# <u>ORIGINAL RESEARCH</u>

# Investigating the Mechanism of Chinese Medicine Formula AACO Against Chronic Heart Failure by Network Pharmacology Analysis and Experimental Validation

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### ABSTRACT

**Background** • A traditional Chinese medicine (TCM) formula, containing *Astragalus membranaceus* (*Fisch.*) *Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L.*, and *Radix ophiopogonis* (AACO), has therapeutic value for the treatment of chronic heart failure (CHF).

**Objective** • This study intends to explore the pharmacological mechanism underlying the activity of the AACO formula against CHF.

**Materials and Methods** • Using the TCM Systems Pharmacology database and Bioinformatics Analysis Tool for Molecular Mechanism of TCM, the active ingredients contained in the herbs of the AACO formula were screened. Meanwhile, the target genes related to these active ingredients were identified and genes correlated with CHF were screened. Protein-protein interaction networks were built to elucidate the relationships between the AACO formula and CHF. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) signal pathway enrichment analysis were carried out using the DAVID database. A "drug-component-target-disease" network was constructed with Cytoscape 3.7.0. The

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#### INTRODUCTION

Chronic heart failure (CHF) presents an increasing overall incidence owing to aging and an increase in the incidence of comorbidities.<sup>1</sup> Improvements in CHF treatment therapeutic effect of the AACO formula was proven by hemodynamic study, echocardiography evaluation, and histological analysis in transverse aortic constrictioninduced CHF mice and was validated *in vitro*.

**Results** • A total of 105 active ingredients and 1026 related targets were screened and identified, and 240 related targets overlapping with CHF were selected. According to GO analysis, the enriched genes participated in gene expression and cardiac contraction regulation by Ca<sup>2+</sup> regulation. From KEGG analysis, the calcium axis was identified as one of the main mechanisms through which the AACO formula exerts an anti-CHF effect. AACO was validated to significantly improve cardiac diastolic and systolic functions *in vivo* via an increase in the rate of Ca<sup>2+</sup> reuptake of the myocardial sarcoplasmic reticulum and improved myocardial contractility *in vitro*.

**Conclusions** • Network pharmacology is a convenient method to study the complex pharmacological mechanisms of TCM. The calcium axis likely participates in the anti-CHF mechanism of AACO. (*Altern Ther Health Med.* [E-pub ahead of print.])

had increased the survival rate between 1980 and 2000, but since then, this positive trend has leveled off.<sup>1</sup> Considering the increasing incidence and undesired survival rate, the treatment of CHF remains challenging.

Chinese herbal formulas are a basic form of Chinese medicine. They have reliable therapeutic effects and have greatly contributed to the health of Chinese people for thousands of years. Chinese herbal formulas usually contain hundreds or thousands of active components and monomers. These active chemicals have synergistic pharmacological effects through different mechanisms, which enables Chinese herbal formulas to show superiority in treating complex diseases. However, the complexity of the active chemicals and their complicated mechanisms of action are difficult to determine. Network pharmacology analyzes data from gene, protein, disease, and medicine databases to clarify the synergistic pharmacological effects of Chinese herbal **Figure 1.** Flowchart of a Network Pharmacology Approach for Showing the Mechanisms Involved in the Activity of the AACO Formula Against CHF



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; CHF, chronic heart failure; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction.

formulas. The network construction of "Chinese herbal formula-components-pharmacological effects-diseases" helps clarify the correlations among components, targets, pathways, and diseases.

Chinese herbal formulas have shown notable curative effects in patients with CHF. The formula, which comprises *Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L.,* and *Radix ophiopogonis* (AACO), is effective in treating CHF.<sup>2,3</sup> This paper aims to elucidate the pharmacological mechanisms of AACO for CHF using network pharmacology analysis and experimental validation as shown in Figure 1.

# MATERIALS AND METHODS

## Active Ingredient Screening of AACO

We screened the active ingredients contained in the AACO formula from the Traditional Chinese Medicine Systems Pharmacology database (TCMSP; URL: https://www.ncbi.nlm.nih.gov) and the Bioinformatics Analysis Tool for Molecular Mechanism of Traditional Chinese Medicine

(BATMAN-TCM; URL: http://bionet.ncpsb.org/batmantcm).<sup>4,5</sup> The pharmacokinetic parameters and the corresponding criteria of active compounds, including oral bioavailability ( $\geq$  30%), drug-likeness ( $\geq$  0.18), and Caco-2 permeability ( $\geq$  -0.4), were identified by Absorption, Distribution, Metabolism, and Excretion (ADME) data.

## Ingredient-Related Target Gene (TG) Prediction

Active ingredient-associated TGs were identified as mentioned in "2.1 Active Ingredient Screening of AACO". We transformed various ID forms of the TGs into UniProt (URL: https://www.uniprot.org/) IDs with the limitation of "*Homo sapiens*" as the species and obtained the official gene names.

# Prediction of transverse aortic constriction-induced CHF Genes

Mouse total RNA was isolated with TRIzol regents. The RNA-seq data can be accessed through the Gene Expression Omnibus (GEO) database (URL: https://www.ncbi.nlm.nih. gov/geo), an open functional genomics data repository of the National Center for Biotechnology Information (NCBI), using accession number GSE217747. Using mouse genome microarray data, we analyzed candidate treatment targets for AACO and AACO-free in transverse aortic coarctation (TAC) model by using the LIMMA package, for the R programming language. Differentially expressed genes (DEGs) referred to those genes with a Q-value and a fold change < .05 and >1.5, respectively.

## **Retrieving CHF-Related TGs**

CHF-related genes were identified by using the Therapeutic Target Database (TTD; URL: https://db.idrblab. org/ttd), Online Mendelian Inheritance in Man (OMIM; URL: http://www.omim.org/), and DisGeNET (URL: http:// www.disgenet.org).<sup>6-8</sup> We transformed various ID forms of the targets into UniProt IDs, with the limitation of "*Homo sapiens*" as the species.

## Constructing the Protein-Protein Interaction (PPI) Networks

PPI networks were constructed to illuminate the correlation of AACO with CHF by analyzing their overlapping targets. The relationships were analyzed by the application of STRING,<sup>9</sup> and visualized using Cytoscape (version 3.7.0), in which the node size was in direct proportion to the degree of centrality acquired from topology analysis.

# **Gene Function Analysis**

We used the DAVID 6.8 database<sup>10</sup> (URL: https://david. ncifcrf.gov/) for gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) signal pathway enrichment analyses. Based on the p-value, the first 20 entries were chosen to create a bubble chart, which was completed using the OmicShare platform (URL: https://www.omicshare.com/).

Table 1.	The	Composition	of	TCM
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	Herbal Components	Herbal Components		Amount		
Formula	Latin name	English name	Traditional Use	(g)	Clinical Manifestations	Function
	Astragalus membranaceus (Fisch.) Bunge	Radix Astragali	To treat qi deficiency syndrome	30	Deficiency of qi and yang	To replenish qi, restore
	Aconitum wilsonii Stapf ex Veitch	Monkshood	To revive the yang for resuscitation	10	marked by cardiac palpitation,	the normal pulse,
AACO	Curcuma longa L.	Turmeric	To promote the flow of qi and eliminate blood stasis	10	shortness of breath, scarcely	nourish yang, and
	Dedin Ophistersonia	Devenfilitation	To nourish yin and promote the production of body	10	perceptible pulse, and	promote the excretion
	Radix Opniopogonis	Dwari iliyturi	fluid, to moisten the lungs, and to ease the mind	10	spontaneous sweating	of body fluid

Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; TCM, Traditional Chinese medicine.

#### Constructing a "Drug-Component-Target-Disease" Network

We built a "drug-component-target-disease" network to obtain considerable insight into the complex correlations among the herbs contained in the AACO formula, the active ingredients, targets, and diseases using Cytoscape 3.7.0.<sup>9</sup>

### **Topology Analysis**

Topology analysis was performed using the "network analyzer" tool in Cytoscape 3.7.0, which yielded betweenness centrality and degree value. We marked the node size and color based on the degree values, from largest to smallest.<sup>9</sup>

### **Experimental Validation**

**Ethical Approval.** All experiments and animal care procedures were reviewed by the Institutional Animal Care and Use Committee and approved by the Shanghai Medical Experimental Animal Care Commission. The study followed the provisions and general recommendations of the Chinese Experimental Animals Administration Legislation. This study was approved by the ethics committee of the Shanghai University of Traditional Chinese Medicine (No. PZSHUTCM2302040001).

**Experimental Animals**. C57BL/6 mice (8–12 weeks old) were ordered from Lingchang BioTech, Shanghai, China (license no. SCXK 2018-0003) and reared in a specific-pathogen-free animal facility.

Model Construction and Drug Intervention. The mice underwent intraperitoneal anesthesia with 2% pentobarbital (35 mg/kg). Mouse breathing was controlled by tracheal intubation and ventilation. The tidal volume was 1.5 ml and the breathing frequency was 90-110 times/min. The surgical area was cleaned, the chest was opened to the second rib through a median thoracic incision, the thymus was separated, and the aortic arch was exposed. According to the diameter of the aortic arch (approximately 1.0-1.1 mm), a 27 G padding needle was used to pad the aorta. The aorta was separated and constricted 0.3 cm after the right common carotid artery. Twodimensional ultrasound revealed that the diameter of the aorta was reduced by 50-55%, resulting in approximately 70% stenosis. The padding needle was extracted after ligation. The mediastinum was sutured in layers and the tracheal intubation was withdrawn after the mice resumed spontaneous breathing. The mice were housed in cages. The sham operation group did not undergo aortic arch ligation; the remaining procedures were the same as described.

After one week of feeding, all mice were administered AACO solution at 0.386  $\mu$ g/g (TCM group), valsartan at

1.029 μg/g (valsartan group), or an equivalent amount of double-distilled water (sham group), once daily for 8 weeks. The dosages administered were chosen according to the "Human and Animal Body Surface Area Dose Equivalent Conversion Ratio Table".<sup>11</sup> The animals were sacrificed 24 hours after the last administration.

**AACO Preparation and Identification**. After purchasing the TCM from Tong Ren Tang, Shanghai, China, we prepared the AACO extract as follows: Using the reflux heating method, AACO (1000 g) was reacted with 90% ethanol for 1.5 hours, followed by filtering with a 120-mesh sieve. After concentrating the filtrate, the residue was decocted with water for 1 h and the sample was re-filtered. Finally, the filtrates obtained from the two steps were mixed and concentrated at 50°C. The mixture was lyophilized and subjected to AACO extraction (110 g). The AACO extract was confirmed by Dr. Cheng Lu per the Pharmacopoeia of the People's Republic of China 2015 Edition. The voucher specimen (No. 20200428) was placed at Shuguang Hospital affiliated with the Shanghai University of Traditional Chinese Medicine, Shanghai, China (Table 1).

UHPLC-Q-Orbitrap High-Resolution Mass Spectrometry (HRMS) Analysis. The AACO extract quality was confirmed by qualitative and quantitative analysis of the major bioactive components through chromatographyquadrupole/electrostatic field orbitrap HRMS (UHPLC-Q/ Exactive; Thermo Fisher Scientific, San Jose, CA, USA). This was followed by the elution of the components with a gradient system composed of aqueous 0.1% formic acid (I) and acetonitrile (II) (0–2 min, 10% II; 2–9 min, 10–95% II).

**Hemodynamic Study**. The mice were anesthetized with 2% pentobarbital. We inserted a catheter (SPR-839; Millar Instruments, Houston, TX, USA) into the carotid artery and then into the left ventricle. After maintaining stability for several minutes, we used AD Instruments Power-Lab4/30 with Lab Chart Pro 7.0 software (MPVS-300; AD Instruments, Colorado Springs, CO, USA) to collect data on the pressure in the aorta and left ventricle.

**Echocardiography**. Mice were anesthetized with 2% pentobarbital. During the evaluation of cardiac function, the heart rate of the mice was maintained at approximately 450 bpm to diminish variation. Systolic function parameters, such as ejection fraction and fractional shortening, and diastolic function parameters, such as E and A waves, E/A ratio, and isovolumic relaxation time (IVRT), were measured using a Vevo 2100 imaging system (Toronto, ON, Canada) with the use of a 22–55 MHz MS450D transducer.

Histological Analysis. Mouse hearts were formaldehydefixed for 24 h, paraffin-embedded, and serially sectioned to 5  $\mu$ m slices. Heart morphology and myocardial fibrosis were analyzed by hematoxylin-eosin and Masson's trichrome staining, respectively.

**Immunohistochemistry**. Following 30 min of blocking with 10% sheep serum in 0.3% Triton X-100-supplemented phosphate-buffered saline, heart slices were immersed in anti-SERCA2a (#9580 Cell Signaling Technology) and -phospholamban (PLN #14562 Cell Signaling Technology) primary antibodies for overnight incubation (4°C). After incubation with a secondary antibody conjugated with diaminobenzidine, the sections were mounted on slides.

Primary Adult Cardiomyocyte (CM) Isolation. Mice were anesthetized with 2% pentobarbital, and the hearts were cut and placed in a buffer consisting of the following materials (volume): NaCl (120 mM), KCl (5.4 mM), NaH<sub>2</sub>PO<sub>4</sub> (1.2 mM), NaHCO<sub>2</sub> (20 mM), MgSO<sub>4</sub> (1.2 mM), glucose (5.6 mM), 2,3-butanedione monoxime (10 mM), taurine (20 mM), pH 7.33.<sup>12</sup> The solution was made by bubbling 95%  $O_2$  and 5%  $CO_2$ for 10 min using and then filtered through a 0.22-micron filter. Meanwhile, gentle cannulation of the heart via the aorta was performed using a small cannula, followed by a 5-minute perfusion with a buffer (2.5 ml/min). The heart was continuously perfused with a fresh collagenase solution (containing 12.5 mg of type II collagenase, 2.5 mg of type XIV protease, 50 µM CaCl, 0.1% BSA, filtered) for approximately 15 minutes until becoming soft. After cutting below the atria, the heart was transferred to a dish containing 5 ml of collagenase solution with calcium, sheared, and the myocardial tissue was transferred to a tube. The supernatant was transferred into a fresh tube containing 5 ml of stopping buffer (12.5 µM CaCl, and 2 ml of FBS) for a 1-minute centrifugation (500 rpm). The resuspended cells were gradually recovered to physiological calcium concentration (1 mM).

Adult Cardiomyocyte Contractility and Calcium Transient. According to the protocol published by Wang and others,12 freshly isolated adult CMs were treated with 30 min of cultivation with Fluo-4 AM (5 µM; Molecular Probes, Grand Island, NY). Next, the CMs were placed in the dish center as close to the electrodes as possible (NaCl 120 mM, KCl 5.4 mM, NaH, PO, 1.2 mM, MgSO, 1.2 mM, HEPES 20 mM, glucose 5.5 mM, CaCl, 1 mM, pH 7.1, filtered). The cells were then settled with 2 ml of beating buffer for 5 minutes. The cells were electrically stimulated at 1 Hz and 30 V. We observed the calcium transients and contractile of the CMs-5-10 rod-shaped CMs per field coverage using an inverted microscope. The following settings were applied: time interval, 1 min; duration, 10 min; exposure time, 25 ms; 200 frames per movie. CM FS was calculated as the percentage of the difference between the maximal and minimal cell length in the maximal cell length. Calcium transients were recorded at 488 nm excitation and 505 nm emission. The analysis was performed using MetaMorph.

Western Blot Analysis. Heart tissue specimen homogenizationwasperformed with a radioimmunoprecipitation lysate buffer supplemented with phosphatase and protease





**Abbreviations**: AACO, *Astragalus membranaceus (Fisch.)* Bunge, *Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis* 



[	Gene	Forward primer	Reverse primer
[	SERCA	5'-GAGAACGCTCACACAAAGACC-3'	5'-CAATTCGTTGGAGCCCCAT-3'
ſ	PLN	5'-AAAGTGCAATACCTCACTCGC-3'	5'-GGCATTTCAATAGTGGAGGCTC-3'
ſ	GAPDH	5'-AGGTCGGTGTGAACGGATTTG-3'	5'-TGTAGACCATGTAGTTGAGGTCA-3'

#### Abbreviations: PCR, polymerase chain reaction

inhibitor cocktails, followed by supernatant collection. After separation on 10% sodium dodecyl sulfate–polyacrylamide gel electrophoresis gels, protein specimens were transferred onto membranes made of polyvinylidene difluoride (Millipore) for 2 h of room temperature sealing with 5% non-fat milk and the subsequent blotting with antibodies (all from Cell Signaling Technology) against SERCA, phospholamban, and GAPDH. Then came 1 h of room temperature incubation of the membranes by adding a horseradish peroxidase-labeled goat anti-rabbit IgG (Beyotime, Shanghai, China) secondary antibody (1:5000 dilution). Protein band visualization and quantification using BeyoECL Star (Beyotime, Shanghai, China) and ImageJ software, respectively.

Quantitative Real-Time Polymerase Chain Reaction Analysis. We used a TRIzol reagent to separate tissue total RNA and transcribed it into cDNA with the use of a Revert Aid First Strand cDNA Synthesis Kit (Life Technologies), after which a TaqMan SYBR kit (Life Technologies) was used for real-time polymerase chain reaction. Primer sequences are listed in Table 2.

#### Statistical Analyses

All experimental data are statistically processed by SPSS (version 20.0; SPSS Inc., Chicago, IL, USA) and presented as mean  $\pm$  standard deviation. Variance homogeneity was analyzed using Levene's test, and data analyses were made with one-way analysis of variance and least significant difference t-tests, with the minimum significance level set at P < .05.

#### RESULTS

# Screening and Collecting the Active Ingredients of the AACO Formula

The contents of calycosin-7-O- $\beta$ -D-glucoside, benzoylnesaconine, benzoylaconine, benzoylhypaconine, astragaloside IV, and ruscogenin were determined by the **Figure 3.** (A) The Heatmap Comparing Gene Expressions Between CHF and AACO Groups (n = 3). (B) The Volcano Plot of p Values of mRNA Weighted Fold Changes in Myocardial Tissue in CHF and AACO Groups. The Perpendicular Line Delimits Up- and Down-Regulation, with Red and Green Plots Representing Significantly Up-Regulated and Down-Regulated mRNAs (Fold Change >1.5, corrected P < .05), Respectively.



**Abbreviations**: AACO, *Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis*; CHF, chronic heart failure

UHPLC-Q/Exactive method as 22.41, 129.59, 14.60, 5.12, 3.20, and 0.0080 µg/ml, respectively (Figure 2).

One hundred and five active compounds were acquired from the TCMSP and BATMAN-TCM databases for the four herbs of AACO, based on chemical similarity. From the TCMSP database, 16 active compounds were obtained from *Astragalus membranaceus (Fisch.) Bunge*, 14 from *Aconitum wilsonii* Stapf ex Veitch, and three from *Curcuma longa L.* From the BATMAN-TCM database, 35 active compounds from *Astragalus membranaceus (Fisch.) Bunge*, 58 from *Aconitum wilsonii* Stapf ex Veitch, 11 from *Curcuma longa L.*, and 22 from *Radix ophiopogonis* were collected. The repetitive active compounds were removed. Eventually, 105 active compounds were obtained, including astragaloside IV, calycosin, benzoylnesaconine, benzoylhypaconine, and benzoylaconine, et al. (Supplementary Table 1).

## DEGs in TAC With and Without AACO

TAC mice treated with and without AACO were analyzed to identify mRNA expression profiles. See Figure 3A for the heatmap of the top 20 genes in TAC with and without AACO. Through volcano plot filtering, 867 DEGs (P < .05, FC > 1.5, Figure 3B), including 494 upregulated and 373 downregulated genes, were identified.





Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; CHF, chronic heart failure

**Figure 5.** (A–B): A Protein-Protein Interaction (PPI) Network was Built to Illuminate the Relationships Among the Shared Target Genes



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; CHF, chronic heart failure

# Prediction of Compound-Related TGs

In total, 492 and 887 predicted targets of the AACO active constituents were acquired from the TCMSP and BATMAN-TCM, respectively. We obtained 1026 targets after deleting the duplicates. Among these, *Astragalus membranaceus (Fisch.) Bunge* had 540, *Aconitum wilsonii* Stapf ex Veitch 274, *Curcuma longa L.* 396, and *Radix ophiopogonis* 244 targets. We identified 12 common targets for the four herbs, namely MAOB, NOS1, OPRK1, PGR, ATP1A1, ADORA2B, RAPGEF2, DRD2, TACR2, IL1B, ESR1, and SCN5A.

## Prediction of CHF-Related TGs

We obtained 883 TGs related to CHF from the TTD, OMIM, and DisGeNET (Figure 4).

# Prediction of Shared TGs Between the AACO Formula and CHF

We mapped 1026 compound-related TGs and 883 CHFrelated TGs to obtain 240 shared TGs by constructing a Venn diagram, which might elucidate the potential mechanisms of action underlying the anti-CHF effect of AACO (Figure 4, Supplementary Table 2).

Finally, a PPI network was constructed to elucidate the relationships between AACO and CHF by analyzing their overlapping targets (Figure 4). This network was composed of 237 nodes and 3,878 edges (Figure 5A). The degree values of the first 20 genes are shown in Figure 5B; the top 10 shared targets were INS, GAPDH, IL6, ALB, VEGFA, TNF, ATP2A2, NOS3, CASP3, and EGFR (Figure 5B).

**Figure 6.** (A–C): GO Analysis of the AACO Targets Involved in the Activity Against CHF. (A) Related Biological Processes, (B) Cell Structures, and (C) Part of Molecular Functions. The Dot Size in the Figure Represents the Gene Number, and the Color Represents the *P*-value. (D) KEGG Analysis of the AACO Targets Involved in the Activity Against CHF. (E) The "Drug-Compound-Target-Disease" Network was Built According to the Screened Compounds, Predicted Targets, and GO/KEGG Analysis. The Dot Size in the Figure Indicates the Gene Number, and the Color Represents the *P* value.



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; CHF, chronic heart failure; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes

## GO and KEGG Enrichment Analyses of the TGs

GO and KEGG analyses of the 240 TGs were performed using the DAVID database. According to GO analysis, the enriched genes related to the biological process were involved in hypoxia, positive gene expression regulation, blood pressure modulation, positive modulation of cytosolic calcium ion concentration, and cardiac muscle contraction regulation by regulating the sequestered calcium ions release (Figure 6A). The enriched genes related to cell structure were involved in the plasma membrane, extracellular space, cytosol, extracellular region, and the calcium channel complex (Figure 6B). Finally, regarding molecular functions, **Figure 7.** The AACO Formula Improved Cardiac Function in CHF Mice. (A–D) M-Mode Echocardiography Results of the Mice in the Four Groups. (E–H) Pulsed-Wave Doppler Mode Echocardiography Results of the Mice in the Four Groups.



**Abbreviations**: AACO, *Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis*; CHF, chronic heart failure.

the enriched genes were involved in enzyme binding, ion channel binding, protein binding, protein homodimerization activity, and drug binding (Figure 6C). KEGG analysis revealed that the TGs were enriched in HIF-1, calcium, cGMP-PKG, adrenergic signaling pathways, and renin secretion (Figure 6D, Supplementary Table 3). Collectively, the calcium axis is one of the main axes involved in the anti-CHF activity of the AACO formula.

### **Network Construction**

The "drug-compound-target-disease" network was built based on the screened compounds, predicted targets, and GO/KEGG analysis (Figure 6E).

# The AACO Formula Improved Cardiac Function in CHF Mice

To test the efficacy of AACO in CHF treatment, we generated CHF mice via transverse aortic constriction. Echocardiography revealed that the ejection fraction, fractional shortening, and E/A ratio were statistically reduced in control mice versus sham mice, and the left ventricle mass and IVRT were markedly enhanced, suggesting that the model was successfully established (Figure 7A-H; Figure 8A–F). The ejection fraction, fractional shortening, E/A

**Figure 8.** The AACO Formula Improved Cardiac Function in CHF Mice. (A–F) Echocardiography Results of the Mice in the Four Groups. (A) EF %, (B) FS%, (C) LV Mass, (D) Correct LV Mass, (E) E/A, and (F) IVRT. (G) Hemodynamic Test Results and the LVEDP of the Mice in the Four Groups. (H) Heart Weight. (I) Heart Weight/Body Weight. \**P* < .05 and \*\**P* < .01: Control Group vs. Other Groups; #*P* < .05 and ##*P* < .01: Valsartan Group vs. Control Group;  $^{\Delta}P$  < .05 and  $^{\Delta}P$  < .01: AACO Group vs. Control Group; (n = 10).



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; CHF, chronic heart failure; E/A, E/A ratio; EF, ejection fraction; GO, gene ontology; IVRT, isovolumic relaxation time; LV, left ventricle; LVEDP, left ventricular end-diastolic pressure; left ventricular end-diastolic pressure

ratio, left ventricle mass, and IVRT were similar between the AACO and valsartan groups, which were improved compared to control mice (Figure 7A-H; Figure 8A–F). In the hemodynamic test, the control mice showed enhanced left ventricular end-diastolic pressure than sham, AACO, and valsartan groups (Figure 8G). Furthermore, a higher heart weight/body weight ratio was determined in the control group as compared to the other three groups (Figure 8H, I).

The CHF CMs were morphologically abnormal, accompanied by hypertrophy, which was in line with the heart function observed (Figure 9A). Masson's trichrome staining showed more severe myocardial fibrosis in control mice compared with sham mice and alleviated myocardial fibrosis in AACO and valsartan groups versus the control group (Figure 9B). Immunohistochemistry showed that the positive staining for SERCA2a and PLN was mainly concentrated in the cytoplasm, showing brown-yellow granules. The staining of SERCA2a was weaker in the control group than in the sham

**Figure 9.** The AACO Formula Inhibited Myocardial Fibrosis. (A) HE Staining. (B) Masson's Trichrome Staining. Scale Bar = 100 µm. a: Sham Group, b: Control Group, c: Valsartan Group, and d: AACO Group. \**P* < .05 and \*\**P* < .01: Control Group vs. Other Groups; #*P* < .05 and ##*P* < .01: Valsartan Group vs. Control Group;  $^{\triangle}P$  < .05 and  $^{\triangle}P$  < .01: AACO Group vs. Control Group (n = 10).



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; HE, Hematoxylin and eosin

**Figure 10.** The AACO Formula Increased SERCA2a Expression and Promoted Calcium Transient and Myocardial Contractility. A–B: The Results of Immunohistochemistry Showed that the Positive Staining of SERCA2a and PLN was Mainly Concentrated in the Cytoplasm, Showing Brown-Yellow Granules. \**P* < .05 and \*\**P* < .01: Control Group vs. Other Groups; #*P* < .05 and ##*P* < .01: Valsartan Group vs. Control Group;  $^{\Delta}P$  < .05 and  $^{\Delta\Delta}P$  < .01: AACO Group vs. Control Group (n = 10).



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis, PLN, Phospholamban; SERCA2a, Sarcoplasmic reticulum calcium ATPase2a

**Figure 11.** (A) Therapeutic Effects of the Drugs on Cardiomyocyte Shortening. ISO, Isoproterenol, a β-Adrenergic Receptor Agonist (100 nM for AVM stimulation). (B) Therapeutic Effects of the Drugs on Cardiomyocyte Ca<sup>2+</sup> Handling. ISO, Isoproterenol, a β-Adrenergic Receptor Agonist (100 nM for AVM stimulation). (C–D) SERCA2a and PLN mRNA Expression in the Calcium Signaling Pathway in the Hearts of the Four Groups. (E–H) SERCA2a and PLN Protein Expression in the Calcium Axis in the Hearts of the Four Groups. \**P* < .05 and \*\**P* < .01: Control Group vs. Other Groups; #*P* < .05 and ##*P* < .01: Valsartan Group vs. Control Group;  $^{\Delta}P$  < 0.05 and  $^{\Delta}P$  < .01: AACO Group vs. Control Group; (n = 10).



Abbreviations: AACO, Astragalus membranaceus (Fisch.) Bunge, Aconitum wilsonii Stapf ex Veitch, Curcuma longa L., Radix ophiopogonis; AVM, arteriovenous malformation; PLN, Phospholamban; SERCA2a, Sarcoplasmic reticulum calcium ATPase2a

group, whereas comparable positivity was observed for the control, AACO, and valsartan groups. PLN staining was similar among the four groups (Figure 10A–D).

### Verification of the Mechanism Identified by Network Pharmacology Analysis

To validate the network pharmacology results, we isolated CMs from transverse aortic constriction mice who were treated with drugs for 8 weeks. The CM contractility test revealed significantly diminished CM contractility in control mice compared to sham mice, with a lower response to isoproterenol, a  $\beta$ -adrenergic receptor agonist (Figure 11A). Besides, significantly reduced CM calcium transients were determined in the control group as compared to the sham

group (Figure 11B). After 8 weeks of AACO administration, CM contractility was significantly enhanced with a higher response to the  $\beta$ -adrenergic receptor agonist compared to the control group (Figure 11A). Significantly improved calcium transients were also found in the AACO group versus the control group (Figure 11B). While AACO and valsartan groups had similar CM contractility or calcium transients (Figure 11A, B). The control group showed reduced SERCA2a gene expression in the myocardium than the sham group, while the AACO group had markedly elevated SERCA2a gene expression than the control group (Figure 11C). PLN gene expression was similar among groups (Figure 11D). Furthermore, the myocardium SERCA2a protein expression was significantly decreased in the control group compared to the sham group, and it was greatly increased in the AACO group compared to the control group. No statistical difference was identified in PLN protein expression among the groups. The SERCA2a/PLN ratio was significantly lower in the control group than sham group and was significantly increased in the AACO group than control and valsartan groups (Figure 11E-F).

### DISCUSSION

CHF has become the most important global public health issue and is the only cardiovascular disease with increasing incidence and high mortality. TCM can treat complex diseases by regulating the interaction of various factors in the human body to maintain the balance of the whole organism. However, the complexities of TCMs have restricted their development. Network pharmacology has been used to investigate the pharmacological mechanisms of TCM treatment of various complex diseases through the analysis of medicine, gene, protein, and disease information databases building an interaction network of "drugcomponent-target-disease".<sup>13,14</sup>

The AACO formula is a clinically proven prescription to treat CHF. This study confirmed that AACO could improve heart function, reduce heart mass, reduce left ventricular enddiastolic pressure, inhibit myocardial fibrosis in transverse aortic constriction mice, and enhance the contractility of CMs and CM calcium transients at the cellular level.

However, the four TCMs in the formula contain hundreds of active ingredients that exert synergistic pharmacological effects at different levels on multiple targets. We applied the network pharmacology method to investigate the mechanism of AACO in CHF treatment, obtained AACO active constituents, and predicted CHF-associated TGs by searching the databases. Through bioinformatic analysis, we found that the calcium axis might be one of the main signaling pathways involved in the activity of AACO against CHF.

The calcium axis is critical in modulating myocardial diastolic and systolic functions<sup>15,16</sup> and includes SERCA2a, PLN, and RyR2. SERCA2a is a myocardial sarcoplasmic reticulum (SR) calcium pump, and disorders in its expression and activity are key pathologies in CHF.<sup>17</sup> Protein kinase A phosphorylates PLN, resulting in the dissociation of PLN

from the binding site of SERCA2a, leading to its inhibitory effects on SERCA2a being reversed. SERCA2a reuptakes Ca2+ from the cytoplasm into the SR, causing CMs to relax and reserve Ca<sup>2+</sup> for subsequent contraction. Pathological changes in any of these steps can cause a decline in myocardial diastolic and systolic functions. Several studies have shown that SERCA2a, PLN, and other calcium regulatory proteins play an extremely crucial role in patients with CHF and animal models.<sup>15,18,19</sup> The significantly reduced expression level and activity of SERCA2a in failed myocardial tissue and disorders in the regulation of PLN all lead to reduced Ca<sup>2+</sup> reuptake into the SR in the diastolic period, reduced SR load, increased intracytoplasmic Ca2+ concentration, and decreased SR Ca<sup>2+</sup> release during the systolic period, resulting in impaired systolic and diastolic functions, which is a characteristic of failed CMs and suggests a poor prognosis.<sup>20,21</sup>

Here, we confirmed that AACO promoted gene expression and protein levels of SERCA2a, while it exerted little influence on PLN expression. Furthermore, we speculated that AACO might affect the phosphorylation of PLN, but this requires further verification.

#### CONCLUSION

Network pharmacology, a practical means for studying the complicated pharmacological mechanisms underlying TCM treatment of various complex conditions, was used in this study to reveal that the calcium axis was the main pathway underlying the effect of AACO against CHF. Further investigations of the key steps in the calcium axis and the application of molecular biology, cell function, morphology, and other technical methods have proven the predicted results of network pharmacology, providing an important basis for TCM treatment of heart failure.

#### AUTHOR DISCLOSURE STATEMENT

All authors have read and approved the final manuscript. The authors declare that they have no conflict of interest. There are no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Cheng Lu as the first author helped with validation, writing, and original draft preparation; Huiling Li helped with software, visualization, and original draft preparation; Xinting Wang helped with validation; Huiying Wang assisted with writing-reviewing and editing; Lei Song helped with validatio; Jingru Zhao helped with software; and Yongming Liu as the corresponding author provided supervision and helped with the conceptualization, validation, reviewing, and editing.

#### DATA AVAILABILITY STATEMENT

All data generated or used during the study are available from the corresponding author by request.

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# **Supplementary Table 1.** The active ingredients of the AACO formula the herbs of the AACO formula

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Molecule Name (the active compounds in the herbs) Isocurcumenol Neocurdione Beta-Elemene Curcumin Curcumol Curdione Curzerene Hederagenin Procurcumenol Weniine 11,14-eicosadienoic acid 3-Acetylaconitine 8-Deoxy-14-Dehydro-Aconosine Aconine Aconitine Benzoylaconine Benzoylhypaconine Benzovlmesaconine Bullatine B Bullatine C Carnosifloside l Corvneine Crassicauline A Delavaconitine Delgrandine

Delphamine Delphatine Delsoline Deltaline Deltoin Deoxyaconitine Deoxyandrographolide Higenamine Hypaconitine Hypaphorine Ignavine Isotalatizidine kaempferol Karakoline Karanjin M-Aminophenol Mesaconitine Mescaline Neojiangyouaconitine Neokadsuranic Acid B Neoline Ortho-Aminophenol P-Aminophenol Para-Aminophenol SalsolinolSitosterol Talatisamine Vilmorrianine C Bifendate (3S,8S,9S,10R,13R,14S,17R)-10,13-dimethyl-17-[(2R,5S)-5-propan-2-yloctan-2-yl]-2,3,4,7,8,9,11,12,14,15,16,17-dodecahydro-1H-cyclopenta[a]phenanthren-3-ol (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol 20-Hexadecanoylingenol 3,5-Dimethoxystilbene 3,9-di-O-methylnissolir 7-O-methylisomucronulatol Acetic Acid Adenine Astragaloside I Astragaloside II Astragaloside III Astragaloside IV Astragaloside V Astragaloside VI Astragaloside VII Astramembrannin I Betaine Beta-Sitosterol Calycosin Canavanine Choline Chrysanthemaxanthin Foliosidine Formononetin Gamma-Sitosterol Guanosine Hederagenin Isorhamnetin Kumatakenin Lupeol Mairin Ouercetin Rhamnocitrin Soyasapogenol B Soyasaponin 1 Sucrose Uridine 6-Aldehydo-Isoophipogonone B Guanosin Methyl Ophiopogonanone A Methyl Ophiopogonanone B Ophiopogon A Ophiopogon B Ophiopogonanone A Ophiopogonanone C Ophiopogonanone EOphiopogonin A Ophiopogonin B Ophiopogonin C Ophiopogonin D Ophiopogonone B Orchinol Stigmasterol Uridine

The active ingredients of the AACO formula. 105 active compounds were obtained, including astragaloside IV, calycosin, benzoylnesaconine, benzoylhypaconine, and benzoylaconine, et al.

NOS

# Supplementary Table 2. The compound-related target

#### genes. The active compounds of the AACO formula compound-related target genes (38,88,98,10R,138,148,17R)-10,13-dimethyl-17-[(2R,5S)-5-propan-2-yloctan-2-yl]-2,4,7,8,9,11,12,14,5,16,17-dodecahydro-1H-cyclopenta[a]phenanthrem-3-ol (3S,8S,9S,10R,13R,14S,17R)-10,13-dimethyl-17-[(2R,5S)-5-propan-2-yloctan-2-yl] 2,3,4,7,8,9,11,12,14,15,16,17-dodecahydro-1H-cyclopenta[a]phenanthren-3-ol ESR1 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol ADRA1B (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol ADRA1D (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol ADRB2 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol AR (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol CA2 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol CALM1 (GaR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol CALM2 (6aR.11aR)-9.10-dimethoxy-6a.11a-dihydro-6H-benzofurano[3.2-c]chromen-3-ol CALM3 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol CHRM4 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol ESR1 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol ESR2 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol GSK3B (6aR.11aR)-9.10-dimethoxy-6a.11a-dihydro-6H-benzofurano[3.2-c]chromen-3-ol NOST (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol PPARD (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol PTGER4 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol PTGS1 (6aR,11aR)-9,10-dimethoxy-6a,11a-dihydro-6H-benzofurano[3,2-c]chromen-3-ol PTK2B 11.14-eicosadienoic acid CÁ2 11,14-eicosadienoic acid NOS3 11,14-eicosadienoic acid PPARD 20-Hexadecanoylingeno CHGA 20-Hexadecanoylingenol NR3C2 20-Hexadecanovlingeno PRKCA 3,5-Dimethoxystilbene ABCC2 3.5-Dimethoxystilbene CDKN1A 3,5-Dimethoxystilbene DNMT1 3,5-Dimethoxystilbene DPYD 3.5-Dimethoxystilbene DPYS 3,5-Dimethoxystilbene HCN2 3,5-Dimethoxystilbene HIF1A 3,5-Dimethoxystilbene HTR2A 3,5-Dimethoxystilbene IL1B 3.5-Dimethoxystilbene PDE3A 3,5-Dimethoxystilbene PDE3B 3,5-Dimethoxystilbene SIRT1 3,9-di-O-methylnissolin ADRA1B 3,9-di-O-methylnissolin ADRA1D 3.9-di-O-methylnissolin ADRA2C 3,9-di-O-methylnissolin ADRB13,9-di-O-methylnissolin ADRB2 3,9-di-O-methylnissolin AR 3.9-di-O-methylnissolin CA2 3,9-di-O-methylnissolin CALM1 3.9-di-O-n thylnissolin CALM2 3,9-di-O-methylnissolin CALM3 3,9-di-O-methylnissolin ESR1 3.9-di-O-methylnissolin ESR2 3,9-di-O-methylnissolin

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Acetic Acid IL10 Acetic Acid MMP12 Acetic Acid MMP3 Acetic Acid MMP8 Acetic Acid MPO Acetic Acid NOS1 Acetic Acid PNMT Acetic Acid PTGS1 Acetic Acid PTGS2 Acetic Acid RELA Acetic Acid REN Acetic Acid SDS Acetic Acid SELP Acetic Acid SERPINE1 Acetic Acid SOD1 Acetic Acid TNF Acetic Acid TPI1 Acetic Acid XDH Aconine ATP2A2 Aconine UCN2 Aconitine CHRM2 Aconitine CHRM4 Aconitine PTGER4 Aconitine PTGS1 Aconitine SLC6A2 Adenine ADORA1 Adenine ADORA2AAdenine ADORA2B Astragaloside I ABCB1 Astragaloside I ALB Astragaloside I ATP1A1 Astragaloside I KCNH2 Astragaloside II ABCB1 Astragaloside II ALB Astragaloside II ATP1A1 Astragaloside II KCNH2 Astragaloside III CXCR4 Astragaloside IV ATP2A2 Astragaloside V CXCR4 Astragaloside VI CXCR4 Astragaloside VII CXCR4 Astramembrannin I CXCR4 Benzovlaconine CHRM2 Benzoylaconine SLC6A2 Benzoylhypa CHRM2 Benzovlhypaconine SLC6A2 Benzoylmesaconine CHRM2 Benzovlmesaconine SLC6A2 Beta-Elemene ADORA1 Beta-Elemene ADRA1A Beta-Elemene ALDH2 Beta-Elemene APOE Beta-Elemene BCL2 Beta-Elemene CAT Beta-Elemene CDKN1A Beta-Elemene CHRM2 Beta-Elemen

CYP2E1 Beta-Elemene EDN1 Beta-Elemene GATM Beta-Elemene IGF1 Beta-Elemene IL1B Beta-Elemene KCNA3 Beta-Elemene KCNIP2 Reta-Flemen KCNQ1 Beta-Elemene LEP Beta-Elemene MIP Beta-Elemene NPPA Beta-Elemene PTGS1 Beta-Elemene PTGS2 Beta-Elemene RHOA Beta-Elemene RYR2 Beta-Elemene SLC6A2 Beta-Elemene SOD1 Reta-Flemen TP53Beta-Elemene TPM1 Betain AKR1B1 Betaine CAD Betain GATM Betaine NOS1 Betaine NOS3 Betaine PIK3CG Betaine PPARG Betaine PTGS1 Betaine PTGS2 Betaine SLC18A3 Betain TGFB2 Betaine TP53 Betaine TPI1 Betaine UCN2 Betaine UTS2R Beta-Sitosterol AR Beta-Sitosterol BAX Reta-Sitostero CYP27B1 Beta-Sitosterol ESR1 Beta-Sitosterol GC Beta-Sitosterol NFKB1 Beta-Sitosterol NR3C1 Beta-Sitosterol NR3C2 Beta-Sitosterol PLN Beta-Sitosterol TBPL1 Bifendate AR Bifendate ESR1 Bifendate GSK3B Bifendate NOS2 Bifendate PTGER4 Bifendate PTGS1 Bullatine B UCN2 Bullatine C CHRM2 Calycosin ADRB2 Calycosin AR Calvcosin CA2 Calycosin CALM1 Calvo CALM2

GSK3B

NOS2

3.9-di-O-methylnissolin

3,9-di-O-methylnissolin

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CALM3 Colucosin
ESR1
Calycosin
ESR2
GSK3B
Calycosin
NOS2
Calycosin
Calvcosin
PIM1
Calycosin
PPARDCalycosin
Calvcosin
PTGER4
Calycosin
PIGSI
PTGS2
Calycosin
PTK2B
ALAS2
Canavanine
ARG1
Canavanine
Canavanine
CAD
Canavanine
ECE1 Canavanina
EDN1
Canavanine
F2RL1
Canavanine
Canavanine
GPT
Canavanine
HMOXI Canavanine
HTR2B
Canavanine
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Curdione CRHR2

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FKBP1B

Curdion

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Curdione NR3C2

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Curdione

LTA

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IL4Curdione

HCN2

HIF1A

HRC

IGF2

IL10

INS

GRK2

G6PD

EDN1

ESR1

ESR2

CRP

CSF2

CD34

ADA

Crassicauline A

Crassicauline A SLC6A2

PDE3B Curdione PDE5A Curdion PDE9A Curdione PIK3CA Curdion PIK3CB Curdion PIK3CD Curdione PIK3CG Curdion PPP3CA Curdione PTGS2 Curdione RYR1 Curdione RYR2 Curdione SEMA4D Curdion SIRT1 Curdione SLC8A1 Curdione SOD1 Curdione SUMO1 Curdione TBPL1 Curdione TNF Curdione TOP2B Curdione TPH2 Curdione UTS2 Curdione VKORC1 Curdion XDH Curzerene ADRA1A Curzeren ADRA1B Curzerene ADRB1 Curzerene ADRB2 Curzerene HTR2A Curzerene NOS3 Curzerene NR3C1 Curzerene PDE3A Curzerene SLC6A2 Curzerene SLC6A4 Delavaconitine CHRM2 Delavaconitine CHRM4 Delavaconitine SLC6A2Delgrandine ADRA2C Delgrandine CHRM2 Delgrandine HTR2A Delgrandine HTR2B Delgrandine KCNJ11 Delgrandine SLC6A2 Delphamine UCN2 Delphatine UCN2 Delsoline UCN2 Deltaline ABCB1 Deltaline ALB Deltaline KCNH2 Deltoin ADRA1B Deltoin ADRB2 Deltoin AR Deltoin CA2 Deltoin CALM1 Deltoin CALM2 Deltoin CALM3 Deltoin ESR1 Deltoin ESR2

Deltoin NOS2 Deltoin PPARD Deltoin PTGER4 Deltoin PTGS1 Deoxyaco CHRM2 onitine Deoxyaco CHRM4 nitine Deoxvaconitine SLC6A2 Deoxyandrographolide AR Deoxyandrographolide ESR1 Deoxyandrographolide NOS2 Deoxyandrographolide NR3C1 Deoxyandrographolide NR3C2 Deoxyandrographolide PTGS1 Foliosidine NQO1 Formononetin ADRA1A netin ADRB2 Formononetin AR Formononetin CA2 Formononetin CALM1 Formononetin CALM2 Formononetin CALM3 Formononetin FSR1 Formononetin ESR2 Formononetin GSK3B Formononetin MAPK14 Formononetin NOS2Formononetin NOS3 Formononetin PIM1 Formononetin PPARD Formononetin PPARG Formononetin PTGER4 Formononetin PTGS1 Formononetin PTGS2 Formononetin PTK2B Formononetin SLC6A2 Formononetin SI C6A4 Gamma-Sitosterol AR Gamma-Sitosterol BAX Gamma-Sitosterol CYP27B1 Gamma-Sitosterol ESR1 Gamma-Sitosterol GC Gamma-Sitosterol NFKB1 Gamma-Sitosterol NR3C1 Gamma-Sitosterol PLN Gamma-Sitosterol TBPL1 Guanosine ADORA1 Guanosine ADORA2A ADORA2B Guanosine BRCA1 DNMT1 Guanosine TBPL1 Hederagenin ADRA1B Hederagenin AR Hederagenin CA2 Hederagenin CHRM2 Hederagenin FSR1 Hederagenin

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Isorhamnetin RELA Isorhamnetin XDH Isotalatizidine CHRM2 Kaempferol ADRA1B Kaempferol AHSA1 Kaempferol AKT1 Kaempferol ARKaempferol AR Kaempferol BAX Kaempferol BCL2 Kaempferol CA2 Kaempferol CA2 Kaempferol CALM1 Kaempferol CALM1 Kaempferol CALM2 Kaempferol CALM2 Kaempferol CALM3 Kaempferol CALM3 Kaempferol CASP3 Kaempferol CHRM2 Kaempferol CRYZ Kaempferol ESR1 Kaempferol ESR1 Kaempferol ESR2 Kaempferol ESR2 Kaempferol GSK3B Kaempferol GSK3B Kaempferol HMOX1 Kaempferol MAPK14 Kaempferol MAPK14 Kaempferol MAPK8 Kaempferol MMP1 Kaempferol NOS2 Kaempferol NOS2 Kaempferol NOS3 Kaempferol NR112 Kaempferol PIK3CG Kaempferol PPARD Kaempferol PPARD Kaempferol PPARG Kaempferol PPP3CA Kaempferol PTGER4 Kaempferol PTGER4 Kaempferol PTGS1 Kaempferol PTGS2 Kaempferol PTGS2 Kaempferol PTK2B Kaempferol PTK2B Kaempferol RELA Kaempferol SCN5A Kaempferol SLC2A4 Kaempferol SLC6A2 Kaempferol TNF Kaempferol TOP2BKaempferol VEGFA Kaempferol XDH Kaempferol PIK3CD

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Karakolin UCN2 Karaniin FSR1 Karanjin PIK3CD Karaniii PTGER4 Karanjin PTGS1 Querco NOS3 Kumatakenin PTGS1 Lupeol BAX Lupeol BCL2 Lupeol CASP3 Lupeol CYP27B1 Lupeol ESR1 Lupeol GC Lupeol NFKB1 Lupeol PLN Lupeol SOD1 Lupeol TRPI 1 Mairin AR Mairin ESR1 Mairin NR3C1 M-Aminophenol ADORA2B M-Aminophenol ANGPT1 M-Aminophenol APOA1 M-Aminophenol M-Aminophenol BMP4 M-Aminophenol CAMK2D M-Aminophenol CHDH M-Aminophenol CRP M-Aminophenol EPO M-Aminophenol FASLG M-Aminophenol HCN2 M-Aminophenol HRC M-Aminophenol IFNG M-Aminophenol IL10 M-Aminophenol IL1B M-Aminophenol IL4 M-Aminophenol M-Aminophenol LGALS3 M-Aminophenol LILRB1 M-Aminophenol LTA M-Aminophenol NRG1 M-Aminophenol PDE3A M-Aminophenol ROCK1 M-Aminophenol SELP M-Aminophenol SIRT1M-Aminophenol TGFB1 Mesaconitine CHRM2 Mescaline ADRA1A Mescaline ADRA1B Mescaline ADRA1D Mescaline ADRA2C Mescaline ADRB1 Mescaline ADRB2 Mescaline ADRB3 Mescaline ANK2 Mescaline CASQ2 Mescaline CAV3 Mescalin

Mescaline GPD1L Mescaline HTR2A Mescaline KCNO1 Mescaline NPPA NOS1 Mescaline PDE3A Mescalin Mescaline Mescaline SLC6A2 Mescaline SLC6A4 Methyl Ophiopogonanone A Methyl Ophiopogonanone A Methyl Ophiopogonanone B Methyl Ophiopogonanone B Methyl Ophiopogonanone B CCR7 Methyl Ophiopogonanone B Methyl Ophiopogonanone B Methyl Ophiopogonanone B Neocurdion ABCC4 Neocurdione ADA RYR2 Neocurdione ADORA1 Neocurdione ADORA2A ADORA2B Neocurdione ADRA1B Neocurdione dione ARID1A Neocurdione Neocurdione ATP1A1 UTS2 Neocurd ATP1A2 Neocurdione ATP2A1 Neocurdione ATP2B4 XDH Neocurdione Neocurdione Neocurdione BNIP3Neocurdione AR CAMK2D Neocurdione CD34 ESR1 Neocurdione CRHR2 Neocurdione CRP Neocurdione Neocurdione CX3CR1 Neocurdion Neocurdione Neocurdione ESR2 Neocurdione FKBP1B Neocurdion Neocurdione AKT1 Neocurdione GRK2 Neocurdione CCR7 Neocurdione Neocurdione CNR2 Neocurdione Neocurdione IL10 Neocurdione Neocurdione

DBH

PTGS2

RYR1

CNR2

SOAT1

AKT1

CAV3

CD36

CNR2

SOAT1

ADRB1

AGT

Neocu

ATM

AVPR2

BCL2

CSF2

EDN1

ESR1

FOXP3

G6PD

GHRL

HCN2

HIF1A

HRC

IGF2

INS

ITPR1

ITPR2

KCNH2 Neocurdione LONP1 Neocurdion LTA Neocurdione MTOR Neocurdione Neocurdione NOS1AP Neocurdione NR3C2 Neocurdione PDE3A Neocurdione PDE3B Neocurd PDE5A ocurdione PDE9A Neocurdione PIK3CA Neocurdi PIK3CB Neocurdione PIK3CD ocurdion PIK3CG PPP3CA Neocurdione Neocurdione RYR1 PTGS2 Neocurdione lione Neocur SEMA4D Neocurdion SIRT1 Neocurdione SLC8A1 Neocurd SOD1 Neocurdione SUMO1 Neocurdione TNFNeocurdione TOP2B Neocurdione TPH2 Neocurdione UCN2 Neocurdione Neocurdione VKORC1 Neocurdione Neojiangyouaconitine CHRM2 Neojiangyouaconitine SLC6A2 Neokadsuranic Acid B AGTR1 Neokadsuranic Acid B Neokadsuranic Acid B Neokadsuranic Acid B NR3C1 Neokadsuranic Acid B NR3C2 Neokadsuranic Acid B PTGER4 Neoline UCN2 Ophiopogon A ATP1A1 Ophiopogon B ATP1A1 Ophiopogonanone A CNR2 Ophiopogonanone A SOATÎ Ophiopogonanone C CNR2 Ophiopogonanone C SOAT1 Ophiopogonanone E Ophiopogonanone E CAV3 Ophiopogonanone E Ophiopogonanone E CD36 Ophiopogonanone E Ophiopogonanone E SOAT1 Ophiopogonin A ATP1A1 Ophiopogonin B ATP1A1 Ophiopogonin C ATP1A1 Ophiopogonin D ATP1A1 Ophiopogonone B

Neocurdion

CRYZ Ophiopogonone B NQO1 Ophiop VEGFA none B Orchinol NR1I2 Orchinol PRKCA Orchinol SCN5A Ortho-Aminophenol ADORA2B Ortho-Aminophenol ANGPT1 Ortho-Aminophenol BMP4 Ortho-Aminophenol CAMK2D Ortho-Aminophenol CHDH Ortho-Aminophenol CRP Ortho-Aminophenol EPO Ortho-Aminophenol FASLG Ortho-Aminophenol HCN2 Ortho-Aminophenol HRCOrtho-Aminophenol IFNG Ortho-Aminophenol II 10 Ortho-Aminophenol IL1B Ortho-Aminophenol II 4 Ortho-Aminophenol IL6 Ortho-Aminophenol LGALS3 Ortho-Aminophenol I II RB1 Ortho-Aminophenol LTA Ortho-Aminophenol NRG1 Ortho-Aminophenol PDE3A Ortho-Aminophenol ROCK1 Ortho-Aminophenol SELP Ortho-Aminophenol SIRT1 Ortho-Aminophenol TGFB1 P-Aminophenol ADORA2B P-Aminophenol ANGPT1 P-Aminophenol BMP4 P-Aminophenol CAMK2D P-Aminophenol CHDH P-Aminophenol CRP P-Aminophenol EPO P-Aminophenol FASLG P-Aminophenol HCN2 P-Aminophenol HRC P-Aminophenol IFNG P-Aminophenol IL10 P-Aminophenol IL1B P-Aminophenol IL4 P-Aminophenol IL6 P-Aminophenol LGALS3 P-Aminophenol LILRB1 P-Aminophenol LTA P-Aminophenol NRG1 P-Aminophenol P-Aminophenol PDE3A P-Aminophenol PTGER4 P-Aminophenol PTGS1 P-Aminophenol ROCK1 P-Aminophenol SELP P-Aminophenol SIRT1 P-Aminophenol TGFB1 Para-Aminophenol ADORA2B

Para-Aminophenol ANGPT1 Para-Aminophenol BMP4 Para-Aminophenol CAMK2D Para-Aminophenol CHDH Para-Aminophenol CRP Para-Aminophenol EPOPara-Aminophenol FASLG Para-Aminophenol HCN2 Para-Aminophenol HRC Para-Aminophenol IFNG Para-Aminophenol IL10 Para-Aminophenol IL1B Para-Aminophenol IL4 Para-Aminophenol IL6 Para-Aminophenol LGALS3 Para-Aminophenol LILRB1 Para-Aminophenol LTA Para-Aminophenol NRG1 Para-Aminophenol PDE3A Para-Aminophenol PTGER4 Para-Aminophenol PTGS1 Para-Aminophenol ROCK1 Para-Aminophenol SELP Para-Aminophenol SIRT1 Para-Aminophenol TGFB1 Procurcumenol AR Procurcumenol ESR1 Procurcum NOX1 Procurcumenol NR3C1 Procurcu PTGER4 Procurcum PTGS1 Procurcum RYR3 Procurcur TGFB1 Quercetin ACACA Quercetin ADRA2C Ouercetin ADRB2 Quercetin AHSA1 Quercetin AKR1B1 Quercetin AKT1 Quercetin AR Ouercetin BAX Quercetin BCL2 Quercetin CA2 Quercetin CASP3 Quercetin CCL2 Ouercetin CDKN1A Quercetin CHEK2 Ouercetin COL1A1 Quercetin COL3A1 Quercetin CRP Ouercetin CXCL2 Quercetin DUOX2 Ouercetin EGFRQuercetin ERBB2 Ouercetin ESR1 Quercetin ESR2 Quercetin GJA1

Quercetir GSK3B Ouercetir HIFIA Quercetii HK2 Ouerce HMOX1 Querceti HSF1 Querce HSPB1 Ouercetir HTR2A Quercetir HTR2B Ouerceti IFNG Quercetir IGF2 Quercetin IL10 Ouercetir II 1A Quercetir IL1B Ouercetir IL6 Quercetir IRF1 Querceti KCNH2 Ouercet MAPK1 Quercetin MAPK14 Ouerce MMP1 Quercet MMP2 Querce MMP3 Querceti MMP9 Querce MPO Ouercetir NCF1 Quercetir NFE2L2 Querce NOS2 Quercetir NOO1 Quercetir NR1I2 Ouercet PARP1 Quercetin PIK3CD Querceti PIK3CG Quercetir PLAT Querc PON1 Ouercetin PPARA Quercetin PPARD Quercetin PPARG Quercetin PRKCA Ouercetin PTEN Quercetin PTGER4 Ouercetin PTGS1 Quercetin PTGS2 Quercetin PTK2B Quercetin RAF1Quercetin RELA Quercetin SCN5A Quercetin SERPINE1 Querce SLC2A4 Quercetir SOD1 Quercetin SPP1 Quercetir TGFB1 Quercetin TNF Quercetir TP53 Quercetin VDR Quercetir VEGFA

Quercetin	Soyasapogenol B	NR3C2
XDH	AR	Stigmasterol
Rhamnocitrin	Soyasapogenol B	PTGS1
AKR1B1	ESR1	Stigmasterol
Rhamnocitrin	Sovasapogenol B	PTGS2
AR	NR3C1	Stigmasterol
Rhamnocitrin	Soyasaponin 1	RYR2
CALM2		Stigmasterol
Phampagitrin	Someanonin 1	SCNEA
CALM2	NID2C1	SCINDA Stimmentenel
Dhamma aitain	Stimmenten 1	Stigmasteror
Rhamhochtrin FCD1	ADODA1	SLC6A2
DI VI	ADORAL	Sugmasteroi
Rhamhocitrin	Stigmasteroi	SODI
ESR2	ADRATA	Stigmasterol
Rhamnocitrin	Stigmasterol	TPM1
GSK3B	ADRA1BStigmasterol	Sucrose
Rhamnocitrin	ADRB1	AKR1B1
MAPK14	Stigmasterol	Sucrose
Rhamnocitrin	ADRB2	COL1A1
NOS2	Stigmasterol	Sucrose
Rhamnocitrin	AKR1B1	CXCR4
PIK3CG	Stigmasterol	Sucrose
Rhamnocitrin	ALDH2	IFNG
PPARG	Stigmasterol	Sucrose
Rhamnocitrin	APOE	MMP9
PTGS1	Stigmasterol	Sucrose
Rhamnocitrin	CAT	PPARG
PTGS2	Stigmasterol	Talatisamine
Salsolinol	CHRM2	CHRM2
ADRA1A	Stigmasterol	Uridine
Salsolinol	CVP2F1	APRT
A DR A 1B	Stigmasterol	Uridine
Salsolinol	FDN1	DNMT1
ADRA1D	Stigmastaral	Uridina
S-laslingl	EED 1	DBVD
Salsolilloi	ESKI	DFID
ADRA2C	Stigmasteroi	Uridine
Salsolinoi	GAIM	ENPPI
ADRBI	Stigmasterol	Uridine
Salsolinol	H1R2A	NOSI
ADRB2	Stigmasterol	Uridine
Salsolinol	IGF1	NQ01
ARRB2	Stigmasterol	Uridine
Salsolinol	IL1B	PON1
ESR1	Stigmasterol	Vilmorrianine C
Salsolinol	KCNA3	ABCB1
NR3C1	Stigmasterol	Vilmorrianine C
Salsolinol	KCNIP2	ACE
NR3C2	Stigmasterol	Vilmorrianine C
Salsolinol	KCNQ1	CHRM2
PTGS1	Stigmasterol	Vilmorrianine C
Salsolinol	LEP	NOS1AP
PTGS2	Stigmasterol	Vilmorrianine C
Salsolinol	MĨP	SLC6A2Wenjine
SLC6A2	Stigmasterol	AR
Sitosterol	NPPA	
AR	Stigmasterol	hsa04012:ErbB signaling pathway
Salsolinol SLC6A2 Sitosterol AR	MIP Stigmasterol NPPA Stigmasterol	SLC6A2Wenjine AR hsa04012:ErbB signaling path

The compound-related target genes. We mapped 1026 compound-related target genes and 883 CHF-related target gene to obtain 240 shared target genes which might elucidate the potential mechanisms of action underlying the anti-CHF effect of AACO.

Supple	mentary '	Tab	le 3.	KEGG	analysis	of	the	AACO
targets	involved	in	the	activity	against	CH	F si	gnaling
pathway	ys the targ	et ge	enes					

CDKN1A

BAD hsa04012:ErbB signaling pathway pathway ADORA1 CAMK2D hsa04012:ErbB signaling pathway CDKN1A hsa04012:ErbB signaling pathway EGFR hsa04012:ErbB signaling pathway pathway ADRA1B FRBB2 hsa04012:ErbB signaling pathway GSK3B pathway hsa04012:ErbB signaling pathway ADRAID MAPK1 hsa04012:ErbB signaling pathway pathway MAPK8 ADRA2C hsa04012:ErbB signaling pathway MTOR hsa04012:ErbB signaling pathway ADRB1 NRG1 hsa04012:ErbB signaling pathway path pathway ADRB2 PIK3CA hsa04012:ErbB signaling pathway PIK3CB hsa04012:ErbB signaling pathway pathway ADRB3 PIK3CD hsa04012:ErbB signaling pathway PIK3CG pathway AGTR1 hsa04012:ErbB signaling pathway pathway ATP1A PRKCA hsa04012:ErbB signaling pathway RAF1 pathway ATP1A2 hsa04020:Calcium signaling pathway ADORA2A hsa04020:Calcium signaling pathway ADORA2B pathway ATP2A1 hsa04020:Calcium signaling pathway ADRA1A hsa04020:Calcium signaling pathway pathway ADRA1B ATP2A2 hsa04020:Calcium signaling pathway ADRA1D pathway hsa04020:Calcium signaling pathway ATP2B4 ADRB1 hsa04020:Calcium signaling pathway pathway ADRB2 BAD hsa04020:Calcium signaling pathway ADRB3 hsa04020:Calcium signaling pathway CALMI AGTR1 hsa04020:Calcium signaling pathway ATP2A1 CALM2 hsa04020:Calcium signaling pathway ATP2A2 hsa04020:Calcium signaling pathway the pathway CALM3 ATP2B4 hsa04020:Calcium signaling pathway athway CALM1 NS hsa04020:Calcium signaling pathway CALM2 athu ITPR1 hsa04020:Calcium signaling pathway CALM3 hsa04020:Calcium signaling pathway pathway ITPR2 CAMK2D hsa04020:Calcium signaling pathway CHRM2 athway hsa04020:Calcium signaling pathway MAPK1 EGFR hsa04020:Calcium signaling pathway pathway FRBB2 NOS3 hsa04020:Calcium signaling pathway HTR2A hsa04020:Calcium signaling pathway PDE3A HTR2B hsa04020:Calcium signaling pathway pathway PDE3B ITPR1 hsa04020:Calcium signaling pathway ITPR2 thway hsa04020:Calcium signaling pathway PDE5A NOS1 hsa04020:Calcium signaling pathway athway pathv PLN NOS2 hsa04020:Calcium signaling pathway pathway PPP3CA NOS3 hsa04020:Calcium signaling pathway PLN pathway RAF1 hsa04020:Calcium signaling pathway PPP3CA hsa04020:Calcium signaling pathway PRKCAhsa04020:Calcium signaling pathway RHOA pathway PTK2B hsa04020:Calcium signaling pathway pathway ROCK1 RYR1 hsa04020:Calcium signaling pathway RYR2 pathway SLC8A1 hsa04020:Calcium signaling pathway RYR3 hsa04020:Calcium signaling pathway ANGPT1 SLC8A1 SLC0A1 hsa04020:Calcium signaling pathway TNNC1 BCL2 hsa04020:Calcium signaling pathway CAMK2D TNNC1

hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling pathway ADRA1A hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022;cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022;cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022;cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022;cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling hsa04022:cGMP-PKG signaling 04066:HIF-1 signaling pathway hsa04066:HIF-1 signaling pathway hsa04066:HIF-1 signaling pathway hsa04066:HIF-1 signaling pathway

hsa04066:HIF-1 signaling pathway EDN1 hsa04066:HIF-1 signaling pathway EGFR hsa04066:HIF-1 signaling pathway EPO hsa04066:HIF-1 signaling pathway ERBB2hsa04066:HIF-1 signaling pathway GAPDH hsa04066:HIF-1 signaling pathway HIF1A hsa04066:HIF-1 signaling pathway HK2 hsa04066:HIF-1 signaling pathway HMOX1 hsa04066:HIF-1 signaling pathway IFNG hsa04066:HIF-1 signaling pathway IGF1 hsa04066:HIF-1 signaling pathway IL6 hsa04066:HIF-1 signaling pathway INS hsa04066:HIF-1 signaling pathway MAPK1 hsa04066:HIF-1 signaling pathway MTOR hsa04066:HIF-1 signaling pathway NFKB1 hsa04066:HIF-1 signaling pathway NOS2 hsa04066:HIF-1 signaling pathway NOS3 hsa04066:HIF-1 signaling pathway NPPA hsa04066:HIF-1 signaling pathway PIK3CA hsa04066:HIF-1 signaling pathway PIK3CB hsa04066:HIF-1 signaling pathway PIK3CD hsa04066:HIF-1 signaling pathway PIK3CG hsa04066:HIF-1 signaling pathway PRKCA hsa04066:HIF-1 signaling pathway SERPINE1 nsa04066:HIF-1 signaling pathway VEGFA hsa04068:FoxO signaling pathway ATM hsa04068:FoxO signaling pathway BNIP3 hsa04068:FoxO signaling pathway CAT hsa04068;FoxO signaling pathway CDKN1A hsa04068:FoxO signaling pathway EGFR hsa04068:FoxO signaling pathway FASLG hsa04068:FoxO signaling pathway IGF1 hsa04068:FoxO signaling pathway IL10 hsa04068:FoxO signaling pathway II 6 hsa04068:FoxO signaling pathway INS hsa04068:FoxO signaling pathway MAPK1 hsa04068:FoxO signaling pathway MAPK14 hsa04068:FoxO signaling pathway MAPK8 hsa04068:FoxO signaling pathway PIK3CA hsa04068:FoxO signaling pathway PIK3CB hsa04068:FoxO signaling pathway PIK3CD hsa04068:FoxO signaling pathway PIK3CG hsa04068:FoxO signaling pathway PTEN hsa04068:FoxO signaling pathway RAF1 sa04068:FoxO signaling pathway SIRT1 hsa04068:FoxO signaling pathway SLC2A4 hsa04068:FoxO signaling pathway TGFB1 hsa04068:FoxO signaling pathway TGFB2 hsa04071:Sphingolipid signaling pathway ADORA1 hsa04071:Sphingolipid signaling nathway

BAX

hsa04071:Sphingolipid signaling pathway BCL2hsa04071:Sphingolipid signaling athu MAPK1 hsa04071:Sphingolipid signaling pathway MAPK14 hsa04071:Sphingolipid signaling pathway MAPK8 hsa04071:Sphingolipid signaling pathway NFKB1 hsa04071:Sphingolipid signaling pathway NOS3 hsa04071:Sphingolipid signaling pathway PIK3CA hsa04071:Sphingolipid signaling pathway PIK3CB hsa04071:Sphingolipid signaling pathway PIK3CD hsa04071:Sphingolipid signaling pathway PIK3CG hsa04071:Sphingolipid signaling othur pathway PRKCA hsa04071:Sphingolipid signaling pathway PTEN hsa04071:Sphingolipid signaling oathway RAF1 hsa04071:Sphingolipid signaling pathway RHOA hsa04071:Sphingolipid signaling pathway ROCKI hsa04071:Sphingolipid signaling pathway TNF hsa04071:Sphingolipid signaling pathway TP53 hsa04210:Apoptosis ATM hsa04210:Apoptosis BAD hsa04210:Apoptosis BAX hsa04210:Apoptosis BCI 2 hsa04210:Apoptosis CASP3 hsa04210:Apoptosis FASLG hsa04210:Apoptosis NFKB1 hsa04210:Apoptosis PIK3CA hsa04210:Apoptosis PIK3CB hsa04210:Apoptosis PIK3CD hsa04210:Apoptosis PIK3CG hsa04210:Apoptosis TNF hsa04210:Apoptosis TP53 hsa04261:Adrenergic signaling in cardiomyocytes ABCC4 hsa04261:Adrenergic signaling in cardiomyocytes ADORA1 hsa04261:Adrenergic signaling in cardiomyocytes ADORA2A hsa04261:Adrenergic signaling in cardiomyocytes ADRAIA hsa04261:Adrenergic signaling in cardiomvocvtes ADRA18 hsa04261:Adrenergic signaling in cardiomyocytes ADRA1D hsa04261:Adrenergic signaling in cardiomyocytes ADRB1 hsa04261:Adrenergic signaling in cardiomyocytes ADRB2 hsa04261:Adrenergic signaling in cardiomyocytes AGTR1 hsa04261:Adrenergic signaling in ardiomyocytes ATP1A1 hsa04261:Adrenergic signaling in cardiomyocytes ATP1A2 hsa04261:Adrenergic signaling in cardiomyocytes ATP2B4

hsa04261:Adrenergic signaling in rdiomyocytes hsa04261:Adrenergic signaling in diomyocytes BCL2 hsa04261:Adrenergic signaling in cardiomyocytes CALM1 hsa04261:Adrenergic signaling in cardiomyocytes CALM2 hsa04261:Adrenergic signaling in cardiomyocytes CALM3 hsa04261:Adrenergic signaling in cardiomyocytes CAMK2Dhsa04261:Adrenergie signaling in cardiomyocytes CHRM2 hsa04261:Adrenergic signaling in cardiomyocytes GHRL hsa04261:Adrenergic signaling in rdiomyocytes HCN2 hsa04261:Adrenergic signaling in cardiomyocytes KCNQ1 hsa04261:Adrenergic signaling in ocytes cardiomy MAPK1 hsa04261:Adrenergic signaling in cardiomyocytes MAPK14 hsa04261:Adrenergic signaling in cardiomyocytes MAPK8 hsa04261:Adrenergic signaling in cardiomyocytes NFKB1 hsa04261:Adrenergic signaling in cardiomyocytes PDF3A hsa04261:Adrenergic signaling in cardiomyocytes PDE3B hsa04261:Adrenergic signaling in cardiomyocytes PIK3CA hsa04261:Adrenergic signaling in cardiomyocytes PIK3CB hsa04261:Adrenergic signaling in cardiomyocytes PIK3CD hsa04261:Adrenergic signaling in IL6 cardiomyocytes PIK3CG hsa04261:Adrenergic signaling in cardiomyocytes PLN hsa04261:Adrenergic signaling in cardiomy ocytes PPARA hsa04261:Adrenergic signaling in cardiomyocytes PRKCA hsa04261:Adrenergic signaling in cardiomyocytes RAF1 hsa04261:Adrenergic signaling in cardiomyocytes RHOA hsa04261:Adrenergic signaling in cardiomyocytes ROCK1 hsa04261:Adrenergic signaling in cardiomyocytes RYR2 hsa04261:Adrenergic signaling in cardiomyocytes SCN5A hsa04261:Adrenergic signaling in cardiomyocytes TNNC1 hsa04261:Adrenergic signaling in cardiomyocytes TPM1 hsa04370:VEGF signaling pathway sa04370:VEGF signaling pathway HSPB1 hsa04370:VEGF signaling pathway MAPK1 hsa04370:VEGF signaling pathway MAPK14 hsa04370:VEGF signaling pathway NOS3 hsa04370:VEGF signaling pathway PIK3CA a04370:VEGF signaling pathway PIK3CB hsa04370:VEGF signaling pathway PIK3CD hsa04370:VEGF signaling pathway PIK3CG hsa04370:VEGF signaling pathway **РРРЗСА** hsa04370:VEGF signaling pathway hsa04722:Neurotrophin signaling PRKCA hsa04370:VEGF signaling pathway

BAD

PTGS2 hsa04370:VEGF signaling pathway RAF1 hsa04370:VEGF signaling pathway VEGFA hsa04380:Osteoclast differentiation IFNG sa04380:Osteoclast differentiation IL1A hsa04380:Osteoclast differentiation II 1B hsa04380:Osteoclast differentiation LILRB1 hsa04380:Osteoclast differentiation MAPK1 hsa04380:Osteoclast differentiation MAPK14 hsa04380:Osteoclast differentiation MAPK8 hsa04380:Osteoclast differentiation NCF1 hsa04380:Osteoclast differentiation NFKB1hsa04380:Osteoclast differentiation NOX1 hsa04380:Osteoclast differentiation PIK3CA hsa04380:Osteoclast differentiation PIK3CB hsa04380:Osteoclast differentiation PIK3CD hsa04380:Osteoclast differentiation PIK3CG hsa04380:Osteoclast differentiation PPARG hsa04380:Osteoclast differentiation PPP3CA hsa04380:Osteoclast differentiation TGFB1 hsa04380:Osteoclast differentiation TGFB2 hsa04380:Osteoclast differentiation TNF hsa04668:TNF signaling pathway CASP3 hsa04668:TNF signaling pathway CCL2 hsa04668:TNF signaling pathway CSF2 hsa04668:TNF signaling pathway CXCL2 hsa04668:TNF signaling pathway EDN1 hsa04668:TNF signaling pathway IL1B hsa04668:TNF signaling pathway hsa04668:TNF signaling pathway MAPK1 hsa04668:TNF signaling pathway MAPK14 hsa04668:TNF signaling pathway MAPK8 hsa04668:TNF signaling pathway MMP3 hsa04668:TNF signaling pathway MMP9 hsa04668:TNF signaling pathway NFKB1 hsa04668:TNF signaling pathway PIK3CA hsa04668:TNF signaling pathway PIK3CB hsa04668:TNF signaling pathway PIK3CD hsa04668:TNF signaling pathway PIK3CG hsa04668:TNF signaling pathway PTGS2 hsa04668:TNF signaling pathway TNF hsa04668:TNF signaling pathway LTA hsa04722:Neurotrophin signaling nthway BAX hsa04722:Neurotrophin signaling BCL2 hsa04722:Neurotrophin signaling CALM1 hsa04722:Neurotrophin signaling pathy CALM2 hsa04722:Neurotrophin signaling CALM3 hsa04722:Neurotrophin signaling pathway CAMK2D hsa04722:Neurotrophin signaling FASLG hsa04722:Neurotrophin signaling GSK3B hsa04722:Neurotrophin signaling MAPK1

MAPK14 hsa04722:Neurotrophin signaling pathway MAPKS hsa04722:Neurotrophin signaling pathway NFKB1 hsa04722:Neurotrophin signali pathway PIK3CA hsa04722:Neurotrophin signaling PIK3CB hsa04722:Neurotrophin signaling . PIK3CD hsa04722:Neurotrophin signaling pathway PIK3CG hsa04722:Neurotrophin signaling RAF1hsa04722:Neurotrophin signaling pathway RHOA hsa04722:Neurotrophin signaling pathway TP53 hsa04750:Inflammatory mediator regulation of TRP channelsCALM1 hsa04750:Inflammatory mediator regulation of TRP channelsCALM2 hsa04750:Inflammatory mediator regulation of TRP channelsCALM3 hsa04750:Inflammatory mediator regulation of TRP channelsCAMK2D hsa04750:Inflammatory mediator regulation of TRP channelsF2RL1 hsa04750:Inflammatory mediator regulation of TRP channelsHTR2A hsa04750:Inflammatory mediator regulation of TRP channelsHTR2B hsa04750:Inflammatory mediator regulation of TRP channelsIGF1 hsa04750:Inflammatory mediato regulation of TRP channelsIL1B hsa04750:Inflammatory mediator regulation of TRP channelsITPR1 hsa04750:Inflammatory mediator regulation of TRP channelsITPR2 hsa04750:Inflammatory mediator regulation of TRP channelsMAPK14 hsa04750:Inflammatory mediator regulation of TRP channelsMAPK8 hsa04750:Inflammatory mediator regulation of TRP channelsPIK3CA hsa04750:Inflammatory mediator regulation of TRP channelsPIK3CB hsa04750:Inflammatory mediator hsa04750:Inflammatory mediator regulation of TRP channelsPIK3CD hsa04750:Inflammatory mediator regulation of TRP channelsPIK3CG hsa04750:Inflammatory mediator regulation of TRP channelsPRKCA hsa04750:Inflammatory mediator regulation of TRP channelsPTGER4 hsa04910:Insulin signaling pathway ACACA hsa04910:Insulin signaling pathway BAD hsa04910:Insulin signaling pathway CALM1 hsa04910:Insulin signaling pathway CALM2 hsa04910:Insulin signaling pathway CALM3 hsa04910:Insulin signaling pathway FASN hsa04910:Insulin signaling pathway GSK3B hsa04910:Insulin signaling pathway HK2 hsa04910:Insulin signaling pathway INS hsa04910:Insulin signaling pathway MAPK1 hsa04910:Insulin signaling pathway MAPK8 hsa04910:Insulin signaling pathway MTOR hsa04910:Insulin signaling pathway PDF3B nsa04910:Insulin signaling pathway PIK3CA hsa04910:Insulin signaling pathway PIK3CB hsa04910:Insulin signaling pathway PIK3CD hsa04910:Insulin signaling pathway PIK3CG hsa04910:Insulin signaling pathway RAF1

hsa04910:Insulin signaling pathway SLC2A4 hsa04915:Estrogen signaling pathway CALM1 sa04915:Estrogen signaling pathway CALM2 hsa04915:Estrogen signaling pathway CALM3 hsa04915:Estrogen signaling pathway EGFR hsa04915:Estrogen signaling pathway ESR1 hsa04915:Estrogen signaling pathway ESR2 sa04915:Estrogen signaling pathy way ITPR1hsa04915:Estrogen signaling athway ITPR2 hsa04915:Estrogen signaling pathway MAPK1 hsa04915:Estrogen signaling pathway MMP2 hsa04915:Estrogen signaling pathway MMP9 hsa04915:Estrogen signaling pathway NOS3 hsa04915:Estrogen signaling pathway OPRM1 hsa04915:Estrogen signaling pathway PIK3CA hsa04915:Estrogen signaling pathway PIK3CB hsa04915:Estrogen signaling pathway PIK3CD nsa04915:Estrogen signaling pathway PIK3CG hsa04915:Estrogen signaling pathway RAF1 hsa04917:Prolactin signaling pathway ESR1 hsa04917:Prolactin signaling pathway ESR2 hsa04917:Prolactin signaling pathway GSK3B hsa04917:Prolactin signaling pathway INS hsa04917:Prolactin signaling pathway IRF1 hsa04917:Prolactin signaling pathway MAPK1 hsa04917:Prolactin signaling pathway MAPK14 hsa04917:Prolactin signaling pathway MAPK8 hsa04917:Prolactin signaling pathway NFKB1 hsa04917:Prolactin signaling pathway PIK3CA hsa04917:Prolactin signaling pathway PIK3CB hsa04917:Prolactin signaling pathway PIK3CD hsa04917:Prolactin signaling pathway PIK3CG hsa04917:Prolactin signaling pathway RAF1 hsa04924:Renin secretion ACE sa04924:Renin secretion ADORA1 sa04924.Renin secretion ADRB1 hsa04924:Renin secretion ADRB2 sa04924:Renin secretion ADRB3 hsa04924:Renin secretion AGT nsa04924:Renin secretion AGTR1 hsa04924:Renin secretion CALM1 hsa04924:Renin secretion CALM2 nsa04924:Renin secretion CALM3 hsa04924:Renin secretion CTSB a04924:Renin secretion ITPR1 sa04924.Renin secretion ITPR2 hsa04924:Renin secretion PDE3A hsa04924:Renin secretion PDE3B hsa04924:Renin secretion PPP3CA sa04924:Renin secretion PTGER4

RFN hsa04930:Type II diabetes mellitus HK2 hsa04930:Type II diabetes mellitus INS hsa04930:Type II diabetes mellitus KCNI11 hsa04930:Type II diabetes mellitus MAPK1hsa04930:Type II diabetes mellitus MAPK8 nsa04930:Type II diabetes mellitus MTOR hsa04930:Type II diabetes mellitus PIK3CA hsa04930:Type II diabetes mellitus PIK3CB hsa04930:Type II diabetes mellitus PIK3CD hsa04930:Type II diabetes mellitus PIK3CG hsa04930:Type II diabetes mellitus SLC2A4 hsa04930:Type II diabetes mellitus TNF hsa04960:Aldosterone-regulated sodium reabsorption ATP1A1 hsa04960:Aldosterone-regulated sodium reabsorption ATP1A2 hsa04960:Aldosterone-regulated sodium reabsorption IGF1 hsa04960:Aldosterone-regulated sodium reabsorption INS hsa04960:Aldosterone-regulated sodium reabsorption MAPK1 hsa04960:Aldosterone-regulated odium reabsorption NR3C2 hsa04960:Aldosterone-regulated sodium reabsorption PIK3CA hsa04960:Aldosterone-regulated sodium reabsorption PIK3CB hsa04960:Aldosterone-regulated odium reabsorption PIK3CD hsa04960:Aldosterone-regulated sodium reabsorption PIK3CG hsa04960:Aldosterone-regulated sodium reabsorption PRKCA hsa04970:Salivary secretion ADRA1A hsa04970:Salivary ADRA1B hsa04970:Salivary secretion ADRA1D hsa04970:Salivary ADRB1 hsa04970:Salivary ADRB2 hsa04970:Salivary secretion ADRB3 hsa04970-Salivary secretion ATP1A1 hsa04970:Salivary secretion ATP1A2 hsa04970:Salivary secretion ATP2B4 hsa04970:Salivary secretion CALM1 hsa04970:Salivary secretion CALM2 hsa04970-Salivary secretion CALM3 hsa04970:Salivary secretion ITPR1 hsa04970:Salivary secretion ITPR2 hsa04970:Salivary secretion NOS1 hsa04970:Salivary secretion PRKCA hsa04970:Salivary secretion RYR3

KEGG analysis of the AACO targets involved in the activity against CHF.

hsa04924:Renin secretion

pathway

BAD