Table S2. Outcomes of molecular docking.

Ingredients	Targets	Affinity	Distance from best mode	
		（kcal/mol）	rmsd l.b.	rmsd u.b.
HF	p38	-8.3	0	0
	ERK1/2	-5.6	0	0
	JNK	-5.0	0	0
	NK-κB	-9.0	0	0