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Supporting Information

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Active Cross-Linkers that Lead to Active Gels**

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Supplementary Materials

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S1 Synthesis of active cross-linker (1) and general method of preparation of gel disks

Materials and methods

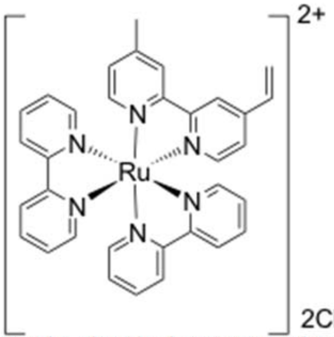
Anhydrous DMF, 4,4’-dimethyl-2,2’-bipyridine (99.5%), N,N-diisopropylethylamine (DIEA), allylamine (98%), and dichloro(*p*-cymene)ruthenium(II) dimmer, 2-hydroxy-4’-(2-hydroxyethoxy)-2-methylpropiophenone (Irgacure 2959), *N*-isopropylacrylamide (NIPAAm) (≥99%) were purchased from Sigma-Aldrich. *O*-benzotriazole-*N*,*N*,*N’*,*N’*-tetramethyl-uronium-hexafluoro-phosphate (HBTU) was purchased from GL Biochem. Sephadex LH-20 was purchased from GE Healthcare.

***N,N’*-diallyl-[2,2’-bipyridine]-4,4’-dicarboxamide**:

4,4’-dicarboxy-2,2’-bipyridine (5 mmoL, 1.22 g) and HBTU (15 mmol, 5.7 g) were charged in a round bottom flask, and anhydrous DMF (15 mL) was added into the flask. The mixture was stirred at room temperature until mixed well. DIEA (30 mmol, 3.8 mL) was added into the mixture and kept stirring for 10 min. Then allylamine (25 mmol, 1.87 mL) was slowly added into the flask. After overnight stirring, the precipitates were collected and washed by ethyl acetate to obtain white crystals as the pure product in a yield of 85%. ^{1}H NMR (400 MHz, DMSO-d_6) δ 9.16 (s, 2H), 8.87 (d, *J* = 4.4 Hz, 2H), 8.82 (s, 2H), 7.87 (d, *J* = 4.4 Hz, 2H), 5.97-5.87 (m, 2H), 5.21 (d, *J* = 17.2 Hz, 2H), 5.12 (d, *J* = 10.4 Hz, 2H), 3.96 (s, 4H) ppm.

The active cross-linker (**1**):

N,N’-diallyl-[2,2’-bipyridine]-4,4’-dicarboxamide (3 mmoL, 967 mg) and dichloro(*p*-cymene)ruthenium(II) dimmer (0.5 mmol, 306 mg) were charged into a two-neck round bottom flask that connected to a condenser. Anhydrous DMF (10 mL) was added into the flask and the solution was purged with N_2 for 30 min. Then the solution was refluxed under N_2 and dark for 12 h. After removing the solvent, the crude product was purified through a Sephadex column by using methanol as the eluent. The active cross-linker (**1**) was obtained as dark red powder in a yield of 61%. ^{1}H NMR (400 MHz, DMSO-d_6) δ 9.69 (d, *J* = 5.2 Hz, 6H), 9.35 (s, 6H), 9.00 (s, 6H), 8.11 (d, *J* = 5.2 Hz, 6H), 5.97-5.90 (m, 6H), 5.26 (d, *J* = 16.8 Hz, 6H), 5.17 (d, *J* = 9.6 Hz, 6H), 4.02 (s, 12H) ppm.



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Scheme S1. The chemical structure of Ru-catalyst **2**.

General method of polymerization

For the production of Gel_1 and Gel_2 disks, the mixture for polymerization was prepared by dissolving monomer (N-isopropylacrylamide and allylamine, respectively), hyper cross-linker **1** and Irgacure 2959 (photo-initiator) in mixed solvent of methanol and DI water. After filling the mixture into a polycarbonate mold, a mask was applied on the top of the mode and the set-up was exposed under an Omicure light source for 10-30 mins. To make Gel_3 and Gel_4 disks, monomer (N-isopropylacrylamide and allylamine, respectively), ruthenium catalyst **2** (Scheme S1), N,N'-methylenebisacrylamide and Irgacure 2959 were dissolved in mixed solvent of methanol and DI water and followed the same procedure of making Gel_1 and Gel_2. The Gel disks were immersed in DI water for dialysis for 3 days before further tests.

S2 UV-vis spectrum of active cross-linker (1)

UV-vis spectrum was recorded on Varian 50 Bio UV-visible spectrophotometer.

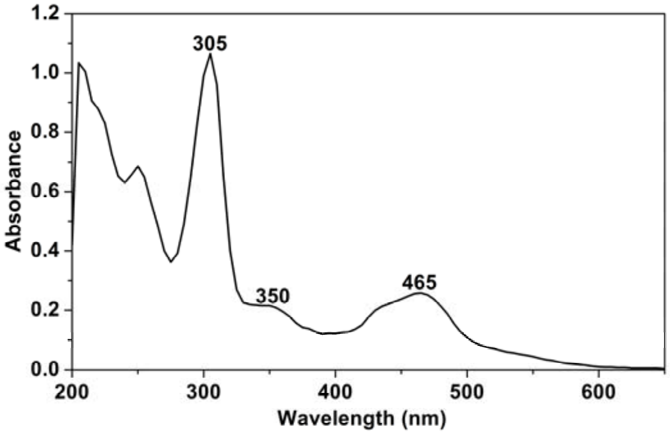

Figure S1. UV-vis absorbance of the Ru-complex (3) at a concentration of 25.5 μmol/L in water.

S3 Rheology

Rheology experiments were performed in the ARES-G2 rheometer with plain plate geometry (25 mm diameter). For gel preparation, when the molar ratio of active cross-linker (**1**) versus NIPAAm is smaller than 0.004, no bulk gel was obtained.

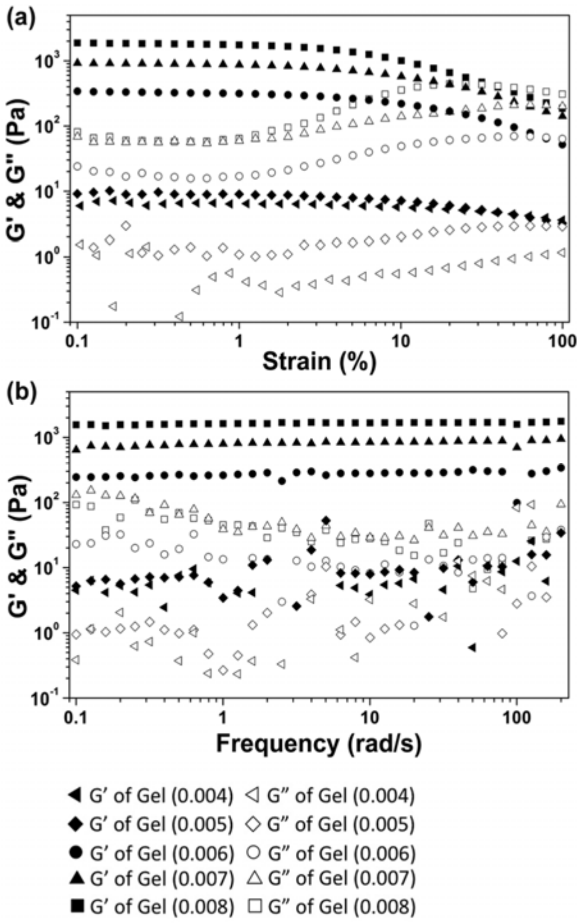

Figure S2. Strain dependence (a) and frequency dependence (b) of dynamic storage modulus (G') and loss modulus (G") of gel series with different molar ratios of active cross-linker (**1**) and monomer NIPAAm.

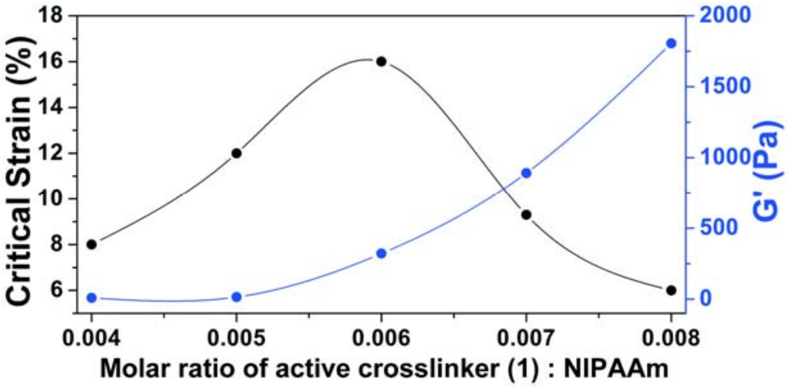

Figure S3. The critical strain (black) and the storage moduli (blue, at 0.5% strain) of the gels versus the mole ratios of active cross-linker (**1**) and monomer NIPAAm applied for polymerizations.

In Figure **S3**, the critical strain initially increases with the molar ratio and reaches a maximum at the ratio of 0.006, after which it decreases. These results suggest that increasing the amount of cross-linker leads to increased brittleness of the gel beyond the optimal density. We also measure the storage modulus (G’) at strain amplitude 0.5%, a value far below the critical strain of the gel, so that the polymer network remains intact. The G’ increases almost exponentially with the amount of cross-linker **3**. In addition, the storage moduli of all five gels are essentially independent of frequency (Fig. **S2**), indicating a highly cross-linked three-dimensional structure within the gel (e.g., a continuous network formation)._Regardless of the amount of cross-linker present, the value of storage modulus/loss modulus (G’/G”) is always about 10, indicating a widely cross-linked structure.

S4 Fluorescent images of Gel_3 and Gel_4

Fluorescent images were recorded on a Marianas Spinning Disk Confocal Microscope which includes a Zeiss Axlovert 200 M inverted microscope, Yokogawa CSU22 Spinning Disk, PhotoMetrics Cascade II, HBO 100W Eplfluorescence Lamp, SlideBook 5, Leica M76 dissecting scope and KL 1500 LCD light source.

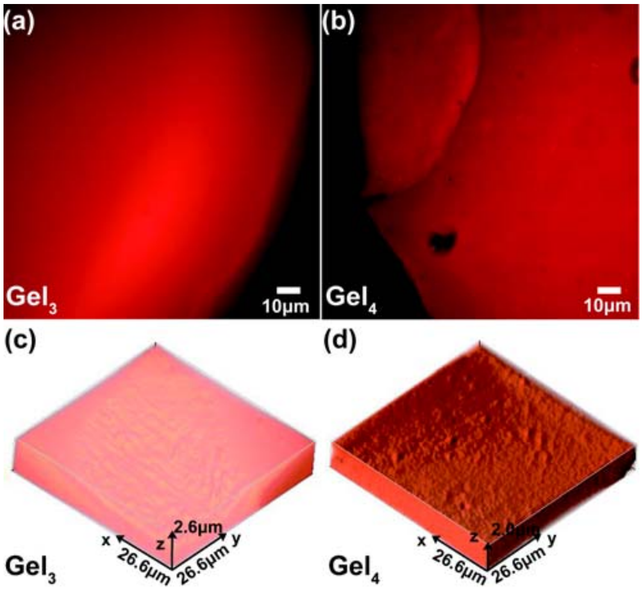

Figure S4. Confocal fluorescent images of (a) Gel_3 and (b) Gel_4 and the 3D rendering images of (c) Gel_1 and (d) Gel_4.

S5 SEM images of Gel_1

The SEM images were recorded on a NVision 40 Dual Beam Focused Ion Beam Imaging System.

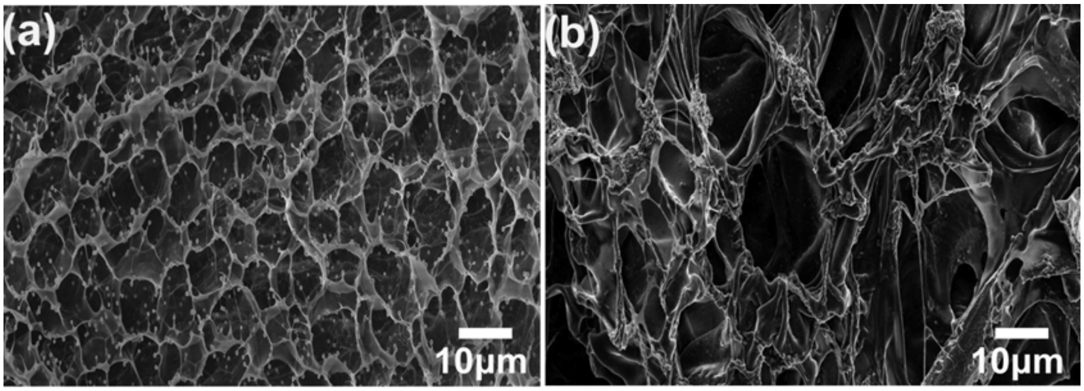

Figure S5. SEM images of freeze dried Gel_1 at reduced state (a) and oxidized state (b).

S6 Single crystal structure of active cross-linker (1)

All operations were performed on a Bruker-Nonius Kappa Apex2 diffractometer, using graphite-monochromated MoKα radiation. All diffractometer manipulations, including data collection, integration, scaling, and absorption corrections were carried out using the Bruker Apex2 software.[1] Preliminary cell constants were obtained from three sets of 12 frames. Data collection was carried out at 120K, using a frame time of 30 sec and a detector distance of 60 mm. The optimized strategy used for data collection consisted of six phi and five omega scan sets, with 0.5° steps in phi or omega; completeness was 99.1 %. A total of 3192 frames were collected. Final cell constants were obtained from the xyz centroids of 9886 reflections after integration.

From the systematic absences, the observed metric constants and intensity statistics, space groupwas chosen initially; subsequent solution and refinement confirmed the correctness of this choice. The asymmetric unit contains one molecule of the complex, two Cl^- ions, and 7.38 (determined by refinement; see below) molecules of water (for the complex, $Z = 2$; $Z' = 1$). The structure was solved using *SuperFlip*,[2] and refined (full-matrix-least squares) using the Oxford University *Crystals for Windows* program.[3] All ordered non-hydrogen atoms were refined using anisotropic displacement parameters. After location of H atoms on electron-density difference maps, the H atoms were initially refined with soft restraints on the bond lengths and angles to regularize their geometry (C---H in the range 0.93--0.98 Å and U_{iso} (H) in the range 1.2-1.5 times U_{eq} of the parent atom), after which the positions were refined with riding constraints.[4] Four of the six amide groups were found to be disordered. The disorder for each of the four pairs was modeled as a two-component disorder, and refined with each sum constrained to be 1.0. The components and their occupancies are: [N(12),C(50),C(51),C(52)/N(112), C(150),C(151),C(152); 0.438/0.562(6)]; [N(104),C(114),C(115),C(116)/O(12),N(4), C(14),C(15),C(16); 0.612/0.388(5)]; [C(124),c(125)/c(24),C(25); 0.529/0.471(15)]; and [N(10),C(41),C(42),C(43)/N(110),C(141),C(142),C(143); 0.408/0.592(11)]. All the modeled disordered components were refined using isotropic displacement parameters. Difference electron-density maps revealed a number of water solvate molecules. Five of the water molecules, O(7) through O(11), were ordered and H atoms could be located. Atom O(12) had a short "self-contact" of 2.22 Å and thus could not be present in amounts greater than 50%; however, since O(12) was hydrogen-bonded to N(4), we chose to constrain its occupancy to that of N(4), 0.388(5). Water molecules assigned as O(13) and O(14) were disordered, and the corresponding H atoms could not be located. Modeling of the disorder was not attempted. The final least-squares refinement converged to $R_1 = 0.0499$ ($I > 2\sigma(I)$, 13102 data) and $wR_2 = 0.1283$ (F^2, 15924 data, 738 parameters). The final CIF is available as supporting material. Two CheckCIF Alert A and three B items arise from the disorder model and the disorder in O atoms O(13) and O(14); accordingly, a validation response from item appears in the CIF.

1. Apex2, Version 2 User Manual, M86-E01078, Bruker Analytical X-ray Systems, Madison, WI, June 2006.

2. Palatinus, L., Chapuis, G.; *J. Appl. Cryst.* **2007**, 40, 786..

3. Betteridge, P. W.; Carruthers, J. R.; Cooper, R. I.; Prout, K.; Watkin, D. J. *J. Appl. Cryst.* **2003**, *36*, 1487; Prout, C.K;. Pearce, L.J. CAMERON, Chemical Crystallography Laboratory, Oxford, UK, 1996.

4. Cooper, R. I.; Thompson, A. L.; Watkin, D. J. *J. Appl. Cryst.* **2010**, *43*, 1100–1107.