

Table 1 Chemical structures and concentrations of major components in SMI

Structure	Component	R ₁	R ₂	Concentration ($\mu\text{g/mL}$)
	Ginsenoside Rg1	Glc	Glc	129.6
	Ginsenoside Re	Glc ² -Rha	Glc	100.6
	Ginsenoside Rf	Glc ² -Glc	H	38.50
	Ginsenoside Rg2	Glc ² -Rha	H	25.58
	Ginsenoside Rb1	Glc ² -Glc	Glc ⁶ -Glc	221.7
	Ginsenoside Rd	Glc ² -Glc	Glc	45.60
	Ginsenoside Rc	Glc ² -Glc	Glc ⁶ -Ara	145.2
	Schisandrin			13.70
	Schisandrol B			0.6574
	Schizandrin B			0.0327
	Ophiopogonin D			0.0054

Table 2 Characterization of the identified altered proteins and relative spot intensity of their spot volumes

Spot number ^a	Protein identity	NCBI accession number	(Theoretical values)pI/kDa	Peptide count	Sequence coverage (%)	Score	Relative spot intensity % (Sham, 100)	
							IR	IR+SMI
Glucose metabolism proteins								
1	Triosephosphate isomerase	124056485	6.89/27	13	43	80	78±31.1*	135±54.3#
2	Pyruvate dehydrogenase E1 component subunit beta	122065728	6.20/40	4	12	58	58±25.0**	106±34.3#
3	Aldose reductase	6978491	6.26/36	16	36	165	61±38.9*	105±54.8
4	L-lactate dehydrogenase B chain	1170739	5.70/37	11	14	85	58±36.4*	106±16.8#
5	Aldolase A	202837	8.31/39	17	38	463	48±26.6*	111±36.9##
Lipid metabolism proteins								
6	Short-chain specific acyl-CoA dehydrogenase	11968090	8.47/45	17	23	296	183±90.1*	121±59.6
7	3-ketoacyl-CoA thiolase	149027157	8.64/38	14	31	140	176±73.4*	98±21.6#
TCA cycle protein								
8	Malate dehydrogenase	81861572	6.16/36	10	23	124	62±25.5*	103±44.2
Rsp-Chain protein								
9	ATP synthase, H ⁺ transporting	149029483	8.24/55	24	34	267	45±34.7*	77±50.4#
10	ATP synthase subunit beta	114562	5.19/56	7	7	173	69±18.3*	100±17.3#
11	Creatine kinase M-type	6978661	6.58/43	13	29	182	208±89.7*	119±84.9
Other proteins								
12	Cytokeratin-6A	123781839	8.06/59	15	24	87	78±11.6*	102±19.1#
13	Tu translation elongation factor	149067905	7.65/44	17	31	321	72±26.0**	108±45.5
14	rCG27551, isoform CRA_a	149041248	8.45/21	5	15	101	75±22.5*	107±32.8

^a The marked spot number in Fig. 2(A). * P<0.05, ** P<0.01 vs. Sham group, # P<0.05, ## P<0.01 vs. IR group

