SUPPORTING INFORMATION

Structural study of a small molecule receptor bound to dimethyllysine in lysozyme

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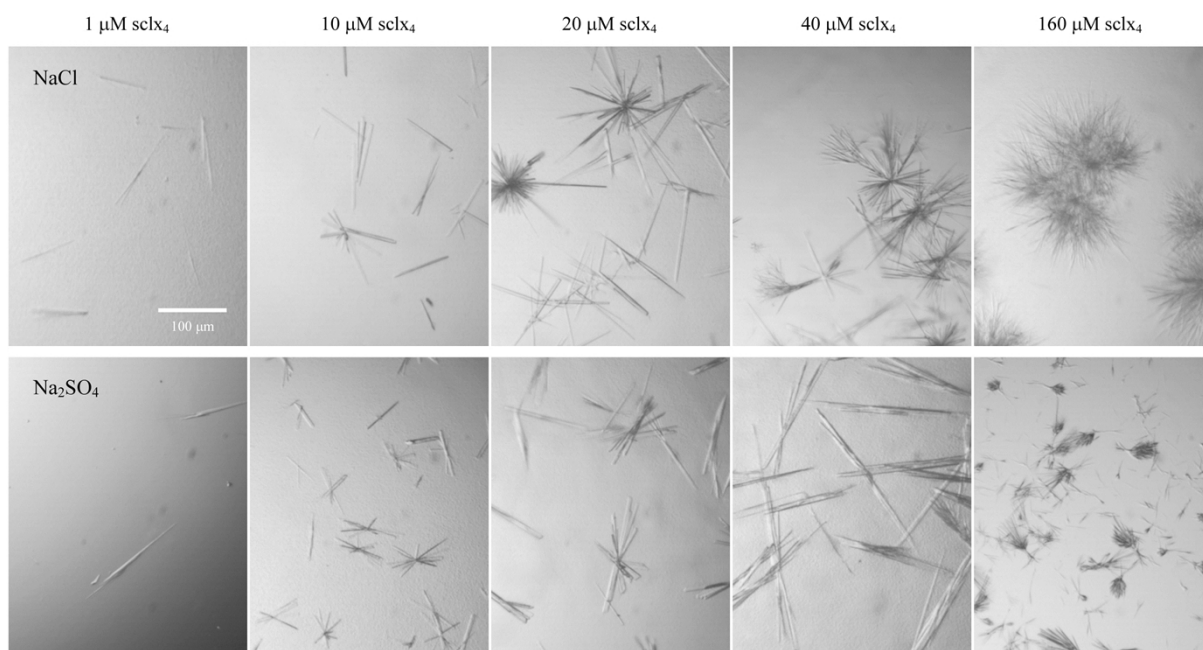
Figure S1. Crystals of the lysozyme-KMe$_2$:sclx$_4$ complex grew in the presence of different concentrations of sclx$_4$. The crystallization drops contained 20 µM lysozyme-KMe$_2$, 1-160 µM sclx$_4$, 20 mM NaCl or Na$_2$SO$_4$ and 10 mM (CH$_3$)$_2$AsO$_2$Na (cacodylate) at pH 6. There was no precipitant (*e.g.* PEG or ammonium sulfate) in the drops. Crystals were evident two days after the experiment set up.
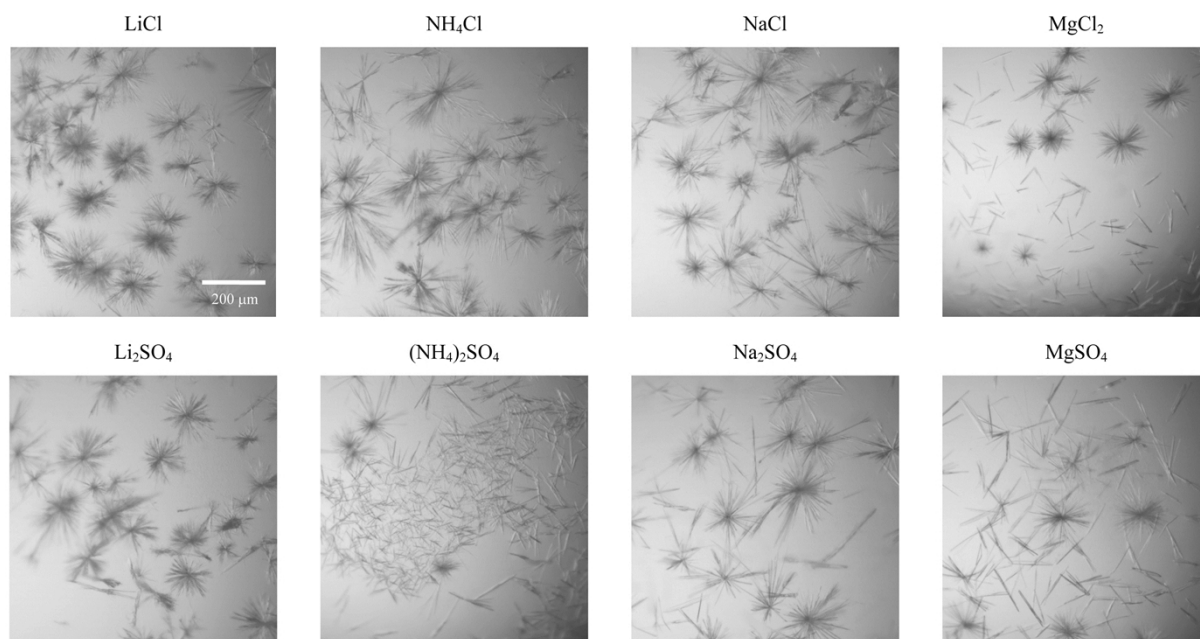
Figure S2. Crystals of the lysozyme-KMe$_2$:sclx$_4$ complex grew in the presence of different chloride- and sulfate-containing salts. The crystallization drops contained 20 µM lysozyme-KMe$_2$, 10 µM sclx$_4$, 20 mM salt and 10 mM (CH$_3$)$_2$AsO$_2$Na (cacodylate) at pH 6. There was no precipitant (*e.g.* PEG or ammonium sulfate) in the drops. Crystals were evident two days after the experiment set up.
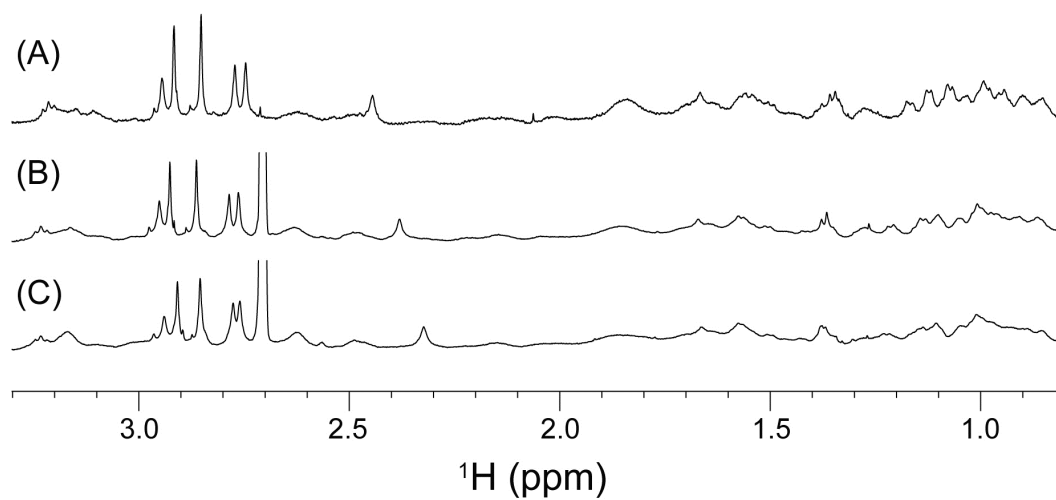
Figure S3. 1D ^{1}H NMR spectra (showing the region corresponding to -NMe$_2$ resonances and further upfield) of lysozyme-KMe$_2$ in (A) 40 mM sodium phosphate, pH 7.4, (B) 40 mM sodium phosphate, 10 % DMSO-d_6, pH 7.4, and (C) 40 mM sodium phosphate, 20 % DMSO-d_6, pH 7.4. The signal at ~2.7 ppm corresponds to DMSO.

Table S1. Summary of crystallization conditions, data collection and refinement statistics

Crystallization Conditions[a]		
[protein], [sclx$_4$] (mM)	0.5, 2.5	0.5, 4.3
PEG 8000 (%)	6	18
Buffer, $(CH_3)_2AsO_2Na$	0.1 M, pH 6.1	0.05 M, pH 6.3
Salts	0.05 M NaCl, 0.1 M MgCl$_2$	
Data Collection[b]		
Space group	$P2_1$	$P2_1$
Cell constants	$a = 45.85$ Å	$a = 44.04$ Å
	$b = 30.20$ Å	$b = 30.28$ Å
	$c = 94.21$ Å	$c = 95.01$ Å
	$\alpha = \gamma = 90º$	$\alpha = \gamma = 90º$
	$\beta = 96.31º$	$\beta = 96.62º$
Resolution (Å)	31.32-1.90 (1.95-1.90)	39.41-2.20 (2.26-2.20)
Wavelength (Å)	0.95372	1.033190
Unique reflections	20709 (19591)	44504 (13557)
Multiplicity	3.6 (3.5)	3.3 (3.3)
I/σ	9.2 (2.6)	7.9 (3.7)
Completeness (%)	94.6 (90.1)	99.6 (98.9)
R_{merge}[c] (%)	8.4 (41.1)	13.0 (73.4)
Solvent content (%)	45.02	49.53
Refinement		
PDB ID	4N0J	4PRU
R_{factor} (%)	16.77	18.00
R_{free} (%)	21.04	23.52
rmsd[d] bonds (Å)	0.01	0.01
rmsd angles (°)	1.19	1.53
# molecules in asymmetric unit		
Protein	2	2
Sclx$_4$	4	4
Na$^+$	1	-
Mg^{2+}	2	-
Cl$^-$	3	-
Glycerol	5	2
Solvent	191	97
Average *B* factors[e] (Å^2)		
Protein	13.12	27.57
Sclx$_4$	17.79	33.56
Na$^+$	16.85	-
Mg^{2+}	19.13	-
Cl$^-$	18.12	-
Glycerol	25.64	38.37
Solvent	23.75	30.65
Ramachandran analysis[f]		
% residues (favoured regions)	97.95	98.0
% residues (allowed regions)	100.0	98.5

[a]The crystallization drops comprised 1 μL each of the protein, ligand and reservoir solution; [b]Values in parentheses correspond to the highest resolution shell; [c]$R_{merge} = \sum_{hkl} \sum_i |I_i(hkl) - \langle I(hkl)\rangle|/\sum_{hkl} \sum_i I_i(hkl)$; [d]root mean square deviation; [e]calculated from the B values of all non-hydrogen atoms; [f]calculated with Molprobity.

Movie S1. Movie of the MD simulation of sclx$_4$ binding to Lys116-Me$_2$. Each frame corresponds to a 100 ps time point over the 10 ns simulation. The simulation was run in explicit solvent but the waters are not shown. The side chains of Asn106 and Arg112 are shown as sticks. Note the formation of hydrogen bonds and salt bridges between these side chains and sclx$_4$.