

Supplementary Figures

Secondary Structure and Solvent Accessibility Prediction

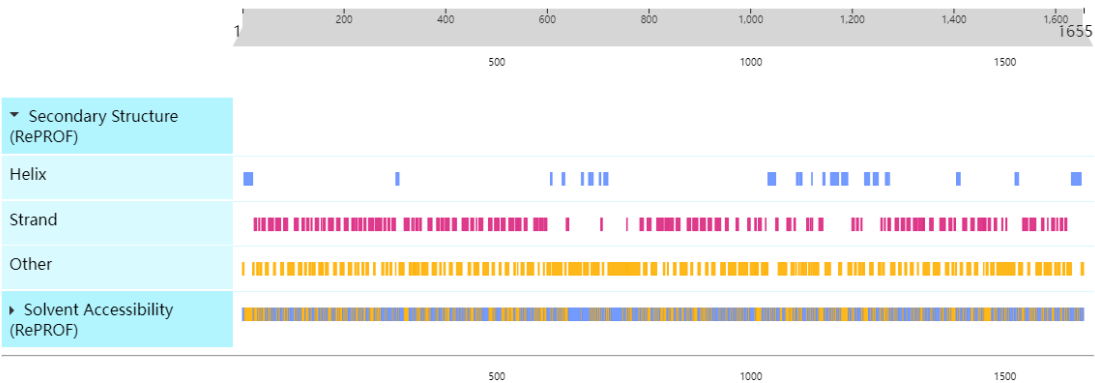


Figure S1. Secondary structure composition of complement C3 protein in Chinese alligator.

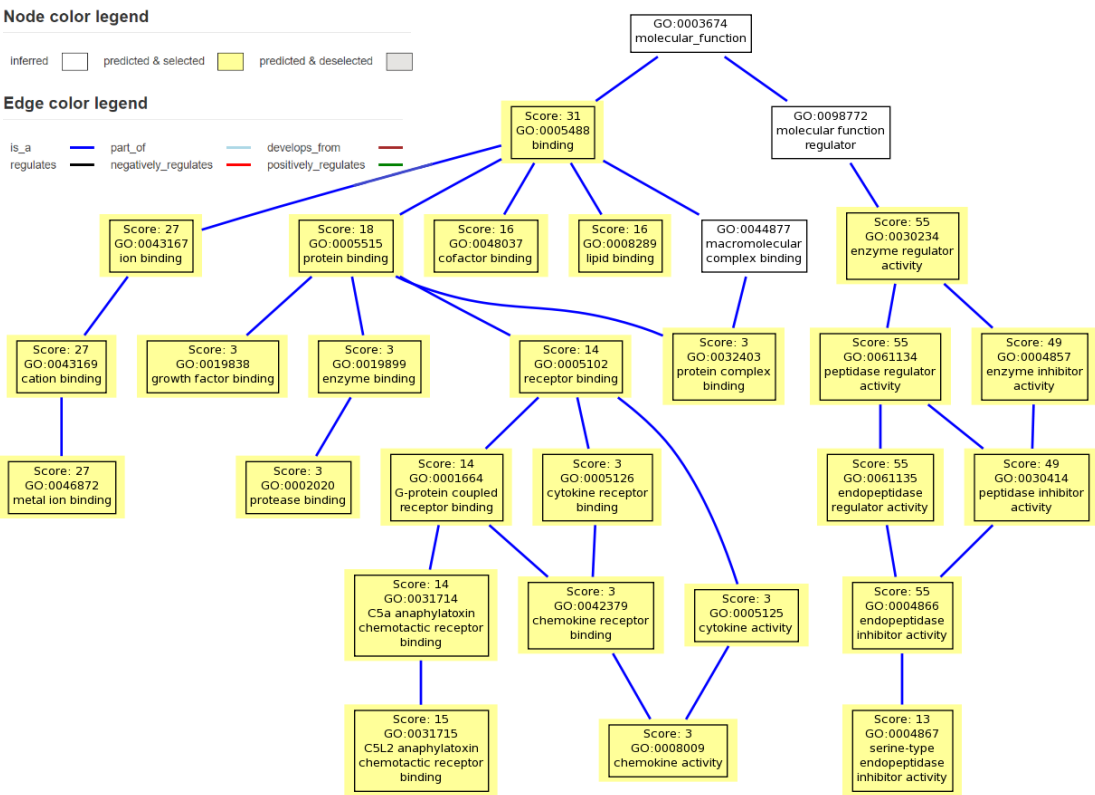


Figure S2. Molecular functional ontology of Chinese alligator complement C3 protein.

1	2	3	4	5	6	7	8	9	10	11	12
1/2	1/4	1/8	1/16	1/32	1/64	1/128	1/256	1/512	1/1024	+	-
1/2	1/4	1/8	1/16	1/32	1/64	1/128	1/256	1/512	1/1024	+	-
1/2	1/4	1/8	1/16	1/32	1/64	1/128	1/256	1/512	1/1024	+	-

Figure S5. Sample configuration scheme for the determination of serum inhibitory concentration of Chinese alligator in 96-well plate.

1	2	3	4	5	6	7	8	9	10	11	12
R1											
R2											
R3											

100μL P/S S+100μL bacteria solution

100μL alligator serum+100μL bacteria solution

100μL FBS+100μL bacteria solution

100μL MHB+100μL bacteria solution

200μL MHB

Figure S6. Sample configuration scheme of 96-well plate for Chinese alligator serum antibacterial experiment.

1	2	3	4	5	6	7	8	9	10	11	12
R1											
R2											
R3											

200μL MHB

90μL bacteria solution+110μL MHB

90μL bacteria solution+90μL MHB+20μL proteinase K

90μL bacteria solution+90μL P/S S+20μL MHB

90μL bacteria solution+90μL Alligator serum+20μL proteinase K

90μL bacteria solution+90μL Alligator serum+20μL MHB

Figure S7. Sample configuration scheme for determination of antibacterial components in Chinese alligator serum in 96-well plate.

Supplementary Tables

Table S1. Parameters used in proteins identification.

Item	Value
Type of search	MS/MS Ion search
Enzyme	Trypsin/P
Fragment Mass Tolerance	± 0.02 Da
Mass Values	Monoisotopic
Variable modifications	Oxidation (M)
Peptide Mass Tolerance	10 ppm
Instrument type	Default
Max Missed Cleavages	2
	Carbamidomethyl(C), TMT6plex (N-term), TMT6plex
Fixed modifications	(K)
Database	uniprot

Table S2. The top 20 pathways of serum protein annotated results in the KEGG database.

KEGG Pathway	Proteins with pathway annotation (488)	Pathway ID
Phagosome	90 (18.44%)	ko04145
PI3K-Akt signaling pathway	85 (17.42%)	ko04151
Leishmaniasis	82 (16.8%)	ko05140
Dilated cardiomyopathy	80 (16.39%)	ko05414
Staphylococcus aureus infection	79 (16.19%)	ko05150
Amoebiasis	70 (14.34%)	ko05146
Viral myocarditis	67 (13.73%)	ko05416
Hematopoietic cell lineage	67 (13.73%)	ko04640

Tuberculosis	66 (13.52%)	ko05152
Systemic lupus erythematosus	65 (13.32%)	ko05322
Natural killer cell mediated cytotoxicity	64 (13.11%)	ko04650
Primary immunodeficiency	64 (13.11%)	ko05340
Complement and coagulation cascades	64 (13.11%)	ko04610
Rheumatoid arthritis	59 (12.09%)	ko05323
Epstein-Barr virus infection	58 (11.89%)	ko05169
Cell adhesion molecules (CAMs)	57 (11.68%)	ko04514
Regulation of actin cytoskeleton	54 (11.07%)	ko04810
Rap1 signaling pathway	53 (10.86%)	ko04015
Pertussis	52 (10.66%)	ko05133
Calcium signaling pathway	50 (10.25%)	ko04020

Table S3. Composition of amino acid residues in complement C3 protein of Chinese alligator, human and cattle.

	Chinese alligator		Human		Cattle	
	Quantity	Proportion	Quantity	Proportion	Quantity	Proportion
Ala (A)	87	5.30%	96	5.90%	95	5.80%
Arg (R)	63	3.90%	82	5.00%	81	4.90%
Asn (N)	68	4.20%	61	3.70%	64	3.90%
Asp (D)	84	5.10%	90	5.50%	102	6.20%
Cys (C)	29	1.80%	27	1.60%	27	1.60%
Gln (Q)	73	4.50%	90	5.50%	88	5.40%
Glu (E)	119	7.30%	123	7.50%	112	6.80%
Gly (G)	96	5.90%	95	5.80%	96	5.90%

His (H)	30	1.80%	28	1.70%	32	2.00%
Ile (I)	103	6.30%	83	5.10%	96	5.90%
Leu (L)	137	8.40%	150	9.10%	144	8.80%
Lys (K)	130	8.00%	113	6.90%	122	7.40%
Met (M)	39	2.40%	35	2.10%	30	1.80%
Phe (F)	62	3.80%	60	3.70%	54	3.30%
Pro (P)	70	4.30%	80	4.90%	74	4.50%
Ser (S)	112	6.90%	106	6.50%	95	5.80%
Thr (T)	107	6.60%	103	6.30%	105	6.40%
Trp (W)	18	1.10%	17	1.00%	17	1.00%
Tyr (Y)	60	3.70%	57	3.50%	62	3.80%
Val (V)	146	8.90%	145	8.80%	143	8.70%
Pyl (O)	0	0.00%	0	0.00%	0	0.00%
Sec (U)	0	0.00%	0	0.00%	0	0.00%
