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Fig. S1. Chemical structural formula of the eight amino acids used in the study.



Fig. S2. The XRD patterns of In/H-Beta-B-10-2, In/H-Beta-B-10-6, and In/H-Beta-B-

30-6.



Fig. S3. (a) N₂ adsorption–desorption isotherms of In/H-Beta-P, In/H-Beta-H, In/H-Beta-R, and In/H-Beta-S samples, the isotherms for In/H-Beta-H, In/H-Beta-R, and In/H-Beta-S are vertically offset by 405, 628, 1169 cm³/g, respectively and (b) BJH desorption pore distributions of In/H-Beta-P, In/H-Beta-H, In/H-Beta-R, and In/H-Beta-S samples, the those for In/H-Beta-H, In/H-Beta-R, and In/H-Beta-S are vertically offset are 0.5, 0.8, 1.4 cm³/g nm, respectively.



Fig. S4. EDX spectrum of In/H-Beta-P catalyst.



Fig. S5. XPS survey spectra of In/H-Beta-P, -H, -R, and -S catalyst.



Fig. S6. FT-IR spectra of In/H-Beta-P in comparison with pure proline.



Fig. S7. The XRD patterns of fresh and used In/H-Beta-P.