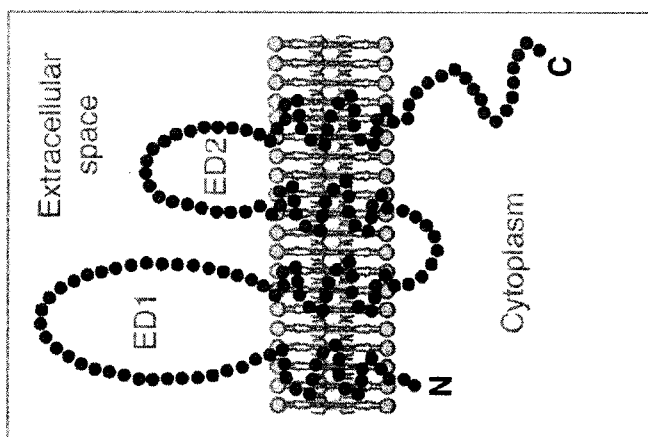


[illegible]

Underlined – Transmembrane domains according to Günzel et. al., Physiol Rev 93:525-569, 2013

Figure 1B

[illegible]

Figure 2A

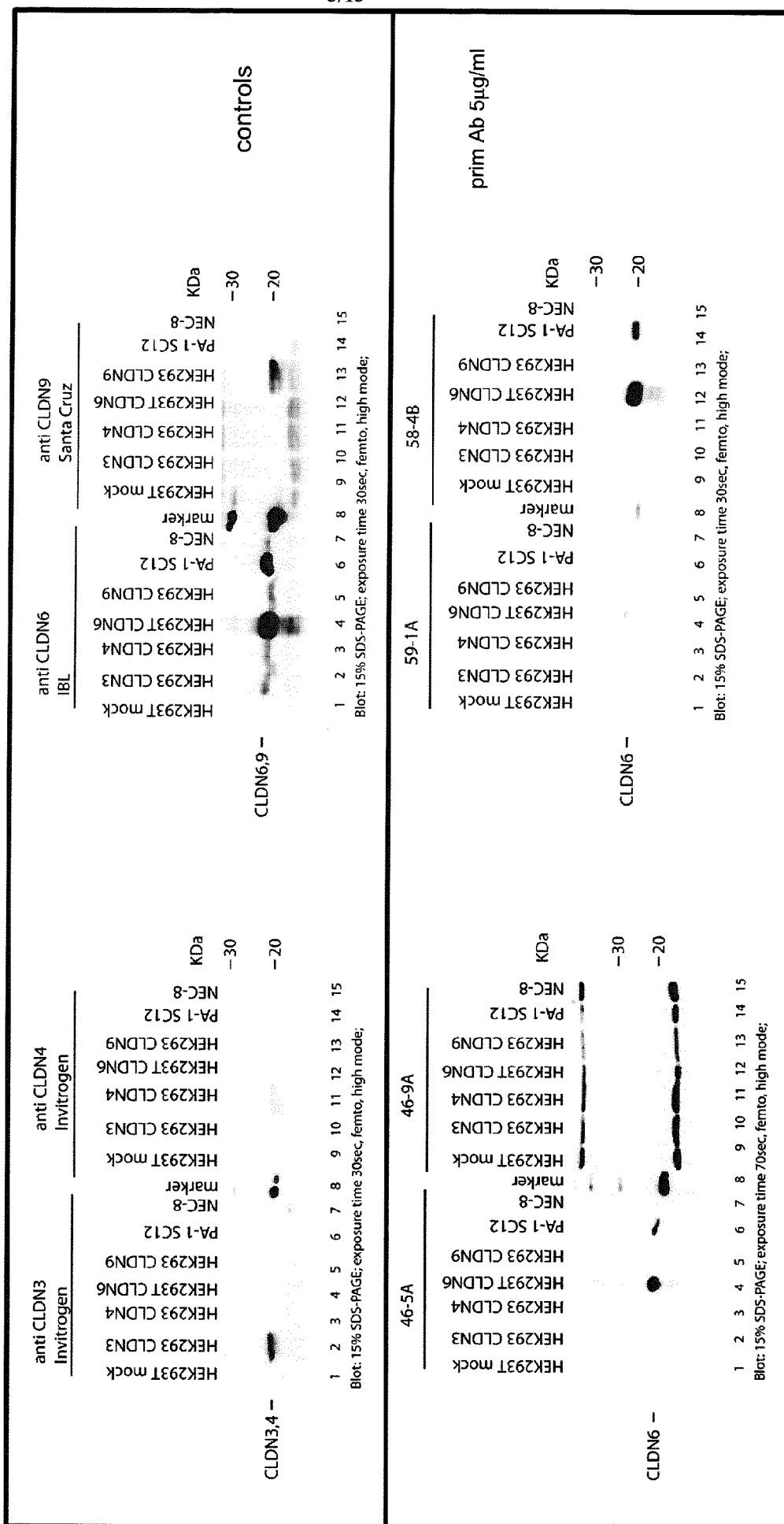
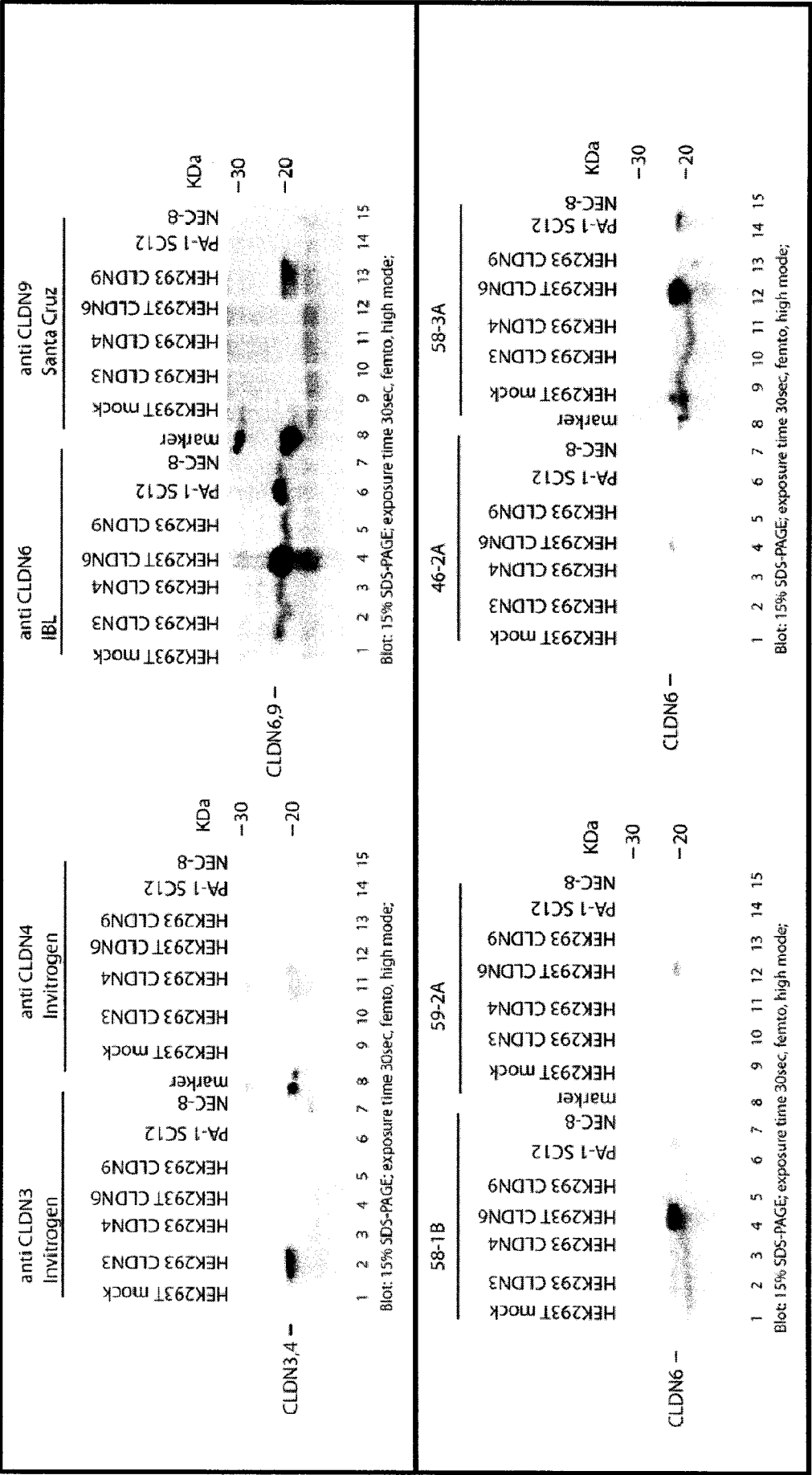


Figure 2B



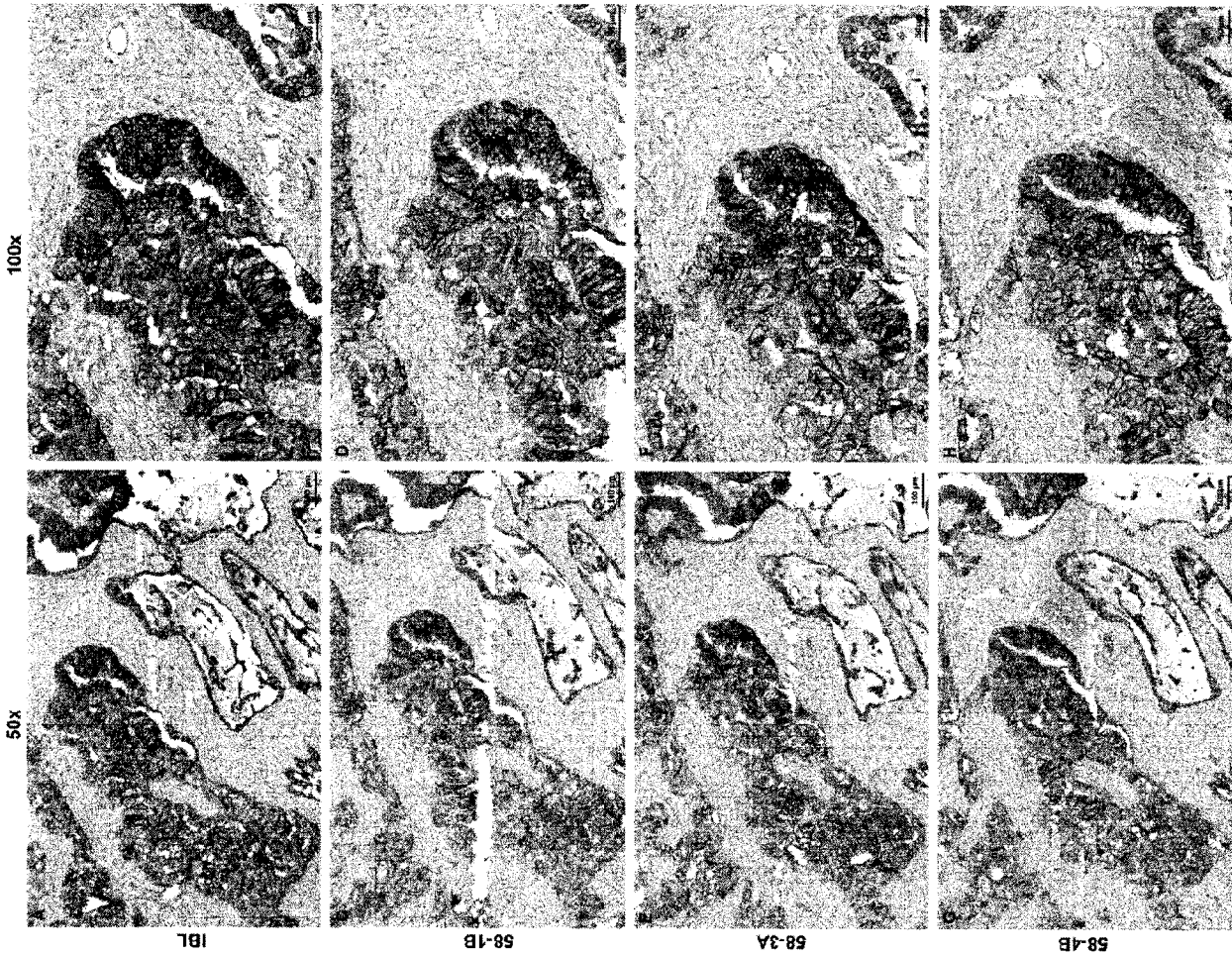


Figure 3

Figure 4A

180
 CLDN 6 human
 CLDN 6 murine
 rec. Protein
 Peptid 1
 Peptid 2
 Peptid 3
 Peptid 4
 Peptid 5
 Peptid 6
 Peptid 7

220
 LLCTCTCPSSGGSGGSHYMARYSTSAPALSRGPSEYPTKNYV
 LLCCACSSGGTQGP RHYMACYSTSP-HSRGPSEYPTKNYV
 ---CTCPSSGGSGGSHYMARYSTSAPALSRGPSEYPTKNYV
 ---CTCPSSGGSGGSHY---
 ---PSGGSGGSHYMAR---
 ---SQGP SHYMARYSTA---
 ---SHYMARYSTSAPALSRGPSEYPTKNYV
 ---ARYSTSAPALSRGPS---
 ---TSAPALSRGPSEYPT---
 ---AISRGPSYPTKNYV

	11-10A 67-3A 67-5B	12-12A 68-30B	37-4A 69-4A	11-13A 12-1A 12-9A 12-14A 25-3A 25-4A 68-12A 68-34A	25-2A 43-1A 59-1A	22-20A	46-2A 52-1A 64-1A	46-5A 58-1B 58-3A 58-4B 58-4B-2 58-9B	rb-ser (IBL)
pep1	X	X	X	X	X				
pep2	X	X	X	X	X				
pep3	X	X		X		X			
pep4	X						X		
pep5	X								
pep6									X
pep7								X	X

X binding of mAB to peptide

Figure 4B

182	220
huCLDN6 C-term	--CTCPGGGQGPSHYMARYSTSAPAIRGPSEYPTKNYV
Peptid 1	---CTCPGGGQGPSHY-----
Peptid 2	-----PSGGGQGPSHYMARY-----
Peptid 3	-----SQGPSHYMARYSTSA-----
Peptid 4	-----SHYMARYSTSAPAIS-----
Peptid 5	-----ARYSTSAPAIRSGPS-----
Peptid 6	-----TSAPAIRSGPSEYPT-----
Peptid 7	-----AISRGPSYPTKNYV-----
	Unconj. Peptide (4aa shift each peptide)

peptide	Biotinylated Peptides (1aa shift each peptide)	46-5A	58-1B	58-3A	58-4B 58-4B-2	rb-anti- CLDN6 IBL
pep4	SHYMARYSTSAPAIS					
pep4A	YMARYSTSAPAIRG					
pep11	ARYSTSAPAIRSGPS					X
pep12	RYSTSAPAIRGPSE					X
pep13	YSTSAPAIRGPSEY					X
pep14	STSAPAIRGPSEYP					X
pep15	TSAPAIRGPSEYPT					X
pep16	SAPAIRGPSEYPTK	X				X
pep17	APAIRGPSEYPTKN	X				X
pep18	PAIRGPSEYPTKNY	X	X	X	X	X
pep19	AISRGPSYPTKNYV	X	X	X	X	X
pep20	ISRGPSYPTKNYV	X	X	X	X	X
pep21	SRGPSEYPTKNYV	X	X	X	X	X
pep22	RGPSYPTKNYV	X	X	X	X	X
pep23	GPSEYPTKNYV	X	X	X	X	<50%
pep24	PSEYPTKNYV	X	X	X	X	<50%
pep25	SEYPTKNYV	X	X	X	X	
pep26	EYPTKNYV	X	X	X	X	
pep27	YPTKNYV					
pep28	PTKNYV					
pep29	PTKNY					
pep30	PTKN					

Figure 4C

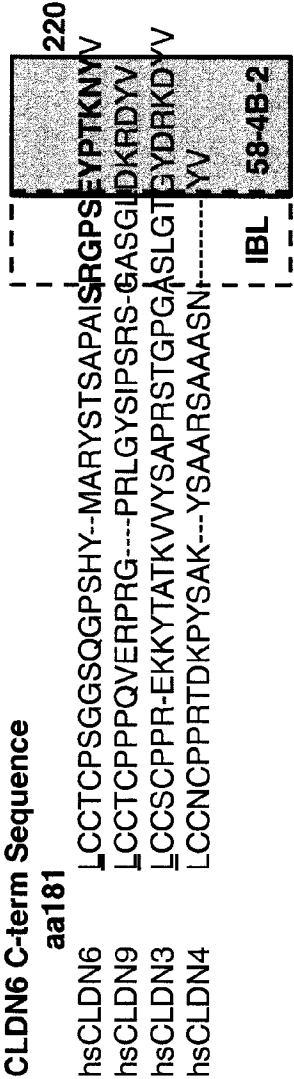


Figure 5A

58-4B variable *kappa* chain
-----FR1----- CDR1-----FR2----- CDR2-----FR3----- CDR3-----FR4-----
DIVLTQNPLTSLVTIGQTASISCKSSQNLLYS DGKTYLNWLLQRPQGSPKRLIY LMS KLD SGVPDRFTGSGSGTDFTLKISRVEAEDLG VYYC WQGT HFPWT FGGG TKLENT

58-4B variable heavy chain
-----FR1----- CDR1-----FR2----- CDR2-----FR3----- CDR3-----FR4-----
EVQLQQSGTVLARP GASVRMS CRTSGYIFTTYW IHVVKERPGQGLVWIGA IIPGNSDT TYNQKFRGKASLTAVTSASTAYLDLSSLTDEDSAVYYC TREFYAT WQG GTTLTVSS

58-1B variable *kappa* chain
-----FR1----- CDR1-----FR2----- CDR2-----FR3----- CDR3-----FR4-----
DVVMTQNPLTSLVTIGQTASISCKSSQNLLYS DGKTYLNWLLQRPQGSPKRLIY LMS KLD SGVPDRFTGSGSGTDFTLKISRVEAEDLG VYYC WQGT HFPWT FGGG TKLEIT

58-1B variable heavy chain
-----FR1----- CDR1-----FR2----- CDR2-----FR3----- CDR3-----FR4-----
EVQLQQSGTVLARP GASVKM SCRTSGYIFTTYW MHWVRRPQGQGLEWIGA IYPENSDA TYNQKFKGKASLTAVTSASTAYLESSLTDEDSAVYYC TREFYAT WQG GTTLTVSS

Figure 5B

58-3A variable *kappa* chain

-----FR1----- --CDR1----- --FR2----- --CDR2----- --FR3----- --CDR3----- --FR4-----
DIVLTQNPLTSLVTIGQTASISCKSS QNLLYSDGKTY LNWLLQRPQGSPKRLIY LMS KLESGVPDRFTGSGSGTEFTLKISRVEAEDLGVVYC WQGT HFPWT FGGG TKLEIS

58-3A variable heavy chain

-----FR1----- --CDR1----- --FR2----- --CDR2-- --FR3----- --CDR3- --FR4-----
EVQLQQSGTVLARPGASVKMSCRTS GYTFTTYW MHWVRRPGQGLEWIGA IYPENSDA TYNQKFKGKASLTAVTSASTAYLELSSLTDEDSAVVYC TREFYAT WQQGTTLT VSS

Figure 6

