```
                                                                                                                                                                  Cap
                                                                                                                                                          <- Insert 1
                                                                                                                                                                 β-A
                 W7,B4                W1,B1                W1,B2                                W1,B3                W1,B4
                   •                    •                    •                    •                    •                    •                    •                    •
  1  LNLDPV--QLTFYAGPN-GSQFGFSLDFHKDSH--GRVAIVVGAPRTLGPS---QEETGGVFLCPWRA-EGGQCPSLLFDLRDETRNVG  AB_HUMAN
  1  FNLDVD--SPAEYSGPE-GSYFGFAVDFFVPSA-SSRMFLLVGAPKANTTQP-GIVEGGQVLKCDWSS--TRRCQPIEFDATGNRDYAK  AV_HUMAN
  1  FNLDAE--APAVLSGPP-GSFFGFSVEFYRPG--TDGVSVLVGAPKANTSQP-GVLQGGAVYLCPWGA-SPTQCTPIEFDSKGSRLLES  A5_HUMAN
  1  FNLDTREDNVIRKYGDP-GSLFGFSLAMHWQLQPEDKRLLLVGAPRGEALPLQRANRTGGLYSCDITA--RGPCTRIEFDNDADPT---  A6_HUMAN
  1  YNVDTE--SALLYQGPH-NTLFGYSVVLHSHG---ANRWLLVGAPTANWLANASVINPGAIYRCRIGKNPGQTCEQLQLGSPNGEPCGK  A4_HUMAN
  1  YNVGLP--EAKIFSGPS-SEQFGYAVQQFINP---KGNWLLVGSPWSGFPE----NRMGDVYKCPVDL-STATCEKLNLQTSTSIPN--  A2_HUMAN
  1  YNLDVR--GARSFSPPRAGRHFGYRVLQVG-------NGVIVGAPGEG-------NSTGSLYQCQSG---TGHCLPVTLRGSN------  AL_HUMAN
     FNLD---------SGP--GS-FGFSV-F-----------LLVGAP-AN---------TG-VY-C-WG---TG-C-PLEFD---------  50%Con

     Cap                                                                                                                                                  Cap
  Insert 1 ------>                                                                  <------ Insert 2 ------>                                      <------ Insert 3
            β-B                  W2,B1                W2,B2                β-C                  β-D                  W2,B3                W2,B4                β-A
                                   •                    •                    •                    •                    •                    •                    •
 81  ------SQTLQTFKARQGLGASVVSWS---DVIVACAPWQHWNVLEKTEEAEKTPVGSCFLAQPE----SGRRAEYSPCRGNTLSRIYV  AB_HUMAN
 83  -------DDPLEFKSHQWFGASVRSKQ---DKILACAPLYHWRTEM---KQEREPVGTCFLQDG------TKTVEYAPCRSQDID----  AV_HUMAN
 83  SLSSSEGEEPVEYKSLQWFGATVRAHG---SSILACAPLYSWRTE---KEPLSDPVGTCYLSTDN----FTRILEYAPCRSDFSW----  A5_HUMAN
 84  ----------SESKEDQWMGVTVQSQGP-GGKVVTCAHRYEKRQHVNTKQESRDIFGRCYVLSQNLREDDMDGGDWSFCDGRLRG----  A6_HUMAN
 84  --------TCLEERDNQWLGVTLSRQPGENGSIVTCGHRWKNIFYI--KNENKLPTGGCYGVPPDL--RTELSKRIAPCYQDYVKK---  A4_HUMAN
 77  ---------VTEMKTNMSLGLILTRNMG-TGGFLTCGPLWAQQCG-----NQYYTTGVCSDISPD-----FQLSASFSPATQPCPS--//  A2_HUMAN
 65  --------------YTSKYLGMTLATDPT-DGSILACDPGLSRTCD-----QNTYLSGLCYLFRQN----LQGPMLQGRPGFQECIKG-//  AL_HUMAN
     --------------K--QWLGATV-S-----G-ILACAP-Y-WR-----------PVG-CYL--------------EYAPCR-Q------  50%Con
                                                                                                                                                                  I domain

     Cap
  Insert 3 ------>                                                                  <------ Cap
                                                                                    Insert 4 ------>
                                W3,B1                W3,B2                W3,B3                β-B                  W3,B4                                W4,B1
                   •                    •                    •                    •                    •                    •                    •                    •
157  ENDFSWDKRYCEAGFSSVVTQ-AGELVLGAPGGYYFLGLLAQAPVADIFSSYR-PGILLWHVSSQSLSFDSSN-PEYFDGYWGYSVAVG  AB_HUMAN
149  ----ADGQGFCQGGFSIDFTK-ADRVLLGGPGSFYWQGQLISDQVAEIVSKYD-PNVYSIKYNNQLATRTAQ--AIFDDSYLGYSVAVG  AV_HUMAN
158  ----AAGQGYCQGGFSAEFTK-TGRVVLGGPGSYFWQGQILSATQEQIAESYY-PEYLINLVQGQLQTRQAS--SIYDDSYLGYSVAVG  A5_HUMAN
159  ----HEKFGSCQQGVAATFTKDFHYIVFGAPGTYNWKGIVRVEQKNNTFFDMNIFEDGPYEVGGETEHDESLV-PVPANSYLGFSLDSG  A6_HUMAN
158  ---FGENFASCQAGISSFYTK--DLIVMGAPGSSYWTGSLFVYNITTN--------------KYKAFLDKQN--QVKFGSYLGYSVGAG  A4_HUMAN
316  -GGDNFQMEMSQVGFSADYSSQNDILMLGAVGAFGWSGTIVQKTSHGHLIF-----------PKQAFDQILQ--DRNHSSYLGYSVAAI  A2_HUMAN
290  QDLTSFNMELSSSGISADLSR--GHAVVGAVGAKDWAGGFLDLKADL---------------QDDTFIGNEPLTPEVRAGYLGYTVTWL  AL_HUMAN
     --------G-CQ-GFSADFTK--D--VLGAPGSYYW-G-L-------------------------Q-F-------P---DSYLGYSVAVG  50%Con

                 W4,B2                W4,B3                W4,B4                W5,B1                W5,B2
     Calcium #1                                                                                   Calcium #2
                   •                    •                    •                    •                    •                    •
243  EFDGDLNTTEYVVGAPTWSWTLGAVEILDS-----YYQRLHRLRAEQMASYFGHSVAVTDVNGDGRHD-LLVGAPLYMESRADRKLAEV  AB_HUMAN
230  DFNGD-GIDDFVSGVPRAARTLGMVYIYDGK----NMSSLYNFTGEQMAAYFGFSVAATDINGDDYAD-VFIGAPLFMDRGSDGKLQEV  AV_HUMAN
239  EFSGD-DTEDFVAGVPKGNLTYGYVTILNGS----DIRSLYNFSGEQMASYFGYAVAATDVNGDGLDD-LLVGAPLLMDRTPDGRPQEV  A5_HUMAN
243  KGIVSKDEITFVSGAPRAN-HSGAVVLLKRDMKSAHLLPEHIFDGEGLASSFGYDVAVVDLNKDGWQD-IVIGAPQYFDR----DGEVG  A6_HUMAN
226  HFRSQ-HTTEVVGGAPQHE-QIGKAYIFSIDE--KELNILHEMKGKKLGSYFGASVCAVDLNADGFSD-LLVGAPMQST------IREE  A4_HUMAN
416  STGE---STHFVAGAPRAN-YTGQIVLYSVNEN-GNITVIQAHRGDQIGSYFGSVLCSVDVDKDTITDVLLVGAPMYMSD----LKKEE  A2_HUMAN
387  PSRQK--TSLLASGAPRYQ-HMGRVLLFQEPQGGGHWSQVQTIHGTQIGSYFGGELCGVDVDQDGETELLLIGAPLFYG------EQRG  AL_HUMAN
     -F-GD--TT-FVSGAPR-N-T-G-V-IL-----------LH-F-GEQMASYFG-SVAAVDVNGDG--D-LLVGAPLYMD-------QEV  50%Con
```

```
     W5,B3                W5,B4                W6,B1                W6,B2                W6,B3        W6,B4
                                                     Calcium #3
326  GRVYLFLQPRGPHALGAPSLLLTGTQL--YGRFGSAIAPLGDLDRDGYNDIAVAAPYGGPSGRGQVLVFLGQSEGLRSRPSQVLDSPFP  AB_HUMAN
313  GQVSVSLYRAS-GDFQT--TKLNGFEV--FARFGSAIAPLGDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQILEGQWA  AV_HUMAN
322  GRVYVYLQHPA-GIEPTPTLTLTGHDE--FGRFGSSLTPLGDLDQDGYNDVAIGAPFGGETQQGVVFVFPGGPGGLGSKPSQVLQPLWA  A5_HUMAN
326  GAVYVYMNQQG-RWNNVKPIRLNGTKD---SMFGIAVKNIGDINQDGYPDIAVGAPYD---DLGKVFIYHGSANGINTKPTQVLKGIS-  A6_HUMAN
304  GRVFVYINSGSGAVMNAMETNLVGSDKY-AARFGESIVNLGDIDNDGFEDVAIGAPQED-DLQGAIYIYNGRADGISSTFSQRIEGLQI  A4_HUMAN
496  GRVYLFTIKKG--ILGQH-QFLEGPEGIENTRFGSAIAALSDINMDGFNDVIVGSPLEN-QNSGAVYIYNGHQGTIRTKYSQKILGSDG  A2_HUMAN
467  GRVFIYQRRQL--GFEEV-SELQGDPGYPLGRFGEAITALTDINGDGLVDVAVGAPLE---EQGAVYIFNGRHGGLSPQPSQRIEGTQV  AL_HUMAN
     GRVYVYL---G----------L-G------GRFGSAIAPLGDIDQDGYNDVAVGAPYE----QGAVYIFNGR-GGL-S-PSQVLEG---  50%Con


                W7,B1                W7,B2        W7,B3
                          Calcium #4
413  T----GSAFGFSLRGAVDIDDNGYPDLIVGAYGANQVAVYRAQP  AB_HUMAN
397  ARSM-PPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRARP  AV_HUMAN
408  ASHT-PDFFGSALRGGRDLDGNGYPDLIVGSFGVDKAVVYRGRP  A5_HUMAN
407  ------PYFGYSIAGNMDLDRNSYPDVAVGSL-SDSVTIFRSRP  A6_HUMAN
391  SK-S-LSMFGQSISGQIDADNNGYVDVAVGAFRSDSAVLLRTRP  A4_HUMAN
581  AFRSHLQYFGRSLDGYGDLNGDSITDVSIGAFG--QVVQLWSQS  A2_HUMAN
550  LS-G-IQWFGRSIHGVKDLEGDGLADVAVGAES--QMIVLSSRP  AL_HUMAN
     --------FG-SL-G--DLDGNGYPDVIVGAFG--QVVVYRSRP  50%Con
```

```
                                                                                PSI                                                                                Hybrid
                                                                                                                                                                   to C435
                                                                                α1    •     α2    •    β1     •          β2    •    α3     •    β3     •    βX     •
  1 ----------------------GPNICTTRGVSSCQQCLAVSPMCAWCSDEALPL----GSPRCDLKENLLKDNCAPESIEFPVSEARVLEDRPLSDKGSG  B3_HUMAN
  1 --------------------QTDENRCLKANAKSCGECIQAGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPRGSKDIKKNKNVTNRSKG  B1_HUMAN
  1 ------------------------QECTKFKVSSCRECIESGPGCTWCQKLNFTGPGDPDSIRCDTRPQLLMRGCAADDIMDPTSLAETQEDHNGGQK---  B2_HUMAN
  1 ELDAKIPSTGDATEWRNPHLSMLGSCQ--PAPSCQKCILSHPSCAWCKQLNFTASGEAEARRCARREELLARGCPLEELEEPRGQQEVLQDQPLSQGARG  B7_HUMAN
    ------------------------N-C-K--VSSCQECI-SGP-CAWC--LNFT--G-P-S-RCD-RE-LLKRGCAPEDIE-PRS-AEVLED-PLSQK--G  50%Con

                    Hybrid                                                                                I-like domain
                                                                                                                                                                   3/10 helix
                 •  βA    βA'•          •  βB          •     β1     •                •     α1     •          •  β2     •          •
 76 D-----SSQVTQVSPQRIALRLRPDDSKNFSIQVRQVEDYPVDIYYLMDLSYSMKDDLWSIQNLGTKLATQMRKLTSNLRIGFGAFVDKPVSPYMYISPP  B3_HUMAN
 82 TAEKLKPEDIHQIQPQQLVLRLRSGEPQTFTLKFKRAEDYPIDLYYLMDLSYSMKDDLENVKSLGTDLMNEMRRITSDFRIGFGSFVEKTVMPYISTTP-  B1_HUMAN
 75 -----------QLSPQKVTLYLRPGQAAAFNVTFRRAKGYPIDLYYLMDLSYSMLDDLRNVKKLGGDLLRALNEITESGRIGFGSFVDKTVLPFVNTHP-  B2_HUMAN
 99 -------EGATQLAPQRVRVTLRPGEPQQLQVRFLRAEGYPVDLYYLMDLSYSMKDDLERVRQLGHALLVRLQEVTHSVRIGFGSFVDKTVLPFVSTVP-  B7_HUMAN
    -----------QLSPQRV-LRLRPGEPQ-F-V-FRRAEDYPVDLYYLMDLSYSMKDDLENVK-LGTDLL--MRELTS--RIGFGSFVDKTVLPFVST-P-  50%Con
                                                                                *

                                                                                I-like domain
                                                                                                                                                                   3/10 helix
    3/10 helix    •          •β3        •   α2      •          •      α3    •   α4     •     β4     •          •
171 EALENPCYDMKTTCLPMFGYKHVLTLTDQVTRFNEEVKKQSVSRNRDAPEGGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVQPND  B3_HUMAN
181 AKLRNPCTSE-QNCTTPFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVAVCGSLIGWRN-VTRLLVFSTDAGFHFAGDGKLGGIVLPND  B1_HUMAN
163 DKLRNPCPNKEKECQPPFAFRHVLKLTNNSNQFQTEVGKQLISGNLDAPEGGLDAMMQVAACPEEIGWRN-VTRLLVFATDDGFHFAGDGKLGAILTPND  B2_HUMAN
191 SKLRHPCPTRLERCQSPFSFHHVLSLTGDAQAFEREVGRQSVSGNLDSPEGGFDAILQAALCQEQIGWRN-VSRLLVFTSDDTFHTAGDGKLGGIFMPSD  B7_HUMAN
    -KLRNPCP-----CQPPFSYKHVLSLTN----FNEEVGKQSISGNLDAPEGGFDAIMQAAVC-E-IGWRN-VSRLLVFTTDDGFHFAGDGKLGGIV-PND  50%Con
                                                                    * *

                                                                                I-like domain                                                                      Hybrid
                                                                                                                                                                   3/10 helix
                 β4•   3/10 helix    •      α5     •        β5    •      α6    •          •β6    3/10 helix•    α7     •     βC     •        βD    •
271 GQCHVGSDNHYSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVVNLYQNYSELIPGTTVGVLSMDSSNVLQLIVDAYGKIRSKVELEVRDLPEELSLSF  B3_HUMAN
279 GQCHLE-NNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKELKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSEGVTISY  B1_HUMAN
262 GRCHLE-DNLYKRSNEFDYPSVGQLAHKLAENNIQPIFAVTSRMVKTYEKLTEIIPKSAVGELSEDSSNVVHLIKNAYNKLSSRVFLDHNALPDTLKVTY  B2_HUMAN
290 GHCHLDSNGLYSRSTEFDYPSVGQVAQALSAANIQPIFAVTSAALPVYQELSKLIPKSAVGELSEDSSNVVQLIMDAYNSLSSTVTLEHSSLPPGVHISY  B7_HUMAN
    GQCHLESNNLYSRSTEFDYPSVGQLAQKLSENNIQPIFAVTE--VPVY-ELSELIPKSAVGELSEDSSNVVQLI-DAYNKLRS-V-LEH--LPEGL--SY  50%Con
                                                                                                    *

                                                                                Hybrid                                                                     PSI I-EGF1
                                                                                                                                                                   to C13
    βD        •  βD'      βD"     •          βE•          •     βF     •          βG    •                •
371 NATCLNNEVIPG----LKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCDCACQAQ  B3_HUMAN
378 KSYCKNGVNGTGEN--GRKCSNISIGDEVQFEISITSNKCPKKDSDSFKIRPLGFTEEVEVILQYICECECQSE  B1_HUMAN
361 DSFCSNGVTHRNQP--RGDCDGVQINVPITFQVKVTATECIQE--QSFVIRALGFTDIVTVQVLPQCECRCRDQ  B2_HUMAN
390 ESQCEGPEKREGKAEDRGQCNHVRINQTVTFWVSLQATHCLPE-PHLLRLRALGFSEELIVELHTLCDCNCSDT  B7_HUMAN
    -S-C-NGV---G----RG-C--V-IGDTVTF-VS-TA--CPQE---SF-IRPLGFTDELIVQV---CDC-CQDQ  50%Con
```