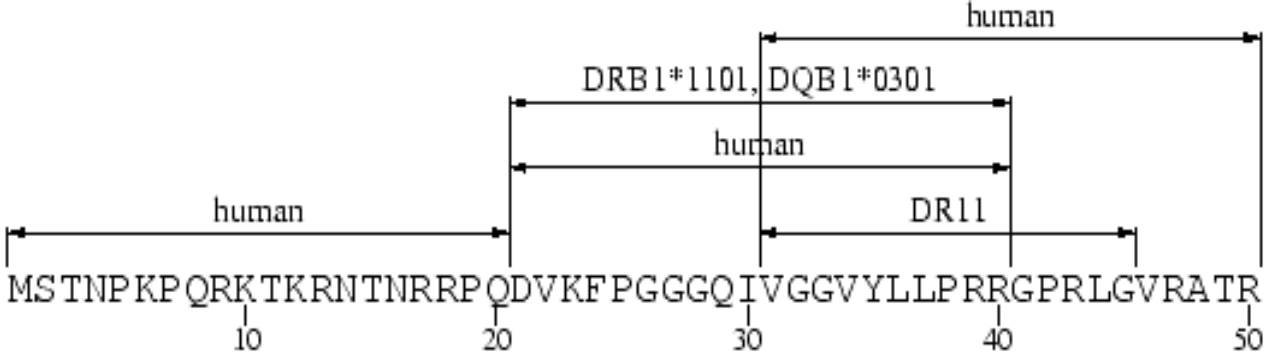
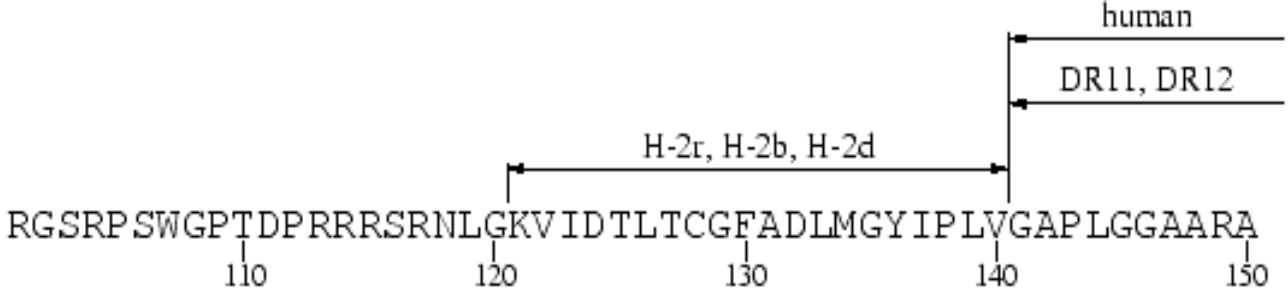
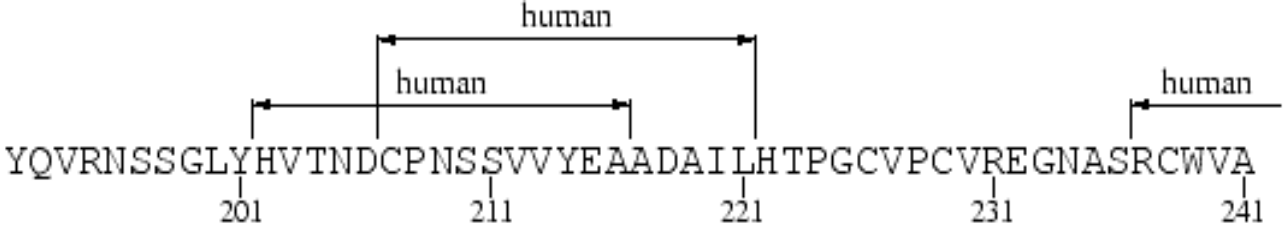

human
DRB1*1101, DQB1*0301
human
human
DR11
MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATR
10
20
30
40
50

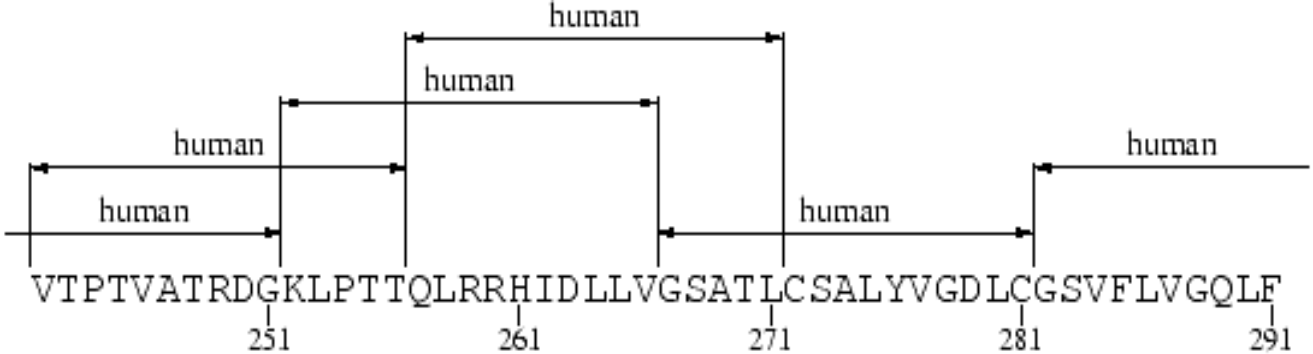
KTSERSQPRGRRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSP

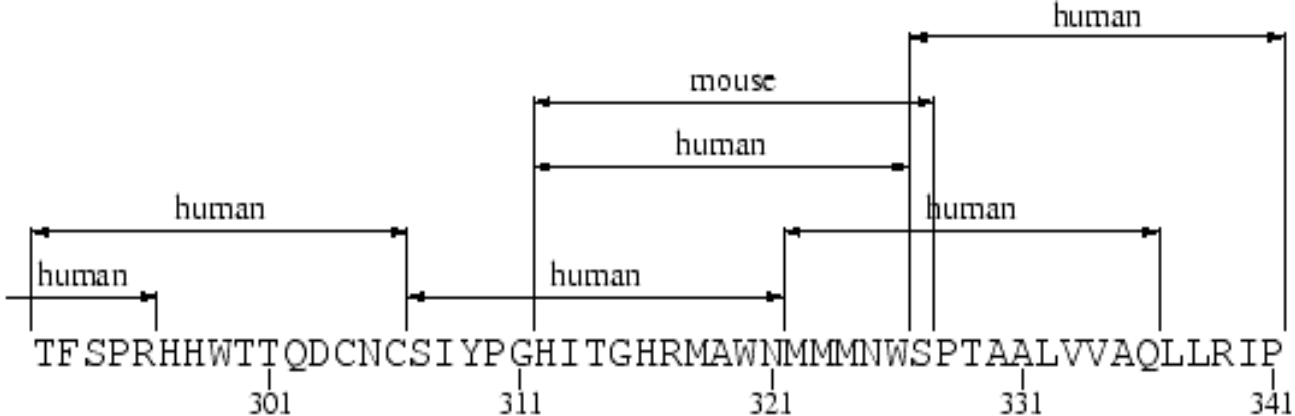
60 70 80 90 100

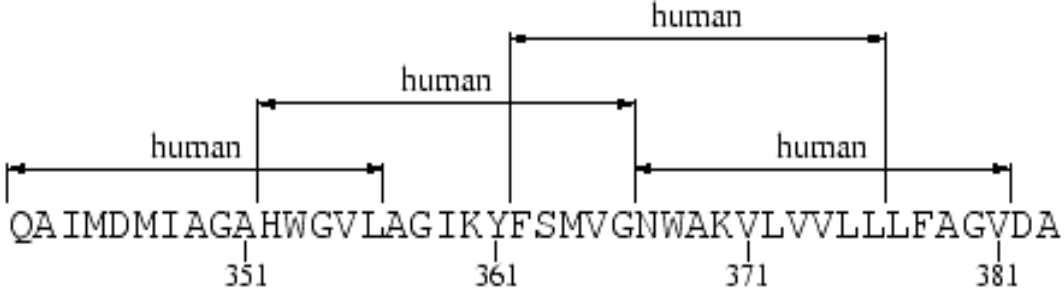

human
DR11, DR12
H-2r, H-2b, H-2d
RGSRPSWGPTDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAARA
110
120
130
140
150

human
DR11, DR12
human
LAHGVRVLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASA
160
170
180
190


human
human
human
YQVRNSSGLYHVTNDCPNSSVVYEAADAILHTPGCVPCVREGNASRCWVA
201
211
221
231
241


human
human
human
human
human
human
VTPTVATRDGKLPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLF
251
261
271
281
291


human
mouse
human
human
human
human
human
TFSPRHHWTTQDCNCSIYPGHITGHRMAWNMMMNWSPTAALVVAQLLRIP
301
311
321
331
341


human
human
human
human
QAIMDMIAGAHWGVLAGIKYFSMVGNWAKVLVVLLLFAGVDA
351
361
371
381

DRB1*1101

ETHVTGGNAGRTTAGLVGLLTPGAKQNIQLINTNGSWHINSTALNCNESL

393 403 413 423 433

NTGWLAGLFYQHKFNSSGCPERLASCRRLTDFAQGWGPISYANGSGLDER

443 453 463 473 483

PYCWHYPPRPCGIVPAKSVCGPVYCFTPSPVVVGTTDRSGAPTYSWGAND

493 503 513 523 533

TDVFVLNNTRPPLGNWFGCTWMNSTGFTKVCGAPPCVIGGVGNNTLLCPT

543 553 563 573 583

DCFRKYPEATYSRCGSGPRITPRCMVDYPYRLWHYPCTINYTIFKVRMYV

593 603 613 623 633

GGVEHRLEAACNWTRGERCDLEDRDRSELSPLLLSTTQWQVLPCSFTTLP

643 653 663 673 683

ALSTGLIHLHQNIVDVQYLYGVGSSIASWAIKWEYVVLLFLLLADARVCS

693 703 713 723 733

CLWMMLLISQAEA

743

ALENLVILNAASLAGTHGLVSFLVFFCFAWYLKGRWVPGAVYALYGMWPL

756 766 776 786 796

LLLLLALPQRAYA

806

LDTEVAASCGGVVLVGLMALTLSPYYKRYISWCMWWLQYFLTRVEAQLHV

819 829 839 849 859

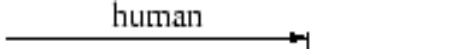
WVPPLNVRGGRDAVILLTCVVHPALVFDITKLLLAIFGPLWILQASLLKV

869 879 889 899 909

PYFVRVQGLLRICALARKIAGGHYVQMAIIKLGALTGTCVYNHLAPLRDW

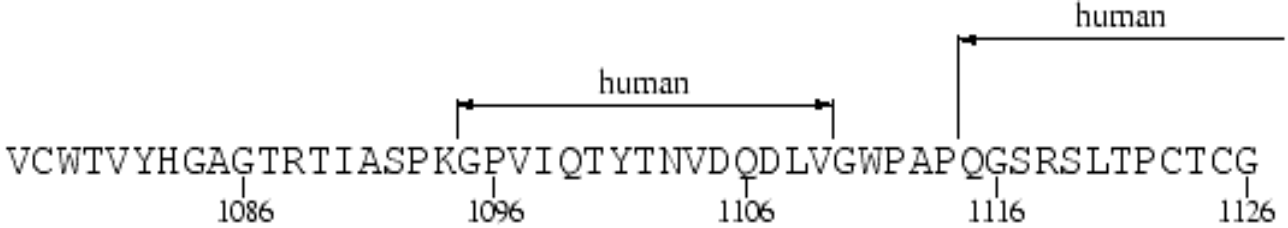
919 929 939 949 959

human
AHNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQE
969
979
989
999
1009

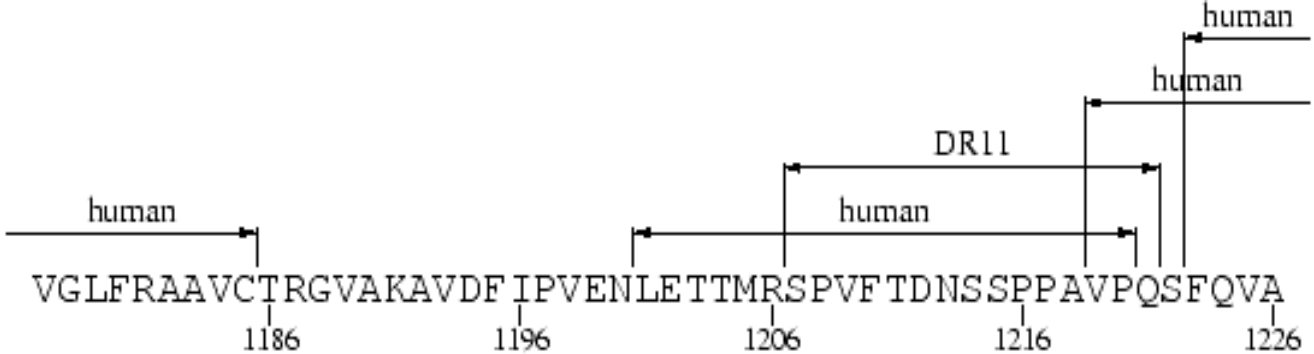

human
ILLGPADGMVSKGWRLL
1019

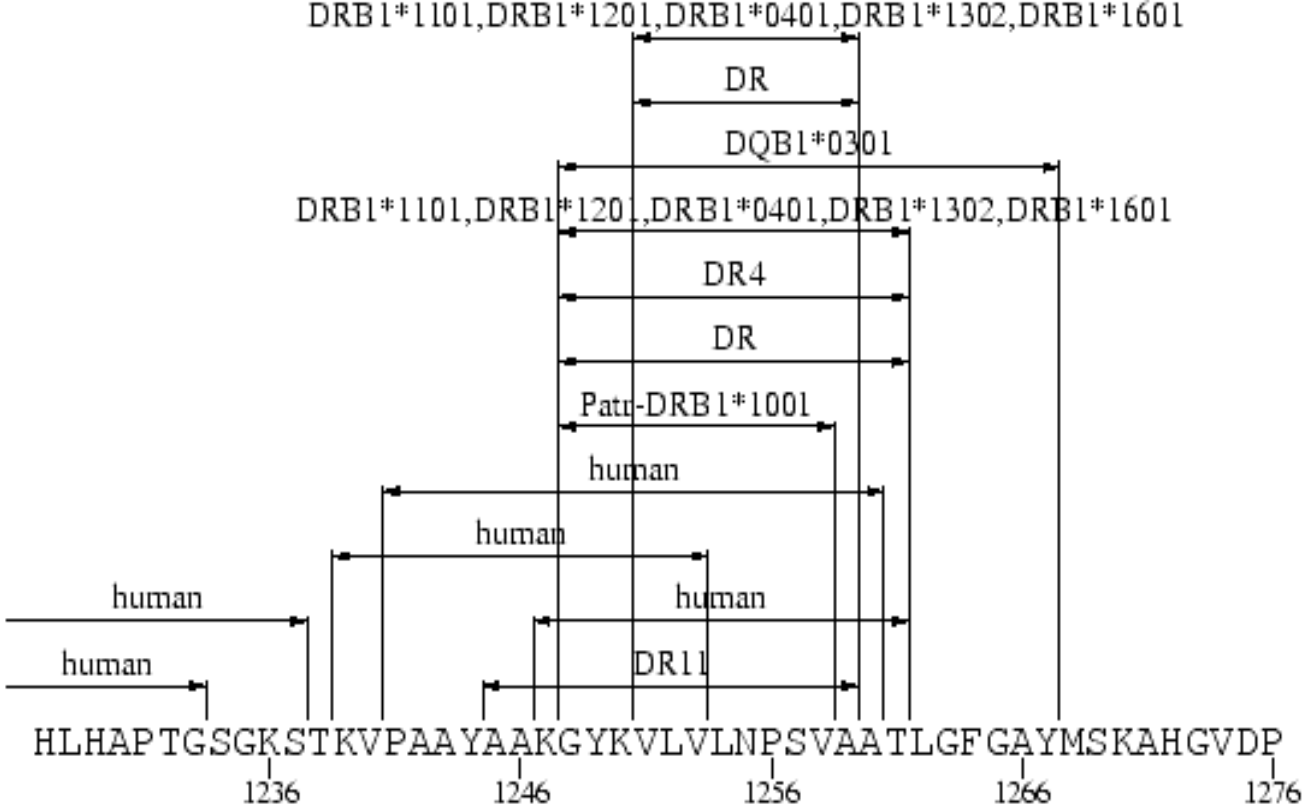
APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCING

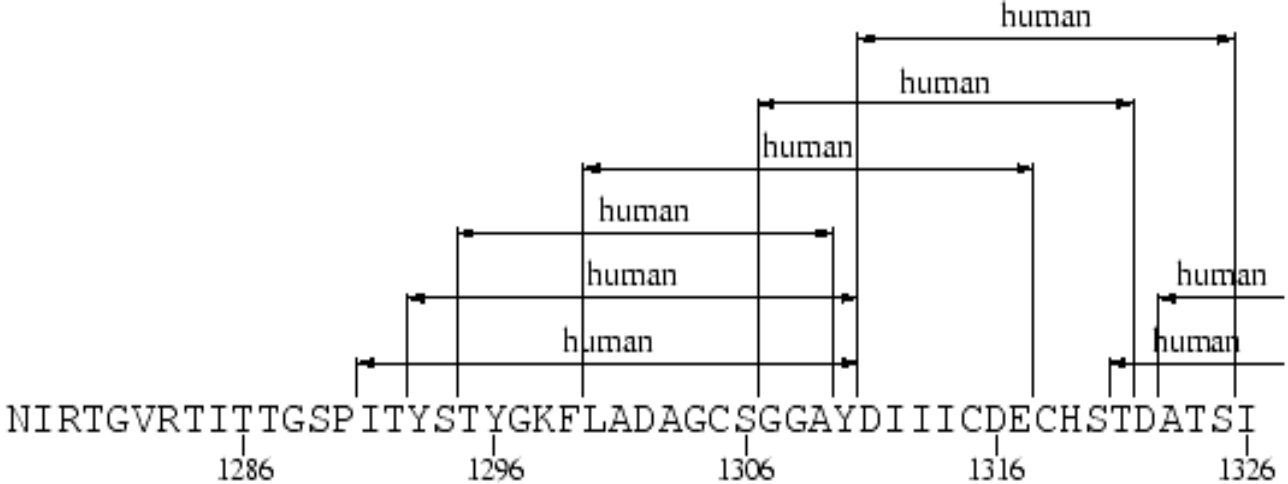
1036 1046 1056 1066 1076


human
human
VCWTVYHGAGTRTIASPKGPVIQTYTNVDQDLVGWPAPQGSRSLTPCTCG
1086
1096
1106
1116
1126

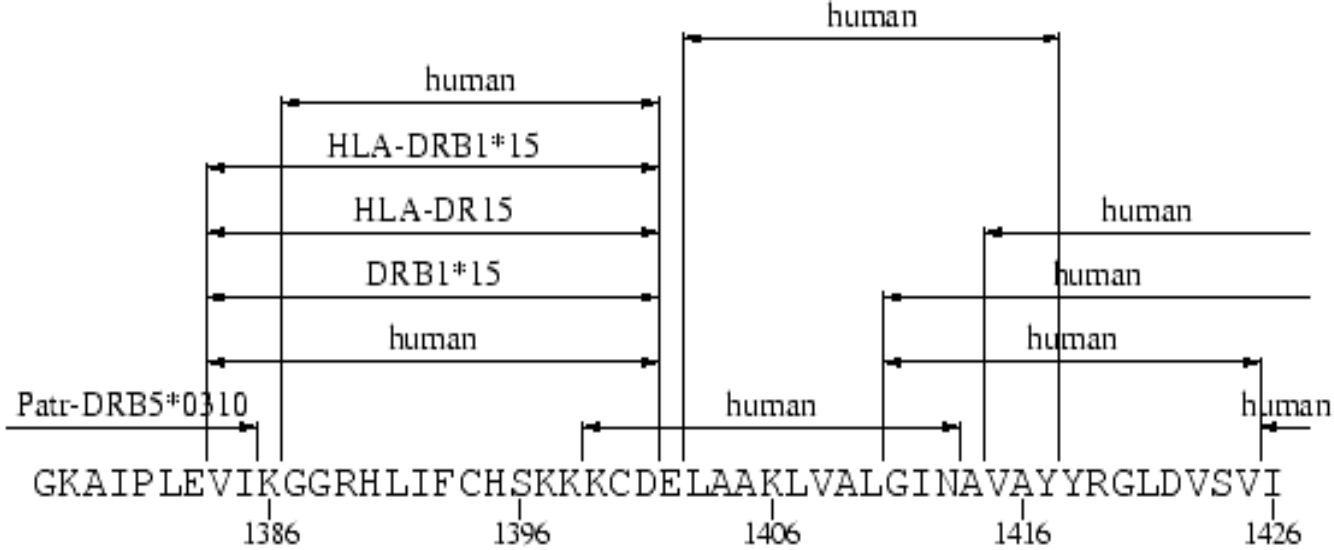
human
human
human
human
human
SSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPTGHA
1136
1146
1156
1166
1176

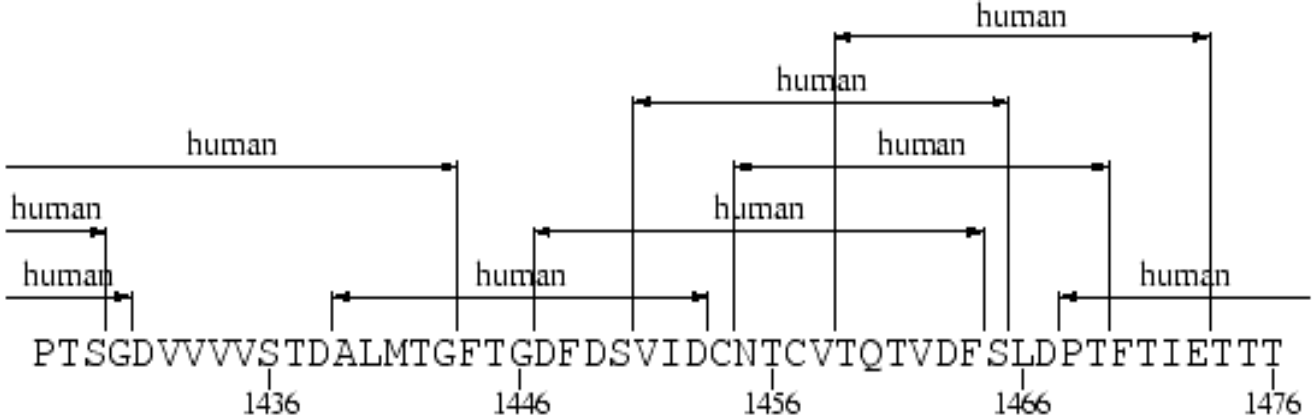

human
human
DR11
human
human
VGLFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVA
1186
1196
1206
1216
1226


DRB1*1101,DRB1*1201,DRB1*0401,DRB1*1302,DRB1*1601
DR
DQB1*0301
DRB1*1101,DRB1*1201,DRB1*0401,DRB1*1302,DRB1*1601
DR4
DR
Patr-DRB1*1001
human
human
human
human
human
DR11
HLHAPTGSGKSTKVPAAYAAKGYKVLVLNPSVAATLGFGAYMSKAHGVDP
1236
1246
1256
1266
1276

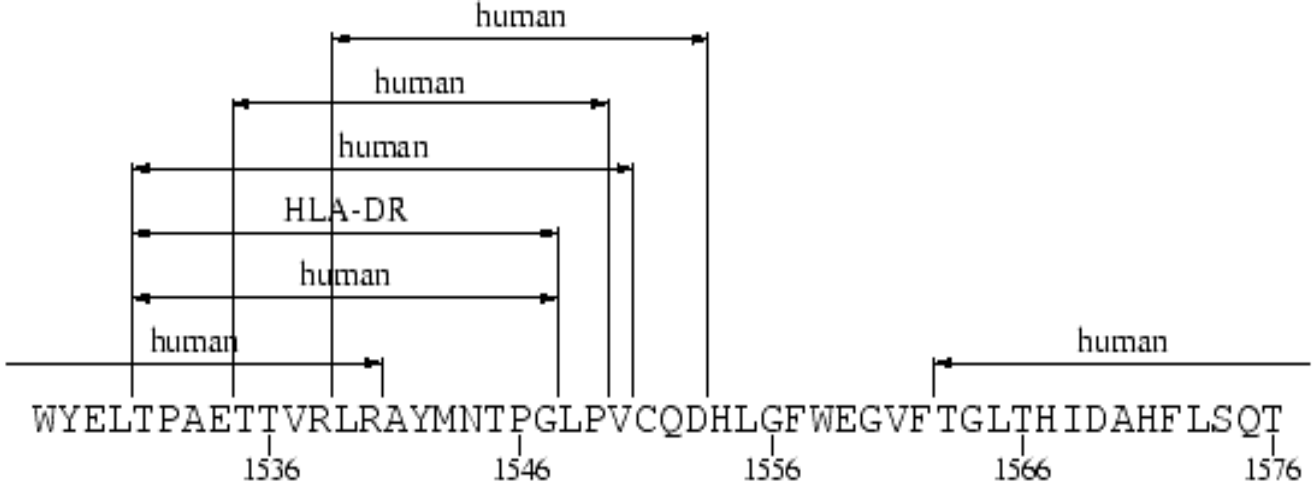

human
human
human
human
human
human
human
human
NIRTGVRTITTGSPITYSTYGKFLADAGCSGGAYDIIICDECHSTDATSI
1286
1296
1306
1316
1326

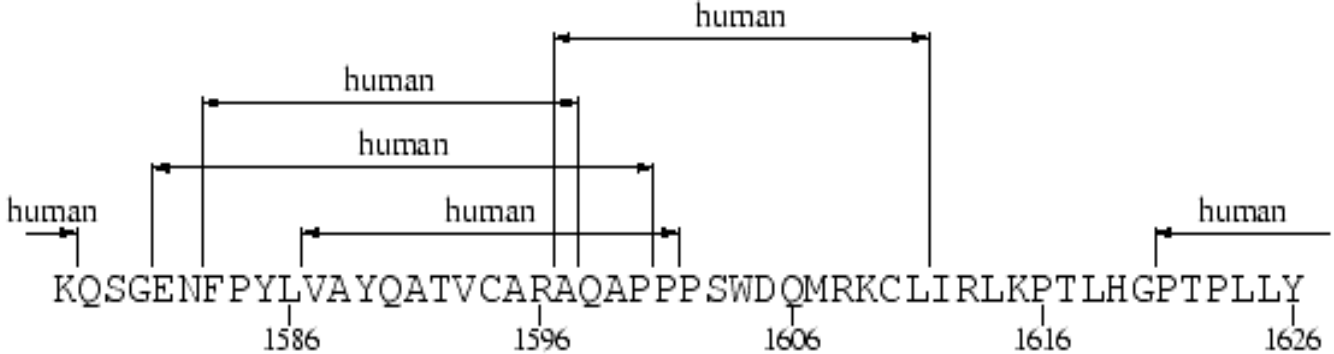
human
human
Patr-DRB5*0310
SGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFY
1336
1346
1356
1366
1376


human
human
HLA-DRB1*15
HLA-DR15
DRB1*15
human
Patr-DRB5*0310
human
human
human
human
human
GKAIPLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVI
1386
1396
1406
1416
1426

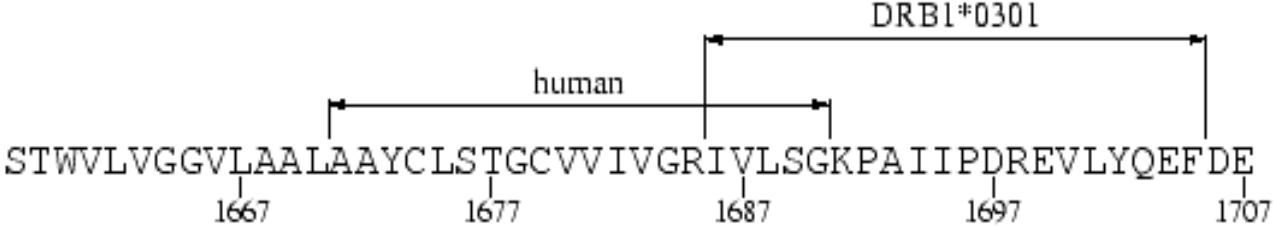

human
human
human
human
human
human
human
human
human
PTSGDVVVVSTDALMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTT
1436
1446
1456
1466
1476

human
human
LPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCA
1486
1496
1506
1516
1526


human
human
human
HLA-DR
human
human
human
WYELTPAETTVRLRAYMNTPGLPVCQDHLGFWEGVFTGLTHIDAHFLSQT
1536
1546
1556
1566
1576


human
human
human
human
human
human
KQSGENFPYLVAYQATVCARAQAPPPSWDQMRKCLIRLKPTLHGPTPLLY
1586
1596
1606
1616
1626

human
human
RLGAVQNEVTLTHPITKYIMTCMSADLEVVT
1636
1646
1656


DRB1*0301
human
STWVLVGGVLAALAAYCLSTGCVVIVGRIVLSGKPAIIPDREVLYQEFDE
1667
1677
1687
1697
1707

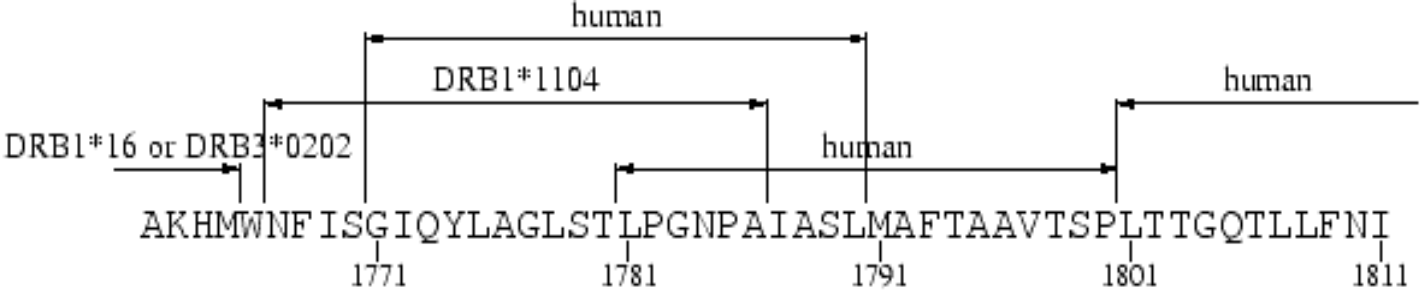
MEEC

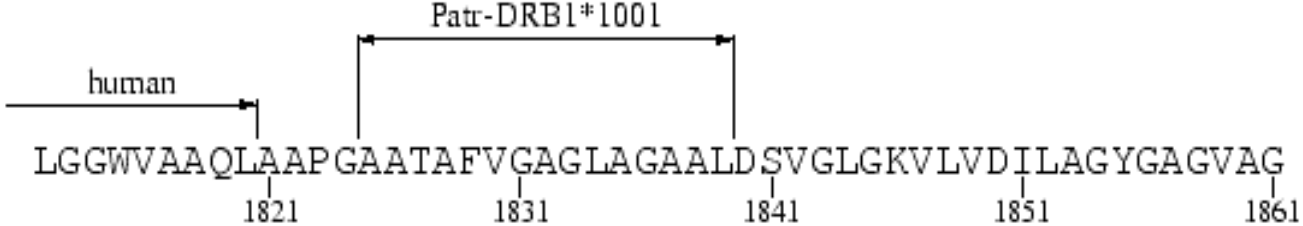
1711

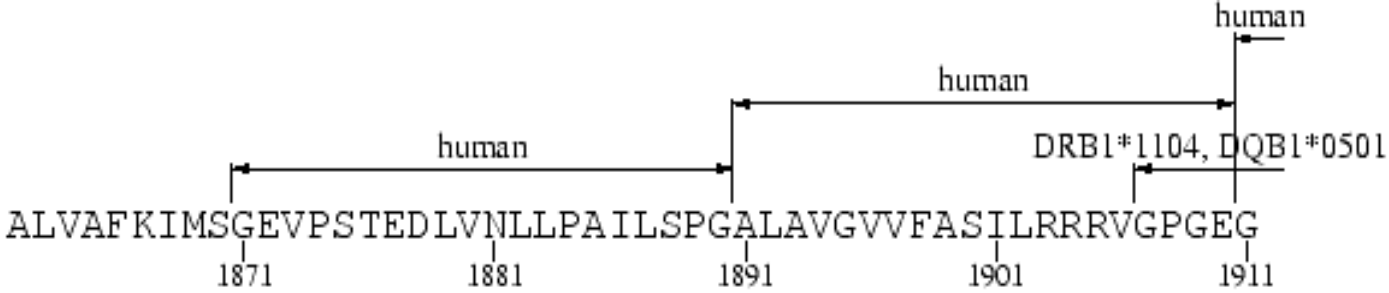
DRB1*16 or DRB3*0202

SQHLPYIEQGMMLAEQFKQKALGLLQTASRHAEVITPAVQTNWQKLEVFW

1721 1731 1741 1751 1761


human
DRB1*1104
human
DRB1*16 or DRB3*0202
human
AKHMWNFISGIQYLAGLSTLPGNPAIASLMAFTAAVTSPLTTGQTLLFNI
1771
1781
1791
1801
1811


Patr-DRB1*1001
human
LGGWVAAQLAAPGAATAFVGAGLAGAALDSVGLGKVLVDILAGYGAGVAG
1821
1831
1841
1851
1861


human
human
human
DRB1*1104, DQB1*0501
ALVAFKIMSGEVPSTEDLVNLLPAILSPGALAVGVVFASILRRRVGPGEG
1871
1881
1891
1901
1911

human
DRB1*1104, DQB1*0501
AVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSSLTVTQLLRRLH
1921
1931
1941
1951
1961

QWISSECTTPC

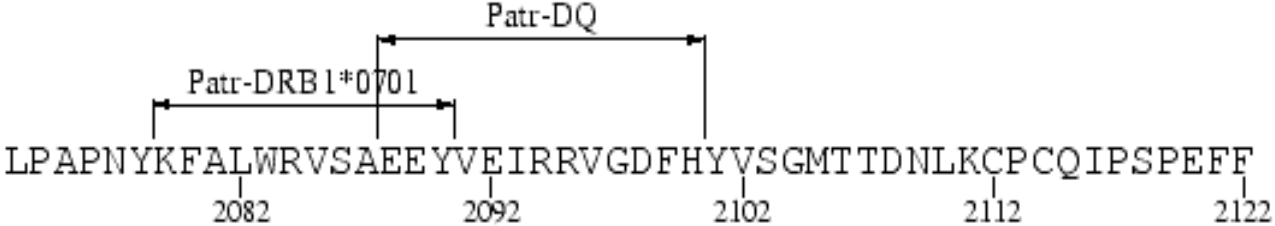
1971

SGSWLRDIWDWICEVLSDFKTWLKAKLMPQLPGIPFVSCQRGYRGVWRGD

1982 1992 2002 2012 2022

GIMHTRCHCGAEITGHVKNGTMRIVGPRTCKNMWSGTFFINAYTTGPCTP

2032 2042 2052 2062 2072

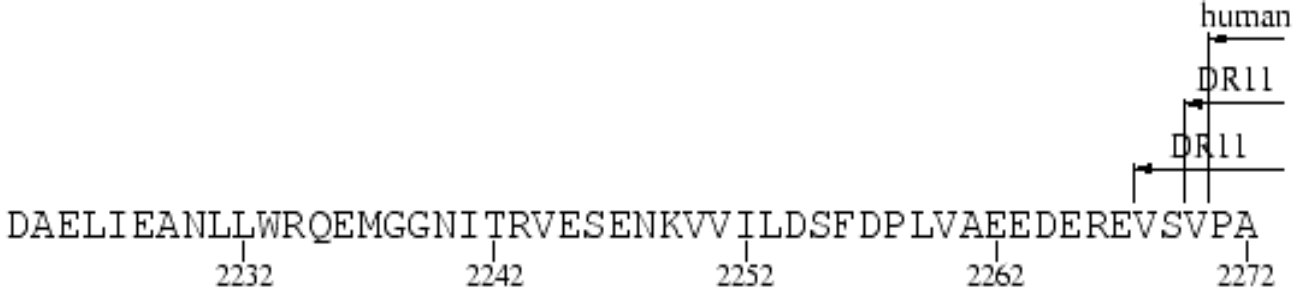

Patr-DQ
Patr-DRB1*0701
LPAPNYKFALWRVSAEEYVEIRRVGDFHYVSGMTTDNLKCPCQIPSPEFF
2082
2092
2102
2112
2122

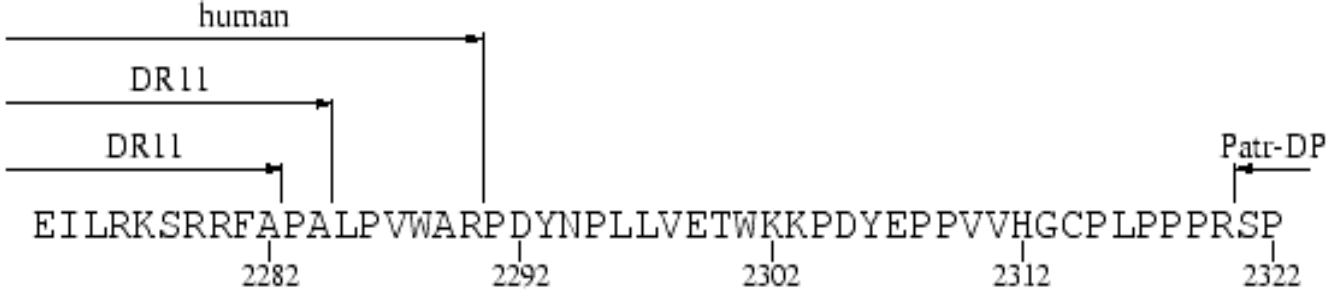
TELDGVRLHRFAPPCKPLLREEVSFRVGLHEYPVGSQLPCEPEPDVAVLT

2132 2142 2152 2162 2172

SMLTDPSHITAEAAGRRLARGSPPSMASSSASQLSAPSLKATCTANHDSP

2182 2192 2202 2212 2222


human
DR11
DR11
DAELIEANLLWRQEMGGNITRVESENKVVILDSFDPLVAEEDEREVSVPA
2232
2242
2252
2262
2272


human
DR11
DR11
Patr-DP
EILRKSRRFAPALPVWARPDYNPLLVETWKKPDYEPPVVHGCPLPPPRSP
2282
2292
2302
2312
2322

Patr-DP

PVPPPRKKRTVVLTESTLPTALAELATKSFGSSSTSGITGDNTTTSSEPA

2332 2342 2352 2362 2372

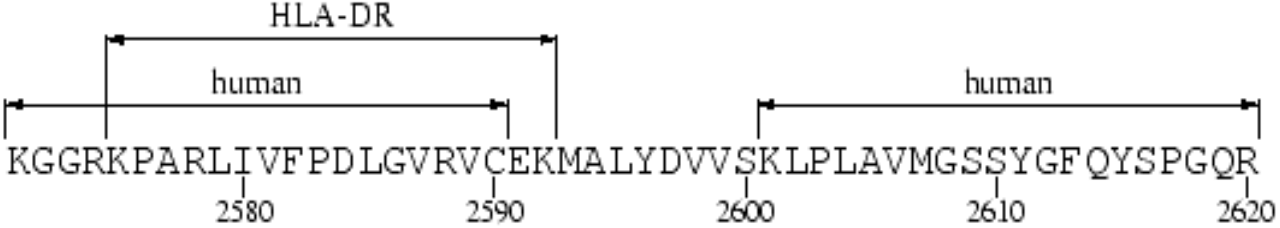
PSGCPPDSDVESYSSMPPLEGEPGDPDLSDGSWSTVSSGADTEDVVCC

2382 2392 2402 2412

Patr-DP
human
SMSYSWTGALVTPCAAEEQKLPINALSNSLLRHHNLVYSTTSRSACQRKK
2430
2440
2450
2460
2470

human
KVTFDRLQVLDSHYQDVLKEVKAAASKVKANLLSVEEACSLAPPHSAKSK
2480
2490
2500
2510
2520

human
FGYGAKDVRCHARKAVAHINSVWKDLLEDSVTPIDTTIMAKNEVFCVQPE
2530
2540
2550
2560
2570

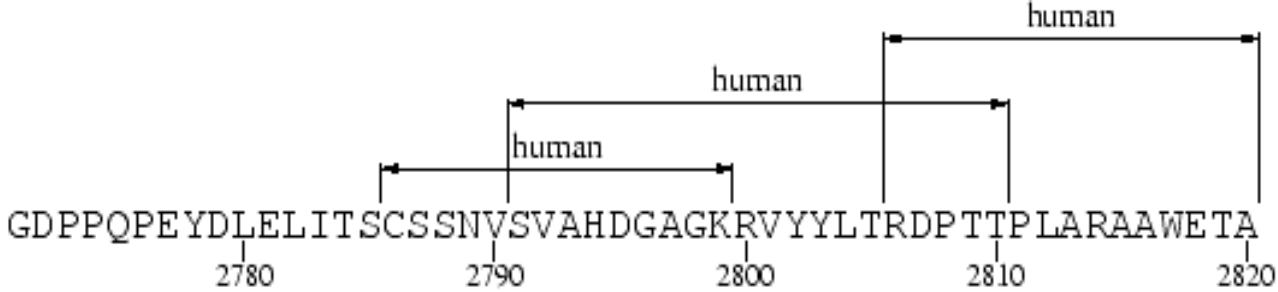

HLA-DR
human
human
KGGRKPARLIVFPDLGVRVCEKMALYDVVSKLPLAVMGSSYGFQYSPGQR
2580
2590
2600
2610
2620

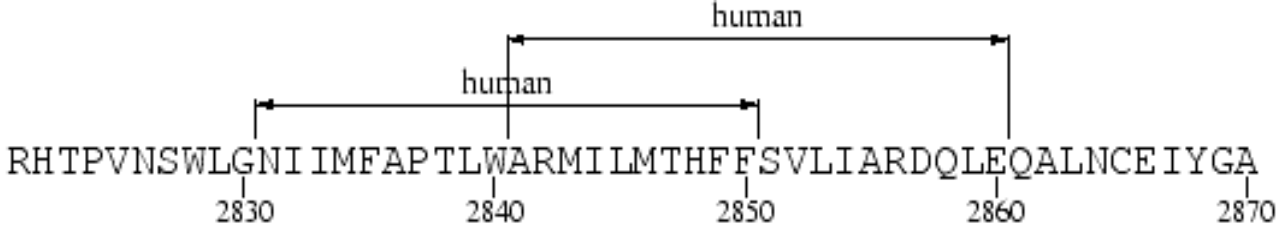
human
human
human
VEFLVQAWKSKKTPMGLSYDTRCFDSTVTESDIRTEEAIYQCCDLDPQAR
2630
2640
2650
2660
2670

human
VAIKSLTERLYVGGPLTNSRGENCGYRRCRASRVLTTSCGNTLTRYIKAR
2680
2690
2700
2710
2720

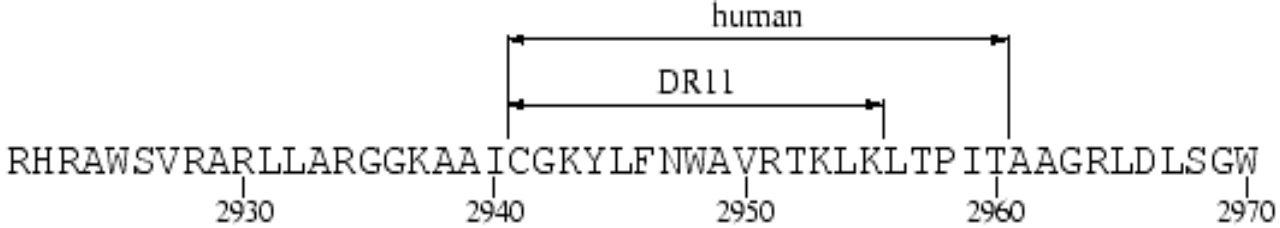
AACRAAGLQDCTMLVCGDDLVVICESAGVQEDAASLRAFTEAMTRYSAPP

2730 2740 2750 2760 2770


human
human
human
GDPPQPEYDLELITSCSSNVSVAHDGAGKRVYYLTRDPTTPLARAAWETA
2780
2790
2800
2810
2820


human
human
RHTPVNSWLGNIIMFAPTLWARMILMTHFFSVLIARDQLEQALNCEIYGA
2830
2840
2850
2860
2870

human
CYSIEPLDLPPIIQRLHGLSAFSLHSYSPGEINRVAACLRKLGVPPLRAW
2880
2890
2900
2910
2920


human
DR11
RHRAWSVRARLLARGGKAAICGKYLFNWAVRTKLKLTPITAAGRLDLSGW
2930
2940
2950
2960
2970

FTAGYSGGDIYHSVSHARPRWFWFCLLLLAAGVGIYLLPNR

2980 2990 3000 3010