

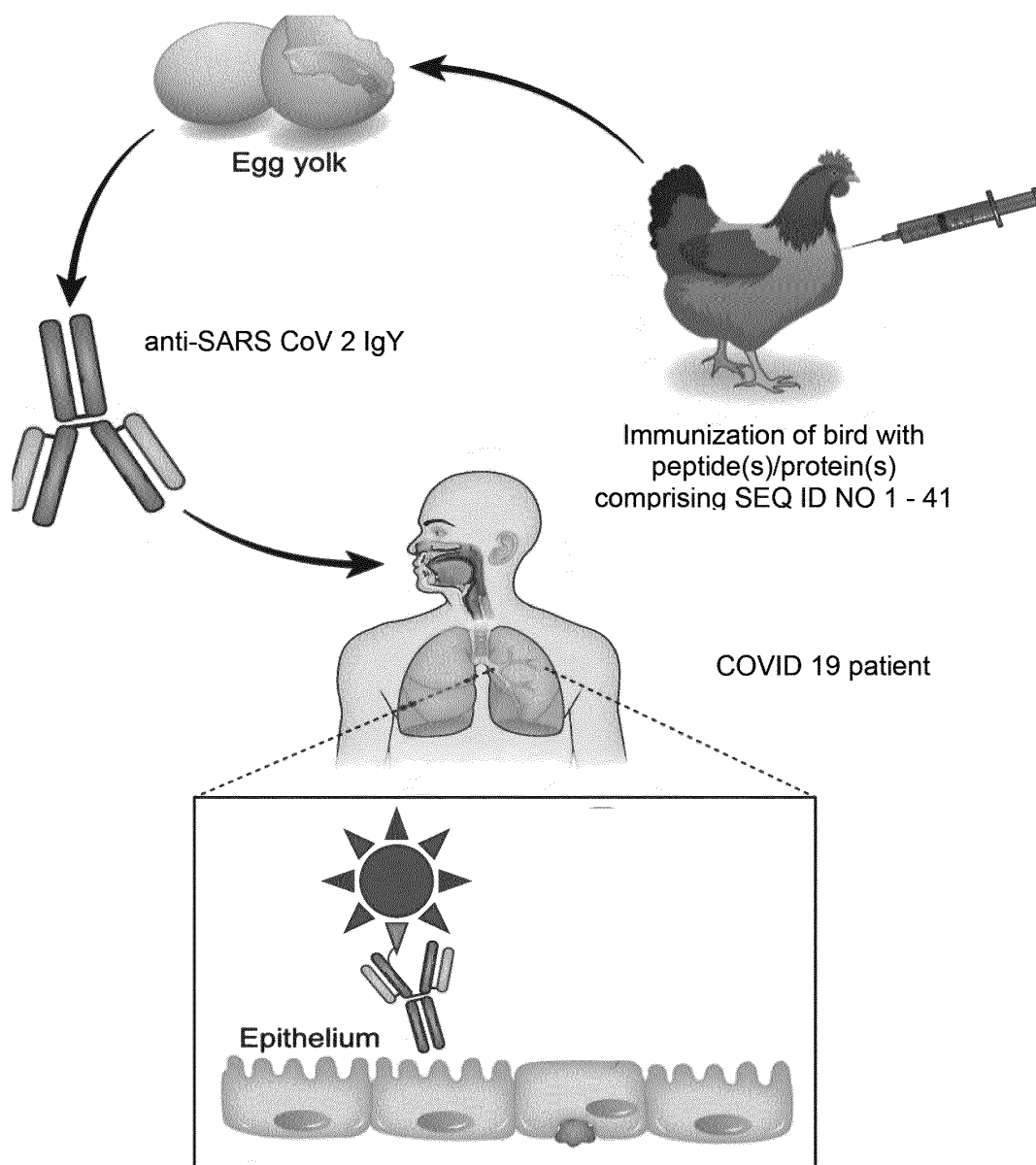


Fig. 1

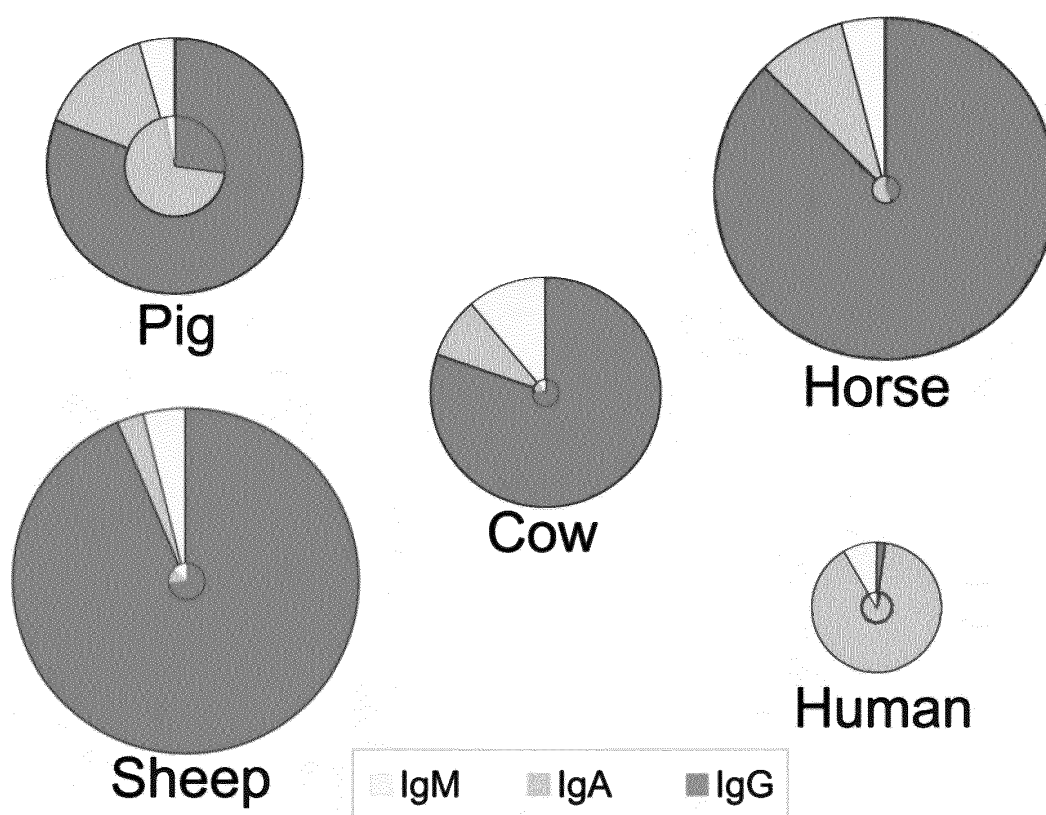


Fig. 2

1.	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
2.	-----VNLTTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	
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10.	-----	
1.	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV	120
2.	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIV	
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1.	NNATNVVIVKCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE	180
2.	NNATNVVIVKCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLE	
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1.	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQT	240
2.	GKQGNFKNLREFVFKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQT	
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1.	LLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTEFLKYNENGTITDAVDCALDPLSETK	300
2.	LLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTEFLKYNENGTITDAVDCALDPLSETK	
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10.	-----	
1.	CTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISN	360
2.	CTLSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISN	
3.	-----RVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISN	
4.	-----PNITNLCPFGEVFNATRFASVYAWNRRKRISN	
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Fig. 3

1.	CVADYSVLYNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD	420
2.	CVADYSVLYNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD	
3.	CVADYSVLYNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD	
4.	CVADYSVLYNSASFSTFKCYGVSP TKLNDLCFTNVYADSFVIRGDEV RQIAPGQTGKIAD	
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10.	-----	
1.	YNYKLPDDFTGCVIAWNSNNLDSKVGGN YNYLRLFRKSNLKPFFERDISTEIQAGSTPC	480
2.	YNYKLPDDFTGCVIAWNSNNLDSKVGGN YNYLRLFRKSNLKPFFERDISTEIQAGSTPC	
3.	YNYKLPDDFTGCVIAWNSNNLDSKVGGN YNYLRLFRKSNLKPFFERDISTEIQAGSTPC	
4.	YNYKLPDDFTGCVIAWNSNNLDSKVGGN YNYLRLFRKSNLKPFFERDISTEIQAGSTPC	
5.	-----	
6.	-----	
7.	-----	
8.	-----SNNLDSKVGGN-----	
9.	-----	
10.	-----QAGSTPC	
1.	NGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN	540
2.	NGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN	
3.	NGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN	
4.	NGVEGFNCYFPLQSYGFQPTNGVG YQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVN	
5.	-----	
6.	-----	
7.	-----	
8.	-----	
9.	-----QPTNGVG YQP-----	
10.	NGVE-----	
1.	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITP	600
2.	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVS VITP	
3.	FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCS-----	
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10.	-----	
1.	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSY	660
2.	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSY	
3.	-----	
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Fig. 3 ctd'

1.	ECDIPIGAGICASYQTQTN SPRRARSVASQ SI IAYTMSLGAENSVAYSNN SI AIPTNFTI	720
2.	ECDIPIGAGICASYQTQTN SPRRARSVASQ SI IAYTMSLGAENSVAYSNN SI AIPTNFTI	
3.	-----	
4.	-----	
5.	ECDIPIGAGICASYQTQTN SPRRARSVASQ SI IAYTMSLGAENSVAYSNN SI AIPTNFTI	
6.	-----	
7.	-----QTNS PRRARSVASQ SI I A-----	
8.	-----	
9.	-----	
10.	-----	
1.	SVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQE	780
2.	SVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQE	
3.	-----	
4.	-----	
5.	SVTTEILPVSMTKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAVEQDKNTQE	
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8.	-----	
9.	-----	
10.	-----	
1.	VFAQVKQIYKTPPIKDFGGFNFSQILP DPSKPSKRSFIEDLL FNKVTLADAGFIKQYGDC	840
2.	VFAQVKQIYKTPPIKDFGGFNFSQILP DPSKPSKRSFIEDLL FNKVTLADAGFIKQYGDC	
3.	-----	
4.	-----	
5.	VFAQVK-----	
6.	-----LPDPSKPSKRSFIEDLL-----	
7.	-----	
8.	-----	
9.	-----	
10.	-----	
1.	LGDI AARDL ICAQKFNGLT VLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAM	900
2.	LGDI AARDL ICAQKFNGLT VLPPLLTDEMI AQYTSALLAGTITSGWTFGAGAALQIPFAM	
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1.	QMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSL SSTASALGKLQDVVNQNAQALN	960
2.	QMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSL SSTASALGKLQDVVNQNAQALN	
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1.	TLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRA	1020
2.	TLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRA	
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Fig. 3 ctd'

1.	SANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPA	1080
2.	SANLAATKMSECVLGQSKRVDFCGKGYHLSFPPQSAPHGVVFLHVTYVPAQEKNFTTAPA	
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4.	-----	
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10.	-----	
1.	ICHDGKAHFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDP	1140
2.	ICHDGKAHFPREGVFSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDP	
3.	-----	
4.	-----	
5.	-----	
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9.	-----	
10.	-----	
1.	LQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	1200
2.	LQPELDSFKEELDKYFKNHTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDL	
3.	-----	
4.	-----	
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9.	-----	
10.	-----	
1.	QELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLGCCSCGSCCKFDEDD	1260
2.	QELGKYEQYIKWP-----	
3.	-----	
4.	-----	
5.	-----	
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8.	-----	
9.	-----	
10.	-----	
1.	SEPVLGKGVKLHYT	1273
2.	-----	
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Fig. 3 ctd'

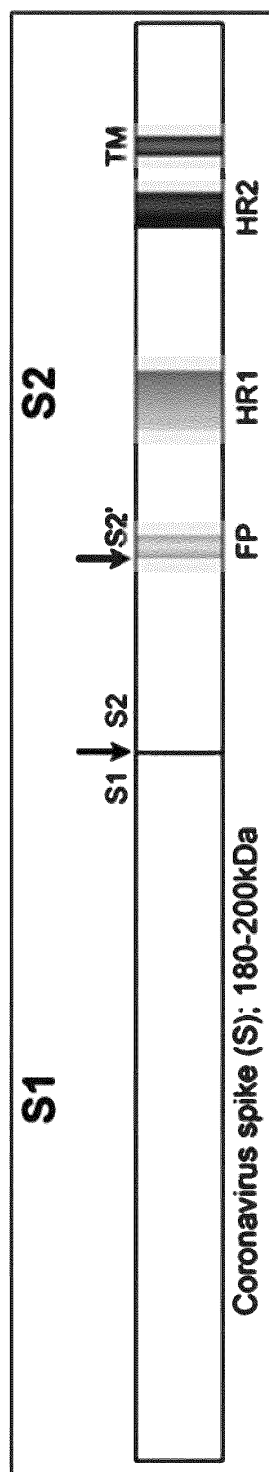


Fig. 4

Anti-SARS-CoV2 IgY ELISA		readout (O.D.)		
Sample		Sample dilution ratio		
		x 1,000	x 10,000	x 100,000
Anti-Spike ecto domain IgY				
antigen expressend in Sf9 cells, native fold		2.726	1.030	0.164
Anti-Spike S1 subunit IgY				
antigen expressend in human cell line, native fold		2.959	1.250	0.211
Anti-Spike RBD IgY				
antigen expressend in human cell line, native fold		1.983	0.489	0.062
Anti-Spike S1 Subunit IgY				
antigen expressed in E. coli, denaturated		0.944	0.174	0.017
Anti-Bovine Coronavirus IgY				
attenuated field reference strain		2.402	0.725	0.089
Control IgY (non immunized chicken)		0.023	0	0

Fig. 5

Virus neutralization test by appearance of cytopathic effect (CPE)

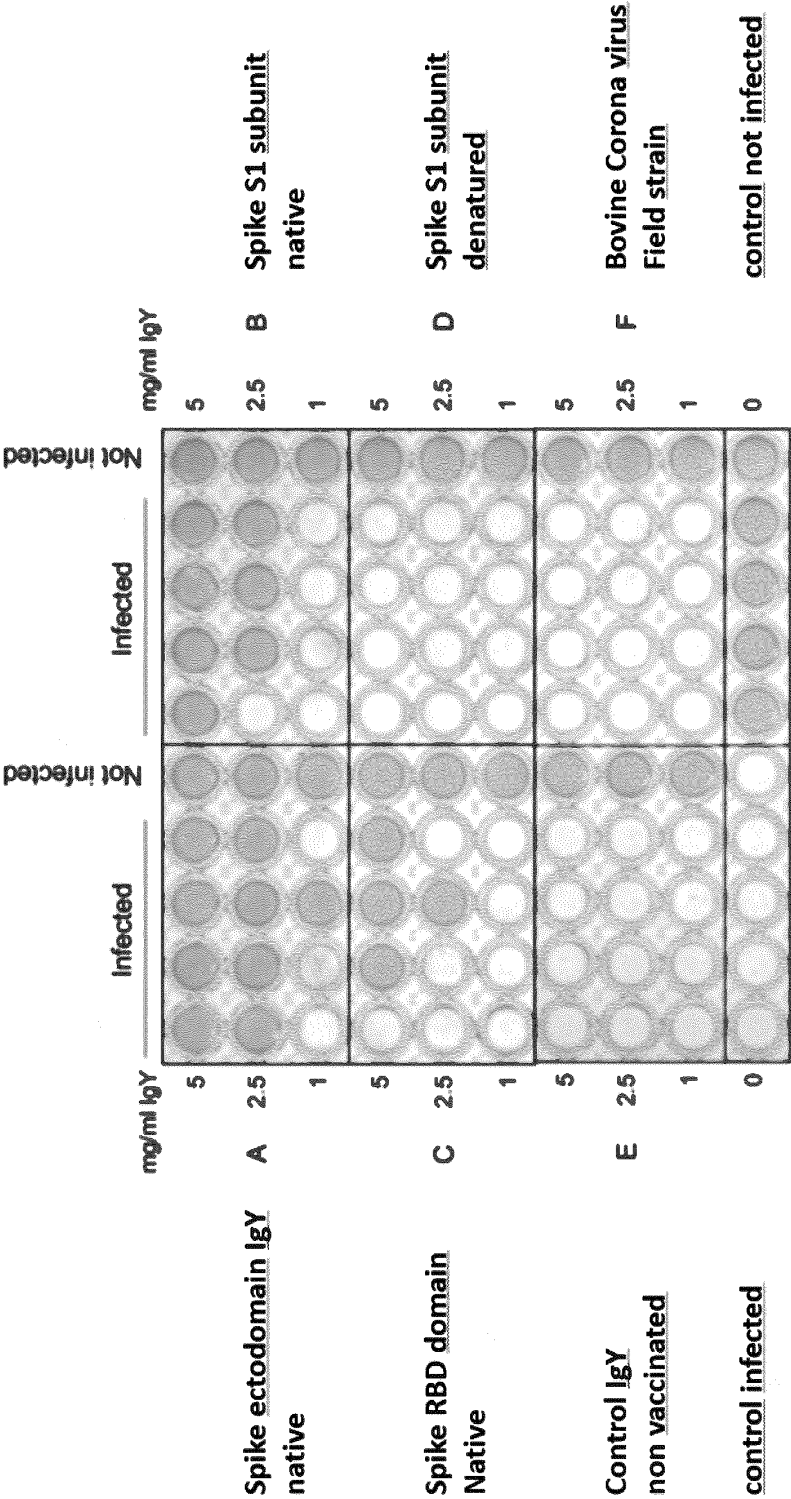


Fig. 6

Anti SARS-CoV2 IgY

antigen	Spike ecto domain native fold	Spike S1 subunit native fold	Spike RBD domain native fold	Spike S1 subunit denatured	bovine corona virus field strain	control non immunized
neutralizing titer (VN50)	x 160	x 40	x10	x10	< 10	<10
Minimum effective IgY dose (total IgY concentration)	62,5 µg/mL	250 µg/mL	1000 µg/mL	1000 µg/mL	> 1000 µg/mL	> 1000 µg/mL

Fig. 7

ConCat1 AA 474-507

(QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS)₈
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP HHHHHH

Epitope partial fold loop2 & sheet – repeat 9; Cter His – 35,6 kDa

QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP GSGS
 QAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQP HHHHHH

ConCat2 AA 474-484 C 480 changed to G

(QAGSTP■NGVE GSGS)₁₉ QAGSTP■NGVE HHHHHH

Linear Epitope loop 2a – repeat 20; Cter His – 30,1 kDa

QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS
 QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS
 QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS
 QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS
 QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE GSGS QAGSTP■NGVE HHHHHH

ConCat3 AA 498-507

Linear Epitope loop 2b – repeat 23; Cter His – 31,1 kDa

(QPTNGVGYQP GSGS)₂₂ QPTNGVGYQP HHHHHH

QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS
 QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS
 QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS
 QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS
 QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP GSGS
 QPTNGVGYQP GSGS QPTNGVGYQP GSGS QPTNGVGYQP HHHHHH

Fig. 8

ConCat4 AA 485-496 C 488 changed to G

Linear Epitope sheet – repeat 22; Cter His – 34,9 kDa

(GFNGYFPLQSYG SGS)₂₁ GFNGYFPLQSYG HHHHHH

GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS
 GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS
 GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS
 GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS
 GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS GFNGYFPLQSYG SGS
 GFNGYFPLQSYG SGS GFNGYFPLQSYG HHHHHH

ConCat5 AA 438-449

Linear Epitope loop 1 – repeat 20; Cter His – 31,3 kDa

(SNNLDSKVGGNY GSGS)₁₉ SNNLDSKVGGNY HHHHHH

SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS
 SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS
 SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS
 SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS
 SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY GSGS SNNLDSKVGGNY
 HHHHHH

ConCat6 AA 677-692

Linear Epitope S1/S2 priming site – repeat 15; Cter His – 30,9 kDa

(QTNSPRRARSVASQSI GSGS)₁₄ QTNSPRRARSVASQSI HHHHHH

QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS
 QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS
 QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS
 QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS
 QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI GSGS QTNSPRRARSVASQSI HHHHHH

Fig. 8 ctd'