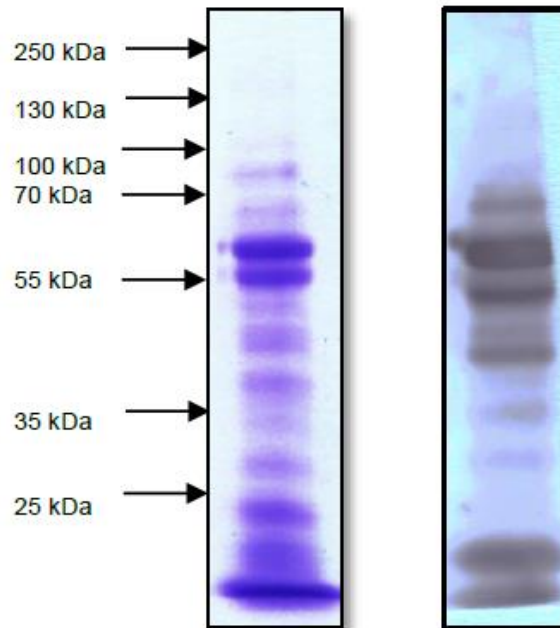
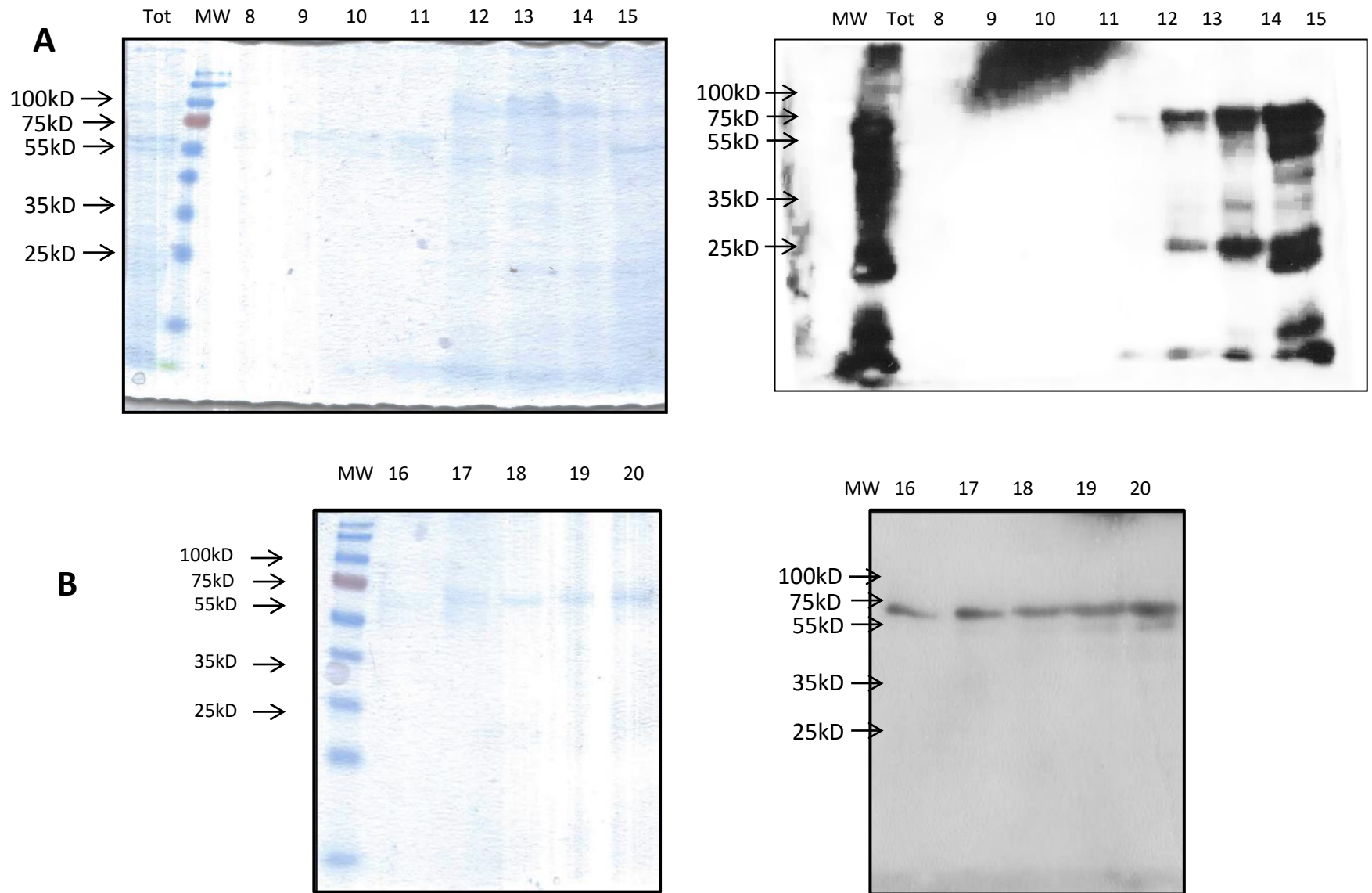


**Supplementary material:** Figures 1-4 show the GroEL protein purification process. Table 1 corresponds to protein identification by liquid chromatography-mass spectrometry.

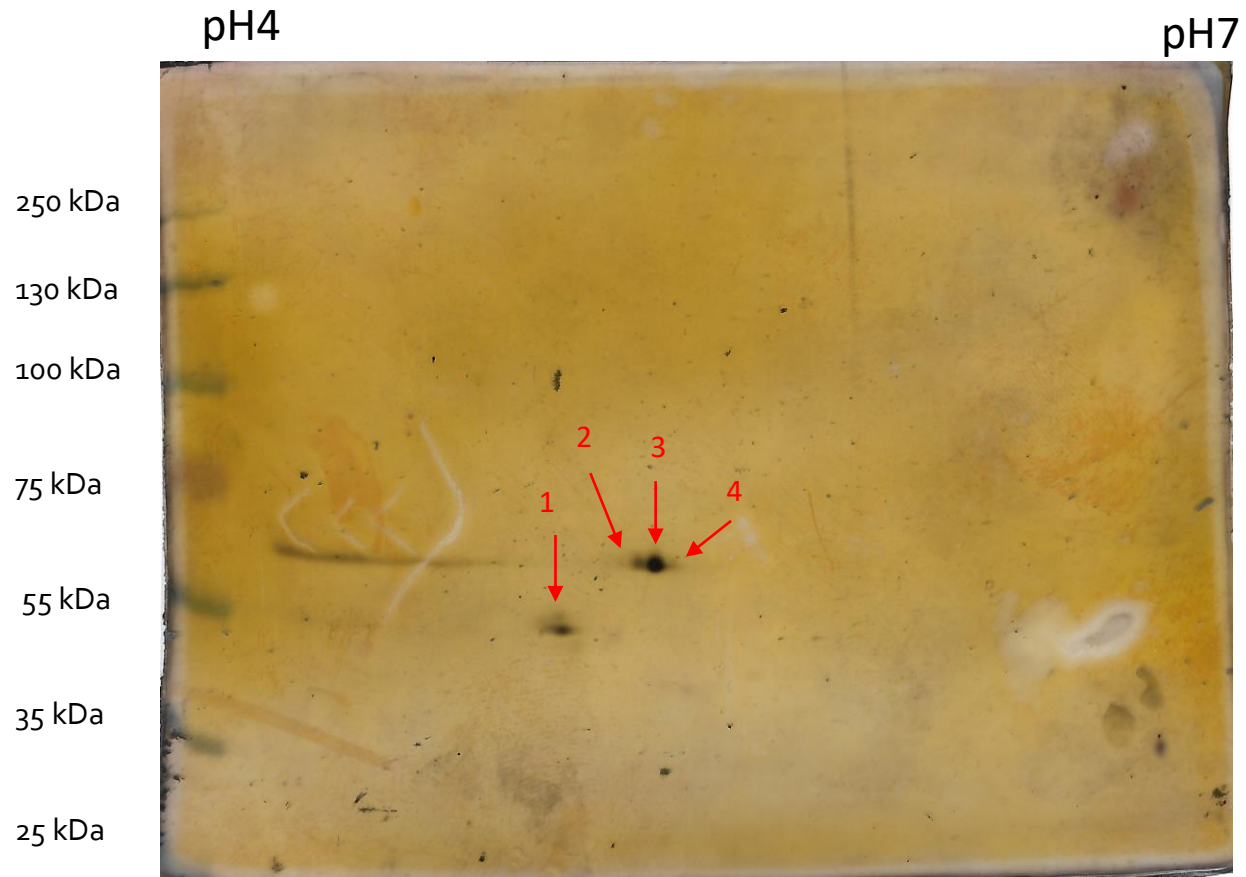


**Fig. 1. *B. canis* proteins from Soluble fraction after sonication.** SDS-PAGE (10%) stained with Coomassie Blue (left) and Western Blot (right) of soluble fraction. Both show the proteins of this fraction and western blot the immunoreactive bands with the aid of an infected dog serum.

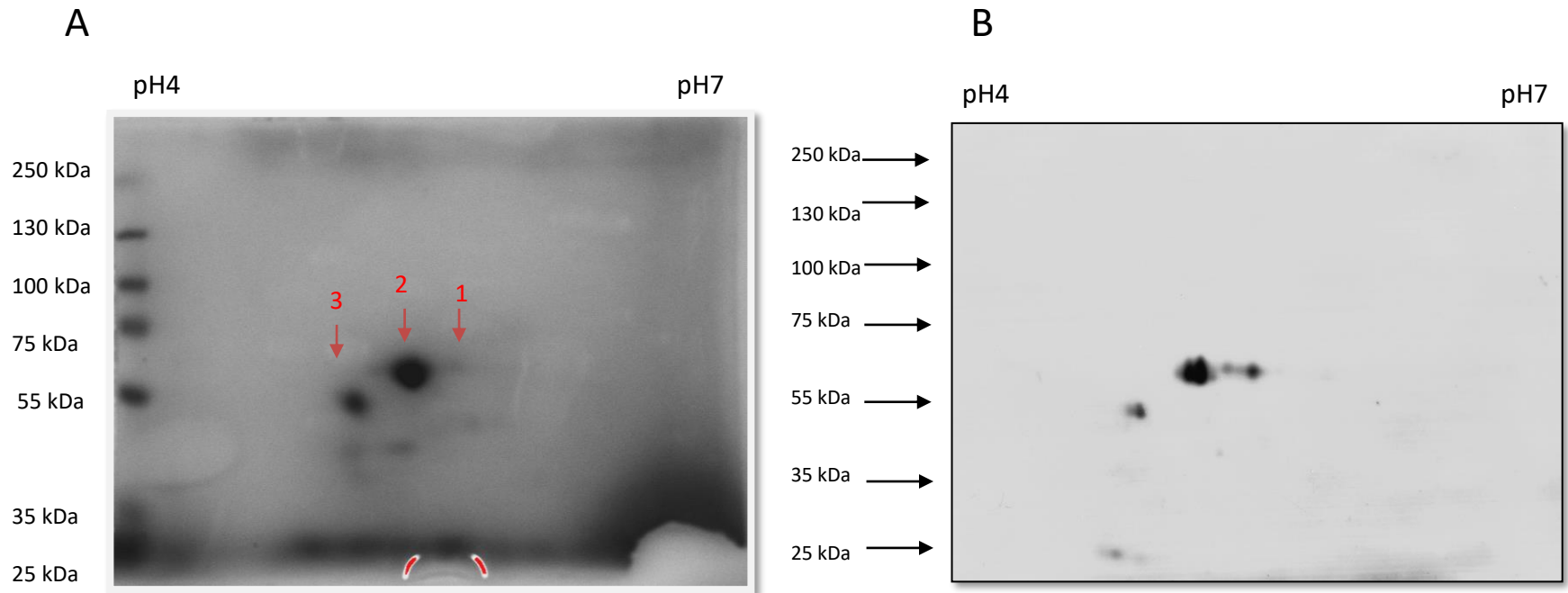


**Fig. 2. SDS-PAGE and Western blot of *B. canis* protein fractionation**

FPLC fractions from the elution were subjected to SDS-PAGE and stained with Coomassie Blue. The gels show the different protein fraction (A and B), and two major protein bands, with a molecular weight between 70 - 55 kDa were observed in fractions 16-20 (B). We can observe the similar bands as in the SDS-PAGE, with a molecular weight between 70-55 kDa in the Enhanced chemiluminescence Western blot



**Fig. 3. Isoelectrofocusing of immunodominant proteins**  
2-D PAGE silver stain of the 19th fraction



**Fig. 4. Isoelectrofocusing of immunodominant proteins**

2-D PAGE of the fraction 20; A, SDS 8% stained with Coomassie Blue; B, western blot of immunodominant proteins, with different isoelectric points.

**Table1. Coverage percentage of the peptides detected by liquid chromatography-mass spectrometry (LC/MS).**

Percentage of coverage for each of the three dots analyzed (coverage), the number of peptides that were identified for the protein (#peptides), the protein name and accession number, the prediction values for the physicochemical characteristics, isoelectric point (PI) and weight (MW). The alignment of the identified peptides within the protein sequence is shown in yellow.

**Sample 1. 64 kDa**

Accession	Description	Score	Coverage	# Peptides	MW [kDa]	calc. pI
A9MDV1	60 kDa chaperonin OS=Brucella canis (strain ATCC 23365 / NCTC 10854) GN=groL PE=3 SV=1 - [CH60_BRUC2]	44.47	29.85	6	57.5	5.15

MAAKDVKFGFR TAREKMLRGV DILADAVKVT LGPKGRNVVI DKSFGAPRIT KDGVSVAKEV  
 ELEDKFENMG AQMLREVASK TNDTAGDGTT TATVLGQAIV QEGAKAVAAG MNPMDLKR**GI**  
**DLAVNEVVAE** **LLK**KAKKINT SEEVAQVGTI SANGAEIIGK MIAEAMQKVG NEGVI TVEEA  
 KTAETELEV V EGMQFDR**GYL** **SPYFVTNPEK** MVADLEDAYI LLHEKKLSNL QALLPVLEAV  
 VQTSKPLLI AEDVEGEALA TLVVNKL RGG LKIAAVKAPG FGDRR**KAMLE** **DIAILTGGQV**  
**I**SEDL**G**IKLE SVTL DMLGRA KKV SISKENT TIVDGAGQKA EIDARVGQIK QQIEETSDY  
 DREKLQERLA KLAGGVAVIR VGGATEVEVK EKKDRVDDAL NATR**AAVEEG** **IVAGGGTALL**  
**R**ASTKITAKG VNADQEAGIN IVRRAIQAPA RQITTNAGEE ASVIVG**KILE** **NTSETFGYNT**  
**ANGEYGLIS** **LGI**VD**PVK**VV R**TALQNAASV** **AGLLITTEAM** **IAELPK**KDAA PAGMPGGMGG MGGMDF

**Table 1 (cont). Sample 2. 64 kDa**

Accession	Description	Score	Coverage	# Peptides	MW [kDa]	calc. pI
A9MDV1	60 kDa chaperonin OS=Brucella canis (strain ATCC 23365 / NCTC 10854) GN=groL PE=3 SV=1 - [CH60_BRUC2]	108.21	51.47	10	57.5	5.15

MAAKDVKFGR TAREKMLRGV DILADAVKVT LGPKGRNVVI DKSFGAPRIT KDGVSVAKEV  
 ELEDKFENMG AQMLREVASK **TNDTAGDGT** **TATVLGQAI** **QEGAK**AVAAG MNPMDLKR**GI**  
**DLAVNEVVAE** **LLK**KAKKINT SEEVAQVGTI SANGEAEIGK MIAEAMQK**VG** **NEGVITVEEA**  
**KTAETELEV** **EGMQFDR**GYL SPYFVTNPEK **MVADLEDAI** **LLHEK**KLSNL QALLPVLEAV  
 VQTSKPLLI AEDVEGEALA TLVVNKLGG LKIAAVKAPG FGDRRK**AMLE** **DIAILTGGQV**  
**ISEDLGIKLE** **SVTLDM**LGRA KKVSIKENT TIVDGAGQKA EIDARVGQIK QQIEETSDY  
 DREKLQERLA KLAGGVAVIR VGGATEVEVK EKKDRVDDAL NATR**AAVEEG** **IVAGGTALL**  
**R**ASTKITAK**G** **VNADQEAGIN** **IVR**RAIQAPA **RQIT**TNAGEE **ASVIVGK**ILE NTSETFGYNT  
 ANGEYGLIS LGIVDPVKVV RTALQNAASV AGLLITTEAM IAELPKKDAAG PAGMPGGMGG MGGMDF

**Table 1 (cont). Sample 3. 55 kDa**

Accession	Description	Score	Coverage	# Peptides	MW [kDa]	calc. pI
A9MDV1	60 kDa chaperonin OS=Brucella canis  (strain ATCC 23365 / NCTC 10854) GN=groL PE=3 SV=1 - [CH60_BRUC2]	322.85	21.98	10	57.5	5.15

MAAKDVKFGR TAREKMLRGV DILADAVKVT LGPKGRNVVI DKSFGAPRIT KDGVSVAKEV ELEDKFENMG  
 AQMLREVASK TNDTAGDGTT TATVLGQAIV QEGAKAVAAG MNPMDLKRGI DLAVNEVVAE LLKKAKKINT  
 SEEVAQVGTI SANGEAEIGK MIAEAMQKVG NEGVITVEEA KTAETELEV EGMQFDR **GYL SPYFVTNPEK**  
 MVADLEDAYI LLHEKKLSNL QALLPVLEAV VQTSKPLLI AEDVEGEALA TLVVNKLKRG LKIAAVKAPG  
 FGDRRKAMLE DIAILTGGQV ISEDLGIK **LE SVTLDMLGRA** KKVSIKENT TIVDGAGQKA EIDARVGQIK  
 QQIEETTSY DREKLQERLA **KLAGGVAVIR** VGGATEVEVK EKKDRVDDAL NATR **AAVEEG IVAGGTALL**  
**RASTKITAKG VNADQEAGIN IVRRAIQAPA RQITTNAGEE ASVIVGK** ILE NTSETFGYNT ANGEYGLIS  
 LGIVDPVKV R **TALQNAASV AGLLITTEAM IAELPK** KDAAG PAGMPGGMGG MGGMDF