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LABOR FÜR KLINISCHE DIAGNOSTIK GMBH & CO. KG

LABOKLIN GmbH & Co. KG , Steubenstraße 4 , 97688 Bad Kissingen

Report No.:	**2201-W-07008**
Date of arrival:	28.01.2022
Date of report:	14.03.2022
Testing started:	28.01.2022
Testing completed:	

Species:	Dog
Breed:	Collie rough
Gender:	Male
Name:	Skabona Blackjack
Stud book No.:	COL 77120
Chip No.:	968000010596845
Date of birth / Age:	23.04.2018
Type of sample:	Swab
Date sample was taken:	26.01.2022
Treating veterinarian:	Dr. Luc Olders (OMV 2004)
Owner / Animal-ID:	Esser, Dr. Simone
IT No. / Report-ID:	---

Degenerative Myelopathy - PCR

Result: Genotype N/DM (exon 2)

Interpretation: The examined animal is heterozygous for the high-risk factor for DM in exon 2 of the SOD1-gene.

Trait of inheritance: autosomal-recessive

Please note: In the Bernese Mountain Dog breed the mutation in exon 1 of the SOD1-gene also occurs in correlation with DM.

Inflammatory pulmonary disease (IPD) - PCR

Unfortunately, there is no valid result from the submitted sample for this genetic test of the combination.

Please send a new EDTA blood sample for a retest.

The test is included in the price of the combination. Therefore, this retest is free of charge when the above mentioned result number is added to the new sample submission as a reference.

MDR1 gene variant - PCR

Result: Genotype N/N (+/+)

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for MDR in the ABCB1-gene.
Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Shepherd, Border Collie, Elo, German Shepherd, Longhaired Whippet, McNab, Old English Sheepdog, Rough/Smooth Collie, Shetland Sheepdog, Silken Windhound, Wäller, White Shepherd

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Please note: in individual cases, heterozygous dogs can show clinical signs!

The DNA-test is run according to the publication of Mealey et al. (2001) "Ivermectin sensitivity in collies is associated with a deletion mutation of the mdr1 gene." and detects the mutation MDR1 nt230 (del4).

Dermatomyositis (DMS) - PCR

Locus A	PAN2	**Aa**
Locus B (MAP3K7CL)		**bb**
Locus C (DLA-DRB1)		**CC**

Assessment of Risk:
The likelihood of an individual dog developing DMS can be classified as low (0%-5%), moderate (33%-50%), or high (90%-100%) based on the genotype combination of Locus A (PAN2), Locus B (MAP3K7CL), and Locus C (DLA-DRB1). Wild type alleles of loci A and B are represented by lower case letters, a and b, while the risk alleles are represented by upper case letters A and B. The risk allele at DLA complex (DLA-DRB1*002:01) is referred to as C, and the lower case letter c represents any alternate allele for DLA-DRB1.

LOW RISK GENOTYPES: aabbCC, aabbCc, AabbCC, AabbCc, aaBbCC, aaBbCc, AaBbCC, AaBbCc, aaBBCc

MODERATE RISK GENOTYPES: AAbbCC, AAbbCc, aaBBCC, AaBBCc, AABbCc

HIGH RISK GENOTYPES: AABbCC, AaBBCC, AABBCC, AABBCc

Scientific studies found correlation between these markers and signs of the disease in the following breeds: Collie, Shetland Sheepdog

rcd2-PRA - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype-allele. It does not carry the causative mutation for rcd2-PRA in the RD3-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Collie

Collie Eye Anomaly (CEA) - PCR

Result: Genotype CEA/CEA

Interpretation: The examined animal is homozygous for the causative mutation for CEA in the NHEJ1-gene.

Trait of inheritance: autosomal-recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Australian Kelpie and Shepherd, Bearded Collie, Border Collie, Boykin Spaniel, Hokkaido, Lancashire Heeler, Longhaired Wippet, Nova Scotia Duck Tolling Retriever, Rough/Smooth Collie, Shetland Sheepdogs, Silken Windhound

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The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material.The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

Premium SNP DNA-profile (ISAG 2020)

001_012:	**AA_AA_GG_AA_GG_GG_GG_AG_GG_CC_GG_GG**
013-024:	**AA_GG_GG_AA_GG_AA_GG_AA_AA_AG_AA_GG**
025-036:	**GG_GG_GG_AA_AA_AA_AA_GG_GG_AG_AG_AG**
037-048:	**AA_GG_AA_AA_GG_AA_AA_GG_GG_AA_AA_AA**
049-060:	**GG_AC_AG_AC_GG_AG_GG_AA_GG_AA_AA_AA**
061-072:	**AC_CC_AG_AA_AG_GG_AA_GG_GG_AA_AA_CC**
073-084:	**GG_CC_AA_AG_AC_GG_GG_GG_AA_AG_AG_CC**
085-096:	**GG_AA_GG_GG_GG_GG_CC_GG_AA_AA_GG_AG**
097-108:	**GG_GG_AA_AA_AA_AA_AG_AA_GG_GG_GG_AA**
109-120:	**GG_GG_AA_GG_AA_GG_AA_GG_AA_AA_AA_AA**
121-132:	**AG_GG_AA_AA_GG_AA_AG_AA_GG_GG_GG_GG**
133-144:	**GG_GG_AA_AA_GG_AG_AA_AA_GG_AA_AG_AG**
145-156:	**AA_AA_AA_GG_GG_AA_GG_CC_.._AA_AA_GG**
157-168:	**AA_GG_GG_AC_AA_AG_AA_AA_GG_.._AA_AA**
169-180:	**AA_GG_CC_AA_GG_GG_AG_GG_AG_AG_AA_GG**
181-192:	**AA_AG_GG_GG_AA_AA_AG_GG_GG_AA_AA_GG**
193-204:	**AA_GG_GG_.._AA_GG_GG_AA_AA_GG_AA_AG**
205-216:	**AA_AA_GG_AG_GG_CC_AA_AG_AA_AA_AG_GG**
217-228:	**AG_GG_GG_CC_AA_AA_GG_GG_GG_AG_AA_AG**
229-230:	**AC_AC**
sex:	**X/Y**

Information on the Premium SNP DNA Profile

The Premium SNP DNA Profile is your animal's genetic fingerprint and uinquely identifies it. It remains the same throughout the animal's life and cannot be manipulated. Every one of the DNA profiles created in our laboratory is saved in our DNA database and is available to you permanently. The DNA profile does not contain any information on traits or diseases of your pet. The Premium SNP DNA Profile evaluates all of the SNPs recommended by the ISAG from (1) the core panel and (2) the auxiliary panel (numbers 001-230). The following table lists the corresponding internationally valid ISAG nomenclature (Cfa_Chromosom:Position) of the examined SNPs.

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Num Panel Chr:Pos

001 1 Cfam_1:3962719	002 1 Cfam_1:20842130	003 1 Cfam_1:70238933	004 1 Cfam_1:80971770	005 1 Cfam_1:106430955
006 1 Cfam_1:119414584	007 1 Cfam_2:2610859	008 1 Cfam_2:38293797	009 1 Cfam_2:77806065	010 1 Cfam_3:1252765
011 1 Cfam_3:24757939	012 1 Cfam_3:73570828	013 1 Cfam_4:31301072	014 1 Cfam_4:64121754	015 1 Cfam_4:75910211
016 1 Cfam_4:86049027	017 1 Cfam_5:5410890	018 1 Cfam_5:26320165	019 1 Cfam_5:85451804	020 1 Cfam_6:11553458
021 1 Cfam_6:33976751	022 1 Cfam_6:64006720	023 1 Cfam_7:76294	024 1 Cfam_7:15011628	025 1 Cfam_7:36555518
026 1 Cfam_8:5291824	027 1 Cfam_8:18121580	028 1 Cfam_8:45852939	029 1 Cfam_8:63196958	030 1 Cfam_9:22610227
031 1 Cfam_9:40096141	032 1 Cfam_9:52710991	033 1 Cfam_9:60437147	034 1 Cfam_10:10652659	035 1 Cfam_10:22409408
036 1 Cfam_10:30034450	037 1 Cfam_10:66922269	038 1 Cfam_11:5318488	039 1 Cfam_11:23907101	040 1 Cfam_11:65603333
041 1 Cfam_12:5579055	042 1 Cfam_12:35306641	043 1 Cfam_12:55201839	044 1 Cfam_12:68125319	045 1 Cfam_13:8704192
046 1 Cfam_13:59896033	047 1 Cfam_14:50063321	048 1 Cfam_14:58465266	049 1 Cfam_15:19299365	050 1 Cfam_15:22834903
051 1 Cfam_16:29634940	052 1 Cfam_16:46884446	053 1 Cfam_16:57958947	054 1 Cfam_17:10649078	055 1 Cfam_17:34462308
056 1 Cfam_17:39124697	057 1 Cfam_18:6745949	058 1 Cfam_18:54361347	059 1 Cfam_19:841347	060 1 Cfam_19:15926130
061 1 Cfam_19:27288167	062 1 Cfam_19:47470564	063 1 Cfam_20:13740894	064 1 Cfam_20:49900586	065 1 Cfam_20:57167714
066 1 Cfam_21:15558670	067 1 Cfam_21:25537675	068 1 Cfam_21:35719434	069 1 Cfam_22:641125	070 1 Cfam_22:26694580
071 1 Cfam_22:55308193	072 1 Cfam_23:42886681	073 1 Cfam_23:50772488	074 1 Cfam_24:23393510	075 1 Cfam_24:29909901
076 1 Cfam_24:47381908	077 1 Cfam_25:2073511	078 1 Cfam_25:33986348	079 1 Cfam_25:47708600	080 1 Cfam_26:20004896
081 1 Cfam_26:35071515	082 1 Cfam_27:2619058	083 1 Cfam_27:22599860	084 1 Cfam_27:41049333	085 1 Cfam_28:9877730
086 1 Cfam_28:18509221	087 1 Cfam_28:38885325	088 1 Cfam_29:251970	089 1 Cfam_29:9625359	090 1 Cfam_29:17561258
091 1 Cfam_29:36319325	092 1 Cfam_30:3896482	093 1 Cfam_30:15542105	094 1 Cfam_30:32852404	095 1 Cfam_31:21068798
096 1 Cfam_31:39391935	097 1 Cfam_32:679380	098 1 Cfam_32:17792284	099 1 Cfam_32:32382778	100 1 Cfam_33:15018500
101 1 Cfam_33:23742061	102 1 Cfam_34:195313	103 1 Cfam_34:24396298	104 1 Cfam_35:15345329	105 1 Cfam_36:3565500
106 1 Cfam_36:12714421	107 1 Cfam_36:23459390	108 1 Cfam_37:9398945	109 1 Cfam_37:15436615	110 1 Cfam_37:27667297
111 1 Cfam_38:9224942	112 1 Cfam_38:17657161	113 1 Cfam_38:20441216	114 2 Cfam_1:72613047	115 2 Cfam_1:74450772
116 2 Cfam_1:119306331	117 2 Cfam_3:10255068	118 2 Cfam_3:37849557	119 2 Cfam_3:43055696	120 2 Cfam_3:43063677
121 2 Cfam_3:64084413	122 2 Cfam_3:90291255	123 2 Cfam_3:91626907	124 2 Cfam_4:42104780	125 2 Cfam_4:67040898
126 2 Cfam_4:70217695	127 2 Cfam_5:13080303	128 2 Cfam_5:36642434	129 2 Cfam_5:44650576	130 2 Cfam_5:55349573
131 2 Cfam_5:64611038	132 2 Cfam_7:3318809	133 2 Cfam_7:6423299	134 2 Cfam_7:15017979	135 2 Cfam_7:76487265
136 2 Cfam_8:6188937	137 2 Cfam_8:19076567	138 2 Cfam_8:24614720	139 2 Cfam_8:52381322	140 2 Cfam_8:67183794
141 2 Cfam_9:20867959	142 2 Cfam_9:32506288	143 2 Cfam_9:50114927	144 2 Cfam_9:56021221	145 2 Cfam_10:8085469
146 2 Cfam_10:14685262	147 2 Cfam_10:39548483	148 2 Cfam_10:47923623	149 2 Cfam_10:57954366	150 2 Cfam_11:1161870
151 2 Cfam_11:62157625	152 2 Cfam_11:70698603	153 2 Cfam_12:6337286	154 2 Cfam_12:8532712	155 2 Cfam_12:23059939
156 2 Cfam_12:40681020	157 2 Cfam_12:70657733	158 2 Cfam_13:40616856	159 2 Cfam_14:55735620	160 2 Cfam_16:29675662
161 2 Cfam_16:58093031	162 2 Cfam_17:9407683	163 2 Cfam_17:12787849	164 2 Cfam_17:57371669	165 2 Cfam_18:10189759
166 2 Cfam_18:16385020	167 2 Cfam_18:16388978	168 2 Cfam_18:31579269	169 2 Cfam_18:47325586	170 2 Cfam_19:30246414
171 2 Cfam_19:40189405	172 2 Cfam_19:42756283	173 2 Cfam_20:6046176	174 2 Cfam_20:45777531	175 2 Cfam_20:48602465
176 2 Cfam_21:22581321	177 2 Cfam_21:29796784	178 2 Cfam_21:31751817	179 2 Cfam_22:20498421	180 2 Cfam_22:33934047
181 2 Cfam_22:37522364	182 2 Cfam_22:39647748	183 2 Cfam_22:61153661	184 2 Cfam_23:44497217	185 2 Cfam_23:48055836
186 2 Cfam_24:18599997	187 2 Cfam_24:27925354	188 2 Cfam_24:30954773	189 2 Cfam_24:43589304	190 2 Cfam_24:45191477
191 2 Cfam_25:4614777	192 2 Cfam_27:20948372	193 2 Cfam_27:34444177	194 2 Cfam_27:42526114	195 2 Cfam_28:9703418
196 2 Cfam_28:12804225	197 2 Cfam_28:34478533	198 2 Cfam_28:35104850	199 2 Cfam_29:4020192	200 2 Cfam_29:4022252
201 2 Cfam_29:19681270	202 2 Cfam_29:22992304	203 2 Cfam_30:10012939	204 2 Cfam_30:11735245	205 2 Cfam_30:27619023
206 2 Cfam_31:20912553	207 2 Cfam_32:13183511	208 2 Cfam_33:15233992	209 2 Cfam_33:22070526	210 2 Cfam_33:22472901
211 2 Cfam_33:22648231	212 2 Cfam_34:24351570	213 2 Cfam_34:34993916	214 2 Cfam_34:37323213	215 2 Cfam_34:41703614
216 2 Cfam_35:15283717	217 2 Cfam_36:288045	218 2 Cfam_36:9241262	219 2 Cfam_36:10084888	220 2 Cfam_36:12723744
221 2 Cfam_36:18627936	222 2 Cfam_37:18338930	223 2 Cfam_37:26611359	224 2 Cfam_37:28611801	225 2 Cfam_37:30110473
226 2 Cfam_37:30902202	227 2 Cfam_38:13098194	228 2 Cfam_38:15271384	229 2 Cfam_38:19172567	230 2 Cfam_38:20930997

Activation Code: **0084DBC003F4C70A**

This activation code is used to display the Labogen Diversity Check online at diversity.labogen.com. The Labogen Diversity Check always shows the most up-to-date genetic breed data from the Premium SNP DNA profile (ISAG 2020).

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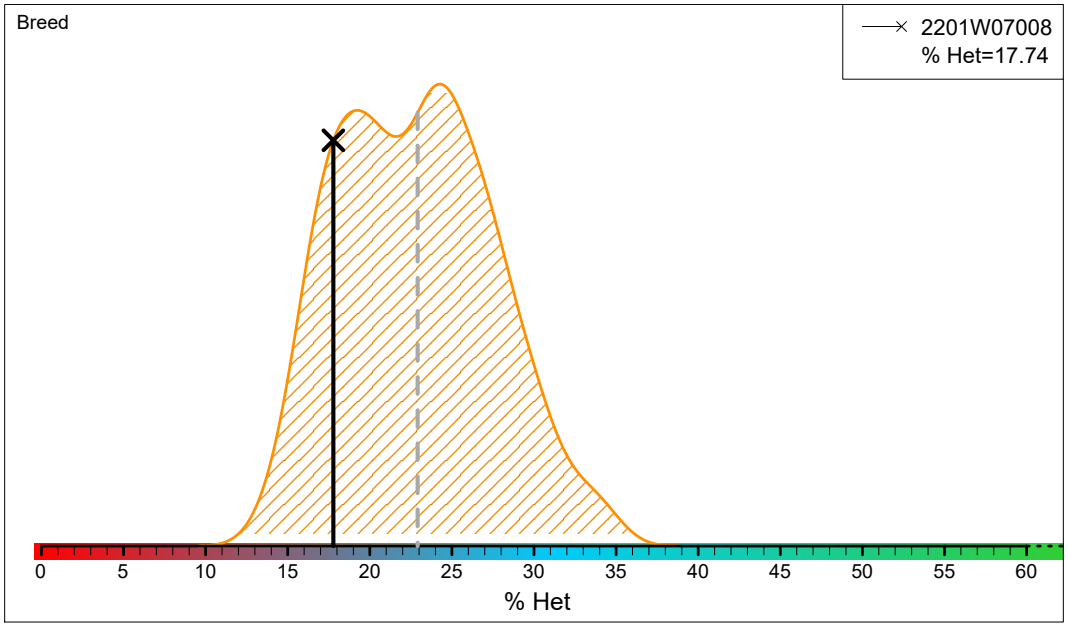
Genetic Variability (Heterozygosity)



This graph shows the genetic variability (heterozygosity) of your animal. Heterozygosity (% Het) describes the percentage of genetic markers (SNPs) for which your dog has inherited different variants from its mother and its father. According to current scientific knowledge, dogs with a high degree of heterozygosity within a breed are less often affected by inbreeding than dogs with a low degree of heterozygosity.
For the calculation of heterozygosity we use the genetic fingerprint (the Premium SNP DNA profile) and hundreds of other genetic markers in your dog's DNA. In the graph, your dog is marked with a cross and a black solid line.
Once LABOKLIN has examined a sufficiently large reference population for your breed, you can see the genetic variability of the entire breed population as an area shaded in orange. The mean value of the breed is marked as a grey dashed line.
Small population sizes and inbreeding can decrease the heterozygosity of a breed. When breeding, animals with a high degree of heterozygosity within their breed might thus contribute to the preservation of the breed's genetic diversity. However, please note that heterozygosity cannot be used to draw any conclusions about individual factors such as genetic diseases or characteristics like coat colour. Maintaining genetic variability can be a building block in responsible dog breeding, but it should not be viewed in isolation. More information can be found on our homepage:
https://shop.labogen.com/en/premium-snp-dna-profile-isag-2020

Breeding club discounts were granted for discountable services!

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These results are based on the sample material submitted to our laboratory.

This was suitable if not stated otherwise. The submitter is responsible for the accuracy of the information regarding the sample. This report can only be transmitted in toto and unchanged. Doing otherwise requires written permission from Laboklin GmbH & Co. KG.

LABOKLIN is an accredited laboratory according to DIN EN ISO/IEC 17025:2018, DAkkS No. D-PL-13186-01-01 and D-PL-13186-1-02. The accreditation applies to all test procedures listed in the accreditation certificate.

Hr. Dipl. Biol. Hubert Bauer
Abt. Molekularbiologie

***** END of report *****

Laboklin App

***** Breeding season has started *****

Bacteriological examination of cervical swabs provides valuable information for assessing the clinical health status of the mare. Culture examination along with pathogen differentiation and resistance testing using the microdilution method supports targeted antibiotic treatment when potentially pathogenic bacterial colonisation is detected.

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Laboklin GmbH & Co. KG, Steubenstraße 4, 97688 Bad Kissingen

Report No.:	**2203-W-23529**
Date of arrival:	29.03.2022
Date of report:	26.03.2024
Testing started:	29.03.2022
Testing completed:	29.03.2022
Status of the report:	Final report

Species:	Dog
Breed:	Collie rough
Gender:	Male
Name:	Skabona Blackjack
Stud book No.:	COL 77120
Chip No.:	968000010596845
Date of birth / Age:	23.04.2018
Type of sample:	EDTA-Blood
Date sample was taken:	26.03.2022
Treating veterinarian:	Dr. Luc Olders (OMV 2004)
Owner / Animal-ID:	Esser, Dr. Simone
IT No. / Report-ID:	---

Inflammatory pulmonary disease (IPD) - PCR

Result: Genotype N/N

Interpretation: The examined animal is homozygous for the wildtype allele. It does not carry the causative mutation for IPD in the AKNA gene.

Trait of inheritance: autosomal recessive

Scientific studies found correlation between the mutation and symptoms of the disease in the following breeds: Collie

The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material.The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

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Breeding club discounts were granted for discountable services!

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Fr. MSc Laura Hübner
Abt. Molekularbiologie

***** END of report *****

***** News from the laboratory *****

Spring is just around the corner. After the winter, remember to check the parasite status of your patients. In addition to the classic parasitological examination we also offer many species-specific parasite profiles. Please also take a look at the publication on parasitology in the current edition of "Parasitology Research": https://link.springer.com/article/10.1007/s00436-024-08181-6

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Laboklin GmbH & Co. KG, Steubenstraße 4, 97688 Bad Kissingen

Report No.:	**2307-W-93407**
Date of arrival:	03.07.2023
Date of report:	26.03.2024
Testing started:	03.07.2023
Testing completed:	06.07.2023
Status of the report:	Final report

Species:	Dog
Breed:	Collie rough
Gender:	Male
Name:	Skabona Blackjack
Stud book No.:	COL 77120
Chip No.:	968000010596845
Date of birth / Age:	23.04.2018
Type of sample:	EDTA-Blood
Date sample was taken:	26.03.2022
Owner / Animal-ID:	Esser, Dr. Simone
IT No. / Report-ID:	---

Additional Order of 03.07.2023 to Report-No. 2203-W-23529 Original Sample received on: 29.03.2022

M-locus* (alleles: Mh, M, Ma+, Ma, Mc+, Mc, m and mosaics) - PCR *

Result: Genotype m/m

Result: Genotype m/m

Interpretation: The examined animal is homozygous for the m-allele for non-merle.

The test detects the alleles Mh (harlequin merle), M (merle), Ma+ and Ma (atypic merle), Mc+ and Mc (cryptic merle) and m (non-merle).

Allelic series: Mh, M, Ma+, Ma, Mc+, Mc > m

The current result is only valid for the sample submitted to our laboratory. The sender is responsible for the correct information regarding the sample material.The laboratory can not be made liable. Furthermore, any obligation for compensation is limited to the value of the tests performed.

There is a possibility that other mutations may have caused the disease/phenotype. The analysis was performed according to the latest knowledge and technology.

The laboratory is accredited for the performed tests according to DIN EN ISO/IEC 17025:2018. (except partner lab tests).

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Breeding club discounts were granted for discountable services!

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*: test performed by partner laboratory

K. Schirl
Fr. MSc Katja Schirl
Abt. Molekularbiologie

***** END of report *****

***** News from the laboratory *****

Spring is just around the corner. After the winter, remember to check the parasite status of your patients. In addition to the classic parasitological examination we also offer many species-specific parasite profiles. Please also take a look at the publication on parasitology in the current edition of "Parasitology Research": https://link.springer.com/article/10.1007/s00436-024-08181-6

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Zertifikat

DNA-Profil - PCR

LABOKLIN-Befund-Nr.:	1906W31614
Hund, Geschlecht:	Skabona Black Jack, männlich
Rasse, Wurftag:	Collie Rough, * 23.04.18
Zuchtbuch-Nummer:	SE29895/2018
Tatoo-Nummer:	---
Chip-Nummer:	968000010596845
Verband:	---
Besitzer:	Esser, Dr. Simone

Von der oben beschriebenen Probe wurde folgendes DNA-Profil erstellt:

AHT 121:	100/100	INU 005:	126/126
AHT 137:	147/147	INU 030:	146/146
AHTH 130:	123/123	INU 055:	210/210
AHTH 171:	221/225	REN 105 L 03:	235/241
AHTH 260:	250/250	REN 162 C 04:	208/208
AHTK 211:	97/97	REN 169 D 01:	212/216
AHTK 253:	288/288	REN 169 O 18:	162/168
CXX 279:	124/126	REN 247 M 23:	266/268
FH 2054:	176/176	REN 54 P 11:	222/222
FH 2848:	234/234	REN 64 E 19:	143/147
INRA 21:	91/91		

Das Ergebnis gilt nur für das im Labor eingegangene Probenmaterial. Die Nomenklatur basiert auf den Werten des ISAG Dog Comparison Test 2006.

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Steubenstr. 4 · 97688 Bad Kissingen
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Bad Kissingen, 18.06.2019

Fr.Dipl.-Biol. Bärbel Gunreben
Abt. Molekularbiologie

Nur gültig mit Originalsiegel
Only valid with original seal.

ilac-MRA DAkkS Deutsche Akkreditierungsstelle D-PL-13186-01-00