

Supplemental Figure 1. Rats on the suspended shelf. For the convenient manipulation of the acupuncture points on the back, rat was placed on the suspended shelf (50 × 45 mm, about 50 cm high from the ground, shown as below), which could easily make it calm and stand still without anesthesia.



Supplemental Table 1. The comparisons of pulmonary dynamic compliance (Cdyn, ml/ kpa) and respiratory rate (RR, breaths/min) within 10min after challenge

	Groups	Min 1	Min 2	Min 3	Min 4	Min 5	Min 6	Min 7	Min 8	Min 9	Min 10
Cdyn	NC	1.066±2. 796	0.463±2. 609	-0.373±2 .496	-2.128±2 .625	-1.53±2.8 36	-2.25±3.1 79	-2.208±3. 117	-4.015±2. 542	-5.605±2. 933	-3.679±3. 747
	AS	-3.629±3. 493	-20.434± 5.057 ^{###}	-23.641± 5.242 ^{###}	-17.95±6 .017 [#]	-12.561± 5.277 [#]	-3.274±5. 035	3.584±5. 266	6.292±5. 018 [#]	5.992±4. 642 [#]	5.698±4. 240
	AA	-0.319±3. 512	3.198±5. 929 ^{**}	7.435±7. 046 ^{**}	3.751±6. 623 ^{**}	4.322±5. 367 ^{**}	3.725±5. 11	8.03±5.6 38	7.889±4. 385	6.86±3.7 44	5.707±3. 458
	NA	1.019±2. 736	0.417±1. 238	-1.095±1 .338	-0.14±1. 154	-0.959±1. 12	-1.923±1. 562	-0.883±1. 109	-0.552±1. 232	-1.503±1. 303	-2.071±1. 656
RR	NC	7.04±2.4 96	2.084±1. 233	1.5±1.30 8	1.871±1. 301	1.974±1. 419	3.238±1. 439	3.934±1. 365	3.898±1. 434	4.352±1. 734	5.465±2. 433
	AS	-28.948± 5.912 ^{###}	-53.031± 8.193 ^{###}	-46.9±6. 911 ^{###}	-39.065± 5.768 ^{###}	-28.048± 2.843 ^{###}	-17.874± 3.708 ^{###}	-13.32±5. 078 ^{###}	-13.033± 4.697 ^{###}	-13.178± 4.731 ^{###}	-12.583± 5.065 ^{###}
	AA	-29.822± 8.505	-48.332± 11.297	-36.24±9 .328	-25.474± 8.025	-21.728± 7.631	-18.959± 6.143	-15.501± 4.685	-15.508± 4.221	-14.934± 4.449	-17.906± 5.674
	NA	4.055±1. 366	0.506±1. 162	1.465±0. 927	2.251±1. 182	2.536±1. 143	3.521±1. 387	3.094±1. 203	3.287±1. 336	4.173±1. 84	6.662±2. 225

Data are shown as means ± SEM. NC: normal control rats (n = 15); AS: asthma model (n = 14); AA: asthma model treated with acupuncture (n = 12); NA: normal rats treated with acupuncture. The values of Cdyn and RR in the tables are expressed as differential values subtracted from the corresponding baseline values (Figure 1). # p < 0.05, ## p < 0.01 when comparing the AS group with the NC group and * p < 0.05, ** p < 0.01 when comparing the AA group with the AS group, , one-way ANOVA followed by LSD post hoc comparisons.

Supplemental Table 2. List of PANTHER biologic process classification

Biological process	Number of process hits	Identified proteins
signal transduction	7	RhoGDI2, S100A8, S100A11, RAGE, Uteroglobin, Annexin A5, Ras suppressor protein 1
oxidation reduction	2	Peroxiredoxin-6, Protein disulfide-isomerase A6
cellular process	10	RhoGDI2, S100A8, S100A11, RAGE, Uteroglobin, Annexin A5, Tubulin alpha-1A chain, Actin, cytoplasmic 1, Actin, alpha skeletal muscle, Cofilin-1
transport	7	Serum albumin, ATP synthase subunit alpha, mitochondrial, Sodium/potassium-transporting ATPase subunit alpha-1, Tubulin alpha-1A chain, Annexin A5, Actin, cytoplasmic 1
cellular component organization	4	Tubulin alpha-1A chain, Actin, cytoplasmic 1, Actin, alpha skeletal muscle, Cofilin-1
response to stimulus	3	S100A8, S100A11, Heat shock-related 70
developmental process	6	RAGE, N(G),N(G)-dimethylarginine dimethylaminohydrolase 2, Tubulin alpha-1A chain, Actin, cytoplasmic 1, Actin, alpha skeletal muscle, Cofilin-1
metabolic process	16	Peroxiredoxin-6; Protein disulfide-isomerase A6; Atic; Psmc6; Glyceraldehyde-3-phosphate dehydrogenase; Anionic trypsin-1; Gamma-enolase; Phosphoglycerate mutase 1; Carbonic anhydrase 2; synthase subunit alpha, mitochondrial; Sodium/potassium-trtransporting ATPase subunit alpha-1
cell cycle	5	S100A8, S100A11, Tubulin alpha-1A chain, Actin, cytoplasmic 1, Actin, alpha skeletal muscle
immune system process	6	Peroxiredoxin-6, S100A8, S100A11, uteroglobin, RAGE, Heat shock-related 70 kDa protein 2
other	4	RAGE, Sodium/potassium-transporting ATPase subunit alpha-1, ATP synthase subunit alpha, mitochondrial, Creatine kinase B-type

The number of process hits is greater than the number of proteins since many proteins are classified as having multiple functions. "Other" category contains biological processes with only 1 hit: homeostatic process, cell adhesion, system process, generation of precursor metabolites and energy.

Supplemental Table 3 (a). Mass spectrometric data of differentially expressed protein spot 24

Reference IPI: IPI00209188.5 SWISS-PROT: Q63495 TREMBL: Q6MG86 ENSEMBL: ENSRNOP00000000508 REFSEQ: NP_445788							
Advanced glycosylation end product-specific receptor precursor			PepCount	UniquePepCount	CoverPercent	MW	PI
			25	6	23.38%	42663.67	5.83
File, Scan(s)	Sequence	MH+	Diff(MH+)	Charge	Rank	XC	DeltaCn
7503_Test,1570	K.GTVVKEETR.R	1019.1343	0.1823	2	1	2.4614	0.353
7503_Test,1576	K.GTVVKEETR.R	1019.1343	0.1303	2	1	2.8472	0.389
7503_Test,1588	K.GTVVKEETR.R	1019.1343	0.5963	2	1	2.7144	0.4287
7503_Test,1860	K.GTVVKEETR.R	1019.1343	0.1753	2	1	2.9238	0.3669
7503_Test,1872	K.GTVVKEETR.R	1019.1343	0.1403	2	1	2.7705	0.423
7503_Test,1878	K.GTVVKEETR.R	1019.1343	0.1893	2	1	2.7504	0.3201
7503_Test,3081	K.VLSPQGDPWDSVAR.I	1527.66322	-0.80178	2	1	4.065	0.6215
7503_Test,3087	K.VLSPQGDPWDSVAR.I	1527.66322	0.95522	2	1	3.9653	0.6064
7503_Test,3093	K.VLSPQGDPWDSVAR.I	1527.66322	0.24722	2	1	4.0732	0.6465
7503_Test,3369	K.VLSPQGDPWDSVAR.I	1527.66322	0.99522	2	1	3.5767	0.597
7503_Test,3375	K.VLSPQGDPWDSVAR.I	1527.66322	0.72622	2	1	3.5194	0.5976
7503_Test,3381	K.VLSPQGDPWDSVAR.I	1527.66322	0.41922	2	1	3.7652	0.6401
7503_Test,3186	R.IGEPLMLSCK.G	1148.39198	1.34298	2	1	2.3798	0.2311
7503_Test,3207	R.IGEPLMLSCK.G	1148.39198	-1.67902	2	1	3.6089	0.3363
7503_Test,3214	R.IGEPLMLSCK.G	1148.39198	-1.85002	2	1	3.4448	0.329
7503_Test,2490	R.RPLNTAPIQPR.V	1263.47427	0.44327	2	1	2.6695	0.4368
7503_Test,2502	R.RPLNTAPIQPR.V	1263.47427	0.28727	2	1	2.631	0.4262
7503_Test,3936	R.SELTVTPAQGGTTPTYSCSFSLGLPR.R	2728.9858	0.3088	3	1	4.0758	0.546
7503_Test,3943	R.SELTVTPAQGGTTPTYSCSFSLGLPR.R	2728.9858	-0.0362	2	1	4.3011	0.611
7503_Test,3945	R.SELTVTPAQGGTTPTYSCSFSLGLPR.R	2728.9858	-0.4462	3	1	4.0494	0.5186
7503_Test,3946	R.SELTVTPAQGGTTPTYSCSFSLGLPR.R	2728.9858	0.2578	2	1	4.5026	0.6591
7503_Test,3951	R.SELTVTPAQGGTTPTYSCSFSLGLPR.R	2728.9858	1.4088	2	1	4.1054	0.6156
7503_Test,3676	R.VYQIPGKPEIVNPASELTANVPNK.V	2579.93287	-0.88213	3	1	5.1792	0.5532
7503_Test,3681	R.VYQIPGKPEIVNPASELTANVPNK.V	2579.93287	1.05187	3	1	4.902	0.5076
7503_Test,3707	R.VYQIPGKPEIVNPASELTANVPNK.V	2579.93287	0.01887	2	1	4.7057	0.6362

Supplemental Table 3 (b). Peptide sequences matched to RAGE (residues 1–342 correspond to the extracellular domain*) are shown below.

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>	<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>
MPTGTVARAW	VLVLALWGAV	AGGQNITARI	GEPLMLSCKG	APKKPTQKLE	WKLNTGRTEA	WKVLSPQGDP	WDSVARILPN	GSLLLPAIGI	VDEGTFR CRA
<u>110</u>	<u>120</u>	<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>	<u>190</u>	<u>200</u>
TNRLGKEVKS	NYRVRVYQIP	GKPEIVNPAS	ELTANVPNKV	GTCVSEGSYP	AGTLSWHLDG	KPLIPDGKGT	VVKEETRRHP	ETGLFTLRSE	LTVTPAQGGT
<u>210</u>	<u>220</u>	<u>230</u>	<u>240</u>	<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>	<u>290</u>	<u>300</u>
TPTYSCSFSL	GLPRRRPLNT	APIQPRVREP	LPPEGIQLLV	EPEGGTVAPG	GTVTLTCAIS	AQPPPQIHWI	KDGTPLPLAP	SPVLLLPEVG	HEDEGIYSCV
<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>	<u>360</u>	<u>370</u>	<u>380</u>	<u>390</u>	<u>400</u>
ATHPSHGPQE	SPPVNIRVTE	TGDEGQAAGS	VDGSGLGTLA	LALGILGGLG	IAALLIGAIL	WRKRQPRLEE	RKAPESQEDE	EERAELNQSE	EAEMPENGAG

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GP

*Reference: Renard, C.; Chappey, O.; Wautier, M. P.; Nagashima, M.; Morser, J.; Scherrmann, J. M.; Wautier, J. L., The human and rat recombinant receptors for advanced glycation end products have a high degree of homology but different pharmacokinetic properties in rats. *J Pharmacol Exp Ther* **1999**, 290, (3), 1458-66.