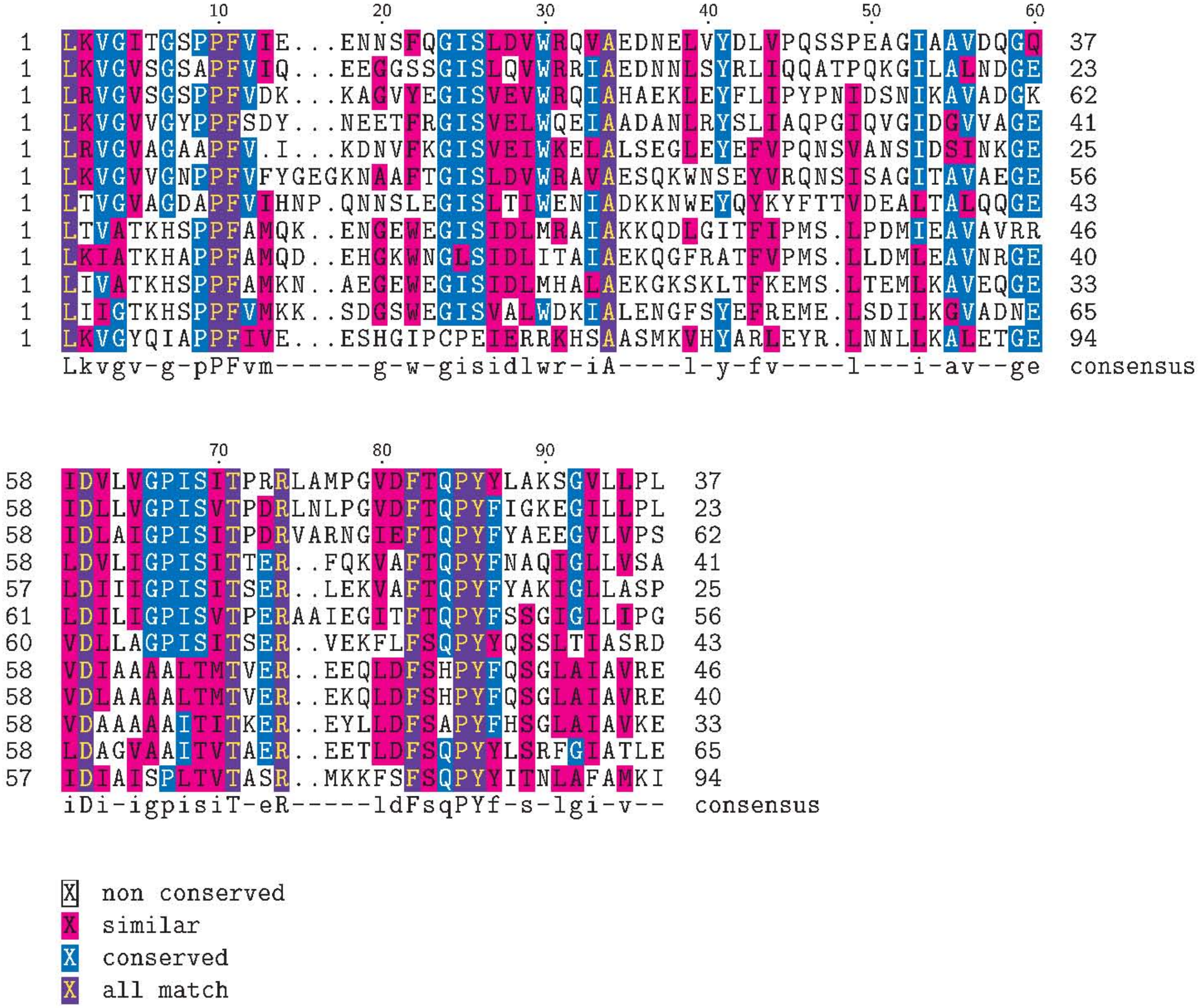
# group 1 S1 region alignment

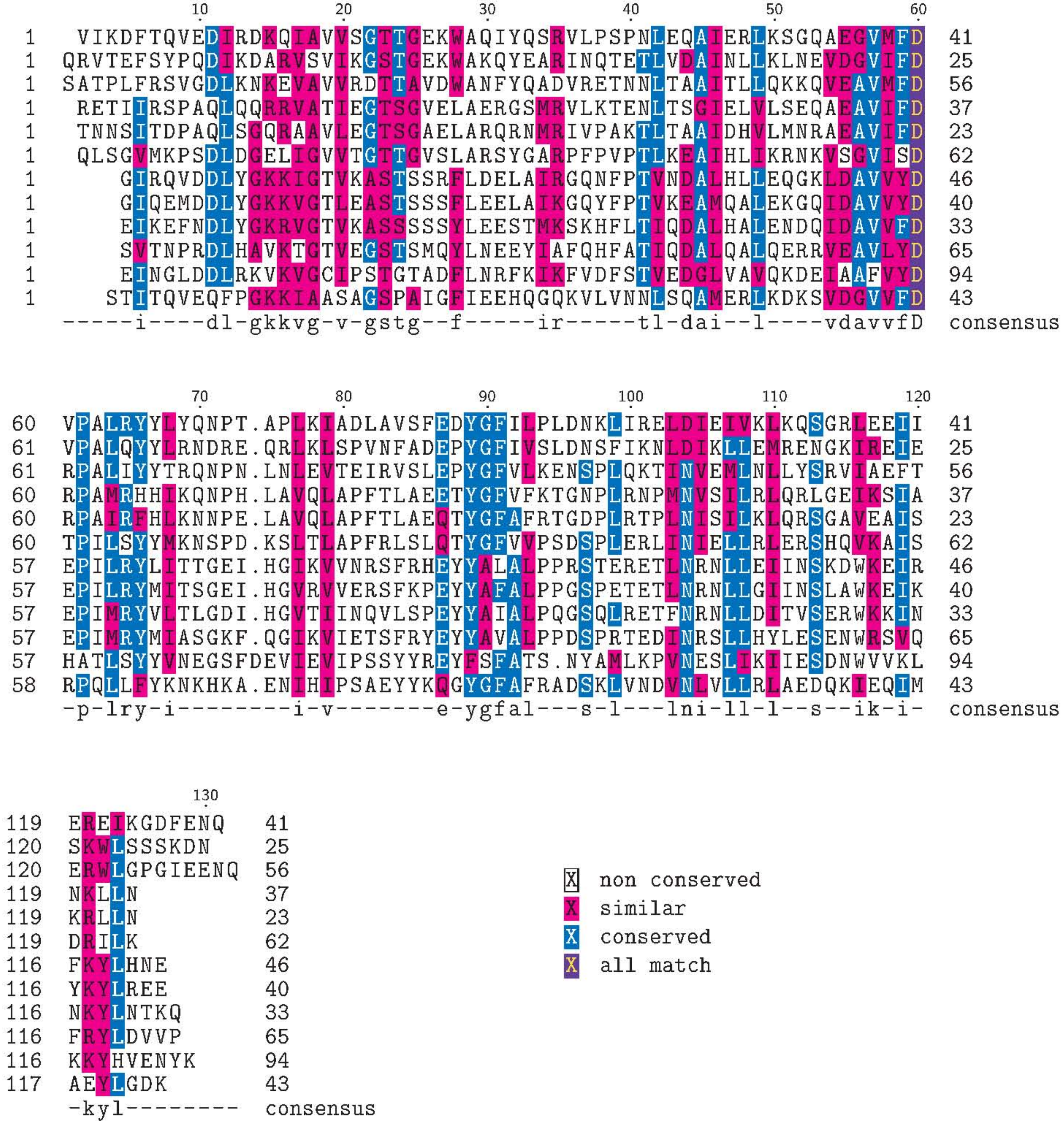


```
                  10        20        30        40        50        60
                   .         .         .         .         .         .
  1   LKVGITGSPPFVIE...ENNSFQGISLDVWRQVAEDNELVYDLVPQSSPEAGIAAVDQGQ  37
  1   LKVGVSGSAPFVIQ...EEGGSSGISLQVWRRIAEDNNLSYRLIQQATPQKGILALNDGE  23
  1   LRVGVSGSPPFVDK...KAGVYEGISVEVWRQIAHAEKLEYFLIPYPNIDSNIKAVADGK  62
  1   LKVGVVGYPPFSDY...NEETFRGISVELWQEIAADANLRYSLIAQPGIQVGIDGVVAGE  41
  1   LRVGVAGAAPFV.I...KDNVFKGISVEIWKELALSEGLEYEFVPQNSVANSIDSINKGE  25
  1   LKVGVVGNPPFVFYGEGKNAAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGE  56
  1   LTVGVAGDAPFVIHNP.QNNSLEGISLTIWENIADKKNWEYQYKYFTTVDEALTALQQGE  43
  1   LTVATKHSPPFAMQK..ENGEWEGISIDLMRAIAKKQDLGITFIPMS.LPDMIEAVAVRR  46
  1   LKIATKHAPPFAMQD..EHGKWNGLSIDLITAIAEKQGFRATFVPMS.LLDMLEAVNRGE  40
  1   LIVATKHSPPFAMKN..AEGEWEGISIDLMHALAEKGKSKLTFKEMS.LTEMLKAVEQGE  33
  1   LIIGTKHSPPFVMKK..SDGSWEGISVALWDKIALENGFSYEFREME.LSDILKGVADNE  65
  1   LKVGYQIAPPFIVE...ESHGIPCPEIERRKHSAASMKVHYARLEYR.LNNLLKALETGE  94
      Lkvgv-g-pPFvm------g-w-gisidlwr-iA----l-y-fv----l---i-av--ge  consensus


                  70        80        90
                   .         .         .
 58   IDVLVGPISITPRRLAMPGVDFTQPYYLAKSGVLLPL  37
 58   IDLLVGPISVTPDRLNLPGVDFTQPYFIGKEGILLPL  23
 58   IDLAIGPISITPDRVARNGIEFTQPYFYAEEGVLVPS  62
 58   LDVLIGPISITTER..FQKVAFTQPYFNAQIGLLVSA  41
 57   LDIIIGPISITSER..LEKVAFTQPYFYAKIGLLASP  25
 61   LDILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPG  56
 60   VDLLAGPISITSER..VEKFLFSQPYYQSSLTIASRD  43
 58   VDIAAAALTMTVER..EEQLDFSHPYFQSGLAIAVRE  46
 58   VDLAAAALTMTVER..EKQLDFSHPYFQSGLAIAVRE  40
 58   VDAAAAAITITKER..EYLLDFSAPYFHSGLAIAVKE  33
 58   LDAGVAAITVTAER..EETLDFSQPYYLSRFGIATLE  65
 57   IDIAISPLTVTASR..MKKFSFSQPYYITNLAFAMKI  94
      iDi-igpisiT-eR-----ldFsqPYf-s-lgi-v--  consensus
```

X non conserved
X similar
X conserved
X all match

# group 1 S2 region alignment



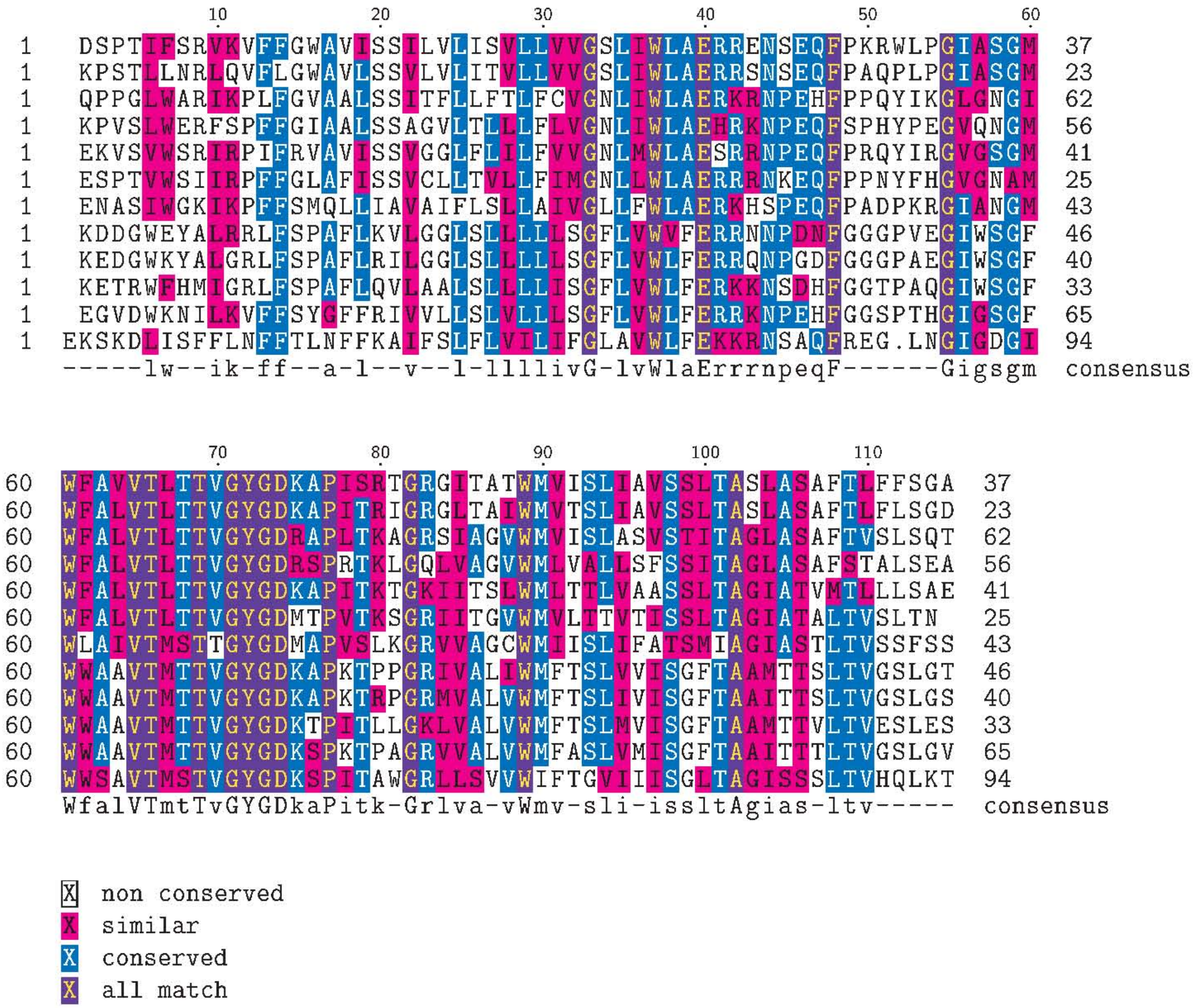
```
                 10        20        30        40        50        60
                  .         .         .         .         .         .
  1     VIKDFTQVEDIRDKQIAVVSGTTGEKWAQIYQSRVLPSPNLEQAIERLKSGQAEGVMFD  41
  1    QRVTEFSYPQDIKDARVSVIKGSTGEKWAKQYEARINQTETLVDAINLLKLNEVDGVIFD  25
  1    SATPLFRSVGDLKNKEVAVVRDTTAVDWANFYQADVRETNNLTAAITLLQKKQVEAVMFD  56
  1     RETIIRSPAQLQQRRVATIEGTSGVELAERGSMRVLKTENLTSGIELVLSEQAEAVIFD  37
  1     TNNSITDPAQLSGQRAAVLEGTSGAELARQRNMRIVPAKTLTAAIDHVLMNRAEAVIFD  23
  1     QLSGVMKPSDLDGELIGVVTGTTGVSLARSYGARPFPVPTLKEAIHLIKRNKVSGVISD  62
  1        GIRQVDDLYGKKIGTVKASTSSRFLDELAIRGQNFPTVNDALHLLEQGKLDAVVYD  46
  1        GIQEMDDLYGKKVGTLEASTSSSFLEELAIKGQYFPTVKEAMQALEKGQIDAVVYD  40
  1        EIKEFNDLYGKRVGTVKASSSSSYLEESTMKSKHFLTIQDALHALENDQIDAVVFD  33
  1        SVTNPRDLHAVKTGTVEGSTSMQYLNEEYIAFQHFATIQDALQALQERRVEAVLYD  65
  1        EINGLDDLRKVKVGCIPSTGTADFLNRFKIKFVDFSTVEDGLVAVQKDEIAAFVYD  94
  1       STITQVEQFPGKKIAASAGSPAIGFIEEHQGQKVLVNNLSQAMERLKDKSVDGVVFD  43
       -----i----dl-gkkvg-v-gstg--f-----ir-----tl-dai--l----vdavvfD  consensus

                 70        80        90       100       110       120
                  .         .         .         .         .         .
 60    VPALRYYLYQNPT.APLKIADLAVSFEDYGFILPLDNKLIRELDIEIVKLKQSGRLEEII  41
 61    VPALQYYLRNDRE.QRLKLSPVNFADEPYGFIVSLDNSFIKNLDIKLLEMRENGKIREIE  25
 61    RPALIYYTRQNPN.LNLEVTEIRVSLEPYGFVLKENSPLQKTINVEMLNLLYSRVIAEFT  56
 60    RPAMRHHIKQNPH.LAVQLAPFTLAEETYGFVFKTGNPLRNPMNVSILRLQRLGEIKSIA  37
 60    RPAIRFHLKNNPE.LAVQLAPFTLAEQTYGFAFRTGDPLRTPLNISILKLQRSGAVEAIS  23
 60    TPILSYYMKNSPD.KSLTLAPFRLSLQTYGFVVPSDSPLERLINIELLRLERSHQVKAIS  62
 57    EPILRYLITTGEI.HGIKVVNRSFRHEYYALALPPRSTERETLNRNLLEIINSKDWKEIR  46
 57    EPILRYMITSGEI.HGVRVVERSFKPEYYAFALPPGSPETETLNRNLLGIINSLAWKEIK  40
 57    EPIMRYVLTLGDI.HGVTIINQVLSPEYYAIALPQGSQLRETFNRNLLDITVSERWKKIN  33
 57    EPIMRYMIASGKF.QGIKVIETSFRYEYYAVALPPDSPRTEDINRSLLHYLESENWRSVQ  65
 57    HATLSYYVNEGSFDEVIEVIPSSYYREYFSFATS.NYAMLKPVNESLIKIIESDNWVVKL  94
 58    RPQLLFYKNKHKA.ENIHIPSAEYYKQGYGFAFRADSKLVNDVNLVLLRLAEDQKIEQIM  43
       -p-lry-i--------i-v-------e-ygfal---s-l---lni-ll-l--s--ik-i-  consensus

                 130
                  .
119    EREIKGDFENQ     41
120    SKWLSSSKDN      25
120    ERWLGPGIEENQ    56
119    NKLLN           37
119    KRLLN           23
119    DRILK           62
116    FKYLHNE         46
116    YKYLREE         40
116    NKYLNTKQ        33
116    FRYLDVVP        65
116    KKYHVENYK       94
117    AEYLGDK         43
       -kyl--------    consensus
```

X non conserved
X similar
X conserved
X all match

# group 1 channel region alignment

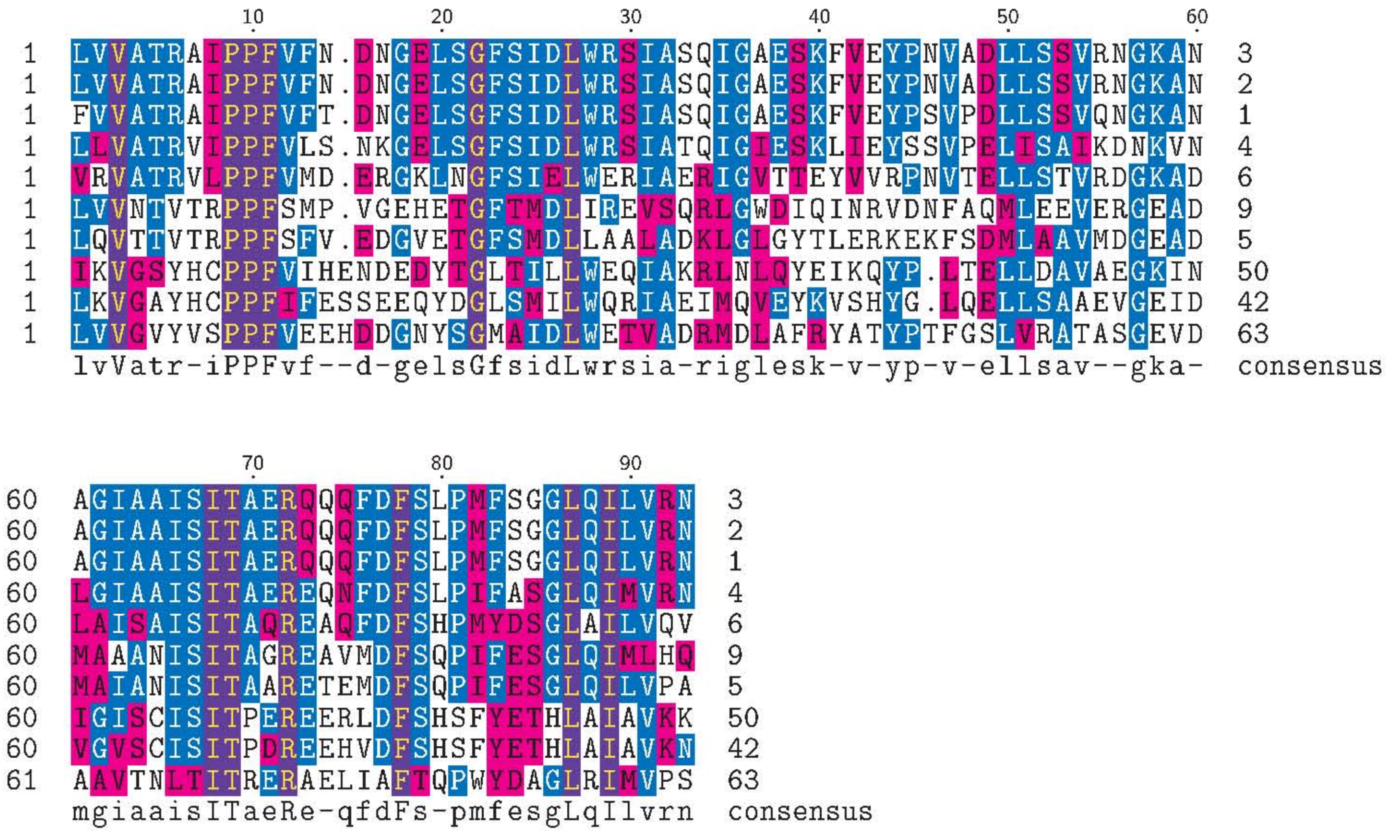


```
                    10        20        30        40        50        60
                     .         .         .         .         .         .
 1   DSPTIFSRVKVFFGWAVISSILVLISVLLVVGSLIWLAERRENSEQFPKRWLPGIASGM  37
 1   KPSTLLNRLQVFLGWAVLSSVLVLITVLLVVGSLIWLAERRSNSEQFPAQPLPGIASGM  23
 1   QPPGLWARIKPLFGVAALSSITFLLFTLFCVGNLIWLAERKRNPEHFPPQYIKGLGNGI  62
 1   KPVSLWERFSPFFGIAALSSAGVLTLLLFLVGNLIWLAEHRKNPEQFSPHYPEGVQNGM  56
 1   EKVSVWSRIRPIFRVAVISSVGGLFLILFVVGNLMWLAESRRNPEQFPRQYIRGVGSGM  41
 1   ESPTVWSIIRPFFGLAFISSVCLLTVLLFIMGNLLWLAERRRNKEQFPPNYFHGVGNAM  25
 1   ENASIWGKIKPFFSMQLLIAVAIFLSLLAIVGLLFWLAERKHSPEQFPADPKRGIANGM  43
 1   KDDGWEYALRRLFSPAFLKVLGGLSLLLLLSGFLVWVFERRNNPDNFGGGPVEGIWSGF  46
 1   KEDGWKYALGRLFSPAFLRILGGLSLLLLLSGFLVWLFERRQNPGDFGGGPAEGIWSGF  40
 1   KETRWFHMIGRLFSPAFLQVLAALSLLLLISGFLVWLFERKKNSDHFGGTPAQGIWSGF  33
 1   EGVDWKNILKVFFSYGFFRIVVLLSLVLLLSGFLVWLFERRKNPEHFGGSPTHGIGSGF  65
 1  EKSKDLISFFLNFFTLNFFKAIFSLFLVILIFGLAVWLFEKKRNSAQFREG.LNGIGDGI  94
    -----lw--ik-ff--a-l--v--l-llllivG-lvWlaErrrnpeqF------Gigsgm  consensus


                    70        80        90       100       110
                     .         .         .         .         .
60  WFAVVTLTTVGYGDKAPISRTGRGITATWMVISLIAVSSLTASLASAFTLFFSGA  37
60  WFALVTLTTVGYGDKAPITRIGRGLTAIWMVTSLIAVSSLTASLASAFTLFLSGD  23
60  WFALVTLTTVGYGDRAPLTKAGRSIAGVWMVISLASVSTITAGLASAFTVSLSQT  62
60  WFALVTLTTVGYGDRSPRTKLGQLVAGVWMLVALLSFSSITAGLASAFSTALSEA  56
60  WFALVTLTTVGYGDKAPITKTGKIITSLWMLTTLVAASSLTAGIATVMTLLLSAE  41
60  WFALVTLTTVGYGDMTPVTKSGRIITGVWMVLTTVTISSLTAGIATALTVSLTN    25
60  WLAIVTMSTTGYGDMAPVSLKGRVVAGCWMIISLIFATSMIAGIASTLTVSSFSS  43
60  WWAAVTMTTVGYGDKAPKTPPGRIVALIWMFTSLVVISGFTAAMTTSLTVGSLGT  46
60  WWAAVTMTTVGYGDKAPKTRPGRMVALVWMFTSLIVISGFTAAITTSLTVGSLGS  40
60  WWAAVTMTTVGYGDKTPITLLGKLVALVWMFTSLMVISGFTAAMTTVLTVESLES  33
60  WWAAVTMTTVGYGDKSPKTPAGRVVALVWMFASLVMISGFTAAITTTLTVGSLGV  65
60  WWSAVTMSTVGYGDKSPITAWGRLLSVVWIFTGVIIISGLTAGISSSLTVHQLKT  94
    WfalVTmtTvGYGDkaPitk-Grlva-vWmv-sli-issltAgias-ltv-----  consensus
```

X non conserved
X similar
X conserved
X all match

# group 2 S1 region alignment



```
             10        20        30        40        50        60
  1  LVVATRAIPPFVFN.DNGELSGFSIDLWRSIASQIGAESKFVEYPNVADLLSSVRNGKAN  3
  1  LVVATRAIPPFVFN.DNGELSGFSIDLWRSIASQIGAESKFVEYPNVADLLSSVRNGKAN  2
  1  FVVATRAIPPFVFT.DNGELSGFSIDLWRSIASQIGAESKFVEYPSVPDLLSSVQNGKAN  1
  1  LLVATRVIPPFVLS.NKGELSGFSIDLWRSIATQIGIESKLIEYSSVPELISAIKDNKVN  4
  1  VRVATRVLPPFVMD.ERGKLNGFSIELWERIAERIGVTTEYVVRPNVTELLSTVRDGKAD  6
  1  LVVNTVTRPPFSMP.VGEHETGFTMDLIREVSQRLGWDIQINRVDNFAQMLEEVERGEAD  9
  1  LQVTTVTRPPFSFV.EDGVETGFSMDLLAALADKLGLGYTLERKEKFSDMLAAVMDGEAD  5
  1  IKVGSYHCPPFVIHENDEDYTGLTILLWEQIAKRLNLQYEIKQYP.LTELLDAVAEGKIN  50
  1  LKVGAYHCPPFIFESSEEQYDGLSMILWQRIAEIMQVEYKVSHYG.LQELLSAAEVGEID  42
  1  LVVGVYYSPPFVEEHDDGNYSGMAIDLWETVADRMDLAFRYATYPTFGSLVRATASGEVD  63
     lvVatr-iPPFvf--d-gelsGfsidLwrsia-riglesk-v-yp-v-ellsav--gka-  consensus

             70        80        90
 60  AGIAAISITAERQQQFDFSLPMFSGGLQILVRN  3
 60  AGIAAISITAERQQQFDFSLPMFSGGLQILVRN  2
 60  AGIAAISITAERQQQFDFSLPMFSGGLQILVRN  1
 60  LGIAAISITAEREQNFDFSLPIFASGLQIMVRN  4
 60  LAISAISITAQREAQFDFSHPMYDSGLAILVQV  6
 60  MAAANISITAGREAVMDFSQPIFESGLQIMLHQ  9
 60  MAIANISITAARETEMDFSQPIFESGLQILVPA  5
 60  IGISCISITPEREERLDFSHSFYETHLAIAVKK  50
 60  VGVSCISITPDREEHVDFSHSFYETHLAIAVKN  42
 61  AAVTNLTITRERAELIAFTQPWYDAGLRIMVPS  63
     mgiaaisITaeRe-qfdFs-pmfesgLqIlvrn  consensus
```

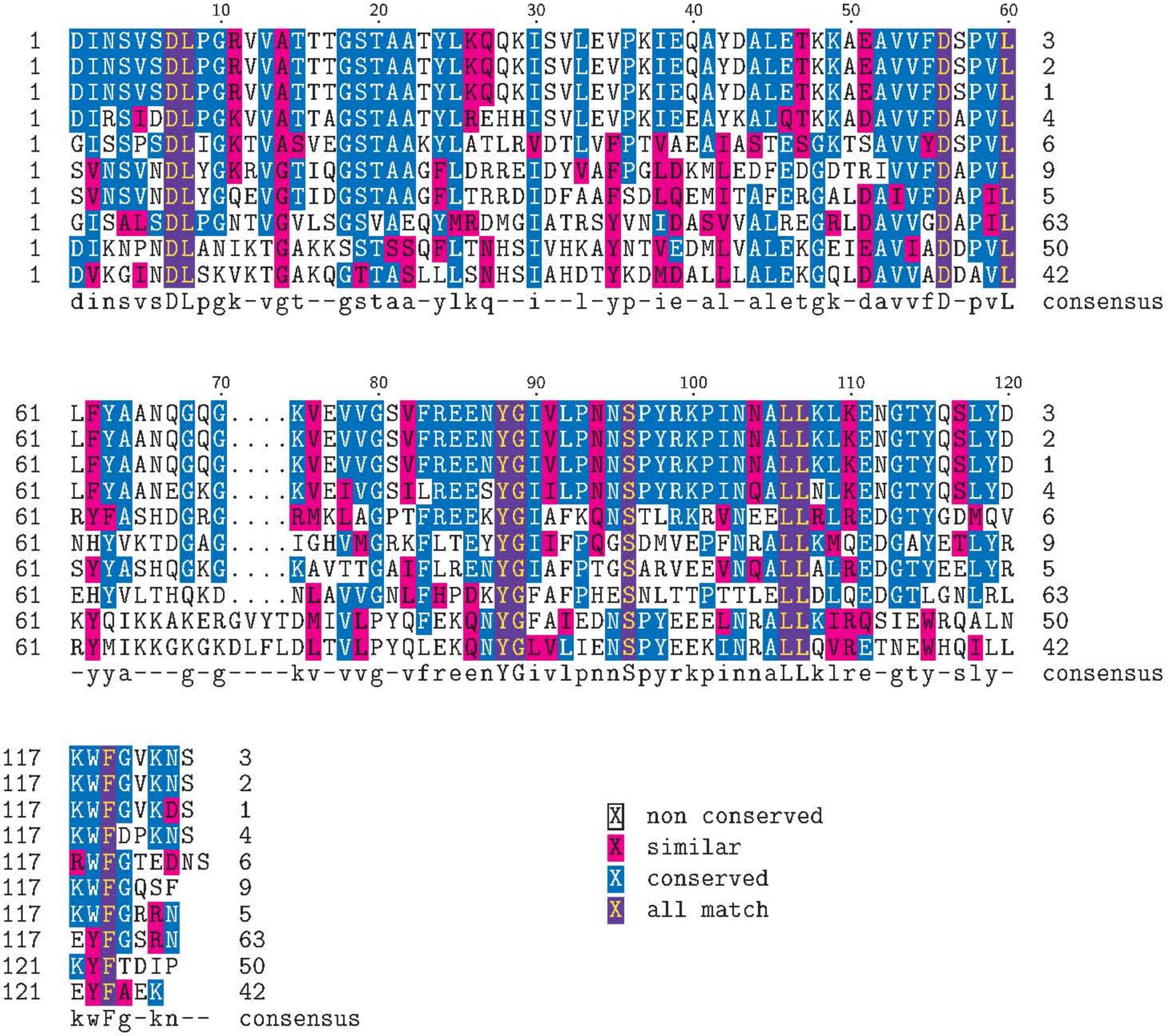
X non conserved

X similar

X conserved

X all match

# group 2 S2 alignment



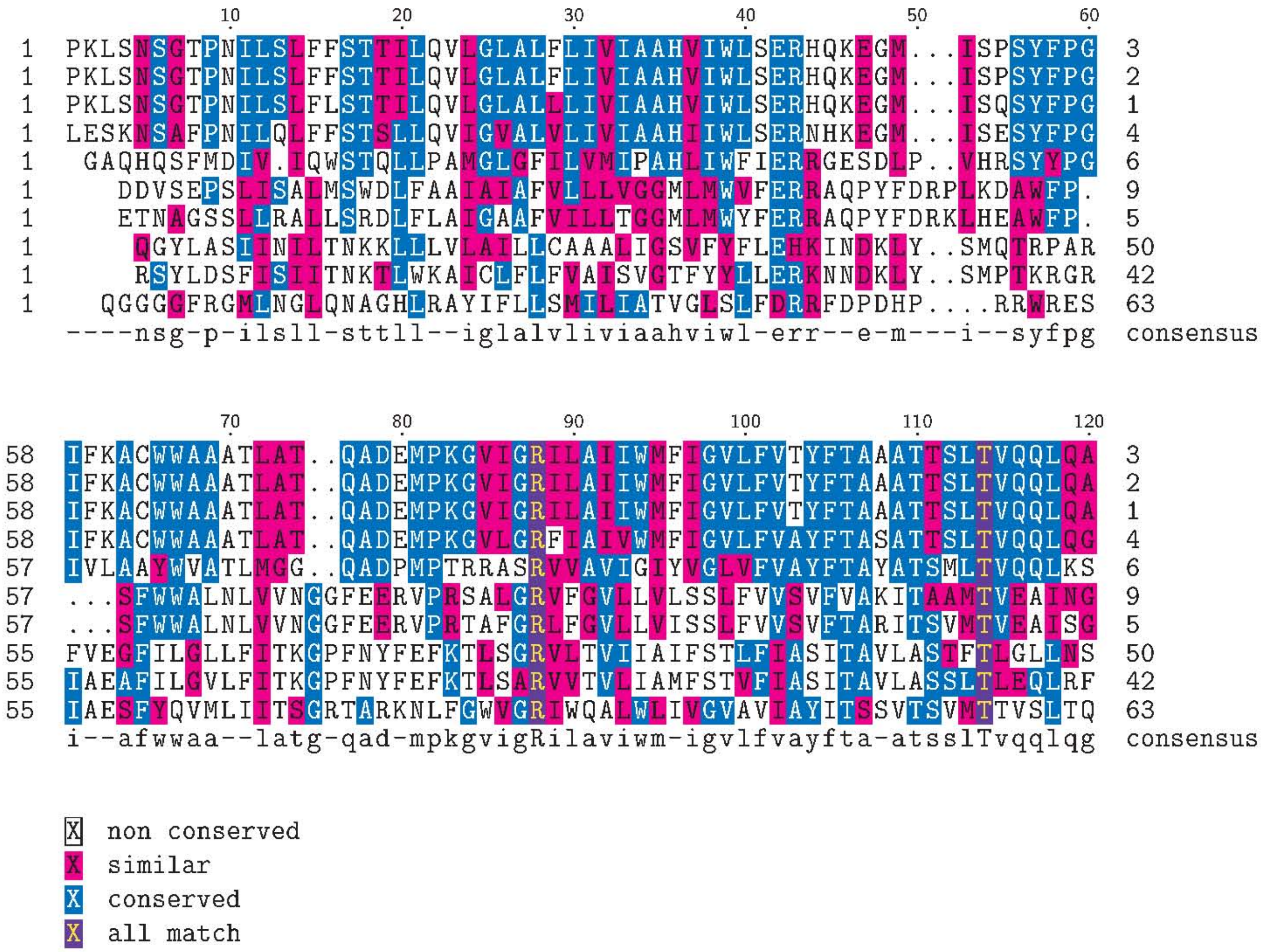
```
                  10        20        30        40        50        60
                   .         .         .         .         .         .
  1  DINSVSDLPGRVVATTTGSTAATYLKQQKISVLEVPKIEQAYDALETKKAEAVVFDSPVL  3
  1  DINSVSDLPGRVVATTTGSTAATYLKQQKISVLEVPKIEQAYDALETKKAEAVVFDSPVL  2
  1  DINSVSDLPGRVVATTTGSTAATYLKQQKISVLEVPKIEQAYDALETKKAEAVVFDSPVL  1
  1  DIRSIDDLPGKVVATTAGSTAATYLREHHISVLEVPKIEEAYKALQTKKADAVVFDAPVL  4
  1  GISSPSDLIGKTVASVEGSTAAKYLATLRVDTLVFPTVAEAIASTESGKTSAVVYDSPVL  6
  1  SVNSVNDLYGKRVGTIQGSTAAGFLDRREIDYVAFPGLDKMLEDFEDGDTRIVVFDAPVL  9
  1  SVNSVNDLYGQEVGTIDGSTAAGFLTRRDIDFAAFSDLQEMITAFERGALDAIVFDAPIL  5
  1  GISALSDLPGNTVGVLSGSVAEQYMRDMGIATRSYVNIDASVVALREGRLDAVVGDAPIL  63
  1  DIKNPNDLANIKTGAKKSSTSSQFLTNHSIVHKAYNTVEDMLVALEKGEIEAVIADDPVL  50
  1  DVKGINDLSKVKTGAKQGTTASLLLSNHSIAHDTYKDMDALLLALEKGQLDAVVADDAVL  42
     dinsvsDLpgk-vgt--gstaa-ylkq--i--l-yp-ie-al-aletgk-davvfD-pvL  consensus

                  70        80        90       100       110       120
                   .         .         .         .         .         .
 61  LFYAANQGQG....KVEVVGSVFREENYGIVLPNNSPYRKPINNALLKLKENGTYQSLYD  3
 61  LFYAANQGQG....KVEVVGSVFREENYGIVLPNNSPYRKPINNALLKLKENGTYQSLYD  2
 61  LFYAANQGQG....KVEVVGSVFREENYGIVLPNNSPYRKPINNALLKLKENGTYQSLYD  1
 61  LFYAANEGKG....KVEIVGSILREESYGIILPNNSPYRKPINQALLNLKENGTYQSLYD  4
 61  RYFASHDGRG....RMKLAGPTFREEKYGIAFKQNSTLRKRVNEELLRLREDGTYGDMQV  6
 61  NHYVKTDGAG....IGHVMGRKFLTEYYGIIFPQGSDMVEPFNRALLKMQEDGAYETLYR  9
 61  SYYASHQGKG....KAVTTGAIFLRENYGIAFPTGSARVEEVNQALLALREDGTYEELYR  5
 61  EHYVLTHQKD....NLAVVGNLFHPDKYGFAFPHESNLTTPTTLELLDLQEDGTLGNLRL  63
 61  KYQIKKAKERGVYTDMIVLPYQFEKQNYGFAIEDNSPYEEELNRALLKIRQSIEWRQALN  50
 61  RYMIKKGKGKDLFLDLTVLPYQLEKQNYGLVLIENSPYEEKINRALLQVRETNEWHQILL  42
     -yya---g-g----kv-vvg-vfreenYGivlpnnSpyrkpinnaLLklre-gty-sly-  consensus

117  KWFGVKNS   3
117  KWFGVKNS   2
117  KWFGVKDS   1
117  KWFDPKNS   4
117  RWFGTEDNS  6
117  KWFGQSF    9
117  KWFGRRN    5
117  EYFGSRN    63
121  KYFTDIP    50
121  EYFAEK     42
     kwFg-kn--  consensus
```

X non conserved
X similar
X conserved
X all match

# group 2 channel region alignment



```
                    10        20        30        40        50        60
                     .         .         .         .         .         .
 1   PKLSNSGTPNILSLFFSTTILQVLGLALFLIVIAAHVIWLSERHQKEGM...ISPSYFPG  3
 1   PKLSNSGTPNILSLFFSTTILQVLGLALFLIVIAAHVIWLSERHQKEGM...ISPSYFPG  2
 1   PKLSNSGTPNILSLFLSTTILQVLGLALLLIVIAAHVIWLSERHQKEGM...ISQSYFPG  1
 1   LESKNSAFPNILQLFFSTSLLQVIGVALVLIVIAAHIIWLSERNHKEGM...ISESYFPG  4
 1    GAQHQSFMDIV.IQWSTQLLPAMGLGFILVMIPAHLIWFIERRGESDLP..VHRSYYPG  6
 1      DDVSEPSLISALMSWDLFAAIAIAFVLLLVGGMLMWVFERRAQPYFDRPLKDAWFP.  9
 1      ETNAGSSLLRALLSRDLFLAIGAAFVILLTGGMLMWYFERRAQPYFDRKLHEAWFP.  5
 1       QGYLASIINILTNKKLLLVLAILLCAAALIGSVFYFLEHKINDKLY..SMQTRPAR  50
 1       RSYLDSFISIITNKTLWKAICLFLFVAISVGTFYYLLERKNNDKLY..SMPTKRGR  42
 1     QGGGGFRGMLNGLQNAGHLRAYIFLLSMILIATVGLSLFDRRFDPDHP....RRWRES  63
     ----nsg-p-ilsll-sttll--iglalvliviaahviwl-err--e-m---i--syfpg  consensus

                    70        80        90        100       110       120
                     .         .         .         .         .         .
58   IFKACWWAAATLAT..QADEMPKGVIGRILAIIWMFIGVLFVTYFTAAATTSLTVQQLQA  3
58   IFKACWWAAATLAT..QADEMPKGVIGRILAIIWMFIGVLFVTYFTAAATTSLTVQQLQA  2
58   IFKACWWAAATLAT..QADEMPKGVIGRILAIIWMFIGVLFVTYFTAAATTSLTVQQLQA  1
58   IFKACWWAAATLAT..QADEMPKGVLGRFIAIVWMFIGVLFVAYFTASATTSLTVQQLQG  4
57   IVLAAYWVATLMGG..QADPMPTRRASRVVAVIGIYVGLVFVAYFTAYATSMLTVQQLKS  6
57   ...SFWWALNLVVNGGFEERVPRSALGRVFGVLLVLSSLFVVSVFVAKITAAMTVEAING  9
57   ...SFWWALNLVVNGGFEERVPRTAFGRLFGVLLVISSLFVVSVFTARITSVMTVEAISG  5
55   FVEGFILGLLFITKGPFNYFEFKTLSGRVLTVIIAIFSTLFIASITAVLASTFTLGLLNS  50
55   IAEAFILGVLFITKGPFNYFEFKTLSARVVTVLIAMFSTVFIASITAVLASSLTLEQLRF  42
55   IAESFYQVMLIITSGRTARKNLFGWVGRIWQALWLIVGVAVIAYITSSVTSVMTTVSLTQ  63
     i--afwwaa--latg-qad-mpkgvigRilaviwm-igvlfvayfta-atsslTvqqlqg  consensus
```

X non conserved
X similar
X conserved
X all match