Analysis the sequences of nAChR-α1 in IMR and IMS strain

```
IMR_1   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMR_2   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMR_3   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMR_4   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMR_5   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSRLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMR_6   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSRLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_1   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_2   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_3   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_4   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSQLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_5   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSRLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130
IMS_6   MLGVVRMERFVVLAMVAVVAGNPEAKRLYNDLLSNYNRLIRPVGNNTDRLTVKMGLKLSRLIDVNLKSQIMTTNMWVEQEWNDYKLKWNPEEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAI   130

IMR_1   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMR_2   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMR_3   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMR_4   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSRSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSRCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMR_5   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMR_6   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_1   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_2   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_3   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_4   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSRSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSRCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_5   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260
IMS_6   IHHTGKVVWKPPATYKSFCEIDVEYFPFDQQTCFMKFGSWSYDGYTVDLRHISQTPDSTEIEMGIDLQDYYLSVEWDVMRVPATRNEKFYSCCEEPYQDIMFNITLRRKTLFYTVNLIIPCIGLSFLSVL   260

IMR_1   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMR_2   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLDVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMR_3   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMR_4   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMR_5   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMR_6   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_1   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_2   VFYLPSDSGEKVSSCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLDVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_3   VFYPPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_4   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_5   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390
IMS_6   VFYLPSDSGEKVSLCISILLSLTVFFLLLAEIIPPTSLTVPLLGKYLLFTMVLVTLSVVVTIIVLNVNFRSPVTHKMTPFWYKVFIQVLPKVLMIERPNKDDSIDDDKPEGVLTGVFDADLGADKYLAYG   390

IMR_1   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMR_2   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMR_3   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALRPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMR_4   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMR_5   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMR_6   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_1   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_2   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_3   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALRPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_4   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVPPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_5   GPEEYSPEYDIPEPPPSRYEPNSAPAPVVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520
IMS_6   GPEEYSPEYDIPEPPPSRYEPNSAPAPSVVPLPLPCFEEPPPPSPLPGPEDDLFSAPGGGCGNALCPRLAGRSPVFERPLREIEKTIEDAKFIAQHVKNKDKFENVIEDWKYVAMVIDRLFLWLFLFACV   520

IMR_1   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMR_2   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMR_3   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMR_4   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMR_5   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMR_6   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_1   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_2   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_3   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_4   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_5   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
IMS_6   IGTCLIILQAPSLYDTTKPIDIVHSKVAKKKLRMMMMGPEED   562
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Analysis the sequences of nAChR-α2 in IMR and IMS strain

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IMR_1   MCFREWLFVFLLILVYALTVARGNPDAKRLYDGLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMR_2   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMR_3   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSDYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMR_4   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGSCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMR_5   MCFREWLFVFLLILVYALTVARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMR_6   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVATTMTK   130
IMS_1   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMS_2   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYSRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMS_3   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMS_4   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMS_5   MCFREWLFVFLLILVYALTMARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130
IMS_6   MCFREWLFVFLLILVYALTVARGNPDAKRLYDDLLSNYNRLIRPVSNNTNTVLVKLGLRLSQLIDLNLKDQILTTNVWLEHEWEDHKFRWDPAEYGGCKELYVPSEHIWLPDIVLYNNADGEYVVTTMTK   130

IMR_1   AVLHFDGKSVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMR_2   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMR_3   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYAVNLIVPCVGISYLS   260
IMR_4   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWVILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMR_5   AVLHFDGKVGWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMR_6   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_1   AVLHFDGKDVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHIDQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_2   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_3   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_4   AVLHFDGKVVWTPPAIFKSSREIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_5   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260
IMS_6   AVLHFDGKVVWTPPAIFKSSCEIDVRYFPFDQQTCFMKFGSWSYDGNQIDLKHINQKAGADMVEVGIDLREYYPSVEWDILGVPAERHEKYYPCCKEPYPDIFFNLTLRRKTLFYTVNLIVPCVGISYLS   260

IMR_1   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMR_2   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMR_3   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMR_4   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMR_5   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSARFNAALAASSL   390
IMR_6   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMS_1   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMS_2   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNTTSAKFNAALAASSL   390
IMS_3   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMS_4   VLVFYLPADTREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGFCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMS_5   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390
IMS_6   VLVFYLPADSREKVVLCITILLSQTMFFLLISEIIPSTSLALPLLGKYLLFTLVLIGLCVVITIGVLNVHYRKPSTHKMAPWVRKLFIRRLPRLLLMRVPEQLLIDMAAKKRLKNATSAKFNAALAASSL   390

IMR_1   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMR_2   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMR_3   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMR_4   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMR_5   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSTTSIVGTF   520
IMR_6   GSSTGSLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_1   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_2   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_3   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDGFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_4   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIRHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_5   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMDNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520
IMS_6   GSSTESLRGRHPYMPGGGPGCNGLHANNGVTNRFNSLVGALSGSVEAMNNGHGHGHPVVVAQDDNLSDAPQRKKYPFELEKAIHNVKFIQHHILREDEFDAEDQDWGFVAMVLDRLFLWIFSITSIVGTF   520

IMR_1   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMR_2   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMR_3   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMR_4   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMR_5   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMR_6   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMS_1   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSD.   555
IMS_2   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSD.   555
IMS_3   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSD.   555
IMS_4   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSD.   555
IMS_5   VILCGAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
IMS_6   VILCEAPALYDDTKPIDLQLSSVAQQQFLPDVTSDF   556
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Analysis the sequences of nAChR-α3 in IMR and IMS strain

```
IMR_1   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMR_2   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMR_3   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMR_4   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMR_5   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMR_6   MRIIYWIIVVLISDCVCNPDAKRLYYDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_1   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_2   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_3   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_4   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_5   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130
IMS_6   MRIIYWIIVVLISDCVCNPDAKRLYDDLLSNYNKLVRPVVNVTDALTVKIKLKLSQLIDVNLKNQIMTTNLWVEQSWNDYKLKWDPKEYGGVEMLHVPSDHIWRPDIVLYNNADGNFEVTLATKATLNYT   130

IMR_1   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMR_2   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMR_3   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMR_4   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMR_5   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMR_6   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMS_1   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTSNLIIPCMGISFLTVLVFYL   260
IMS_2   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMS_3   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMS_4   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMS_5   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260
IMS_6   GRVEWKPPAIYKSSCEIDVEYFPFDEQTCVMKFGSWTYDGFQVDLRHIDEVFGSNVVNIGVDLSEFYTSVEWDILEVPAVRNEKFYTCCDEPYLDITFNITMRRKTLFYTVNLIIPCMGISFLTVLVFYL   260

IMR_1   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMR_2   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMR_3   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMR_4   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMR_5   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMR_6   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_1   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_2   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_3   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_4   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_5   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390
IMS_6   PSDSGEKVSLSISILLSLTVFFLLLAEIIPPTSLVVPLLGKFVLFTMILDTFSICVTVVVLNVHFRSPQTHTMAPWVKRVFIHILPKLLVMRRPHYPVDKRGLAASCQRIMVRTCNGNVELRDSSLFPHH   390

IMR_1   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMR_2   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMR_3   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMR_4   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMR_5   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMR_6   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_1   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_2   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_3   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_4   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_5   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520
IMS_6   AAPPALPSELLNTPAQYVFQHSSRDTEPTIIGSSCEIHGAPPALSQLFPDTLGENGCGGVTPEPSPNENGSAVPTSSSHHLPQRWHHCPELHKAFDGVRYIADHTKKEEDSTKVKEDWKYVAMVLDRLFL   520

IMR_1   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMR_2   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMR_3   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMR_4   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMR_5   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMR_6   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_1   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_2   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_3   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_4   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_5   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
IMS_6   WIFTLAVLVGSAGIILQAPTLYDDRRPIDVQLSDIASTTSKPQVTTTTL   569
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Analysis the sequences of nAChR-α4 in IMR and IMS strain

```
IMR_1   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNGYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNTADGNYEVT   130
IMR_2   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_3   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_4   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_5   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_6   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_1   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_2   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_3   MIFVFALILLKSSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRPIRPVVNNTETLVVLLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_4   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWGPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_5   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_6   MIFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130

IMR_1   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYSPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMR_2   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMR_3   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMR_4   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMR_5   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMR_6   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_1   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_2   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_3   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCPMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_4   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQGCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_5   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260
IMS_6   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITMRRKTLFYTVNLIIPCVGI   260

IMR_1   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVSVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_2   TFLTVLVFYLPSDSGEKVSLSSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_3   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_4   TFLTGLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_5   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_6   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_1   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_2   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_3   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_4   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAKIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_5   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_6   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTISICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390

IMR_1   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_2   FSDGCPMEHKCSPKENRNMYKGNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_3   FSDGCPMEHKYSPKENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_4   FSDGCPMEHKCSPRENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_5   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_6   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_1   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_2   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_3   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_4   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_5   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_6   FSDGCPMEHKCSPKENRNMYKSNDCNHFHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520

IMR_1   PIYSINRDKILDAL   534
IMR_2   PIYSINRDKILDAL   534
IMR_3   PIYSINRDKILDAL   534
IMR_4   PIYSINRDKILDAL   534
IMR_5   PIYSINRDKILDAL   534
IMR_6   PIYSINRDKILDAL   534
IMS_1   PIYSINRDKILDAL   534
IMS_2   PIYSINRDKILDAL   534
IMS_3   PIYSINRDKILDAL   534
IMS_4   PIYSINRDKILDAL   534
IMS_5   PIYSINRDKILDAL   534
IMS_6   PIYSINRDKILDAL   534
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Analysis the sequences of nAChR-α5 in IMR and IMS strain

```
IMR_1   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMR_2   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMR_3   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMR_4   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMR_5   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMR_6   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_1   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_2   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_3   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_4   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_5   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130
IMS_6   MRLLSDNRIFALLCVHSLLSFVSVICDGVEYALMRTLMENYDSSIRPAKNSTQSLKVEFGVSLHHIIDVDEKNQILTTNCWITQVWTDHHLLWNISDFDEITVLRIPYHKVWRPDIILYNNADSQYNSAV   130

IMR_1   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMR_2   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMR_3   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMR_4   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMR_5   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMR_6   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_1   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_2   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_3   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_4   INTNVIVKHDGESTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_5   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260
IMS_6   INTNVIVKHDGEVTWLSHGIYRSSCDIDVEYFPFDIQSCAMKWASWTYDGYMLDLVKQTEEGDVSNYQANGEFDLIGFDSIKNVITYSCCEEPYPDITYFIRLRRRPMFYVFNLILPCILINCIALLVFY   260

IMR_1   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMR_2   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMR_3   VPSESGEKVTLGISALLSMTVFLMTIRETTPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMR_4   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMR_5   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMR_6   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_1   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_2   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_3   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_4   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_5   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390
IMS_6   VPSESGEKVTLGISALLSMTVFLMTIRETLPPTEKTPLISMYYGVSICLVTLASGLSVVTLNIYHRGVRGTKVPGIIKATMLGKLARCLFLQFEPRKKNSQEARRCGPKMQINYTKPDRWTTMNDEYRYN   390

IMR_1   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMR_2   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMR_3   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMR_4   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMR_5   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMR_6   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_1   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_2   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_3   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_4   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_5   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
IMS_6   SPKFIMRHSAQPAETTATSTGSRSFETQFMRMLQRVNVTVEQNELRLLDQERREQTELEWKQVALVMDRLLLWIFIILTAISTTVILRGSPYGP   484
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Analysis the sequences of nAChR-α6 in IMR and IMS strain

```
IMR-1   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNDGTCLY   140
IMR-2   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFDITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNDGTCLY   140
IMR-3   MIRADSYFVLVVLMTQFGDSNQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMR-4   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFDITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNDGTCLY   140
IMR-5   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPSRVWKPDILMYNSADEKFDGTFHTNVLVRNDGTCLY   140
IMR-6   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMS-1   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMS-2   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWDSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMS-4   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMS-5   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNNGTCLY   140
IMS-6   MIRADSYFVLVVLMTQFGDSHQGRHERRLLDKLLDSYNVLERPVANESAALLVRFGITLQQIIDVDEKNQILTTNAWLNLEWVDYSLGWNSSDYGGVKDLRITPNRVWKPDILMYNSADEKFDGTFHTNVLVRNDGTCLY   140

IMR-1   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMR-2   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMR-3   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMR-4   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMR-5   IPPGILKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMR-6   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMS-1   IPPGIFKSTCKIDITWFPFDDQRCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMS-2   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMS-4   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMS-5   IPPGIFKSTCKIDITWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLN   280
IMS-6   IPPGIFKSTCKIDVTWFPFDDQKCDMKFGSWTYDGFQLDLQLKSEEGGDLSDFIPNGEWYLLGMPGKRNVLYYQCCPEPYVDITFQIQIRRRTLYYFFNLIVPCVLISSMALLGFTLPPDSGEKLTLGVTILLSLTVFLD   280

IMR-1   LVAESMETTSDAVPLLGTYFNCIMFTVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMR-2   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMR-3   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMR-4   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMR-5   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMR-6   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMS-1   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDGLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMS-2   LVAESMETTSDAVPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMS-4   LVAETLEQVSDAHPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420
IMS-5   LVAESMETTSDAVPLLGTYFNCIMFMVASSVVLTVLVLNYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNDSTNTTCHQRQGITVSQSVDET   420
IMS-6   LVAESMETTSDAVPLLGTYFNCIMFMVASSVVLTVLVLSYHHRTPENHKMSGFVQKLFLEYLPWVLRMGRPGKKITLKTISISHRMRELEIRERSSRSLLANILDLDDDLQRFRANVNNSTNTTCHQRQGITVSQSVDET   420

IMR-1   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMR-2   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMR-3   AMCSIAQREMQHVLRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMR-4   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMR-5   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMR-6   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMS-1   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMS-2   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMS-4   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMS-5   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
IMS-6   AMCSIAQREMQHILRELRFITGRLRKKDEEAEVISDWKFAAM   462
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Analysis the sequences of nAChR-α7 in IMR and IMS strain

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IMR_1   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMR_2   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMR_3   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMR_4   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMR_5   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMR_6   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_1   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_2   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_3   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_4   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_5   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130
IMS_6   MVRIGVVLVLCLLWTPQESSQGPHEKRLLHTLLDTYNTLERPVANESEPLQLSFGLTLMQIIDVDEKNQLLITNIWLKLEWNDVNLRWNPSEFGNVRDLRIPPHRLWKPDILMYNSADEGFDGTYPTNVV   130

IMR_1   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMR_2   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMR_3   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMR_4   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMR_5   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMR_6   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMS_1   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMS_2   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTSPPDS   260
IMS_3   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMS_4   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMS_5   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQQDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260
IMS_6   VRSNGSCSYIPPGIFKSTCKIDITWFPFDDQRCEMKFGSWTYDGFQIDLQLQDEGGGDISSFITNGEWDLLGVPGKKNVIYYNCCPEPYIDITFVIIIRRRTLYYFFNLIVPCVLIASMAVLGFTLPPDS   260

IMR_1   GEKLSLSVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMR_2   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMR_3   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMR_4   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFQCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMR_5   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPQSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMR_6   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_1   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_2   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_3   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_4   GEKLSSGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_5   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390
IMS_6   GEKLSLGVTILLSLTVFLNMVAETMPATSDAVPLLGTYFNCIMFMVASSVVSTILILNYHHRNADTHEMSPWIKLLFLKWFPCILRMSRPEPETPVSGSGESARKLQLRELELKERSSKSLLANVLDIDD   390

IMR_1   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMR_2   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMR_3   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMR_4   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMR_5   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMR_6   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_1   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_2   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_3   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_4   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_5   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
IMS_6   DFRHAPIPPPAPHGYLPRHGVGVGGHPHEDGHTGTLLHATSASCLGPHRELALILKELRVITEKIRKEEEDAAVTNDWKFAAMVVDRLCLIIFTLFTVIATIAVLMSAPHIIVN   504
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Analysis the sequences of nAChR-α8 in IMR and IMS strain

```
IMR_1   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_2   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_3   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_4   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_5   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMR_6   MLFVFALILLKLHYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_1   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_2   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEASLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_3   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_4   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_5   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130
IMS_6   MLFVFALILLKLSYHPENVNGLKQIEANPDAKRLYDDLLSNYNRLIRPVVNNTETLVVQLRLKMSQLLEVSLKSQVMTTNVWVEQKWNDYKLRWDPNEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVT   130

IMR_1   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMR_2   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMR_3   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLAVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPWVGI   260
IMR_4   LMTKATLNYTGDVLWRPPAIYKSSCEMNALYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMR_5   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMR_6   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFGEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_1   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_2   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_3   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_4   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDVLEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_5   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260
IMS_6   LMTKATLNYTGDVLWRPPAIYKSSCEMNVLYFPFDEQSCLMKFGSWTYNGFQIDLKHMEQVYGSNLVNVGVDLSEFHLSVEWDILEVPARRNEEYYPCCTEPYSDITFNITVRRKTLFYTVNLIIPCVGI   260

IMR_1   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_2   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_3   TFLTGLGFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_4   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSTCVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_5   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMR_6   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLVTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPDDLYLENLSDASYVNDGDFRDS   390
IMS_1   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_2   TFLTVLVSYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_3   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_4   TFLTVLVFYLPSDSGEKASLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_5   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLSICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390
IMS_6   TFLTVLVFYLPSDSGEKVSLCSSILVSLTVFFLLLAEIIPPTSLAVPLLGKYLLFTMTLVTLPICVTVCVLNVHFRSPSTHKMSPWVKTVFLHFMPRLLMMRRPPYSPNDLYLENLSDASYVNDGDFRDS   390

IMR_1   FSDGCPMEHKGSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_2   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_3   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_4   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_5   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMR_6   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_1   FSDGCPMEHKCSPRENRNMYKGNDCNHSHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERALIDRQLSTFLYGENQM   520
IMS_2   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_3   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_4   FSDGCPMEHKCSPKENRNMYKSNDCNHPHYGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_5   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAPDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520
IMS_6   FSDGCPMEHKCSPKENRNMYKSNDCNHPHHGAQAQDLENVIPRHLSDDLLAALEGVRFIAQHIKDADKDNEVIEDWKYVSMVMDRFFLWIFTVACIGGTCIIMFQAPSLYDERAPIDRQLSTFLYGENQM   520

IMR_1   PIYSINRDKILDAL   534
IMR_2   PIYSINRDKILDAL   534
IMR_3   PIYSINRDKILDAL   534
IMR_4   PIYSINRDKILDAL   534
IMR_5   PIYSINRDKILDAL   534
IMR_6   PIYSINRDKILDAL   534
IMS_1   PIYSINRDKILDAL   534
IMS_2   PIYSINRDKILDAL   534
IMS_3   PIYSINRDKILDAL   534
IMS_4   PIYSINRDKILDAL   534
IMS_5   PIYSINRDKILDAL   534
IMS_6   PIYSINRDKILDAL   534
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Analysis the sequences of nAChR-β1 in IMR and IMS strain

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IMR_1   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMR_2   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMR_3   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMR_4   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMR_5   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMR_6   MKTSLVATLNLLMTGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_1   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_2   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_3   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_4   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_5   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130
IMS_6   MKTSLVATLNLLMIGLILPCLCSEDEERLVRDLFRGYNKLIRPVQNITEKVDVRFGLAFVQLINVNEKNQIMKSNVWLRLVWNDYQLRWDETDYGGIGVLRLPPDKVWKPDIVLFNNADGNYEVRYKSNV   130

IMR_1   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMR_2   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMR_3   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMR_4   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWRSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMR_5   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMR_6   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_1   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDRVSLALYNNKNFVDLSDYWKSGTWGIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_2   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_3   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWRSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_4   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKALFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_5   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260
IMS_6   LIYPHGEVLWIPPAIYQSSCTIDVTYFPFDQQTCIMKFGSWTFNGDQVSLALYNNKNFVDLSDYWKSGTWDIIEVPAYLNTYPGVPTETDITFYIIIRRKTLFYTVNLILPTVLISFLCVLVFYLPAEAG   260

IMR_1   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMR_2   EKVTLGISILLSLVVFLLLASKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMR_3   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMR_4   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMR_5   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMSTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMR_6   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMS_1   EKVTLGISILLSLVVFLLLVSKILPPTSLVGPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTEPPKNLAQASS   390
IMS_2   EKVTLGISILLALGVFLLLVSKTLPPTSLVGPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTGLPKNLAQASS   390
IMS_3   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMS_4   EKVTLGISILLSLVVFLLLVSKIPPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMS_5   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390
IMS_6   EKVTLGISILLSLVVFLLLVSKILPPTSLVLPLIAKYLLFTFIMNTVSILVTVIIINWNFRGPRTHRMPVWIRSVFLYYLPIILLMKRPKKTRLRWMMEMPSMTNVSSVPPHPHYGSPTELPKNLAQASS   390

IMR_1   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMR_2   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMR_3   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMR_4   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYTQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMR_5   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMR_6   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_1   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_2   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_3   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_4   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_5   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
IMS_6   KSKTEVMELSDFHHPNCKINRKASVERRESPSSDSLLLSPEASKATEAVEFIVEHLRNEDQYIQIREDWKYVAMVIDRLQLYIFFIVTTVGTVGIMMDAPHIFEYVDQDRIIEIYRGK   508
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