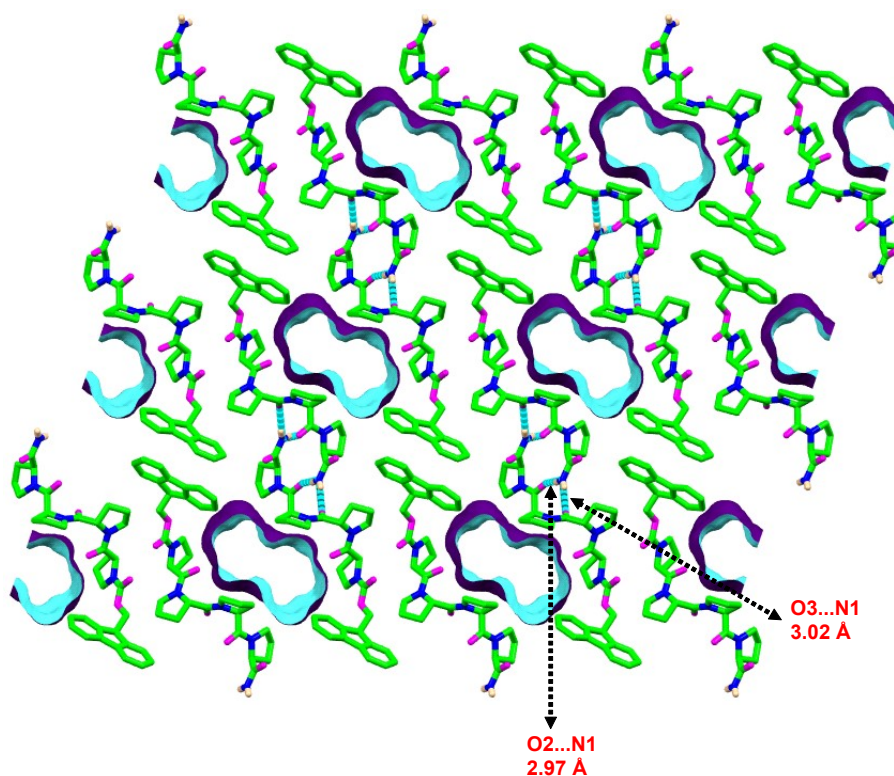
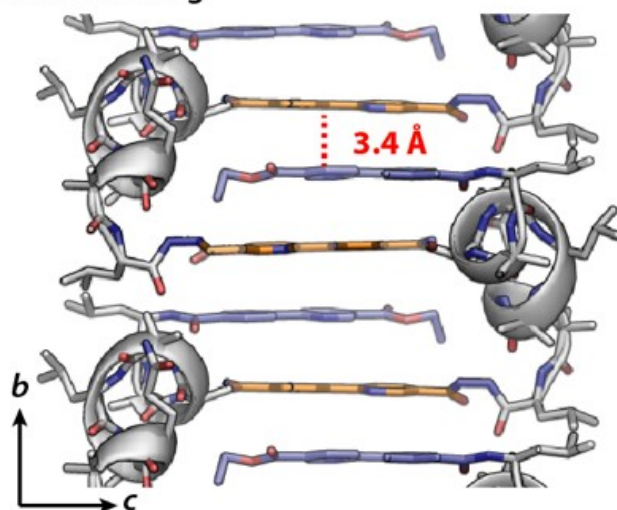


Figure S6. Higher-order crystal packing diagram of PP4 displaying hydrogen-bonded porous framework and the solvent-accessible channels (viewed along the b-axis). The solvent ethanol molecules are removed for structural clarity.

a. π - π stacking



b. Inter-chain hydrogen-bonds

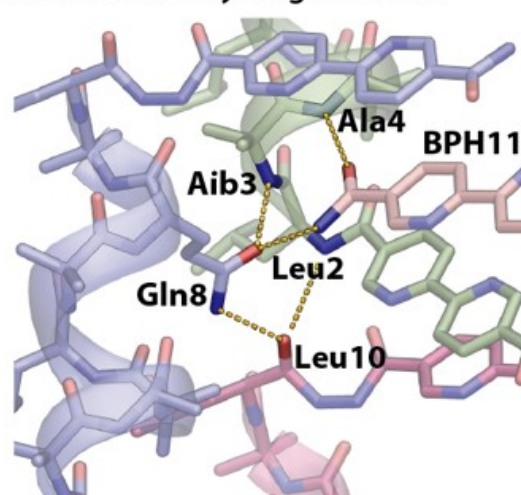


Figure S7. Views of the π - π stacking and inter-chain H-bonding contributing to the structure of UIC-1 (SP1).