

A Peptides related to the extracellular juxtamembrane region adjacent to TMD1 of human iRhom2

Peptide	Amino acids	Sequence
Peptide 1	431-447	AQHVTTLQLVLRNKGVE-C-Biotin/KLH
Peptide 2	426-447	APVGFAQHVTTLQLVLRNKGVE-C-Biotin/KLH
Peptide 3	431-459	AQHVTTLQLVLRNKGVEVKYIQQENFWV-C-Biotin/KLH
Peptide 4	426-459	APVGFAQHVTTLQLVLRNKGVEVKYIQQENFWV-C-Biotin/KLH

B Peptides related to Loop1 of human iRhom2

Peptide	Amino acids	Sequence
Peptide 5	474-498	KLH/Biotin-C-SP-Abu-IRKDGQIEQLVLRERDLERDSG
Peptide 6	508-548	KLH/Biotin-CIQTQRKD-Abu-SETLATFVKWQDDTGPPMDKSDLGQKRTSGAV
Peptide 7	578-600	TEQARSNHTGFLHMD-Abu-EIKGRPC-Biotin/KLH

C Peptides related to C-terminus of human iRhom2

Peptide	Amino acids	Sequence
Peptide 8	824-839	YIYPINWPWIEHLT-Abu-F-C-Biotin/KLH
Peptide 9	819-839	LVLWLYIYPINWPWIEHLT-Abu-F-C-Biotin/KLH
Peptide 10	824-856	YIYPINWPWIEHTCFPFTSRFCEKYELDQVLH-C-Biotin/KLH
Peptide 11	819-856	LVLWLYIYPINWPWIEHTCFPFTSRFCEKYELDQVLH-C-Biotin/KLH

D Peptides related to the extracellular juxtamembrane region adjacent to TMD1 of human iRhom1

Peptide	Amino acids	Sequence
Peptide 1b	433-449	SQHETVDSVLRNRGVYE-C-Biotin
Peptide 2b	428-449	APVGFSQHETVDSVLRNRGVYE-C-Biotin
Peptide 3b	433-461	SQHETVDSVLRNRGVYENVKYVQQENFWI-C-Biotin
Peptide 4b	428-461	APVGFSQHETVDSVLRNRGVYENVKYVQQENFWI-C-Biotin

Fig. 1

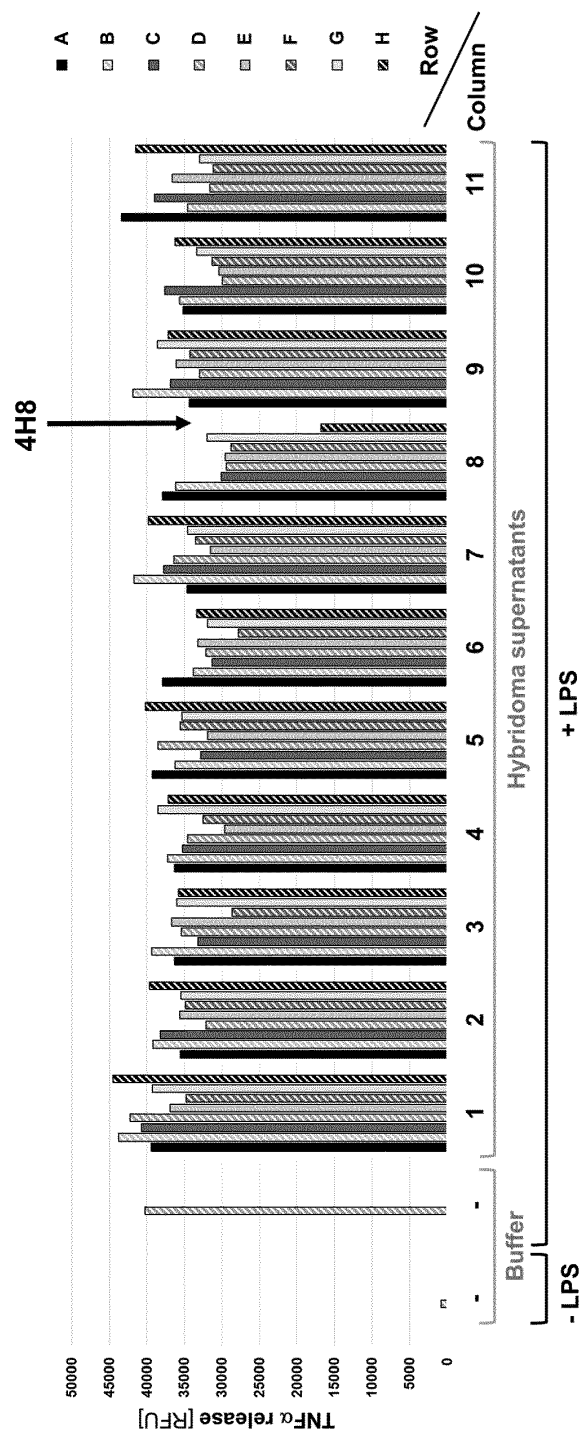


Fig. 2

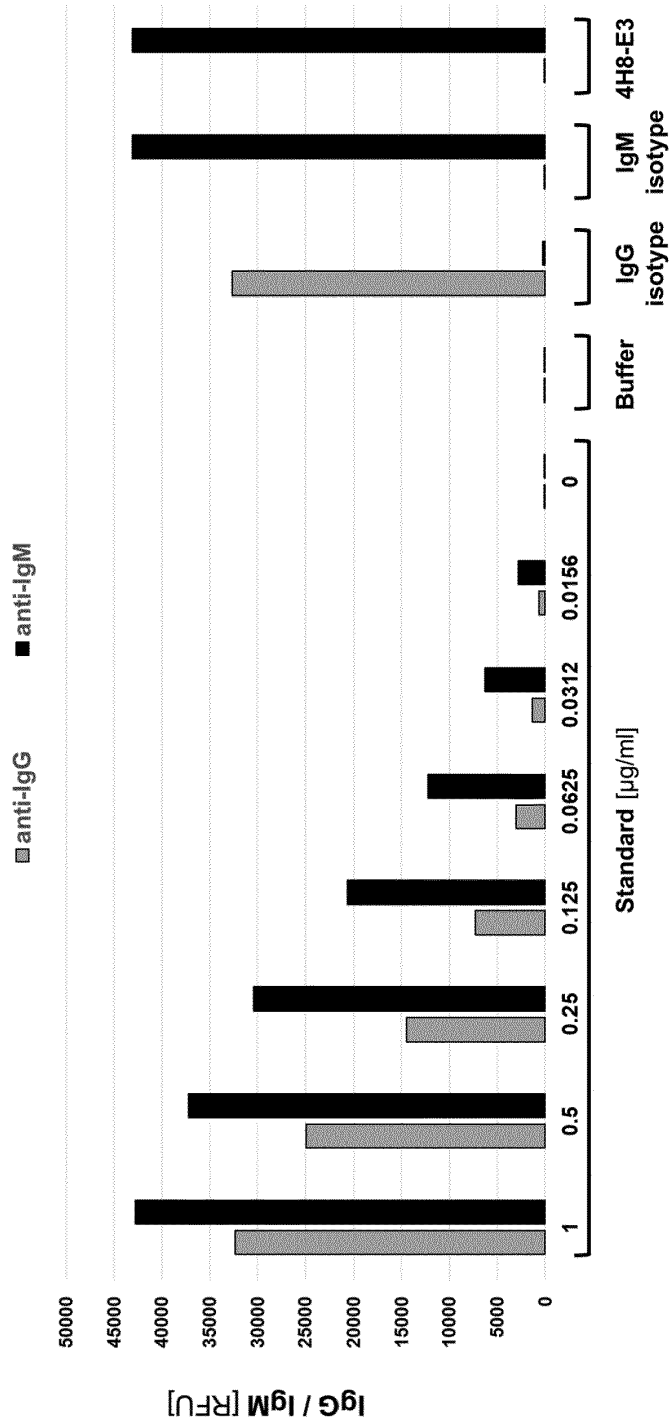


Fig. 3

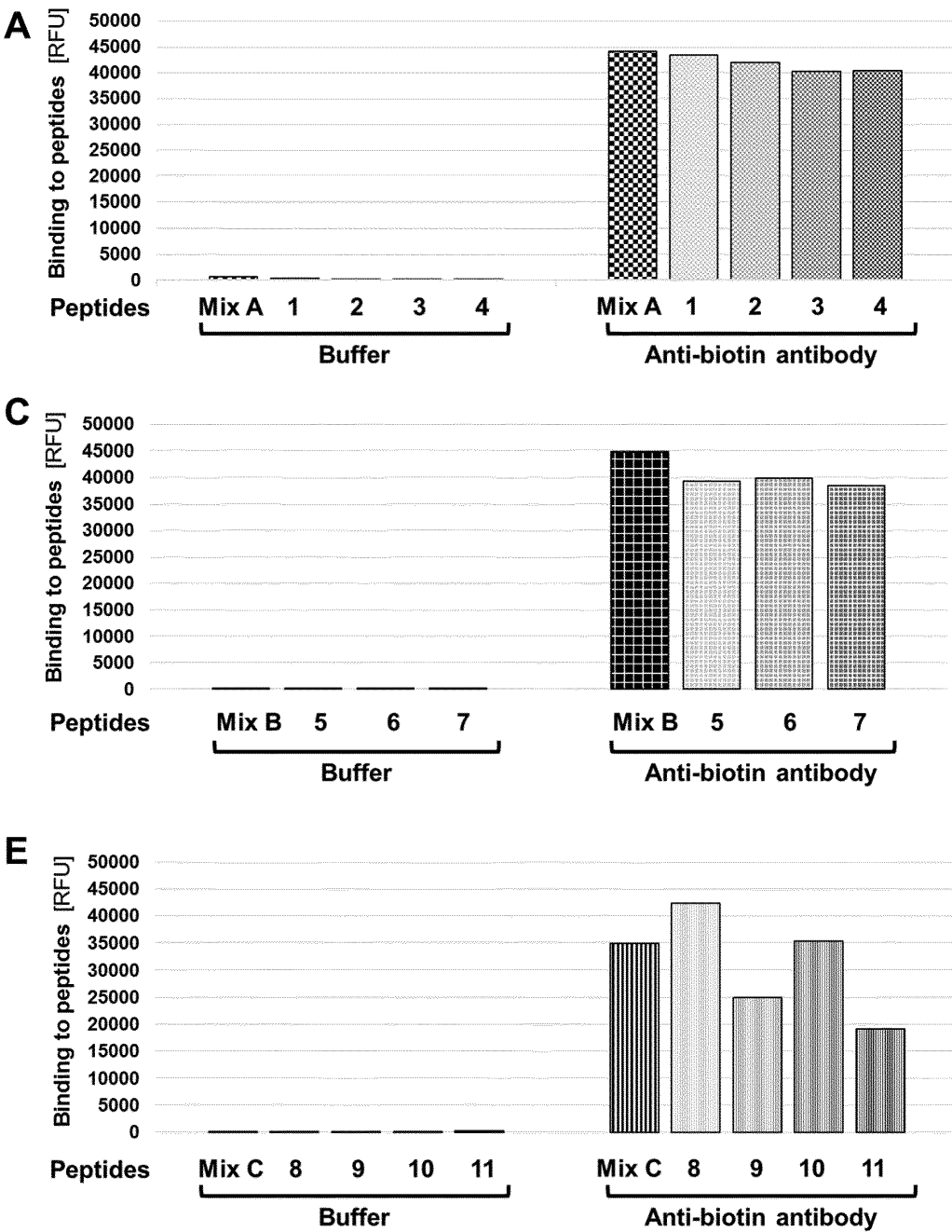


Fig. 4

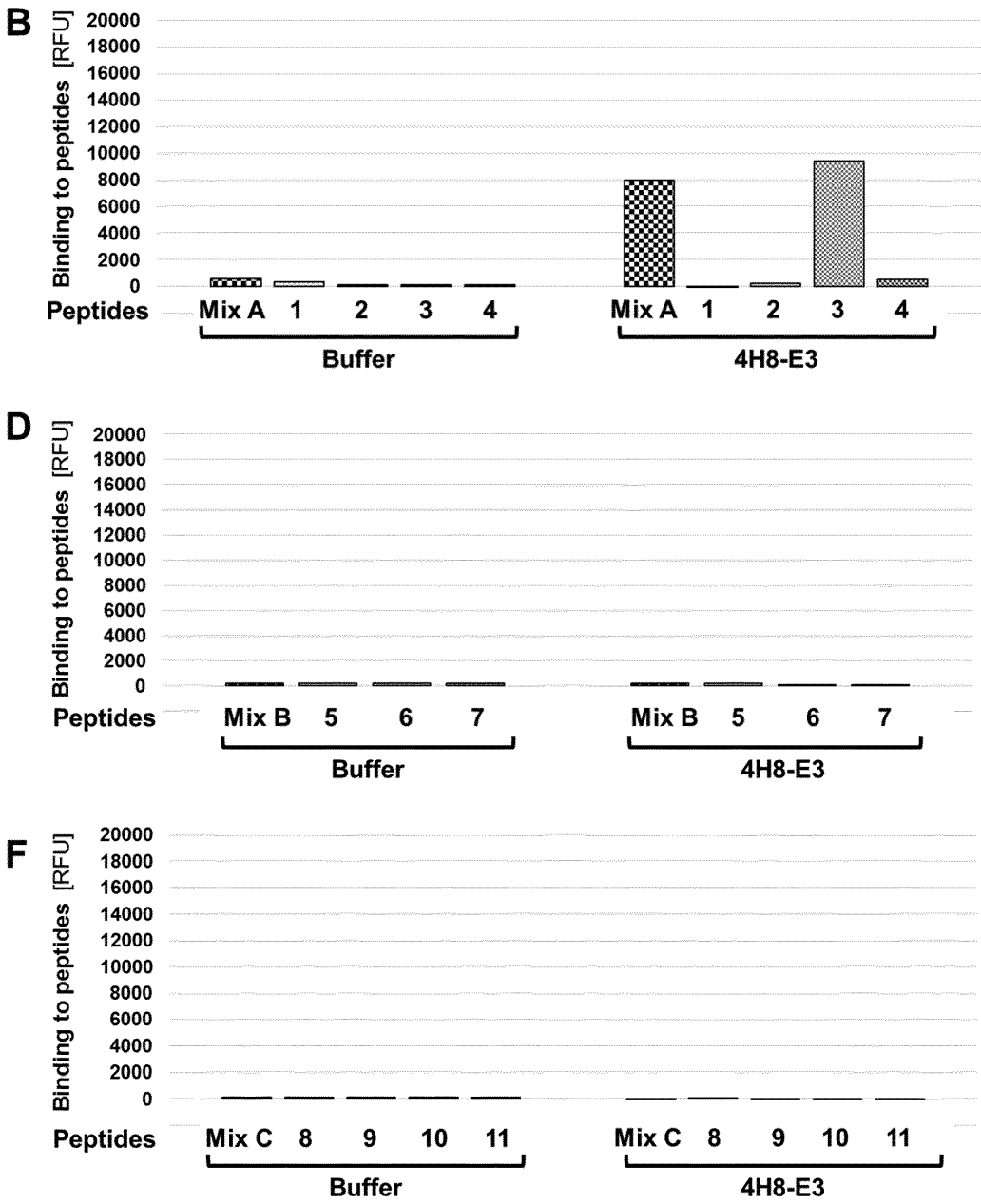


Fig. 4 ctd'

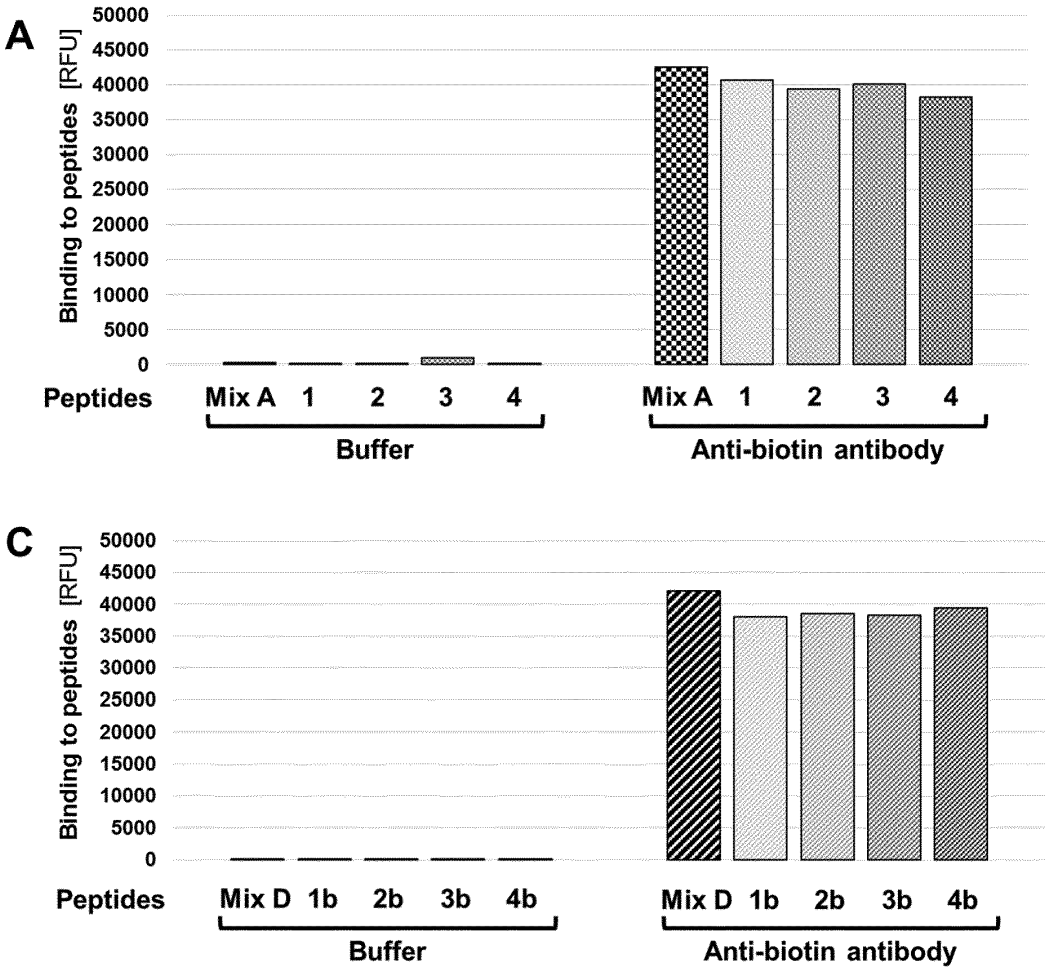


Fig. 5

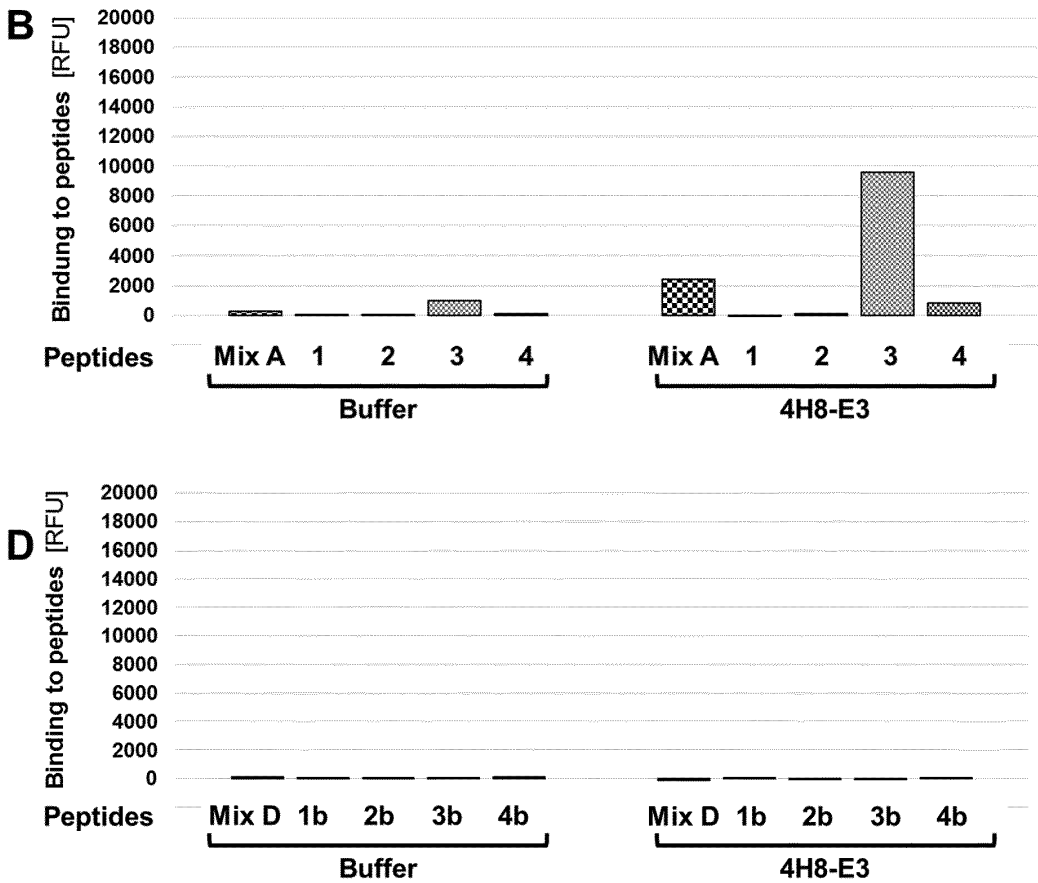


Fig. 5 ctd'

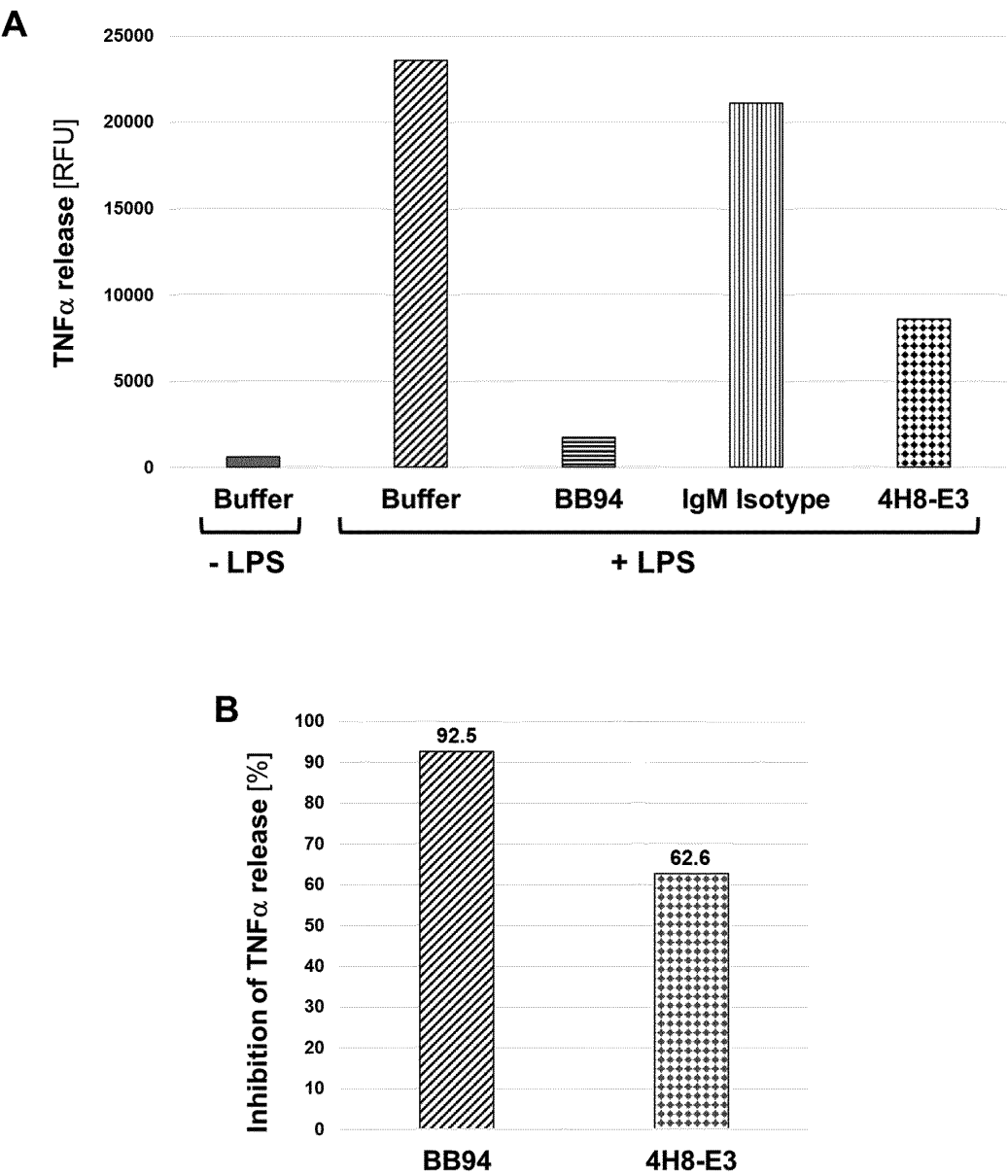
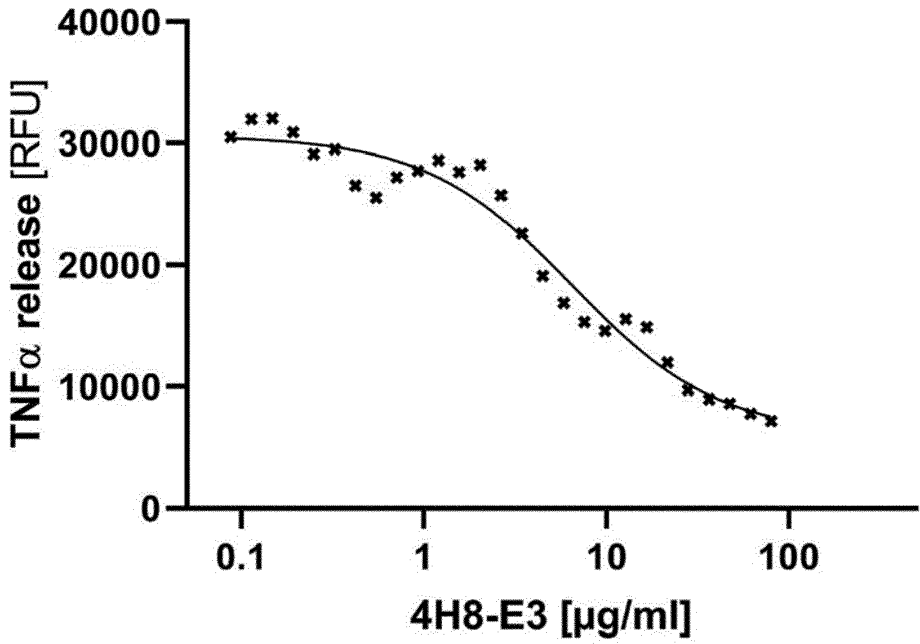
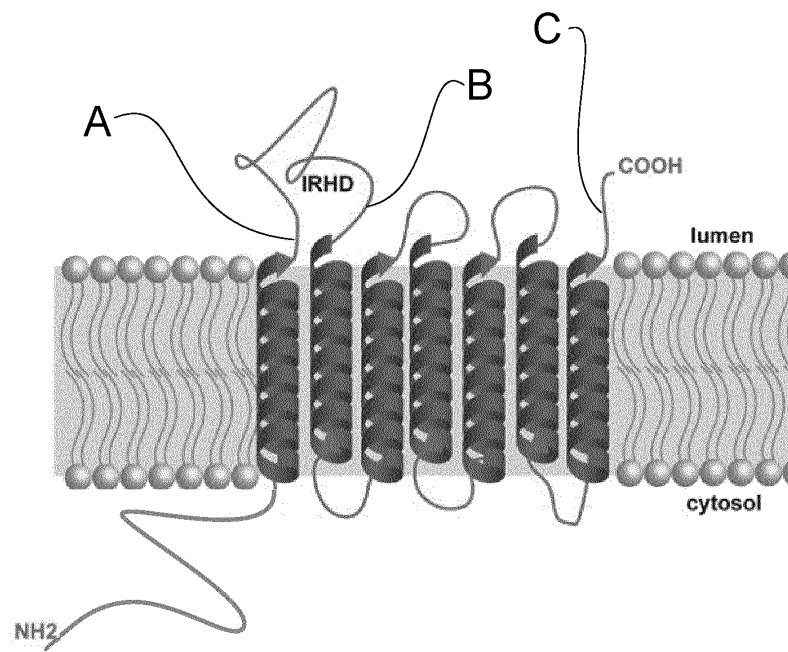


Fig. 6



Fig, 7



Name	Posistions	length
N terminus	1 – 409	409
TMD1	410 – 430	21
JMD with Loop1	431 – 660	230
TMD2	661 – 681	21
Loop2	682 – 692	11
TMD3	693 – 713	21
Loop3	714 – 715	2
TMD4	716 – 736	21
Loop4	737 – 747	11
TMD5	748 – 768	21
Loop5	769 – 773	5
TMD6	774 – 794	21
Loop6	795 – 802	8
TMD7	803 – 823	21
C-terminus	824 – 856	32

Fig. 8

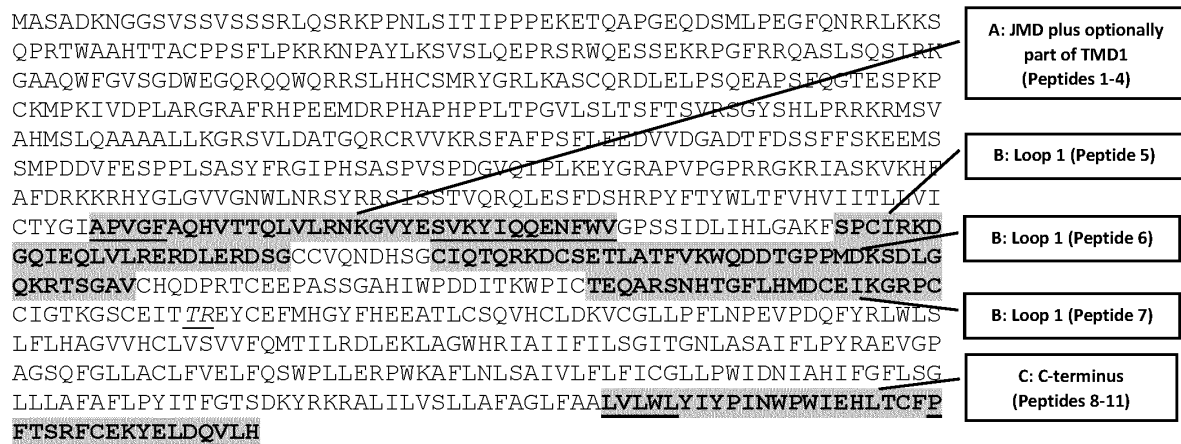


Fig. 9

iRhom2	1	MASADKNGGSSVSSSSRLQSRKPPNLSITIPPEKETQAPGEQDSMLPE	50
iRhom1	1	MSEARRD-----STSSLQRKKPPWLKLDIP-----SAVP-	29
iRhom2	51	GFQNRRLKKSQPRTWAAHTTACPPSFLPKRKNPAYLKSQVSLQEPRSRWQE	100
iRhom1	30	-----LTAEEPSFLQPLRRQAFLRVSM--PAETAHI	59
iRhom2	101	SSE----KRPGRFRQASLSQSIRKGAQWFGVSGDWEGRQQWQRRSLHH	146
iRhom1	60	SSPHHELRRPVLQRQTSITQTIIRRGTDWFGVSKD-SDSTQKWQRKSI RH	108
iRhom2	147	CSMRYGRLKASCQRDLPLSQEAPSFGQTESPK-----PCK--MPKIVDP	189
iRhom1	109	CSQRYGKLPQVLRDLPLSQDNVSLTSTETPPPLYVGPCQLGMQKIIDP	158
iRhom2	190	LARGRAFRHPPEE-MDRPHAPHPLTPGVLSLTSFTSVRSYGSHLP-RRKR	237
iRhom1	159	LARGRAFRVADDTAEGLSAPHTPVTPGAASLCFSSSRSFGHRLPRRRKR	208
iRhom2	238	MSVAHMSLQAAAAALLKGRSVLDATGQRCRVVKRSFAFP SFLEEDVVDGAD	287
iRhom1	209	ESVAKMSFRAAAALMKGRSVRDGTFRRAQ--RRSFTPASFEEDTDFPD	256
iRhom2	288	TFDSSFFSK-----EEMSSMPDDVFESPLSA-SYFRGI PHSA-----	324
iRhom1	257	ELDTSFFAREGILHEELSTYPDEVFESPEAALKDWEKAPEQADLTGGAL	306
iRhom2	325	--SPVSPDGVQIPL-----KEYGRAPVP-----GPRRGKRI	353
iRhom1	307	DRSELEERSHMLPLERGWKRQKEGAAAPQPKVRLRQEVVSTAGPRRGQRI	356
iRhom2	354	ASKVKHFAFDRKKRHYGLGVGNWLNRSYRRSISSTVQRQLESEFDSHRPY	403
iRhom1	357	AVPVRKL-FAREKRPYGLGMVGRLTNRTYRKIDSFVKRQIEDMDHRRPF	405
iRhom2	404	FTYWLTFFVHVITLLVICTYGIAPVGFAQHVTTLQVLRLNKGVIYESVKYIQ	453
iRhom1	406	FTYWLTFFVHSLVTLAVCIYGIAPVGFSQHETVDSVLRNRGVYENVKYVQ	455
iRhom2	454	QENFWVGPSSIDLHLGAKFSPCIRKDGQIEQLVLRERDLERDSGCCVQN	503
iRhom1	456	QENFWIGPSSSEALHLGAKFSPCMRQDPQVHSFIRSAREKHSACCVRN	505
iRhom2	504	DHSGCIQTQRKDCSETLATFVKWQDDTGPPMDKSDL-GQKRTSGAVCHQD	552
iRhom1	506	DRSGCVQTSEEECSSTLAVVWKWPIHPSAP---ELAGHKRQFGSVCHQD	551
iRhom2	553	PRTCEEPASSGAHIWPDITKWPICTEQARSNHTGFLHMDCEIKGRPCCI	602
iRhom1	552	PRVCDEPSSDPHEWPEDITKWPICTKNSAGNHTNHPHMDCVITGRPCCI	601
iRhom2	603	GTKGSCEITTREYCEFMHGYFHEEATLCSQVHCLDKVCGLLPFLNPEVPD	652
iRhom1	602	GTKGRCEITSREYCDFMRGYFHEEATLCSQVHCDMDVCGLLPFLNPEVPD	651
iRhom2	653	QFYRLWLSLFLHAGVVHCLVSVVFQMTILRDLEKLAGWHRIAIIFILSGI	702
iRhom1	652	QFYRLWLSLFLHAGILHCLVSI CFQMTVLRDLEKLAGWHRIAIYLLSGV	701
iRhom2	703	TGNLASAIFLPYRAEVGPAGSQFGLLACLFVELFQSWPLLERPWKAFNL	752
iRhom1	702	TGNLASAIFLPYRAEVGPAGSQFGILACLFVELFQSWQILARPWRAFFKL	751
iRhom2	753	SAIVLFLFICGLLPWIDNIAHIFGFLSGLLLAFAFLPYITFGTSDKYRKR	802
iRhom1	752	LAVVLFLLFTFGLLPWIDNFAHISGFISGLEFLSFAFLPYISFGKFDLYRKR	801
iRhom2	803	ALILVSLLAFAAGLFAALVLWLYIYPINWPWIEHLTCFPFTSRFCEKYELD	852
iRhom1	802	CQIIIFQVVFLGLLAGLVVLFYVYPVRCEWCEFLTICIPFTDKFCEKYELD	851
iRhom2	853	QVLH	856
iRhom1	852	AQLH	855

Fig. 10