

Supplementary Information

**Surfactant-like peptide gels are based on cross- $\beta$  amyloid fibrils**

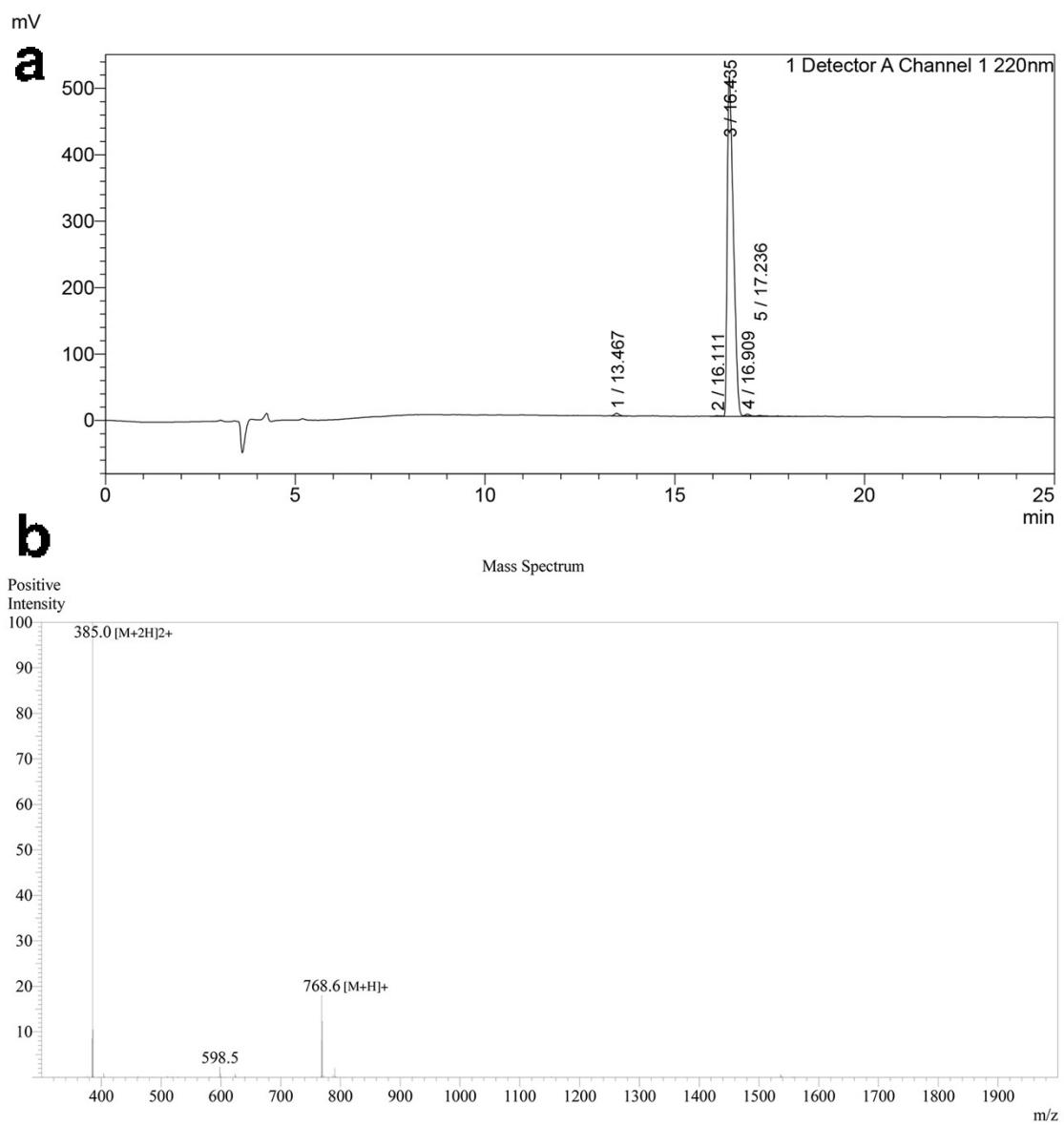
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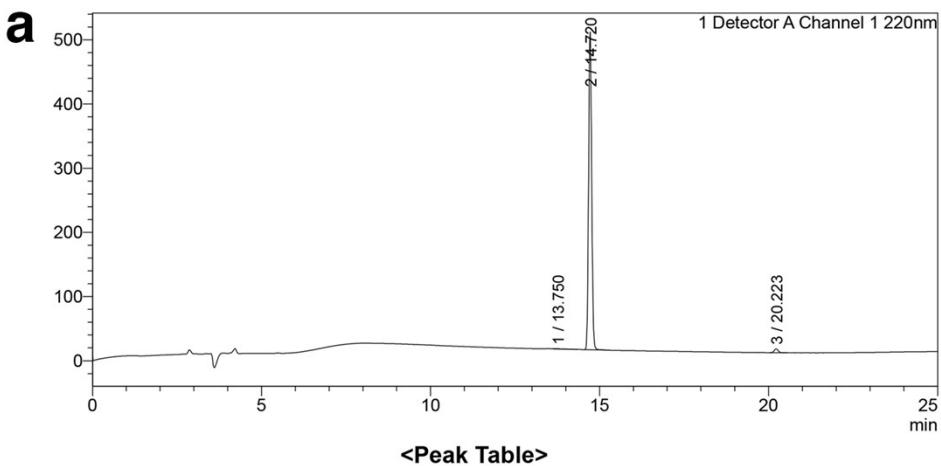
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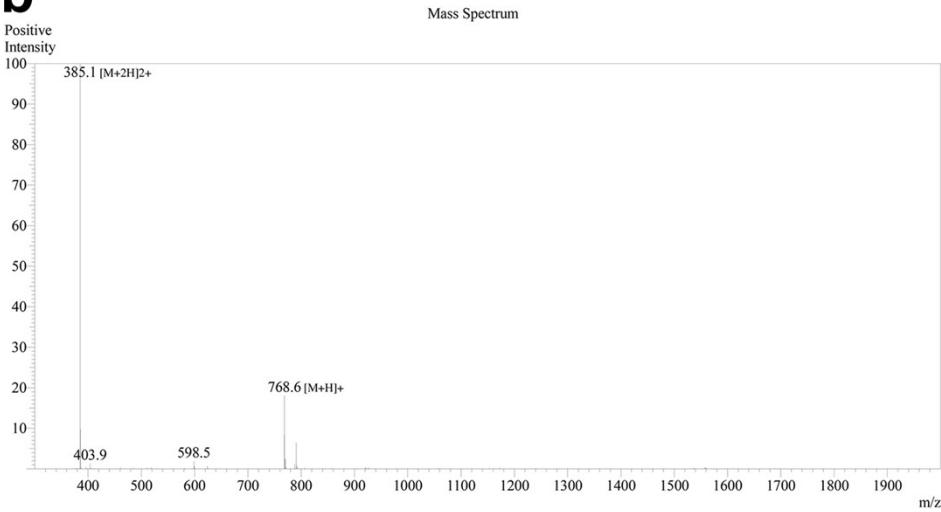
**Fig. S1** Analytical HPLC (a) and ESI-MS (b) data for peptide **L2**, Ac-KLIIIK-NH<sub>2</sub>. Peptide purity was estimated at 98.6%. Calculated monoisotopic mass for Ac-KLIIIK-NH<sub>2</sub>, 767.6 Da; experimental mass from mass spectrum, 767.6 Da.



Detector A Channel 1 220nm

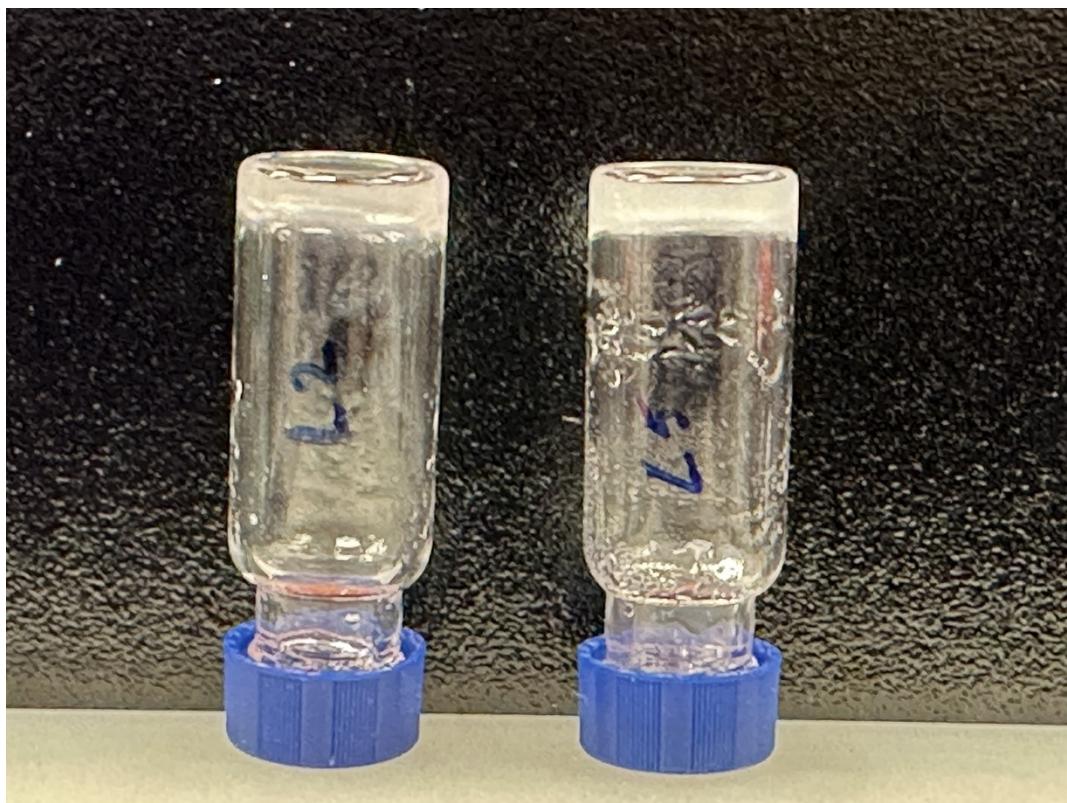
| Peak# | Ret. Time | Area    | Height | Area%   |
|-------|-----------|---------|--------|---------|
| 1     | 13.750    | 11848   | 565    | 0.368   |
| 2     | 14.720    | 3158174 | 495365 | 98.107  |
| 3     | 20.223    | 49101   | 5944   | 1.525   |
| Total |           | 3219123 | 501873 | 100.000 |

**b**

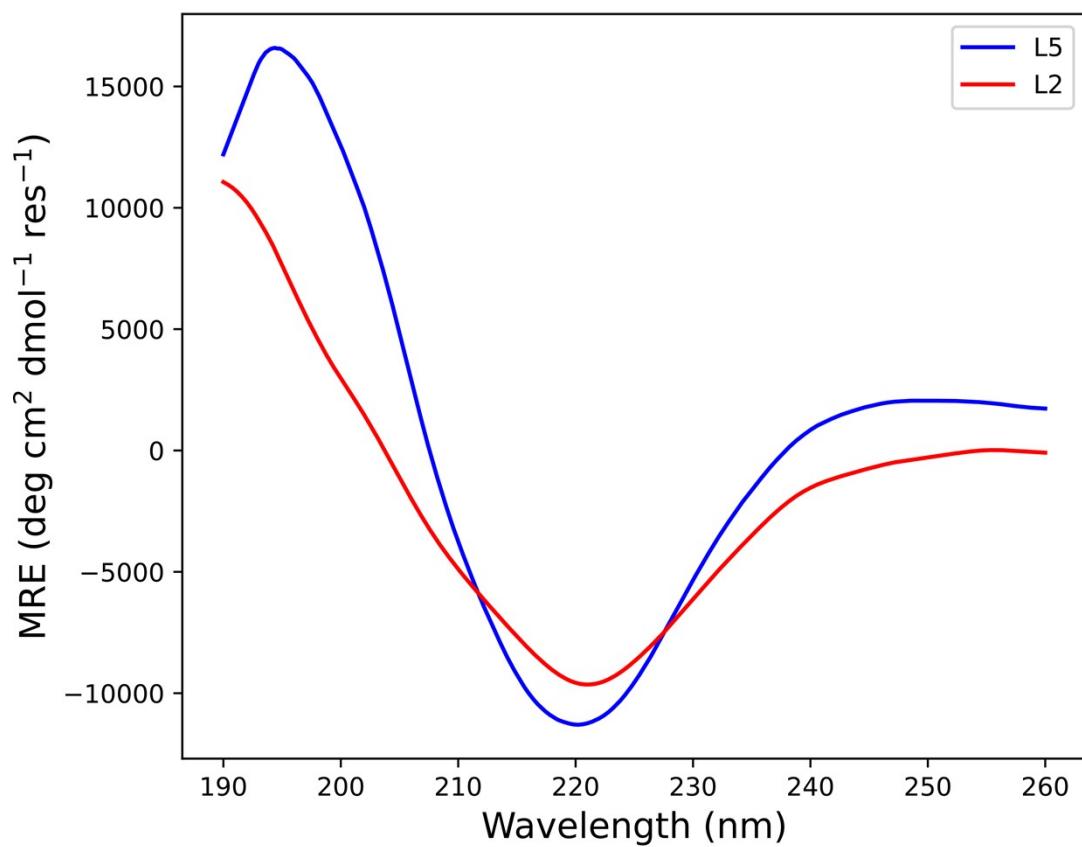


|                       |              |                     |           |                 |                 |
|-----------------------|--------------|---------------------|-----------|-----------------|-----------------|
| Sample Information    |              | Interface           | :ESI      | Equipment       | :ZJ22010150     |
| Month-Day Processed : | 07/15/22     | Nebulizing Gas Flow | :1.5L/min | Interface Bias  | :+4.5 kV        |
| Time Processed :      | 17:26:55     | CDL Temp            | :250      | Drying Gas Flow | :5 L/min        |
| Injection Volume :    | 0.1          | Block Temp          | :200      | T.Flow          | :0.2 mL/min     |
| Sample Name :         | KIILK        |                     |           | B.conc          | :50%H2O/50%MeOH |
| Sample ID :           | L4596HG100-1 |                     |           |                 |                 |
| Theoretical MW :      | 768.05       |                     |           |                 |                 |
| Observed MW :         | 768.2        |                     |           |                 |                 |

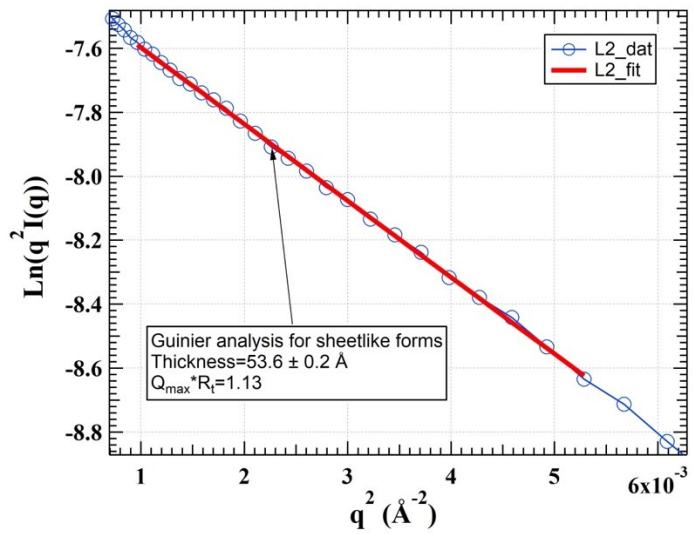
**Fig. S2** Analytical HPLC (a) and ESI-MS (b) data for peptide **L5**, Ac-KIIILK-NH<sub>2</sub>. Peptide purity was estimated at 98.1%. Calculated monoisotopic mass for Ac-KIIILK-NH<sub>2</sub>, 767.6 Da; experimental mass from mass spectrum, 767.6 Da.



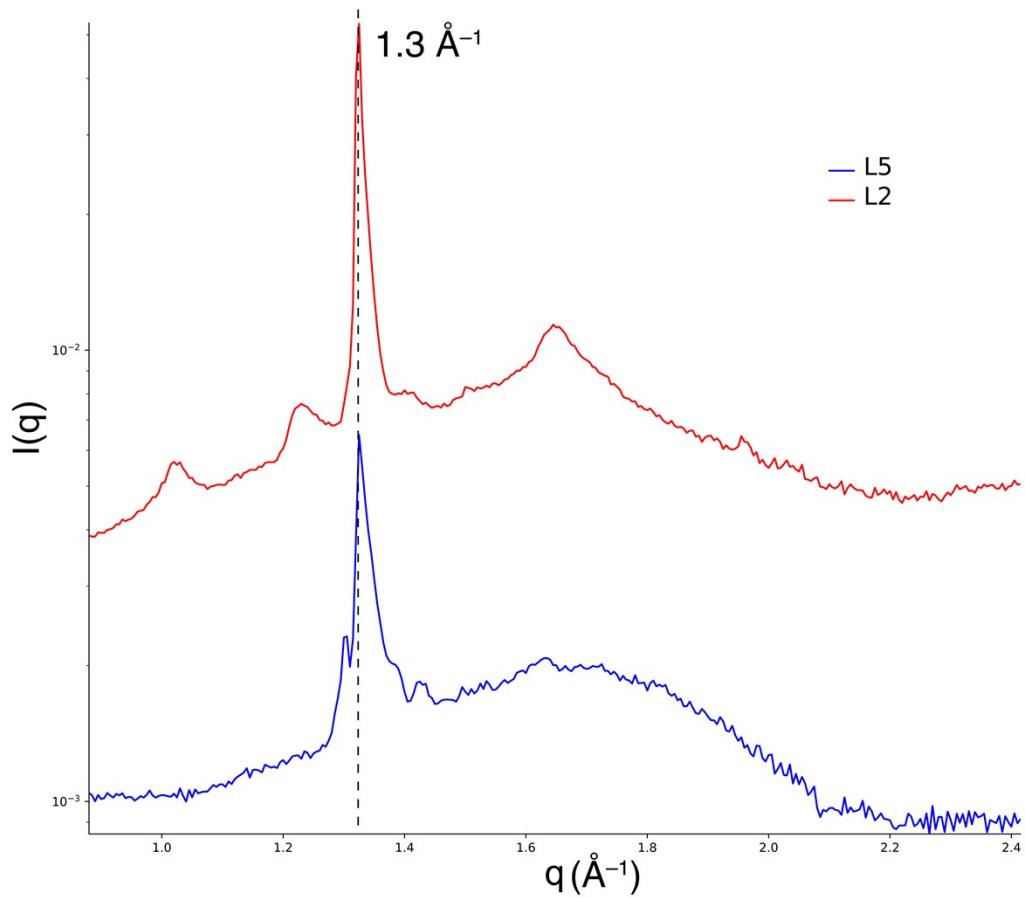
**Fig S3.** Inversion test for hydrogel formation from solutions of peptides **L2** (left) and **L5** (right) incubated for seven days at ambient temperature (32 mM in ddH<sub>2</sub>O).



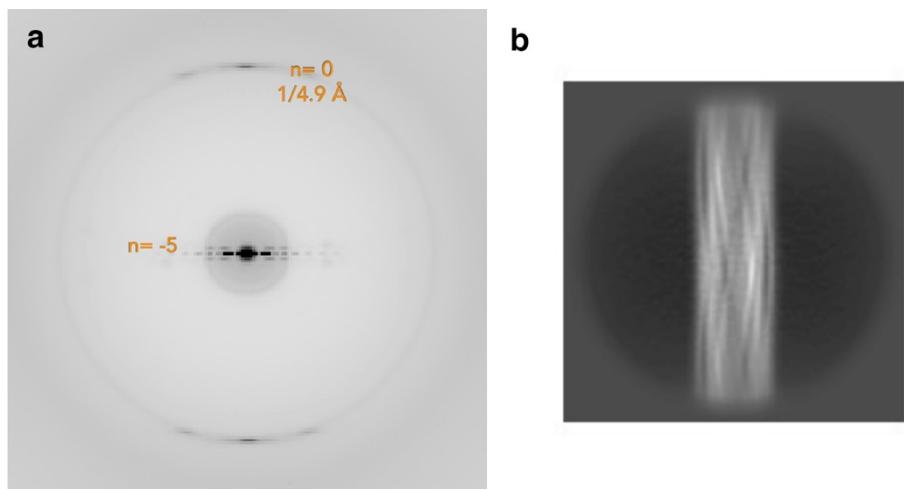
**Fig. S4** Circular dichroism (CD) spectropolarimetry of bola-like peptides; Ac-KLIIIK-NH<sub>2</sub> (**L2**) and Ac-KIIILK-NH<sub>2</sub> (**L5**). Samples were incubated in ddH<sub>2</sub>O for 2 weeks and diluted to a concentration of 25 mM.



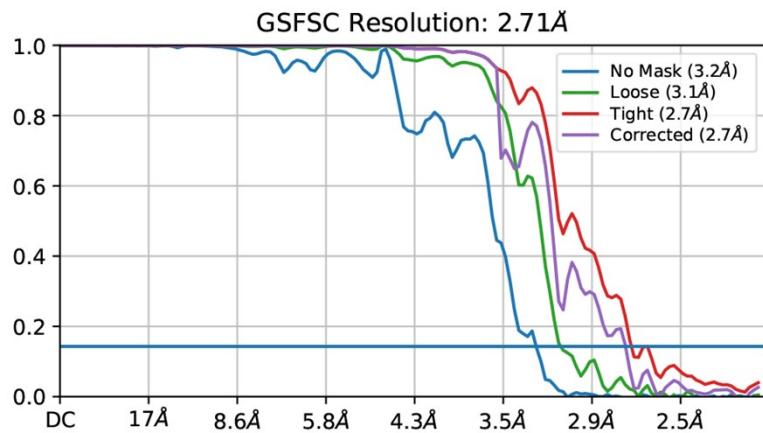
**Fig. S5** Modified Guinier analysis for sheet-like forms applied to the experimental SAXS scattering data for the L2 (32 mM) in ddH<sub>2</sub>O.



**Fig. S6** Synchrotron wide-angle X-ray scattering (WAXS) measurements for peptide assemblies in aqueous solution (32 mM). The line indicates the position of the momentum transfer ( $q$ ) associated with a Bragg distance ( $d$ ) of  $\sim 4.7 \text{ \AA}$ , which corresponds to the hydrogen-bonding distance between strands in a cross- $\beta$  fibril.



**Fig. S7** Averaged power spectra (**a**) and representative class average (**b**) derived from cryo-EM analysis of Ac-KIIILK-NH<sub>2</sub> (**L5**) filaments. The positions of the indexed layer lines and associated Bessel orders are highlighted in the power spectrum.



**Fig. S8** “Gold-standard” map:map Fourier Shell Correlation (FSC) calculation for the L5 nanotube using a 0.143 criterion.

**Table S1** Cryo-EM and refinement statistics for the Ac-KI<sub>3</sub>LK-NH<sub>2</sub> (**L5**) nanotubes.

| Parameter                               | Ac-KI <sub>3</sub> LK-NH <sub>2</sub> ( <b>L5</b> ) |
|---|---|
| <b>Data collection and processing</b>   |   |
| Voltage (kV)                            | 300   |
| Electron exposure (e-/ Å <sup>2</sup> ) | 48.0  |
| Pixel size (Å)                          | 1.08  |
| Particle images (n)                     | 702,524   |
| <b>Helical symmetry</b>                 |   |
| Point group                             | C5  |
| Helical rise (Å)                        | 4.94  |
| Helical twist (°)                       | -1.77   |
| <b>Map resolution (Å)</b>               |   |
| Reconstruction software                 | CryoSPARC   |
| Model:map FSC (0.5)                     | 3.1   |
| Map:map FSC (0.143)                     | 2.7   |
| <b>Refinement and Model validation</b>  |   |
| <b>Map sharpening method</b>            |   |
| DeepEMhancer                            |   |
| RSCC                                    | 0.86  |
| Bond lengths rmsd (Å)                   | 0.013   |
| Bond angles rmsd (°)                    | 1.759   |
| Clashscore                              | 0.18  |
| Ramachandran Favored (%)                | 98.9  |
| Ramachandran Outlier (%)                | 0   |
| MolProbity score                        | 0.57  |
| <b>Deposition ID</b>                    |   |
| PDB (model)                             | 9CZ3  |
| EMDB (Map)                              | 46060   |