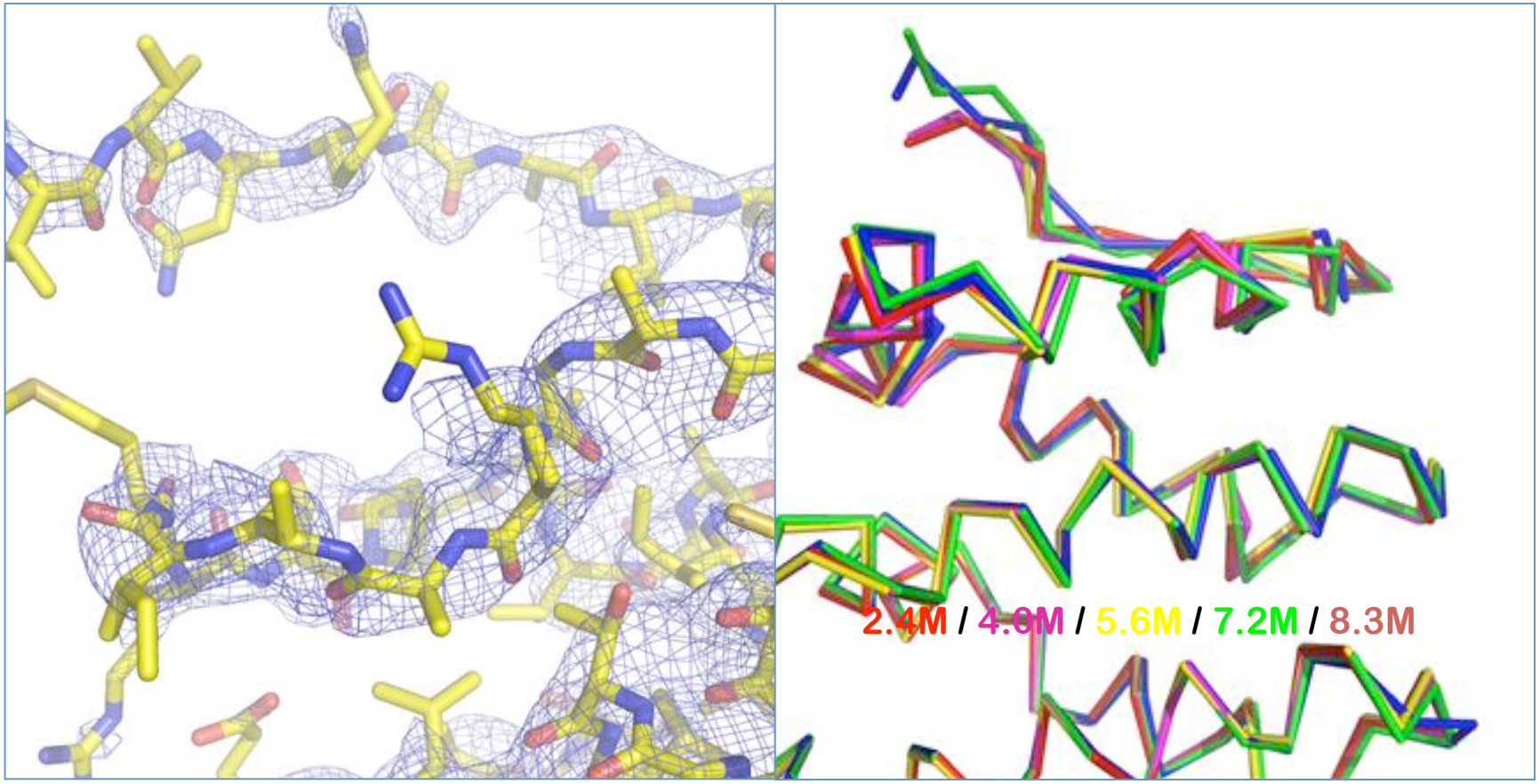

Figure S1. Disordered N-terminal Vs. Urea Conc**.** A. 8.3M Urea model, 2Fo-Fc map with 1.0δ cut off . B. The overlap of the N-terminal at different urea concentration.

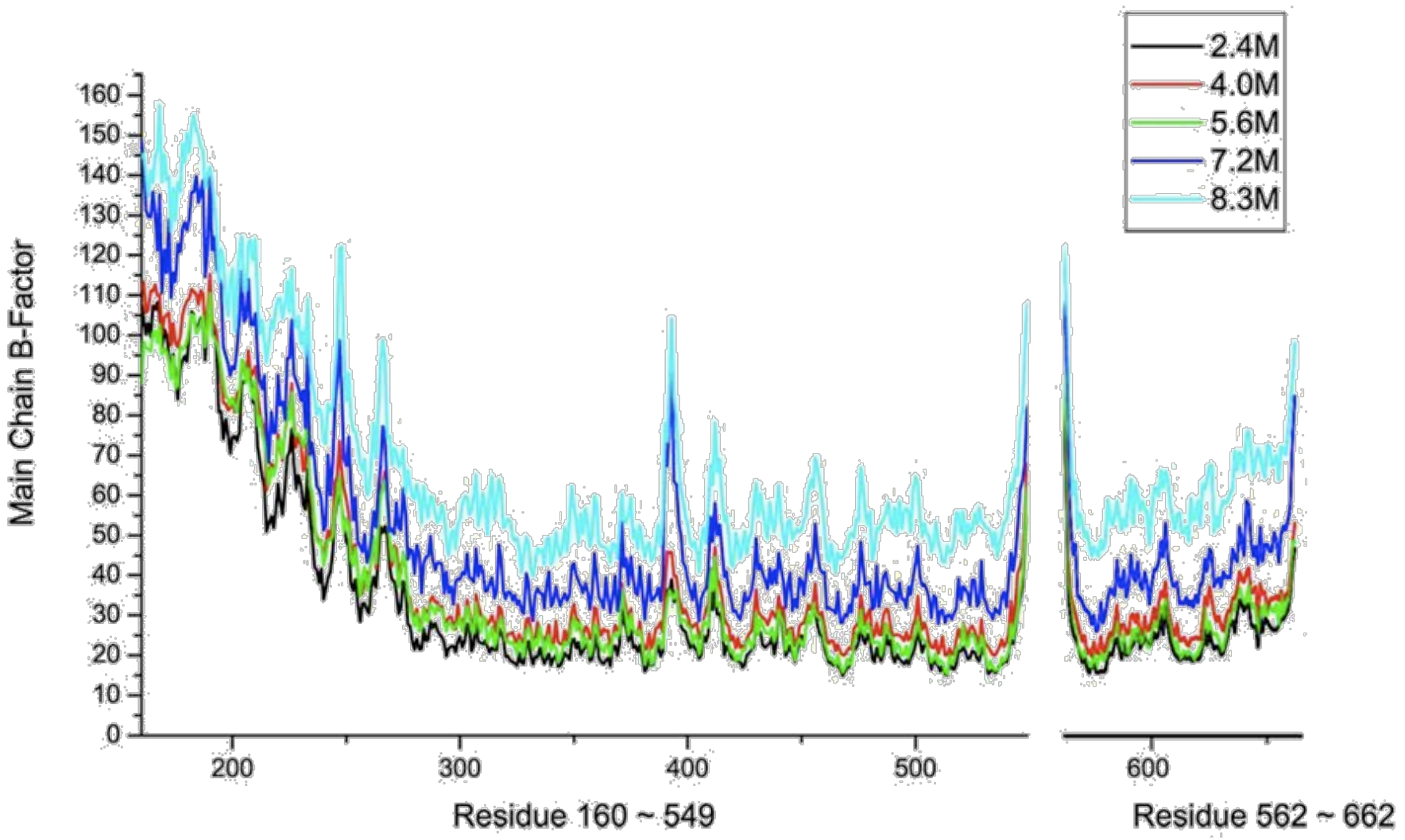

Figure S2. Increased B - factor Vs. Urea Conc.

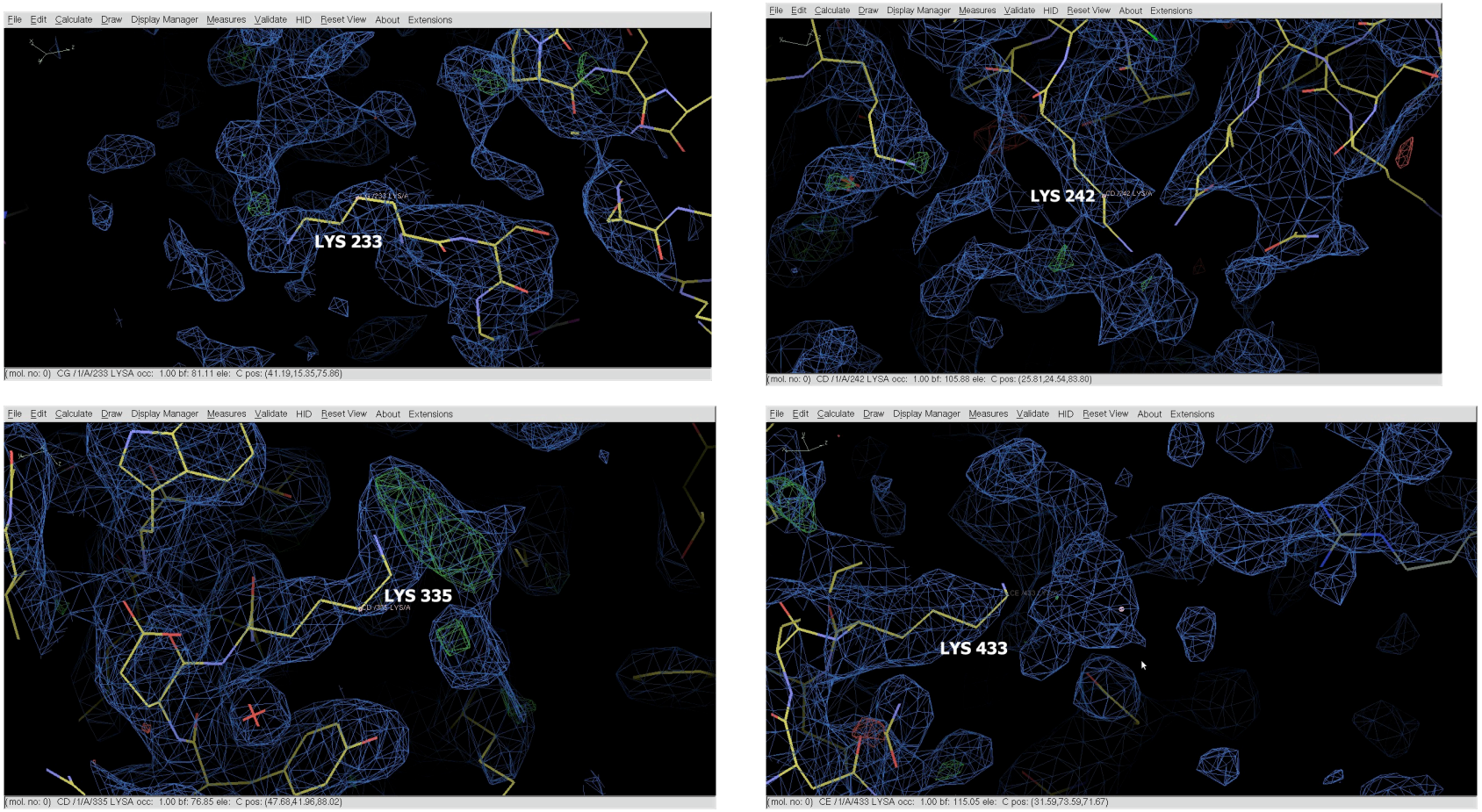

Figure S3. Modified side chains of Lys residues from cross-linked structures. Due to low occupancy, no continuous density was oberserved between two side chains of Lys residues.

Table S1. Data processing statistics

Data Set	2.4 M	4.0 M	5.6 M	7.2 M	8.3 M
Wavelength(Å)	1.0000	1.0000	1.0000	1.0000	1.0000
Resolution(Å)	50.0 ~ 1.9	50.0 ~ 2.1	50.0 ~ 2.0	50.0~2.15	50.0 ~ 2.4
Completeness (%)	96.6(90.3)	99.3(93.2)	86.1(75.7)	100(99.7)	99.6(94.9)
R_{sym} (last shell)	7.2% (68.0%)	12.0% (91.5%)	6.1% (65.5%)	10.7% (93.2%)	6.5% (73.4%)
I/δ (last shell)	26.1(2.7)	21.2(1.6)	27.5(3.0)	16.4(2.1)	29.1(1.6)
Redundancy (last shell)	7.4(6.2)	13.1(7.4)	6.6(7.0)	7.2(6.6)	8.0(5.3)

$$Rsym = \sum_{hkl}\sum_{i=1}^{n} | I_i(hkl) - I_i(\overline{h}\overline{k}\overline{l}) | / \sum_{hkl}\sum_{i=1}^{n} I_i(hkl)$$

Table S2. Model refinement statistics

Data Set		2.4 M	4.0 M	5.6 M	7.2 M	8.3 M
Resolution(Å)		50.0 ~ 1.9	50.0 ~ 2.1	50.0 ~ 2.0	50.0~2.15	50.0 ~ 2.4
Space Group		$C222_1$	$C222_1$	C2	$C222_1$	$C222_1$
Cell		a=64.185 b=102.587 c=187.092 α=β=γ=90	a=64.185 b=102.618 c=187.255 α=β=γ=90	a=64.271 b=102.719 c=187.559 α=γ=90, β=90.14	a=64.154 b=102.441 c=186.871 α=β=γ=90	a=64.748 b=102.606 c=187.392 α=β=γ=90
Reflections used/free		45018/2288	33978/1700	70232/3542	30952/1594	22898/1169
R / R_{free} (%)		17.3/21.8	18.8/23.6	18.7/23.2	19.3/24.8	18.9/24.7
Number of atoms		4342	4227	8630	4092	4056
Number of Ureas		19	49	42+34	44	56
Number of Waters		511	268	898	145	90
RMSD	Bond lengths	0.008Å	0.003Å	0.004Å	0.002Å	0.003Å
	Bond angles	1.017°	0.642°	0.725°	0.564°	0.606°
Ramachandran favorite		95.0%	94.1%	94.9%	93.2%	93.0%

*R-factor = ∑(|Fo - Fc|)/ ∑|Fo|; R-free = R factor for a selected subset of the reflections that was not included in refinement calculations.

Table S3. Buffer systems for CD measurements

pH	
8.5	20 mM Tris-HCl, 50 mM NaCl
9.5	25 mM $Na_2B_4O_7$, 50 mM NaCl
10.5	25 mM $NaHCO_3$, 50 mM NaCl
11.5	20 mM KCl, 0.00316 M NaOH
12.0	20 mM KCl, 0.01 M NaOH
12.5	20 mM KCl, 0.0316 M NaOH
13.0	20 mM KCl, 0.1 M NaOH

Table S4. Buffer conditions for PCR

Final Urea Concentration (M)	0.0	0.32	0.32	0.64	0.64	0.96	0.96	1.28	1.28
10× PCR Buffer (μL)	5.0								
10 mM Forward Primer (μL)	2.5								
10 mM Reverse Primer (μL)	2.5								
Template (μL)	1.0								
10 mM dNTP (μL)	1.0								
Taq (μL)	2.0								
8.0 M Urea (μL)		2.0	2.0	4.0	4.0	6.0	6.0	8.0	8.0
50% PEG 8K (μL)			2.0		5.0		8.0		10.0
ddH_2O	add to 50.0 μL								

Table S5. PCR experiments

Cycle step	Temperature	Time	Cycles
Initial denaturation	95°C	5 min	1
Denaturation	95°C	30 sec	30
Annealing	55°C	30 sec	
Extension	72°C	45 sec	
Final extension	72°C	10 min	1