Supplementary material for

Pancreatic ductal deletion of S100A9 alleviates acute pancreatitis by targeting VNN1-mediated ROS release to inhibit NLRP3 activation

Hong Xiang^{1,*}, Fangyue Guo^{1,2,*}, Xufeng Tao^{3,*}, Qi Zhou^{1,2}, Shilin Xia¹, Dawei Deng⁴, Lunxu Li⁴, Dong Shang^{1,2,4,#}

¹Laboratory of Integrative Medicine, First Affiliated Hospital of Dalian Medical University, Dalian, 116011, China;

²Institute (College) of Integrative Medicine, Dalian Medical University, Dalian, 116044, China;

³School of Chemical Engineering, Dalian University of Technology, Dalian, 116024, China;

⁴Department of General Surgery, First Affiliated Hospital of Dalian Medical University, Dalian, 116011, China.

* These authors contributed equally to this work.

[#]Corresponding Author: Dong Shang, Laboratory of Integrative Medicine, First Affiliated Hospital of Dalian Medical University, Dalian, 116011, China; shangdong@dmu.edu.cn

Supplementary Table S1 Primer sequences used for qPCR assay				
Gene	species	Primers (5'-3')		
0 11	•	Forward: CCTGGGCATGGAGTCCTGTG		
β-actin	Human	Reverse: TCTTCATTGTGCTGGGTGCC		
		Forward: ATGATGGCTTATTACAGTGGCAA		
IL-1β	Human	Reverse: GTCGGAGATTCGTAGCTGGA		
		Forward: AAGCCAGAGCTGTGCAGATGAGTA		
IL-6	Human	Reverse: TGTCCTGCAGCCACTGGTTC		
		Forward: CACTGTGTGTGTAAACATGACTTCCAA		
IL-8	Human	Reverse: TGTGGTCCACTCTCAATCACTCTC		
		Forward: TCTTCATTGACCAAGGAAATCGG		
IL-18	Human	Reverse: TCCGGGGTGCATTATCTCTAC		
		Forward: AAATTGCTAGAGACCGAGTGTCCT		
S100A8	Human	Reverse: CACGCCCATCTTTATCACCA		
		Forward: TCCACCAATACTCTGTGAAGCTG		
S100A9	Human	Reverse: CCTCCATGATGTGTTCTATGACC		
		Forward: GGTCAGGCCCTACCATTGAG		
HSPA1B	Human	Reverse: TCCTTGAGTCCCAACAGTCCA		
		Forward: AAGCTATGTCGCCTTTACGGACAC		
HSPA8	Human	Reverse: CATCATCAAATCTGCGTCCAATC		
		Forward: ACCGTCTCGCTATAGCCGTTTG		
HNRNPH2	Human	Reverse: CATCACTTCATCGGCTGAGCA		
		Forward: GGTTCCAAGGGCTATGGATTTGTA		
PABPC1	Human	Reverse: GCCCTAGCTCCAAGTTCAGCTTC		
		Forward: CCATGGACTCTGTCCGTTCT		
TUBB4A	Human	Reverse: CCCTTTGCCCAGTTGTTG		
		Forward: CTGAGCAACTCATCACAGGCAAG		
TUBA1C	Human	Reverse: CCATGAGCAGCGAGGTGAAC		
		Forward: CAAGACTCCCAGCCGGGTTA		
TBC1D2	Human	Reverse: GGAATTCCCAGCGCTTCATC		
		Forward: TGGCACTTTCGGAACCCAGTA		
VNN1	Human	Reverse: TCAGACTAAACAAGCGTCCGTCAG		
		Forward: CATCCGTAAAGACCTCTATGCCAAC		
β-actin	Mouse	Reverse: ATGGAGCCACCGATCCACA		
		Forward: AAATCTCGCAGCAGCACATCAA		
IL-1β	Mouse	Reverse: CCACGGGAAAGACACAGGTAGC		
		Forward: CCTTCTTGGGACTGATGATGCTG		
IL-6	Mouse	Reverse: TTGGGAGTGGTATCCTCTGTGA		
		Forward: CAGGCCTGACATCTTCTGCAA		
IL-18	Mouse	Reverse: TCTGACATGGCAGCCATTGT		
		Forward: ATGGCTGGGATTCACCTCAAGAAC		
CXCL1	Mouse	Reverse: AGTGTGGCTATGACTTCGGTTTGG		
		Forward: CACTGGTCCTGCTGCTGCTG		
CXCL2	Mouse	Reverse: GCGTCACACTCAAGCTCTGGATG		
		Forward: ATCCCCAGCGGTTCCATCTCG		
CXCL5	Mouse	Reverse: CGTTGCGGCTATGACTGAGGAAG		
		Forward: CAGCTGCCTTAACCCCATC		
CXCR2	Mouse	Reverse: CTTGAGAAGTCCATGGCGAAA		

Samples	Total spectrogram number	Number of identification spectrogram	Identification of peptide number	Identification of protein number	Unique-2
lgG	4713	493	154	56	32
IP	15232	420	80	20	13

Supplementary Table S2 Statistical data of protein identification

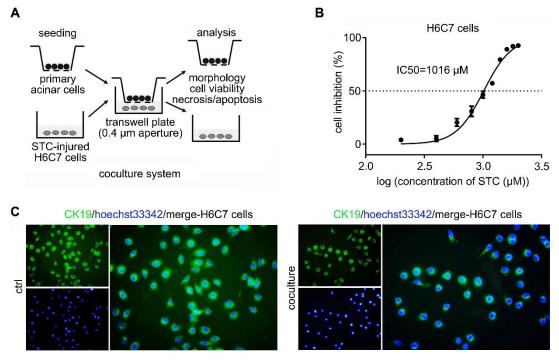
Accession	Names	Length	Mass	Unused	Coverage(%)
sp P0DMV9 HS71B_HUMAN	Heat shock 70 kDa protein 1B	641	70051.60	3.33	9.20
sp P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein	646	70897.60	14.69	13.78
sp P55795 HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	449	49229.30	2.00	3.79
sp P11940 PABP1_HUMAN	Polyadenylate-binding protein 1	636	70670.40	10.43	9.43
sp P04350 TBB4A_HUMAN	Tubulin beta-4A chain	444	49585.50	2.00	2.70
sp Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain	449	49894.90	2.08	4.45
sp Q9BYX2 TBD2A_HUMAN	TBC1 domain family member 2A	928	105412.80	6.14	4.31
sp O95497 VNN1_HUMAN	Pantetheinase	513	57011.20	2.28	4.09
sp P04432 KVD39_HUMAN	Immunoglobulin kappa variable 1D-39	117	12737.30	2.00	13.68
sp P0DOX7 IGK_HUMAN	Immunoglobulin kappa light chain	214	23378.90	2.00	8.41
sp P01860 IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3	377	41286.60	7.24	15.38

Supplementary Table S3 Unique proteins of pull-down in S100A9 IP group

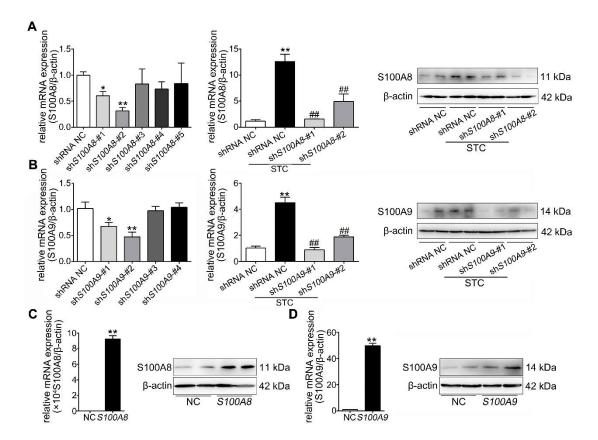
Supp	lementary [·]	Table S4	Contact list	between	S100A9	and VNN1
------	------------------------	----------	--------------	---------	--------	----------

The residues in S100A9	The residues in VNN1	Interaction type
Oxygen atom of carboxyl group of Glu92	Nitrogen atoms of guanidine group of Arg259	Salt bridge
Nitrogen atom of amino group of Lys57	Oxygen atoms of carboxyl group of Glu324	Salt bridge
Sulfur atom of thioether group of Met94	Nitrogen atom of imidazolyl group of His228	Hydrogen bond
Oxygen atom of backbone of Gly100	Oxygen atom of hydroxyl group of Ser309	Hydrogen bond
Nitrogen atom of backbone of Gly102	Oxygen atom of hydroxyl group of Ser309	Hydrogen bond
Oxygen atom of backbone of Glu92	Nitrogen atom of imidazolyl group of His310	Hydrogen bond
Nitrogen atom of imidazolyl group of His105	Oxygen atom of backbone of His310	Hydrogen bond
Nitrogen atom of imidazolyl group of His103	Oxygen atom of hydroxyl group of Ser311	Hydrogen bond
Oxygen atom of carboxyl group of Glu92	Carbon atom of backbone of Val313	Hydrogen bond
Oxygen atom of carboxyl group of Glu92	Nitrogen atom of backbone of Val314	Hydrogen bond
Oxygen atom of carboxyl group of Glu52	Nitrogen atom of amido group of Asn315	Hydrogen bond
Carbon atom of sidechain of Lys57	Oxygen atom of backbone of Ser321	Hydrogen bond
Nitrogen atom of amino group of Lys57	Oxygen atom of backbone of Ile323	Hydrogen bond
Nitrogen atom of guanidine group of Arg85	Oxygen atom of backbone of Phe431	Hydrogen bond
Nitrogen atom of guanidine group of Arg85	Oxygen atom of amido group of Gln434	Hydrogen bond

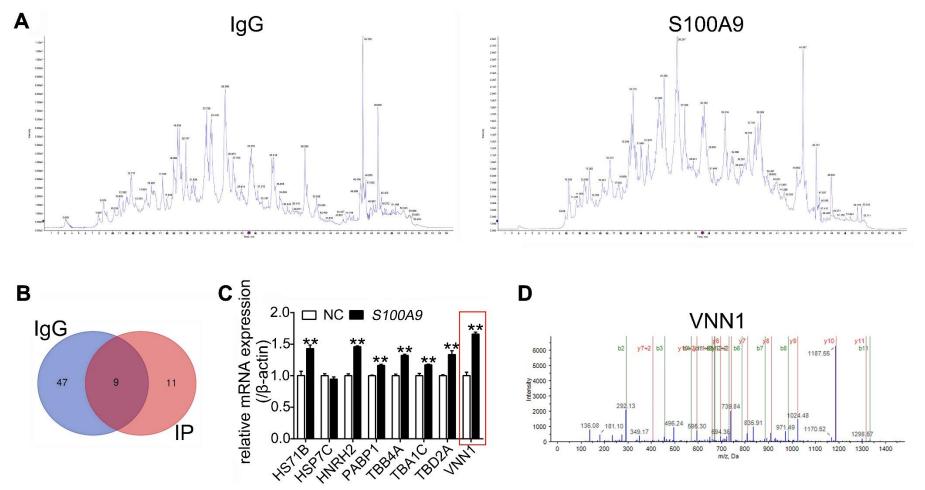
Compounds	Chemical groups in compound	The residues in S100A9	Interaction type
	Oxygen atom in one hydroxyl group (hydrogen bond acceptor)	Side chain nitrogen atom of Arg85	Hydrogen bond
$C_{42}H_{60}N_4O_6$	Oxygen atom in one hydroxyl group (hydrogen bond donor)	Side chain oxygen atom of Glu92	Hydrogen bond
	Carbon atom (hydrogen bond donor)	Backbone oxygen atom of His103	Hydrogen bond
	Others	Gly97, Gly100, Ala89, Trp88 and Val58	Hydrogen bond
	Oxygen atom (hydrogen bond acceptor)	Side chain nitrogen atom of Lys51	Hydrogen bond
C28H29F3N4O5S	Nitrogen atom (hydrogen bond donor) Nitrogen atom	Backbone oxygen atom of Trp88 Side chain oxygen atom of Glu92	Hydrogen bond Salt bridge
	Others	Val58, Ile62, Leu49, Phe48 and Leu109	Hydrogen bond
	Nitrogen atom (hydrogen bond donor)	Side chain oxygen atom of Glu92	Hydrogen bond
	Sulfur atom (hydrogen bond acceptor)	Backbone nitrogen atom of Gly102	Hydrogen bond
C30H32N4O6S4	Oxygen atom (hydrogen bond acceptor)	Backbone nitrogen atom of His105	Hydrogen bond
	Others	Leu109, Ala89, Trp88, Gly97 and Gly100	Hydrogen bond



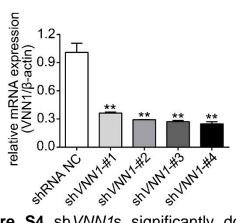
Supplementary Figure S1 (A) Pattern diagram of the coculture system for STC-injured ductal cells and primary acinar cells. (B) MTT results showed that the IC50 value of STC in H6C7 cells was 1016 μ M (n = 6). (C) IF staining proved that the expression of the ductal cell marker CK19 clearly decreased in STC-treated H6C7 cells. Data are presented as the mean ± SEM.



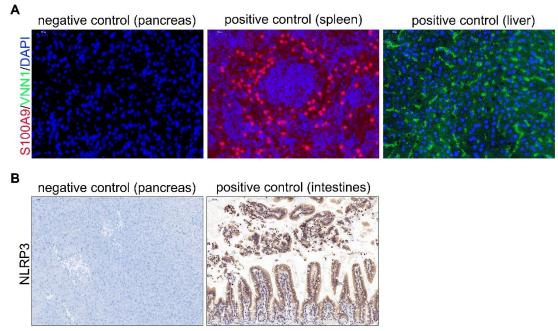
Supplementary Figure S2 (A) sh*S100A8*-#1 and -#2 significantly downregulated S100A8 mRNA (n = 3) and protein expressions. (B) sh*S100A9*-#1 and -#2 significantly downregulated S100A9 mRNA (n = 3) and protein expressions. (C) S100A8 mRNA and protein expression levels were upregulated in S100A8-overexpressing H6C7 cells (n = 3). (D) S100A9 mRNA and protein expression levels were upregulated in S100A9-overexpressing H6C7 cells (n = 3). Data are presented as the mean ± SEM; *P < 0.05 and **P < 0.01 *vs.* shRNA NC or NC group; ##P < 0.01 *vs.* shRNA NC+STC.



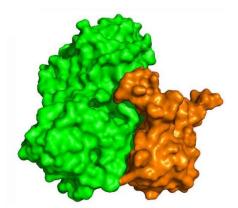
Supplementary Figure S3 (A) LC-MS/MS was performed to identify and analyze the binding proteins of S100A9. (B) 56 and 20 kinds of proteins were identified in the IgG and S100A9 pull-down samples, respectively. (C) Gene expression levels of 8 proteins (HS71B, HSP7C, HNRH2, PABP1, TBB4A, TBA1C, TBD2A and VNN1) in S100A9-overexpressing H6C7 cells were detected by qPCR (n = 3). (D) Mass spectrogram of the VNN1 protein. Data are presented as the mean \pm SEM; **P < 0.01 *vs.* NC group.



Supplementary Figure S4 sh*VNN1*s significantly downregulated S100A9 mRNA level compared to shRNA NC group (n = 3). Data are presented as the mean \pm SEM; ^{**}P < 0.01 *vs.* shRNA NC group.



Supplementary Figure S5 (A-B) Negative and positive controls of S100A9, VNN1 and NLRP3 expressions.



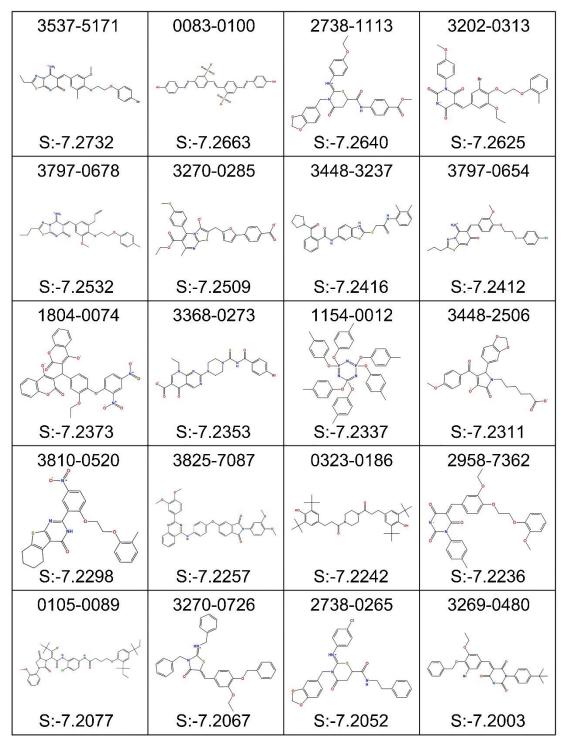
Supplementary Figure S6 Binding model between the S100A9 protein and the VNN1 protein; the surfaces of S100A9 and VNN1 are colored orange and green, respectively.

0683-0021	0884-0014	2372-3991	3948-1149
-0+2-5-6+0	o Justico	-2-01-0-C-04	the for
S:-10.8913	S:-8.5406	S:-8.2299	S:-8.2043
3948-1191	0249-0003	2324-0140	3232-0780
the on	tota	oftedo	ampfinia
S:-8.1575	S:-8.0931	S:-8.0680	S:-8.0591
3289-7235	3861-0047	3797-0694	3537-5285
proport	optoration	the cont	at and
S:-8.0092	S:-7.9737	S:-7.9408	S:-7.9036
0927-0035	2040-0304	3232-0776	0669-0140
anor		8-74-78-	
S:-7.8888	S:-7.8013	S:-7.7541	S:-7.7270
4011-0808	2036-0830	3948-0977	2324-0157
strand	Diggingid	A Charles and the second	offer
S:-7.7152	S:-7.6875	S:-7.6810	S:-7.6803

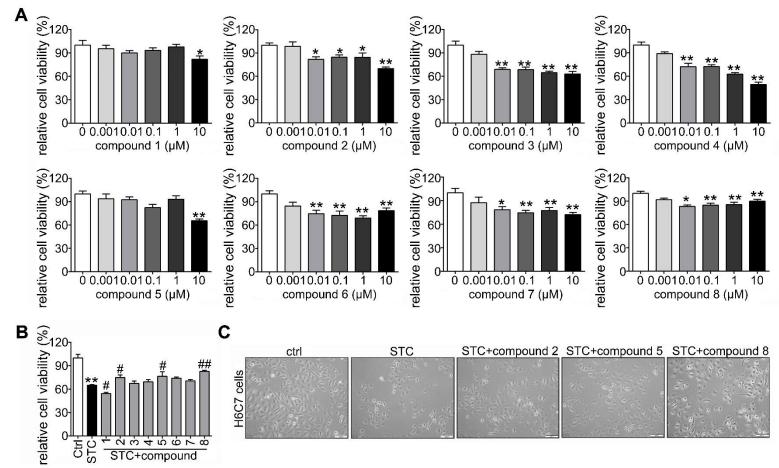
2185-0036	3894-0003	2324-0151	2030-0071
La Casaçar	offererese	000000	
S:-7.6740	S:-7.6408	S:-7.6389	S:-7.6349
3948-1099	3948-1042	2033-0102	3819-1354
tit of the	+ital-o		AT CYCO
S:-7.5964	S:-7.5867	S:-7.5851	S:-7.5820
0105-0143	3257-1297	3773-3548	2368-0020
fact	John a	Xiano	that.
S:-7.5818	S:-7.5771	S:-7.5752	S:-7.5750
2036-0525	0940-0013	2036-0823	3202-0346
Honorton	8-02-0-6-8	digtoratory	
S:-7.5608	S:-7.5265	S:-7.5255	S:-7.5175
4013-2645	3448-6069	2324-0213	1477-0001
Girand	Jagdoro.	fright.	0470 ⁴ 40
S:-7.5161	S:-7.5141	S:-7.5076	S:-7.5034

2030-0098	0868-0307	3272-1306	0669-0063
	traout	and - for the	aotolatao
S:-7.5001	S:-7.4941	S:-7.4911	S:-7.4846
2144-0834	0242-0428	3229-0011	3202-0363
	or the share		
S:-7.4844	S:-7.4756	S:-7.4705	S:-7.4633
2214-0085	0927-0007	0149-0038	3797-0804
			- Brocher
S:-7.4591	S:-7.4447	S:-7.4371	S:-7.4349
2897-1797	3948-1182	3229-0544	0683-0042
abraha	131		
S:-7.4319	S:-7.4275	S:-7.4193	S:-7.4152
0927-0042	2029-0063	2958-7372	3773-4815
	3 jorook		-kitchC
S:-7.4139	S:-7.4089	S:-7.4053	S:-7.4013

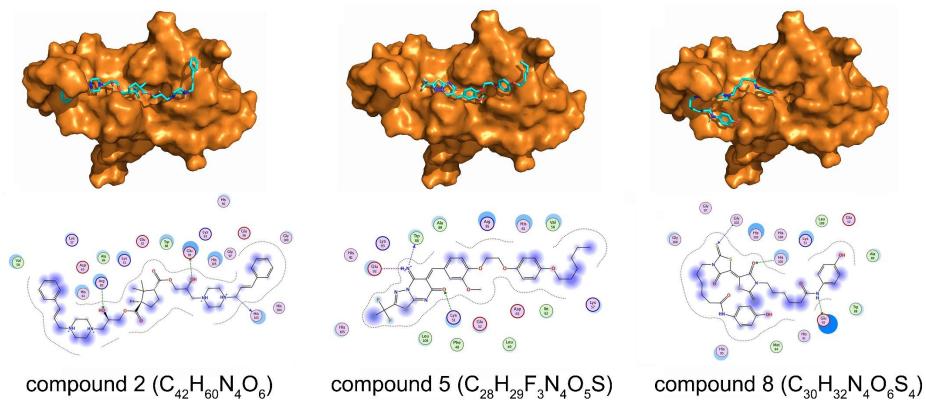
1762-0597	3773-0729	3184-1221	3706-2051
	the for		
S:-7.3981	S:-7.3947	S:-7.3868	S:-7.3852
2641-1586	2897-0360	0102-0089	2425-3824
	$\rightarrow \rightarrow $	H Cee o Con M-O Con M-	rokarat
S:-7.3775	S:-7.3720	[ັ] S:-7.3577	S:-7.3517
2958-7523	3235-0305	3797-0798	2030-0099
	offero	Joseph Color	
S:-7.3485	S:-7.3385	S:-7.3286	S:-7.3274
3948-1036	3389-1064	2958-7463	0878-7200
AT A CARACTER AND CONC		ottenot	pta
S:-7.3232	S:-7.3223	S:-7.3214	S:-7.3059
3537-5212	3948-1140	3797-0764	2368-0284
rice o	+3+0-00		
S:-7.2984	S:-7.2984	S:-7.2961	S:-7.2832



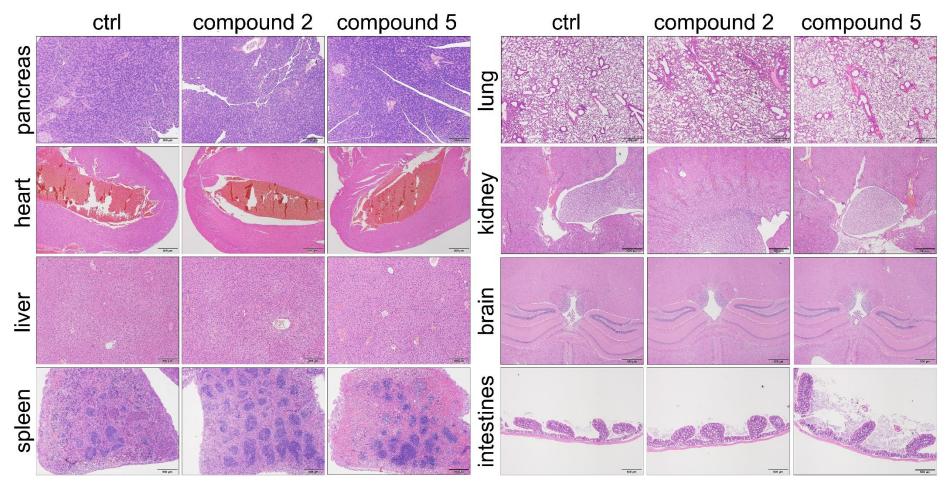
Supplementary Figure S7 Structures and docking scores of the top 100 inhibitors of the S100A9-VNN1 interaction.



Supplementary Figure S8 (A) Toxicities of the top 8 compounds *in vitro* (n = 6). (B) Pharmacodynamics of the top 8 compounds *in vitro* (n = 6). (C) Compounds 2, 5 and 8 decreased STC-induced H6C7 cells injury. Data are presented as the mean \pm SEM; *P < 0.05 and **P < 0.01 *vs.* ctrl group; #P < 0.05 and ##P < 0.01 *vs.* STC group.



Supplementary Figure S9 Binding models of C₄₂H₆₀N₄O₆, C₂₈H₂₉F₃N₄O₅S and C₃₀H₃₂N₄O₆S₄ with S100A9 protein.



Supplementary Figure S10 HE staining results of pancreas, heart, liver, spleen, lung, kidney, brain and intestines also proved that compounds 2 and 5 have no obvious toxicities at the doses of 10 mg/kg/day for 2 days.