

**Table 1.** Identification by mass spectrometry of canine follicular fluid proteins separated by 2D-PAGE

Gene	AC <sup>1</sup> N <sup>o</sup>	Protein name	Exp <sup>2</sup>	Theo <sup>2</sup>	Score <sup>3</sup>	P N <sup>o</sup> 2	SC (%) <sup>4</sup>
			pI <sup>2</sup> /Mr <sup>2</sup>				
A2AP	P28800	Alpha-2-antiplasmin	6,08/57	5.36/54	10.17	1	2.2
ACTG	Q9UVW9	Actin-gamma	5,49/42	5.36/41	20.22	2	4.8
AHSG	P12763	Alpha-2-HS-glycoprotein	4,66/57	5.16/38	10.14	1	3.6
APOA1	P02648	Apolipoprotein A-I	5,05/48	5.06/30	10.16	1	3.4
APOA1	P02648	Apolipoprotein A-I	5,07/24	5.06/30	296.41	30	72.2
APOA1	P02648	Apolipoprotein A-I	6,20/21	5.06/30	50.23	5	24.1
APOA1	P02648	Apolipoprotein A-I	5,07/62	5.06/30	40.24	4	14.3
APOA4	Q32PJ2	Apolipoprotein A-IV	5,44/38	5.17/42	50.21	5	9.7
AT3	P41361	Antithrombin-III	5,14/55	7.08/52	80.20	8	8
AZGP1	Q3ZCH5	Zinc-alpha-2-glycoprotein	4,8/33	4.98/33	30.14	3	10.4
C4	P01030	Complement C4	7,48/31	6.13/101	34.19	4	4
CFB	P81187	Complement factor B	7,04/59	7.07/85	20.21	2	3.8
CFB	P81187	Complement factor B	6,38/102	7.5/85	20.26	2	3.8
CLU	P25473	Clusterin	5,05/33	5.56/51	10.16	1	3.6
CLU	P25473	Clusterin	5,3/31	5.56/51	20.16	2	6.1
FGG	P02679	Fibrinogen gamma chain	5,8/48	5.27/51	56.25	6	14.3
GC	Q3MHN5	Vitamin D-binding protein	5,17/54	5.24/53	70.29	7	9.5
GSN	Q3SX14	Gelsolin	6,01/88	5.45/80	20.24	2	5.5
HP	P19006	Haptoglobin	5,31/33	5.68/36	60.21	6	15.8
HP	P19006	Haptoglobin	5,47/33	5.68/36	50.30	5	21
HPR	Q28801	Haptoglobin-related protein	5,75/33	7.61/38	10.15	1	5.8
ICA	Q29545	Inhibitor of carbonic anhydrase	6,29/77	5.85/77	50.20	5	3.6
PON1	P27169	Paraoxonase/arylesterase 1	5,13/42	4.96/39	20.27	2	7.9
RBP4	P18902	Retinol-binding protein 4	5,45/20	5.33/21	40.21	4	12
TF	Q29443	Serotransferrin	7,05/72	6.69/77	42.25	5	7.7

The experimental position of identified spots is shown in Figure 5.

<sup>1</sup> AC is an accession number from the UniProt database

<sup>2</sup> Exp: Experimental; Theo: Theoretical; pI: Isoelectric point; Mr: Molecular weight; P N<sup>o</sup>: Peptid number; SC: Sequence coverage

<sup>3</sup> Score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event, it is based on NCBIInr database using the MASCOT searching program

<sup>4</sup> Sequence coverage (%) is based on number of peptide masses matched in NCBIInr databases