Supplementary Table 1. Comparison and assessment of the models of the tertiary structures of SAPCD2 and SAPCD2X1 generated by different programs.

	SAPCD2		**SAPCD2X1**	
Prediction software	**Predicted model**	**SAVES v6.0 verification**	**Predicted model**	**SAVES v6.0 verification**
SWISS-MODEL	no matching templates	——	no matching templates	——
AlphaFold		ERRAT:93.8865 VERIFY:Fail 34.01% WHATCHECK:21,32,39,41 is wrong; PROCHECK:errors:5; warning:2; pass:2 Ramachandran plot: 70.2% in (A,B,L); 5.9% in disallowed regions	——	——
I-TASSER		ERRAT:92.487 VERIFY:fail 62.18% WHATCHECK:1,2,22,23,28,33		ERRAT:76.2019 VERIFY:fail 54.01% WHATCHECK:

		,40,43 is wrong; PROCHECK:errors:6; warning:2;pass:1 Ramachandran plot: 72.4% in (A,B,L);4.3% in disallowed regions		1,2,22,23,28,33,36,40,43,44 is wrong; PROCHECK:errors:8; warning:1;pass:0 Ramachandran plot: 50.9% in (A,B,L); 5.0% in disallowed regions
QUARK	>300,cannot be modeled	——	>300, cannot be modeled	——
ROBETTA	model_21142_1	ERRAT:91.906 VERIFY:pass 80.46% WHATCHECK:1,2,22,33,40,43 is wrong; PROCHECK:errors:3; warning:3; pass:3 Ramachandran plot: 87.9% in (A,B,L); 0.0% in disallowed regions	model_18305_1	ERRAT:87.1671 VERIFY:pass 82.55% WHATCHECK:1,2,22,33,40,43,44 is wrong; PROCHECK:errors:4; warning:2; pass:3 Ramachandran plot: 91.7% in (A,B,L); 0.3% in

			disallowed regions
model_21142_2	ERRAT:92.2078 VERIFY:pass 80.96% WHATCHECK:1,2,33,40,43 is wrong; PROCHECK:errors:3; warning:2; pass:4 Ramachandran plot: 88.2% in (A,B,L); 0.0% in disallowed regions	model_18305_2	ERRAT:90.6634 VERIFY:Fail 79.48% WHATCHECK: 1,2,33,40,42 is wrong; PROCHECK:errors:2; warning:3; pass:4 Ramachandran plot: 88.2% in (A,B,L); 0.3% in disallowed regions
model_21142_3	ERRAT:92.2078 VERIFY:pass 82.99% WHATCHECK:1,2,33,40,42 is wrong;	model_18305_3	ERRAT:88.6978 VERIFY:Pass 82.55% WHATCHECK: 1,2,33,40,43,44 is wrong;

	PROCHECK:errors:2; warning:3; pass:4 Ramachandran plot: 90.4% in (A,B,L); 0.0% in disallowed regions		PROCHECK:errors:0; warning:4; pass:5 Ramachandran plot: 91.1% in (A,B,L); 0.0% in disallowed regions
model_21142_4	ERRAT:91.9271 VERIFY:Fail 76.90% WHATCHECK:1,2,33,40,42 is wrong; PROCHECK:errors:4; warning:1; pass:4 Ramachandran plot: 88.8% in (A,B,L); 0.3% in disallowed regions	model_18305_4	ERRAT:92.8218 VERIFY:Fail 79.01% WHATCHECK:1,2,33,40,43,44 is wrong; PROCHECK:errors:2; warning:4; pass:3 Ramachandran plot: 82.0% in (A,B,L); 0.3% in disallowed regions
	ERRAT:90.5263 VERIFY:Fail		ERRAT:90.5797 VERIFY:Fail

	model_21142_5	77.92% WHATCHECK :1,2,33,40,43 is wrong; PROCHECK:errors:0; warning:5; pass:4 Ramachandran plot: 88.8% in (A,B,L); 0.3% in disallowed regions	model_18305_5	79.48% WHATCHECK: 1,2,33,40,42,43 is wrong; PROCHECK:errors:4; warning:2; pass:3 Ramachandran plot: 90.5% in (A,B,L); 1.2% in disallowed regions

Supplementary Table 2. GO annotations of sapcd2.

all molecular function	all biological process	all cellular component
catalytic activity	cell cycle	extracellular region
enzyme regulator activity	cellular component organization	plasma membrane
signaling receptor activity	establishment of localization	synapse
signaling receptor binding	cell population proliferation	cell junction
transporter activity	cell differentiation	cell projection
structural molecule activity	cell death	cytoplasmic vesicle
cytoskeletal protein binding	developmental process	endosome
DNA binding	reproduction	vacuole
RNA binding	immune system process	golgi apparatus
DNA-binding transcription factor activity	nervous system process	endoplasmic reticulum
transcription factor binding	response to stimulus	cytosol
small molecule binding	signaling	mitochondrion
metal ion binding	DNA metabolic process	nucleus
carbohydrate binding	RNA metabolic process	chromosome
carbohydrate derivative binding	protein metabolic process	protein-containing complex
lipid binding	carbohydrate metabolic process	cytoskeleton
	carbohydrate derivative metabolic process	
	lipid metabolic process	
	homeostatic process	
	catabolic process	
	behavior	