

```

TTR_95      -----MLYAVVFL--FSFAGFPSFL--NAICTTSHVTVTGQLGCGERALK--NVIVELRE      49
TTR_07      -----MLT--LKVTFGLLLVTFAYCKMQMTVVRGQVACSDKSAI--NVHIELRE      46
TTR_32      -----MRLTLTFI--II--SGISIPITALKMKSVGVNGTVICDGKPVN--DAWIELYS      48
TTR_47      -----MILVHILCLFLHLVIGDQIKFAEKISTHSTAIGKILLCGNTSAN--DVKVKLFR      52
TTR_16      -----MEWILFILLPT---IANA--LFPLSRVQRVAVQGILLCEGRPLP--NHQIILID      47
TTR_41      -----MFHILLCLFNFSGIFGVL--GGLIGRTQSAGIEGLMCDGKPLP--GVLIKLYD      51
TTR_08      -----MIRQILLTTFLIPSIVGAA--GGLVGRTQSAGAKGYLMCNGVPES--GVLIKLYD      52
TTR_90.     MQRKSTFLFLIFT-----IFHQQVIVISFRQQSVGIRGRLLCGNQSLP--NTQIKLWN      51
TTR_76      -----MFIFLA-----LSITLCSVNAFRTQSAGVGTLMCGNSPLK--NTKVKLWD      44
TTR_79      -----MKAVLFL-----FLTILSISNGMRLQAVQVKGQLKCGDKPAS--GVKVKLWD      45
TTR_62      -----MKVVIV-----LLALLSGVVSFRSQSVAVRGRMLCNSNPAS--NVRIKLWE      44
TTR_77      -----MHFWLLFL-----ILGVVTFSTAMRQQAVAVKGLKCGTAPAR--NIRVKLWD      46
TTR_61      -----MQLAYAGHKCVMIHGTVRCHKDPSRNLNVEVRVVD      35
TTR_05      -----MDHQIVVA--F---LLILLSLRIVGKSECMQIVGTLVCPQKSMLAGNVQIDLK      49
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TTR_95      HDI-----LDPDDSLNTKSDNKGYFTIYGEECEVG-----S-IEPYLRIIHNCEDG      95
TTR_07      ADT-----WDPDDSLATHSDRNGRFVSGQEDEIG-----SIIEPYLRITHSCNDG      93
TTR_32      ERNA-----GKSNVAVLAKTKTNEQGHFMKGSSTKD-----MFDPQFTISHKCRTK      94
TTR_47      KAS-----DDIGEVHSTDQTTLNHFQIKGDTVGR-----EQDIEPVIRFYHRCDD      100
TTR_16      HDSSSEIVLELDPDDIMAMNVTQGRGVFFVHGNETENS-----TIDPVLVVRHKCNDG      100
TTR_41      DDRG-----IDTDLMAKGGKSDSKGHFRISGYTSEIT-----TIDPKLNIYHDCND      98
TTR_08      DDRG-----LDFDDFMGETVDSRGFFEITGRNAEVT-----PIDPKINIYHDCNDG      99
TTR_90.     KNK-----IGTDDQLAATKTKADGSYELKGGIGSIF-----GMDVVLTIYHDCDDG      97
TTR_76      EDA-----IDMDLLEEGRTAQGHFELSGYTSEIT-----TINPILKIYHDCNDR      90
TTR_79      EDDG-----PDPDVLSEGGTDRDGNFNLEGSTRELT-----SIDPVLKIYHDCDDG      92
TTR_62      EDSG-----PDPDDLQGGYTDQNGDFLLQGDVELT-----PIDPVFKVYHDCDDG      91
TTR_77      EDTG-----PDPDLLAQGYTDDQGMFMLQGDTAELT-----TIDPVFKAYHDCND      93
TTR_61      RDGL-SIAKIIDPDDLMGVFTFSEDGSQLDGGCEDIDWIPGIPNPEPYLQILHYCNRQ      94
TTR_05      EDLSL-P----WETHDQMGRTWSHSDGSMISGCGADFG----PFNEPDPYIIIEHKCPSV      100
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TTR_95      ILS---EN-CIITDDFPINQDI-----GKIYKLGIVSLNIARMNHKKHCH---      137
TTR_07      VID---PK-CRIMDDYQIPKEYI-----NDIYNMGIVSLNIAQEGREKKCI---      135
TTR_32      -----L-CTRRVFLRIPDKYFTLSSEPYEMVDIGVDMKKKFLTEIKTCPT--      139
TTR_47      LKKDLKKV--GYRTFAISYPKEYVVTIGKVPRKQFDIGKLNLIQIIPRESRDMKFVD      154
TTR_16      GI-----P-CDREWRLGIPVKYISNEGDEHIMDIGILNAEVVFGYGEKRDCLL--      147
TTR_41      WVV---IP-CQRKISVMIPDKYVSSGKTPKQFYNAGNIELSGKFKGETRDCVH--      147
TTR_08      WNV---P-CQRKISIMIPDDYIAIGNAPTPLYDVGTIELAGKYNGETRDCIH--      146
TTR_90.     IM-----P-CKRKRVALRIPSYVTRSDVVRQWFNAGDLNMEFKFPDEGRSCIN--      144
TTR_76      IM-----P-CQRKVAFRIPSSYVSSGKKVNEFFDIDGTVMQIIFEKETRDCIHR-      138
TTR_79      IK-----P-GKRKVKLRIPKQYISAGSTAKKPFDIGVNLLEAIFAKEERDLI---      138
TTR_62      LK-----P-GKRKLFKIPQSYITNGKTPKKVFDIGTLNLETIFHHEERELIVS-      139
TTR_77      LK-----L-GQRKLLKIPSSYISEGKTAKKVFDIGVNLLETIFPV-----      133
TTR_61      TGEII-----KLPPFGIF-----VPNTYEVGIVDLDLPIQASSAKNNT--      132
TTR_05      LRSTIGNIGSTRKTQFALTKVF-----MPKIILNIGKVFLLDSDL-----      139
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**Supplemental Data Figure 7. Amino acid sequence alignment of WbTTR proteins bound by 5H1 or 18H7 IgE mAbs.** Amino acid sequence alignment of all WbTTR proteins bound by at least one human IgE mAb. Amino acid conservation across aligned proteins is indicated as follows: “\*” identical; “:” strongly similar; “.” weakly similar.