Supporting information

Antimicrobial Amphiphilic Random Copolymers From Bio-Based Methacrylates: Effect of Chemical Composition on Activity and Selectivity

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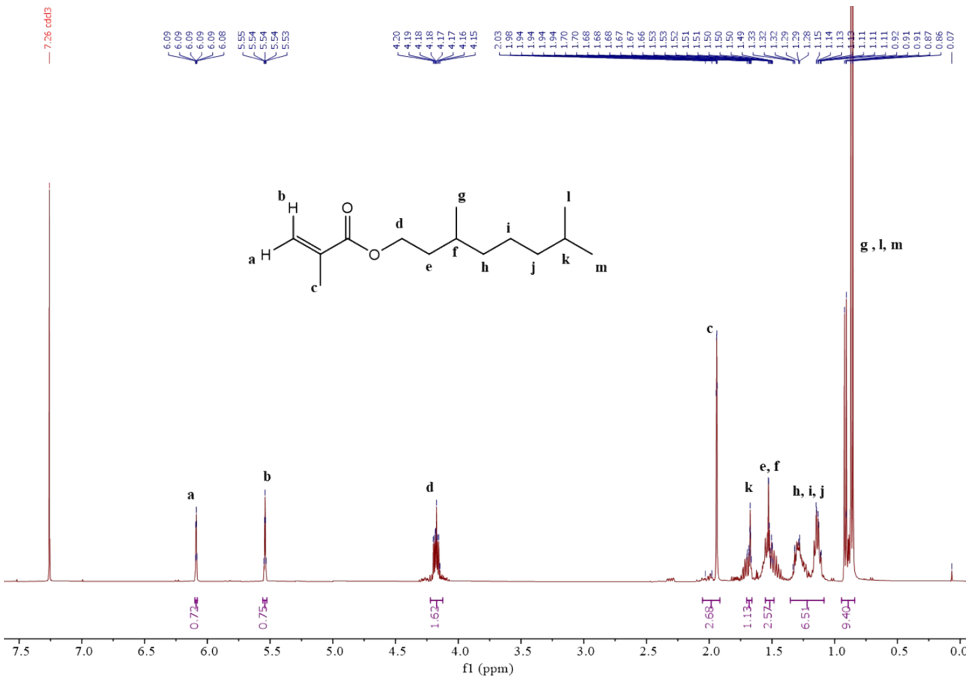

Figure S1. ^{1}H NMR spectrum of THGA monomer in Chloroform-D_1.

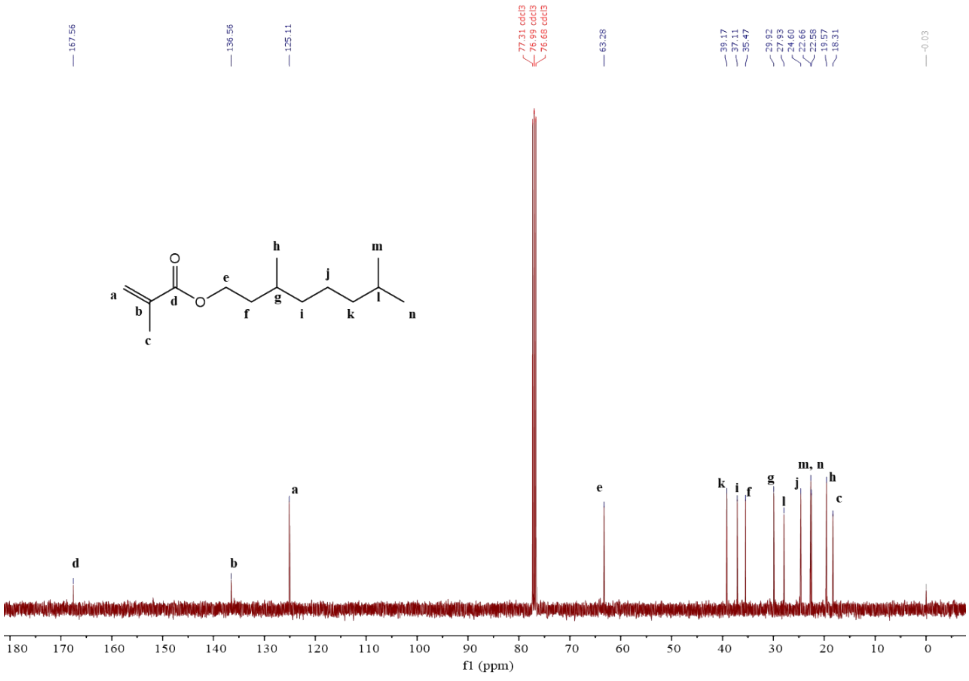

Figure S2. ^{13}C NMR spectrum of THGA monomer in Chloroform-D_1.

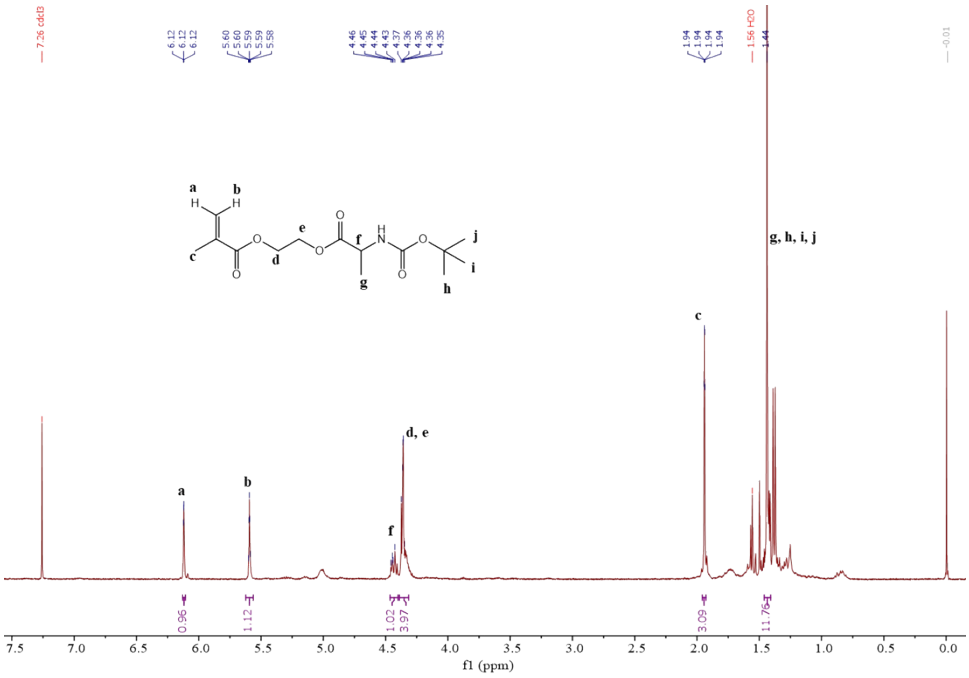

Figure S3. ^{1}H NMR spectrum of Boc-Ala-Hema monomer in Chloroform-D_1.

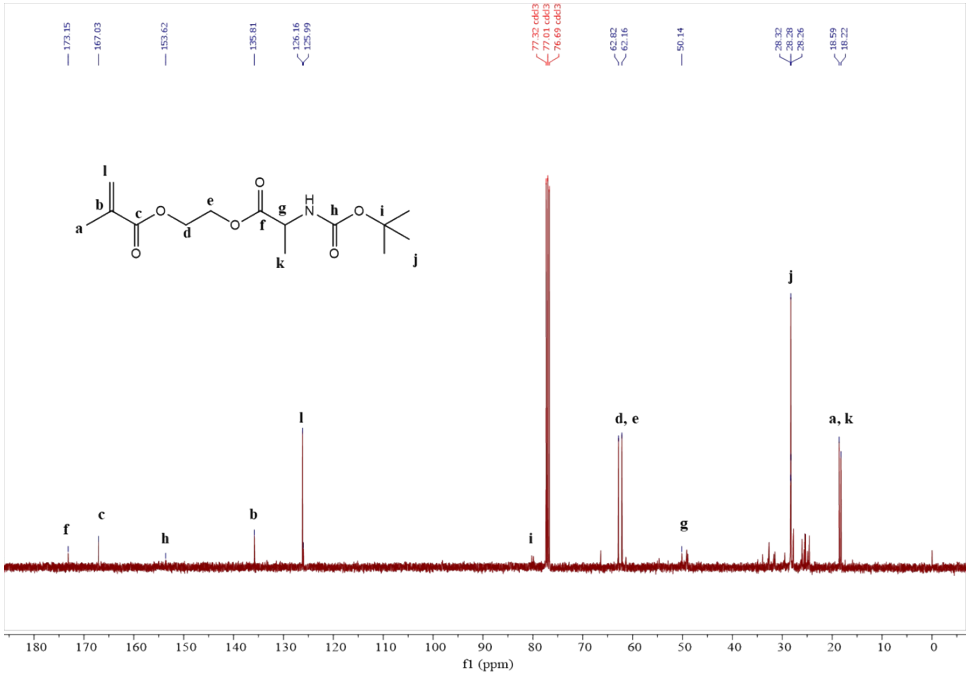

Figure S4. ^{13}C NMR spectrum of Boc-Ala-Hema monomer in Chloroform-D_1.

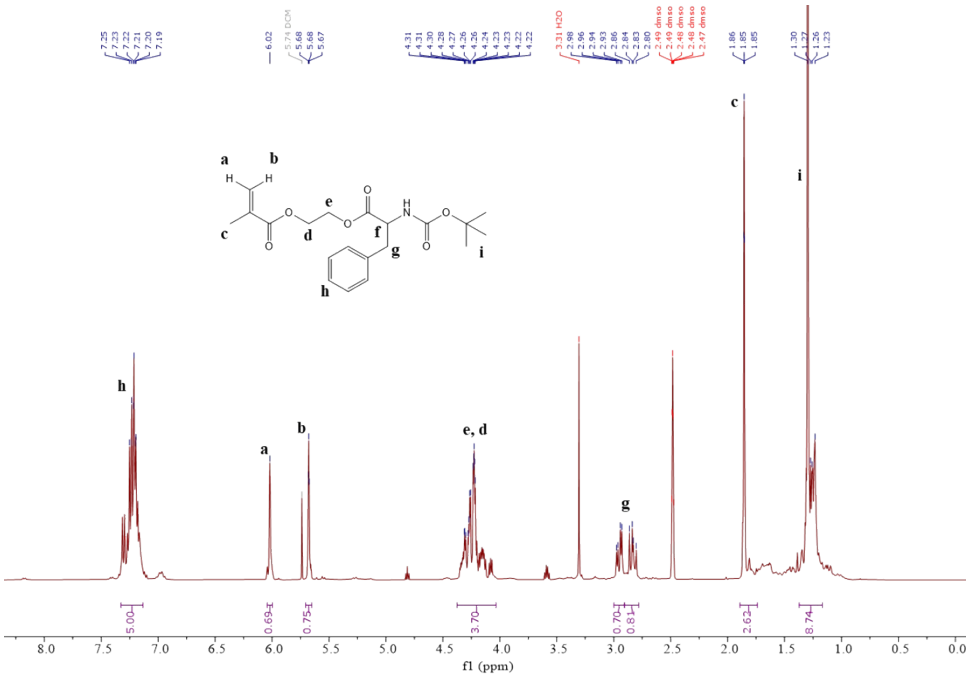

Figure S5. ^{1}H NMR spectrum of Boc-Phe-Hema monomer in DMSO-D_6.

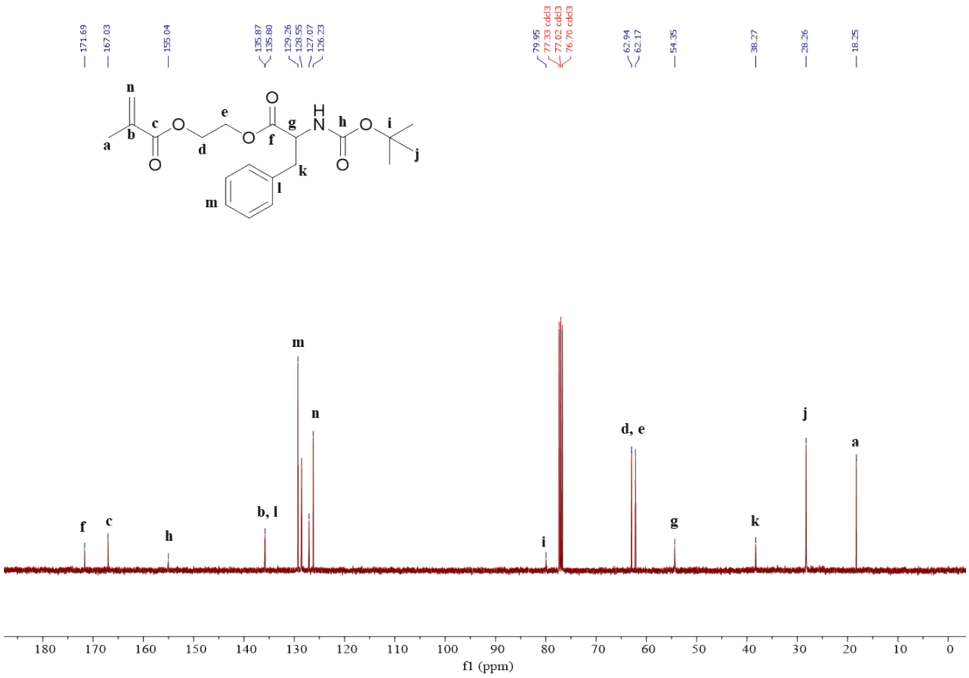

Figure S6. ^{13}C NMR spectrum of Boc-Phe-Hema monomer in Chloroform-D_1.

Converting Boc-Amino Acid DCHA Salts to Free Acids

1. Dissolve the Boc-amino acid DCHA salt in dichloromethane (DCM).
2. Extract the DCM solution with ice-cold aqueous $KHSO_4$ solution 3 times.
3. Dry the organic layer over $NaSO_4$ and filter.
4. Evaporate the solvent under reduced pressure. Dry the resulting residue in vacuo.

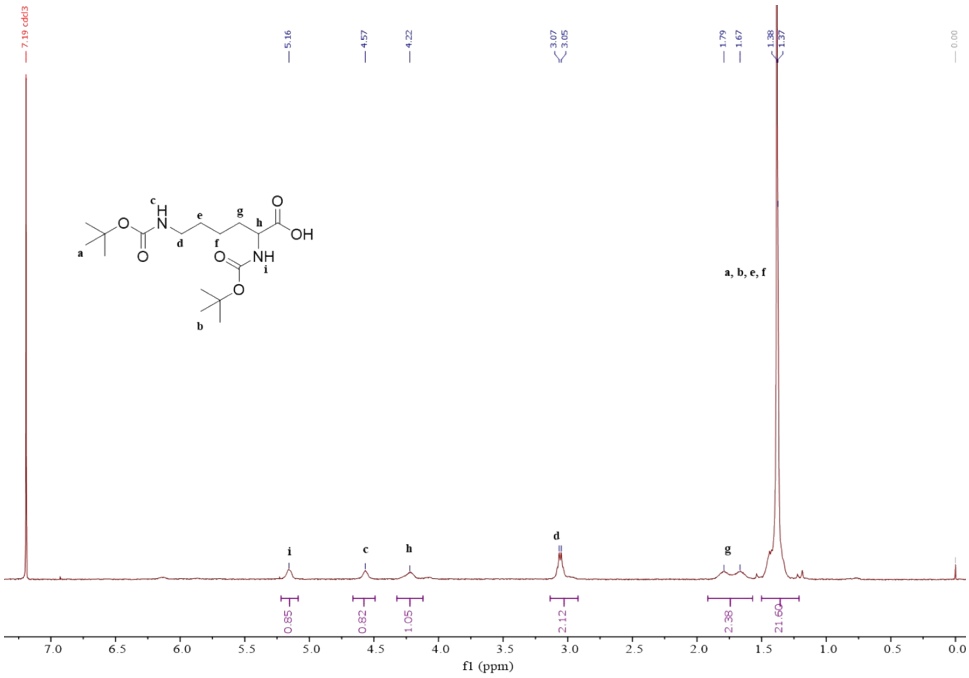

Figure S7. ^{1}H NMR spectrum of Boc-Lys(boc)-OH free acid in Chloroform-D_1.

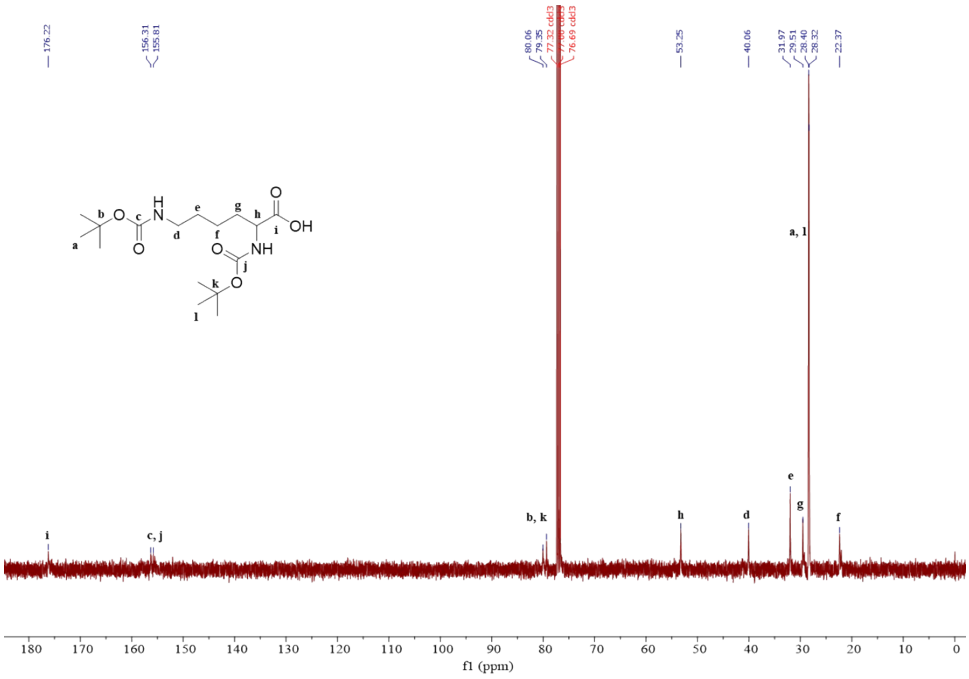

Figure S8. ^{13}C NMR spectrum of Boc-Lys(boc)-OH free acid in Chloroform-D_1.

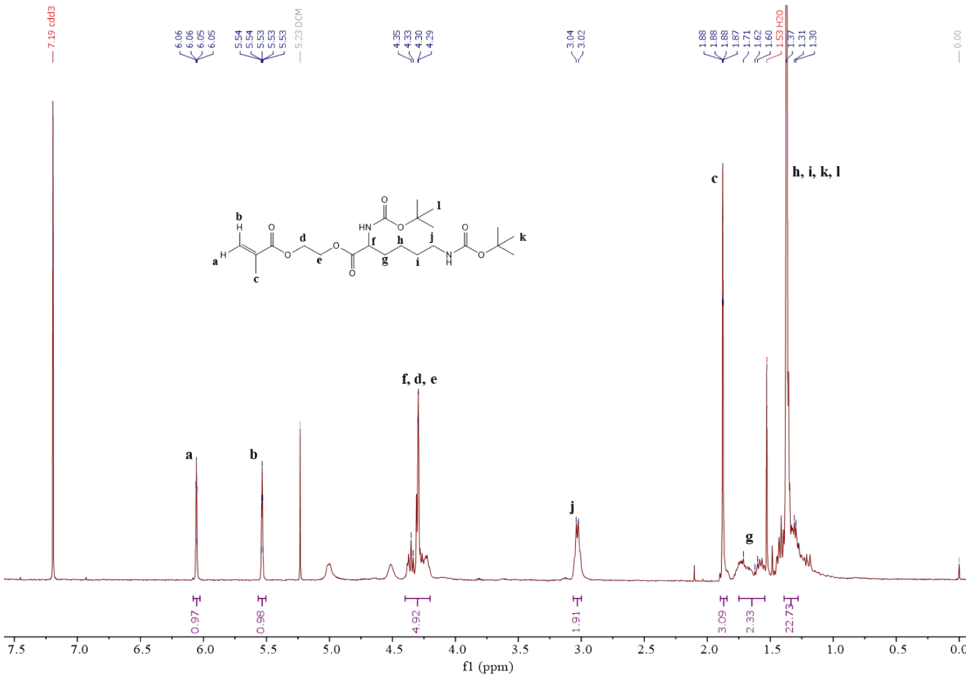

Figure S9. ^{1}H NMR spectrum of Boc-Lys(boc)-Hema monomer in Chloroform-D_1.

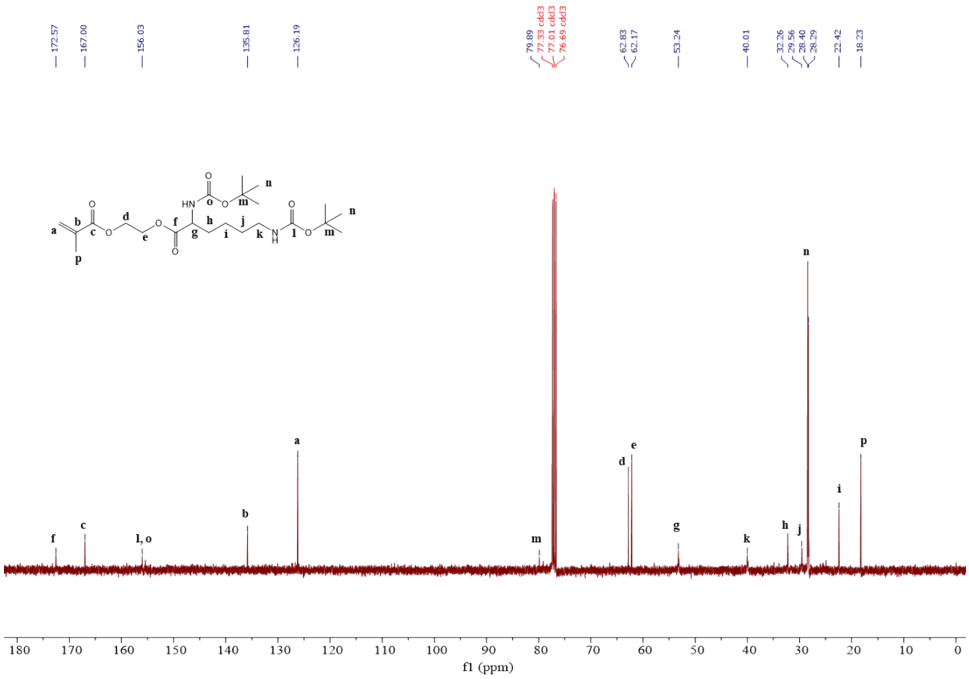

Figure S10. ^{13}C NMR spectrum of Boc-Lys(boc)-Hema monomer in Chloroform-D_1.

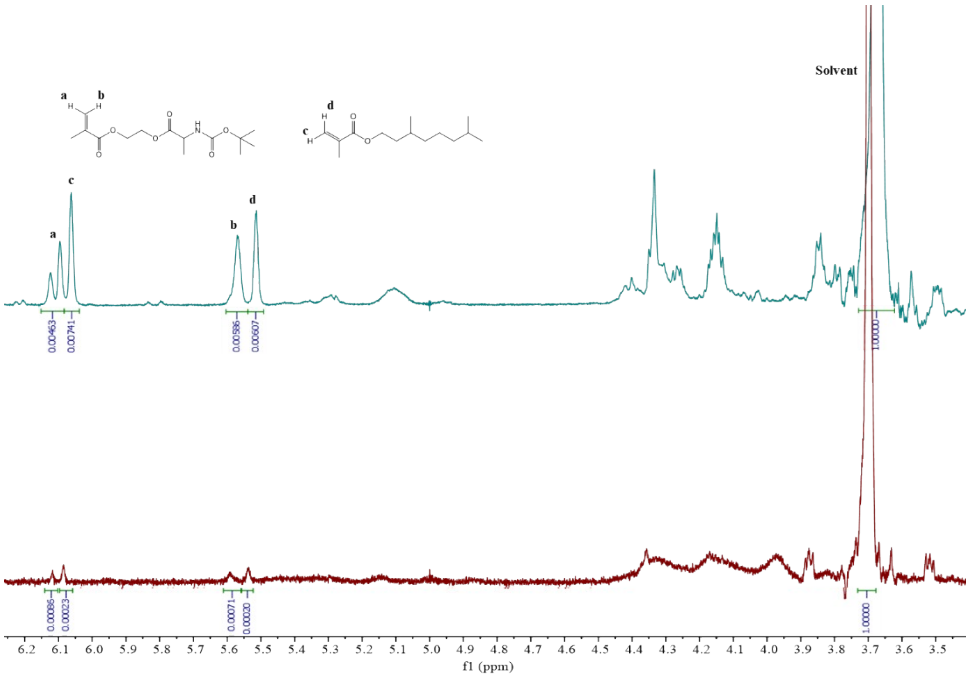

Figure S11. The ^{1}H NMR spectrum in Chloroform-D_1 used to calculate the monomer conversion rate, before the reaction (top) and after the reaction (bottom), taking P(A-r-T)5 as an example.

Peaks a and b in **Figure S11** represent a proton from the Boc-Ala-Hema double bond, and peaks c and d represent a proton from the THGA double bond. We determined the conversion of the monomer by comparing the changes in the double bond protons before and after the reaction, as follows: Assuming that the solvent does not change before and after the reaction, and the total content is set to 1, the conversion rate of THGA is

{[(0.00741+0.00607)/2-(0.00023+0.00020)/2]/ (0.00741+0.00607)/2}*100 % = 96.8 %;

and the conversion rate of Boc-Ala-HEMA is

{[(0.00463+0.00586)/2-(0.00086+0.00071)/2]/ (0.00463+0.00586)/2}*100 % = 85.0 %;

the overall monomer conversion rate is 96.8 %*0.5+85.0 %*0.5 = 90.9 %.

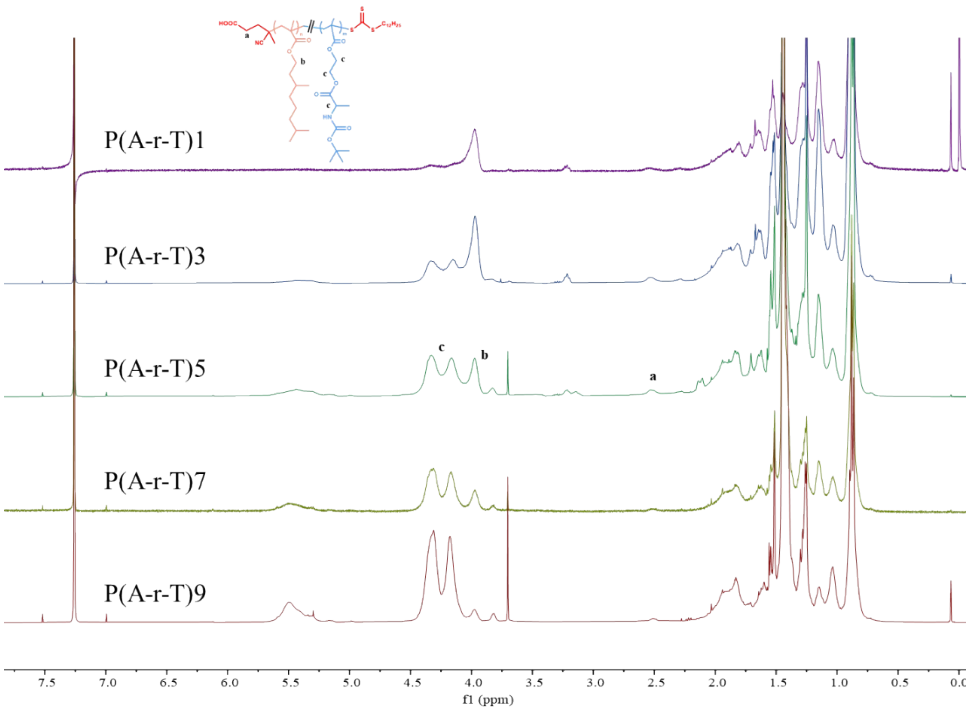

Figure S12. ^{1}H NMR spectrum of random copolymers (with boc protection) with different feed ratios of Ala and THGA in chloroform-D_1.

The calculation method takes P(A-r-T)5 as an example as follows: Peak a of **Figure S13** accounts for 2 protons from the R group of the RAFT agent. Comparing the integration of this peak to those from side chains of monomer give the DP for the polymer.

For instance, peak b constitutes 2 protons of the THGA monomers. Therefore, the average number of THGA units per polymer chain equates to 6.96. Similarly, the peak c constitutes 5 protons of the Ala-Hema monomers. Therefore, the average number of Ala-Hema per polymer chain equates to (17.98/5)*2 = 7.19.

DP is the average total number of monomer units per polymer chain and is the sum of these values (6.96+7.19=14.15). This is rounded to a DP value of 14.

MP_{THGA} (mole percentage of hydrophobic side chains) is simply the number of THGA containing units divided by the total number of monomer units (DP) and would be 6.96/14.15 = 49%

To work out the M_n of the polymer, you take the number of each of the relevant repeat units and multiply by the relevant molecular weight of monomers (THGA = 228.38 g mol^{-1}and Ala-Hema=303.36 g mol^{-1}) then add the molecular weight of the RAFT agent (403.67 g mol^{-1}). This would be as follows: (6.96*228.38)+(7.19*303.36)+403.67 = 4180 g mol^{-1}.

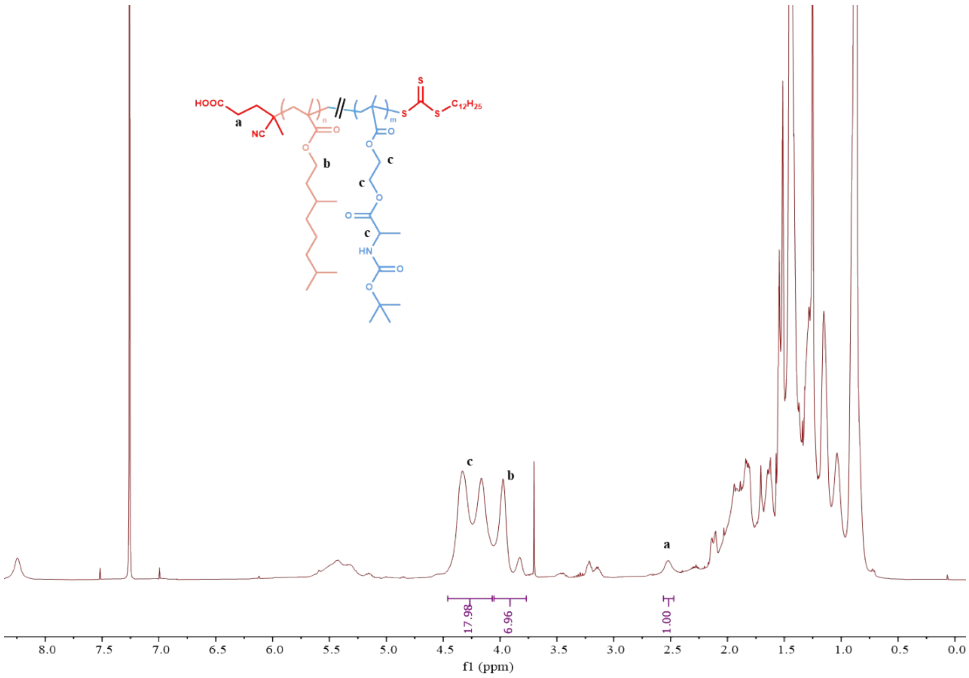

Figure S13. ^{1}H NMR spectrum of P(A-r-T)5 (with boc protection) in chloroform-D_1.

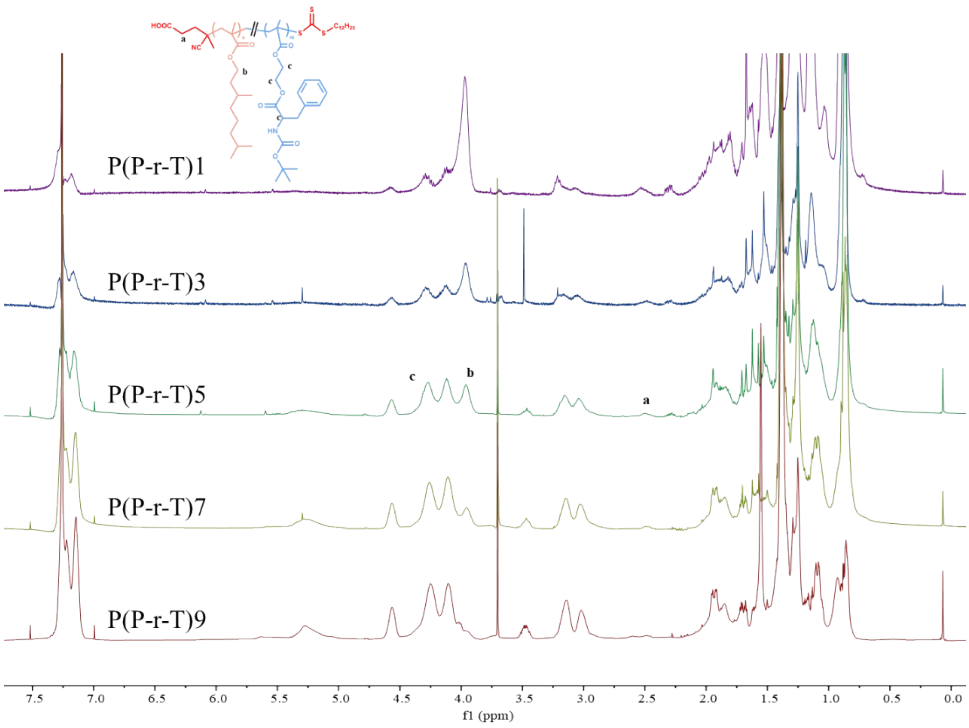

Figure S14. ^{1}H NMR spectrum of random copolymers (with boc protection) with different feed ratios of Phe and THGA in chloroform-D_1.

The calculation method takes P(P-r-T)5 as an example as follows: Peak a of **Figure S15** accounts for 2 protons from the R group of the RAFT agent. Comparing the integration of this peak to those from side chains of monomer give the DP for the polymer.

For instance, peak b constitutes 2 protons of the THGA monomers. Therefore, the average number of THGA units per polymer chain equates to 7.11. Similarly, the peak c constitutes 5 protons of the Phe-

Hema monomers. Therefore, the average number of Phe-Hema per polymer chain equates to (20.84/5)*2 = 8.34.

DP is the average total number of monomer units per polymer chain and is the sum of these values (7.11+8.34=15.45). This is rounded to a DP value of 15.

MP_{THGA} (mole percentage of hydrophobic side chains) is simply the number of THGA containing units divided by the total number of monomer units (DP) and would be 7.11/15 = 47%

To work out the M_n of the polymer, you take the number of each of the relevant repeat units and multiply by the relevant molecular weight of monomers (THGA = 228.38 g $mol^{-1}$and Phe-Hema=379.45 g mol^{-1}) then add the molecular weight of the RAFT agent (403.67 g mol^{-1}). This would be as follows: (7.11*228.38)+(8.34*379.45)+403.67 = 5190 g mol^{-1}.

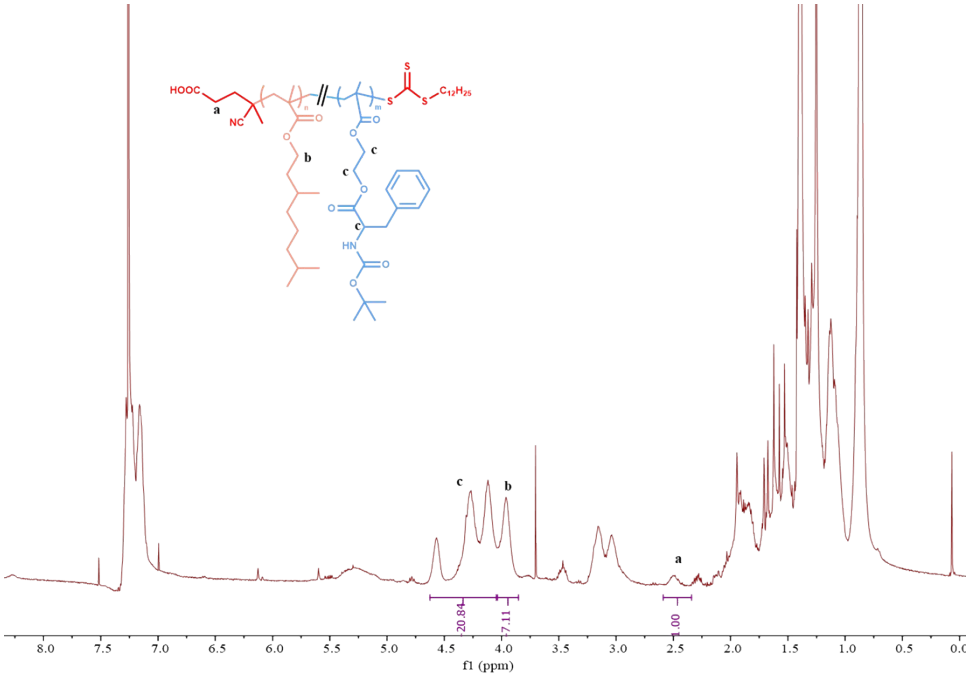

Figure S15. ^{1}H NMR spectrum of P(P-r-T)5 (with boc protection) in chloroform-D_1.

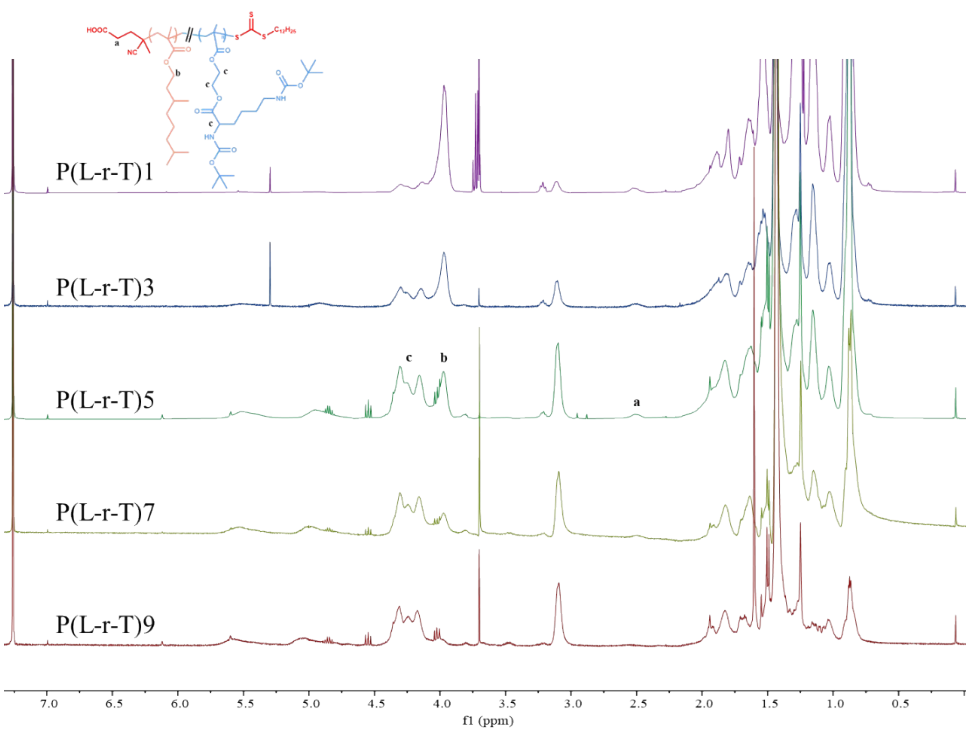

Figure S16. ^{1}H NMR spectrum of random copolymers (with boc protection) with different feed ratios of Lys and THGA in chloroform-D_1.

The calculation method takes P(L-r-T)5 as an example as follows: Peak a of **Figure S17** accounts for 2 protons from the R group of the RAFT agent. Comparing the integration of this peak to those from side chains of monomer give the DP for the polymer.

For instance, peak b constitutes 2 protons of the THGA monomers. Therefore, the average number of THGA units per polymer chain equates to 7.91. Similarly, the peak c constitutes 5 protons of the Lys-Hema monomers. Therefore, the average number of Lys-Hema per polymer chain equates to (19.26/5)*2 = 7.70.

DP is the average total number of monomer units per polymer chain and is the sum of these values (7.70+7.91=15.61). This is rounded to a DP value of 16.

MP_{THGA} (mole percentage of hydrophobic side chains) is simply the number of THGA containing units divided by the total number of monomer units (DP) and would be 7.91/16 = 50.7%

To work out the M_n of the polymer, you take the number of each of the relevant repeat units and multiply by the relevant molecular weight of monomers (THGA = 228.38 g mol^{-1}and Lys-Hema=460.57 g mol^{-1}) then add the molecular weight of the RAFT agent (403.67 g mol^{-1}). This would be as follows: (7.91*228.38)+(7.70*460.57)+403.67 = 5760 g mol^{-1}.

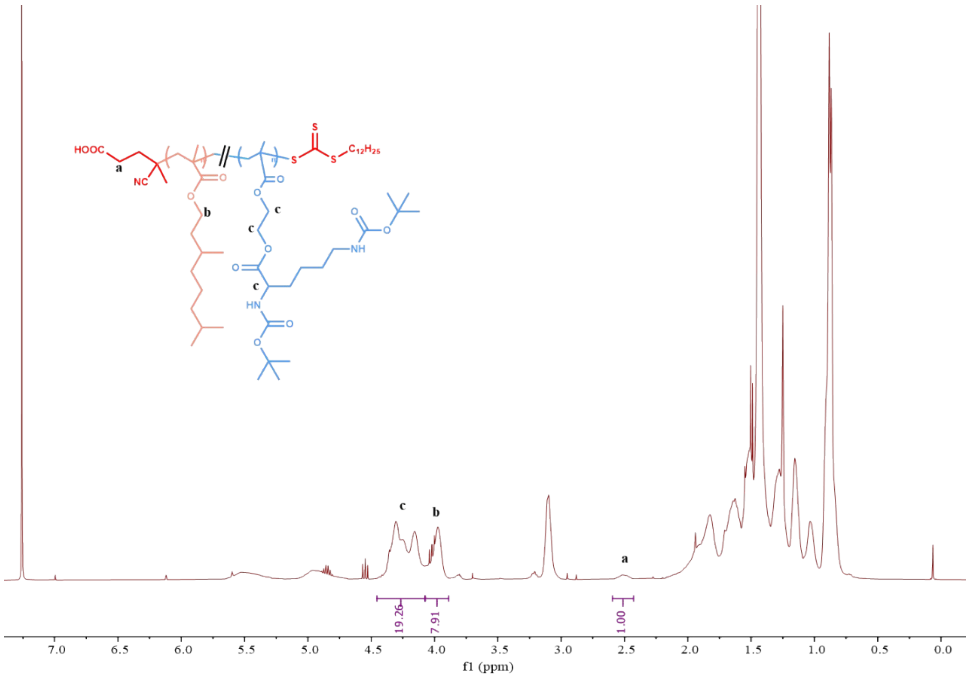

Figure S17. ^{1}H NMR spectrum of P(L-r-T)5 (with boc protection) in chloroform-D_1.

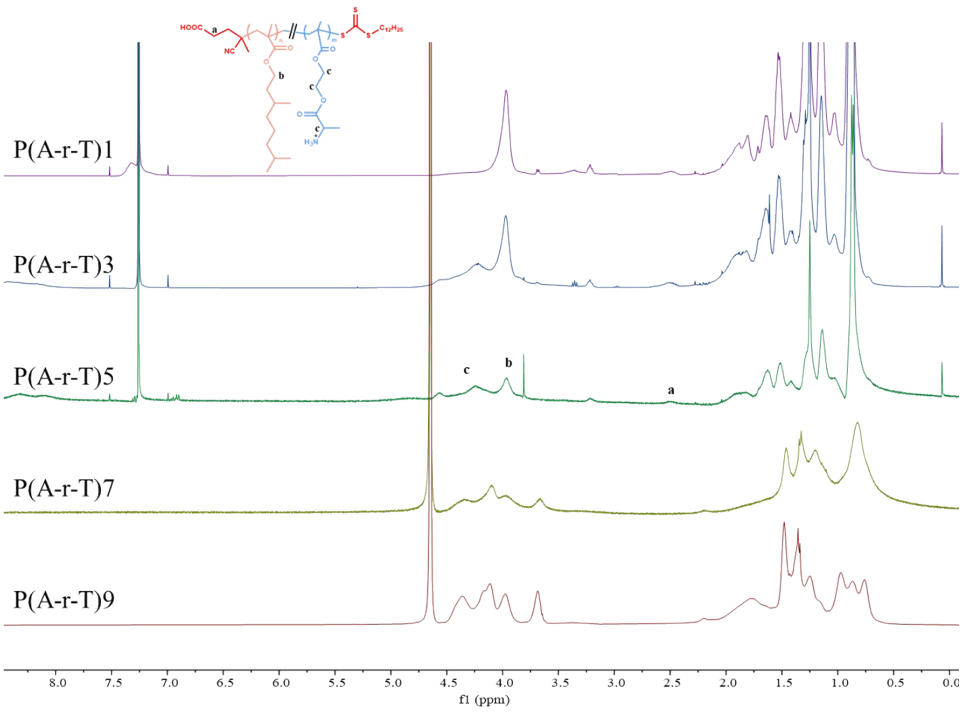

Figure S18. ^{1}H NMR spectrum of random copolymers (without boc protection) with different feed ratios of Ala and THGA (P(A-r-T)1, P(A-r-T)3, P(A-r-T)5 in chloroform-D_1; P(A-r-T)7, P(A-r-T)9 in D_2O).

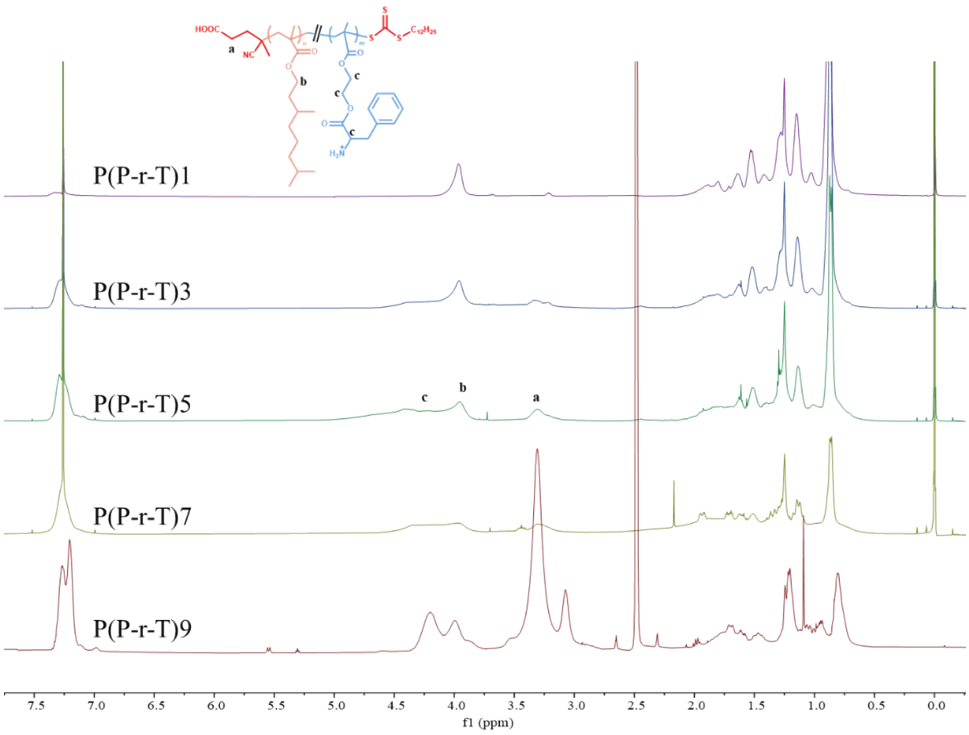

Figure S19. ^{1}H NMR spectrum of random copolymers (without boc protection) with different feed ratios of Phe and THGA in chloroform-D_1.

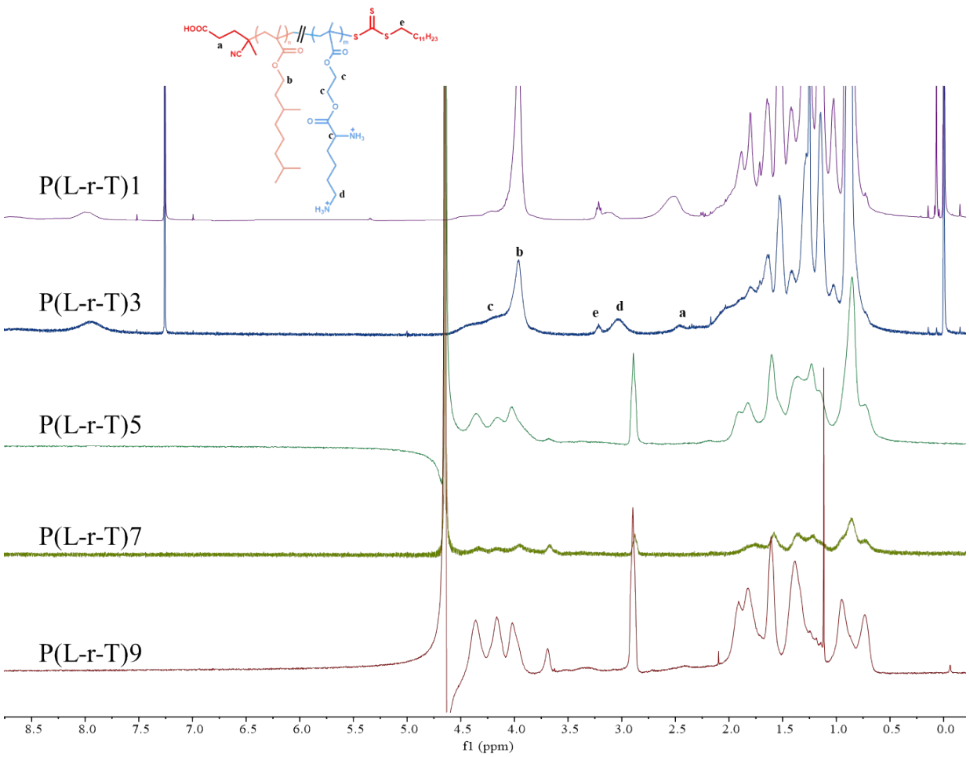

Figure S20. ^{1}H NMR spectrum of random copolymers (without boc protection) with different feed ratios of Lys and THGA (P(L-r-T)1, P(L-r-T)3in Chloroform-D_1; P(L-r-T)5, P(L-r-T)7, P(L-r-T)9 in D_2O).

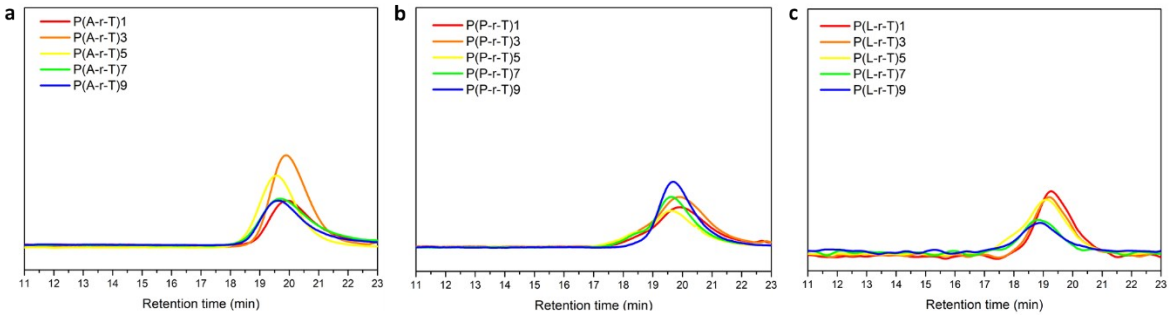

Figure S21. Size exclusion chromatography (SEC) traces of the Boc protected copolymer of Ala (a) Phe (b) Lys (c) dissolved in THF.

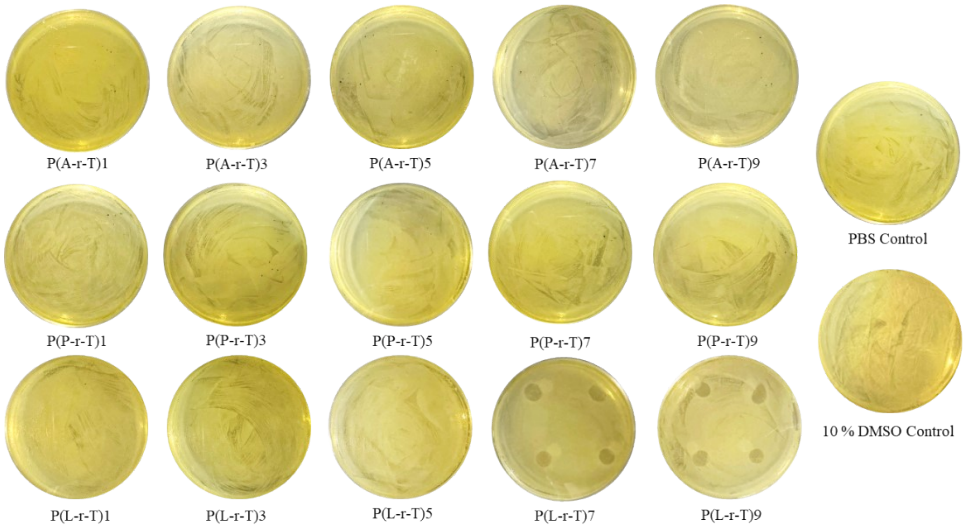

Figure S22. Zone of inhibition of random copolymers with varying cationic monomers and monomer feed ratios against *E. coli* (ATCC 25922).

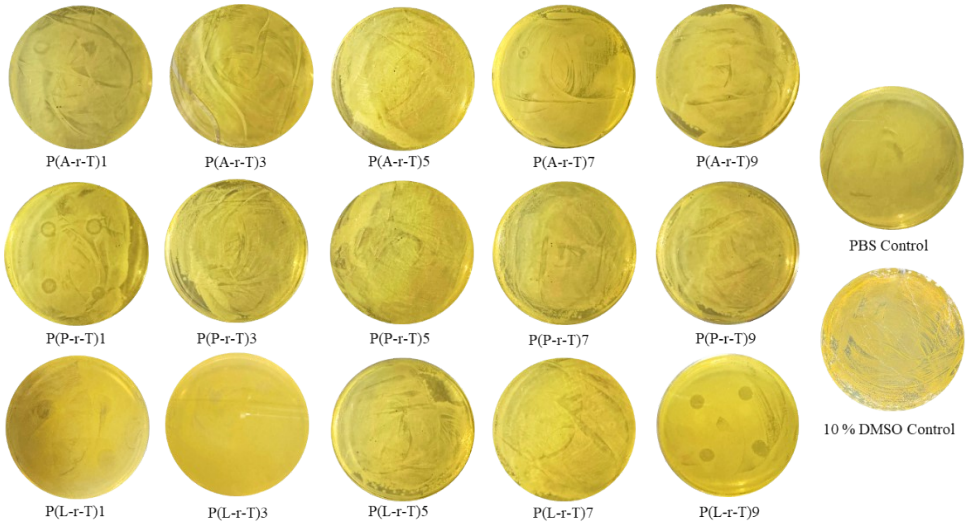

Figure S23. Zone of inhibition of random copolymers with varying cationic monomers and monomer feed ratios against *S. aureus* (ATCC 25922).