Electronic Supplementary Material (ESI) for Food & Function.

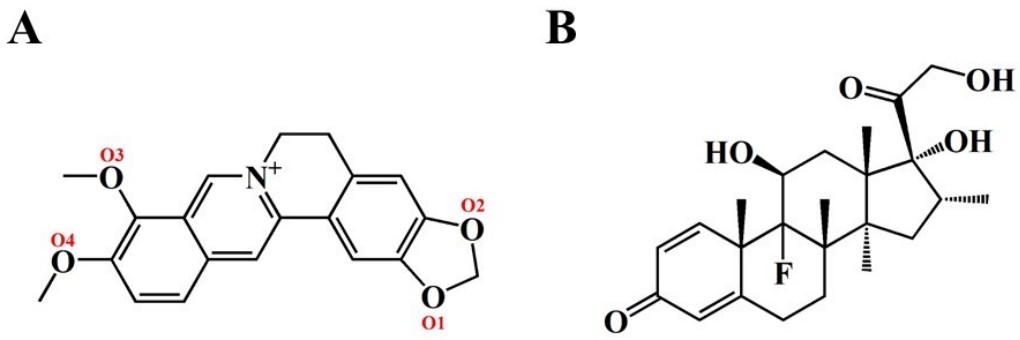

Fig. S1 Structures of berberine (A) and dexamethasone (B).

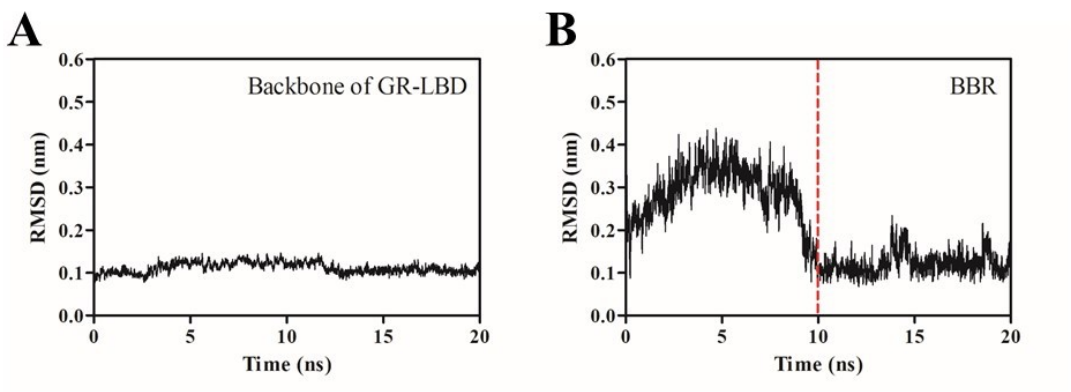

Fig. S2 The result of molecular dynamics simulation. (A) Ligand binding domain of glucocorticoid receptor, GR-LBD. (B) Berberine, BBR.

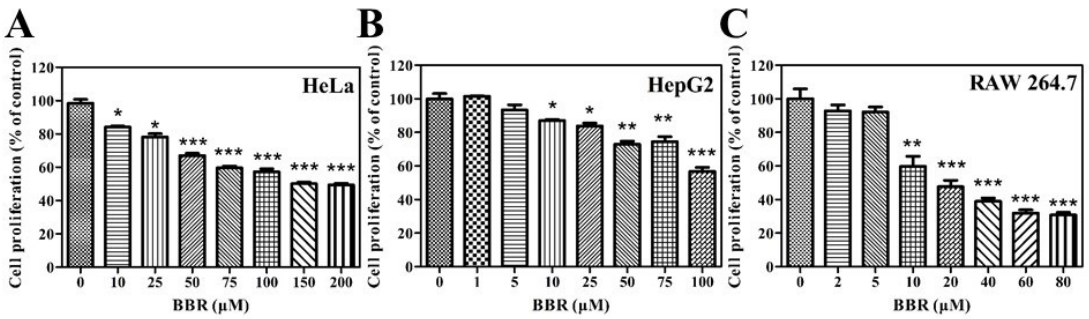

Fig. S3 Cytotoxicity analysis of berberine (BBR) in HeLa (A), HepG2 (B), and RAW 264.7 (C) cells. Data are expressed as mean ± SEM, *$p < 0.05$, **$p < 0.01$, and ***$p < 0.001$ compared with the DMSO control groups.

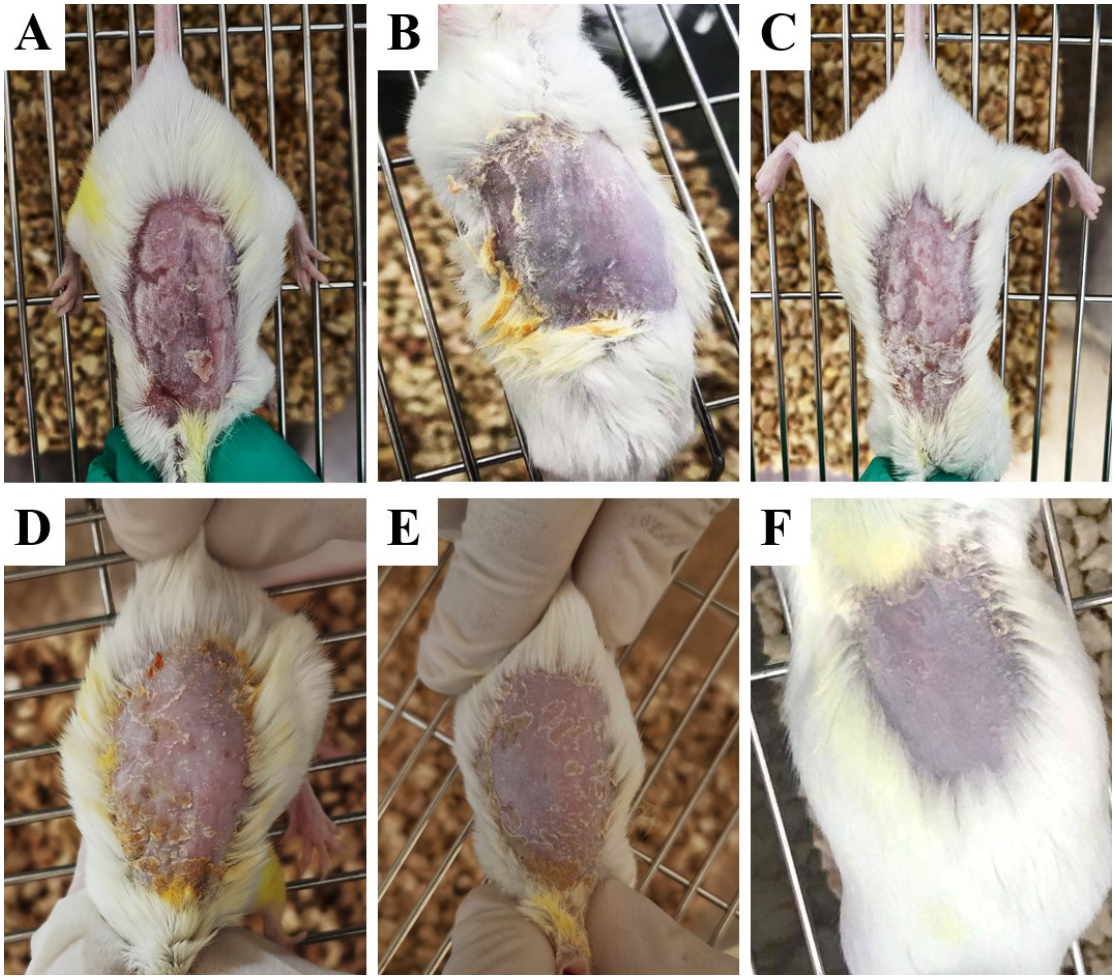

Fig. S4 Photographs of the clinical appearance of mice treated with berberine (BBR) and dexamethasone (DEX). (A) DNCB-induced ACD model group (DNCB-sensitized mice). (B) Dexamethasone-treated group (0.1% in 50 μL saline solution). (C) Berberine-treated group (10 mg/kg). (D) Berberine-treated group (20 mg/kg). (E) Berberine-treated group (40 mg/kg). (F) Berberine (40 mg/kg) combined with dexamethasone (0.1% in 50 μL saline solution)-treated group.

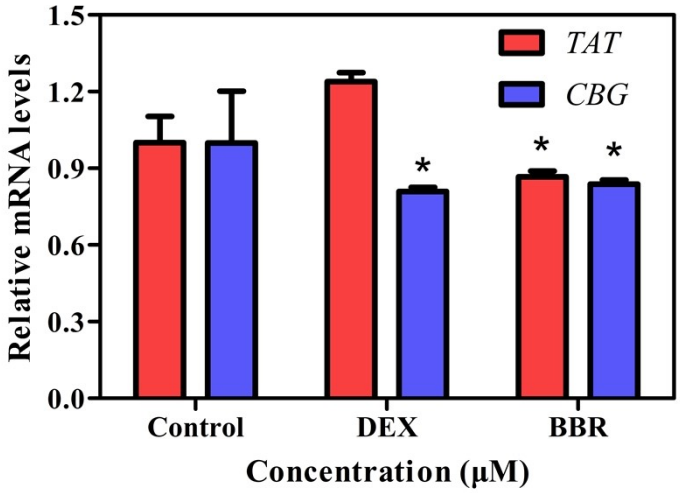

Fig. S5 The gene expressions of tyrosine aminotransferase (*TAT*) and corticosteroid-binding globulin (*CBG*) in primary liver cells isolated from ACD mice treated with dexamethasone (DEX, 0.1% in 50 μL saline solution) or berberine (BBR, 40 mg/kg). The healthy mice served as the control group. *$p < 0.05$ compared with the control group.

Table S1 Primers for real-time quantitative PCR

Gene	Primer
TATF	CTGAAGTTACCCAGGCAATGAAAG
TATR	TAATAAGAAGCAATCTCCTCCCGAC
CBGF	CACCAACCAGGCAAATTTCT
CBGR	GGACGTCAGGTTTAGGGTGA
PEPCKF	CAAGACGGTTATCGTCAGCA
PEPCKR	GAACCTGGCATTGAACGCTT
HPRTF	GAAGAGCTATTGTAATGACC
HPRTR	GCGACCTTGACCATCTTTG