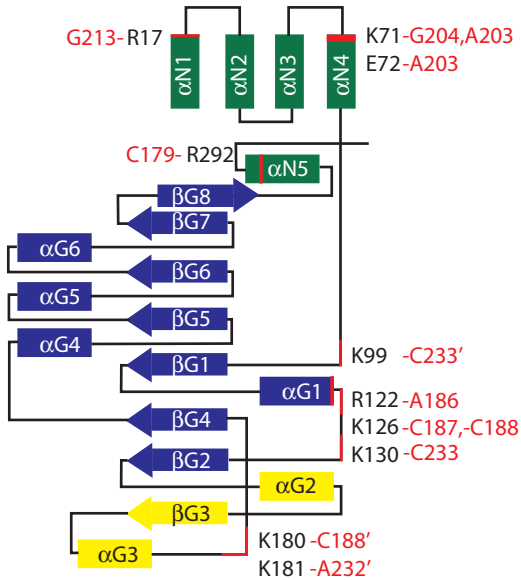
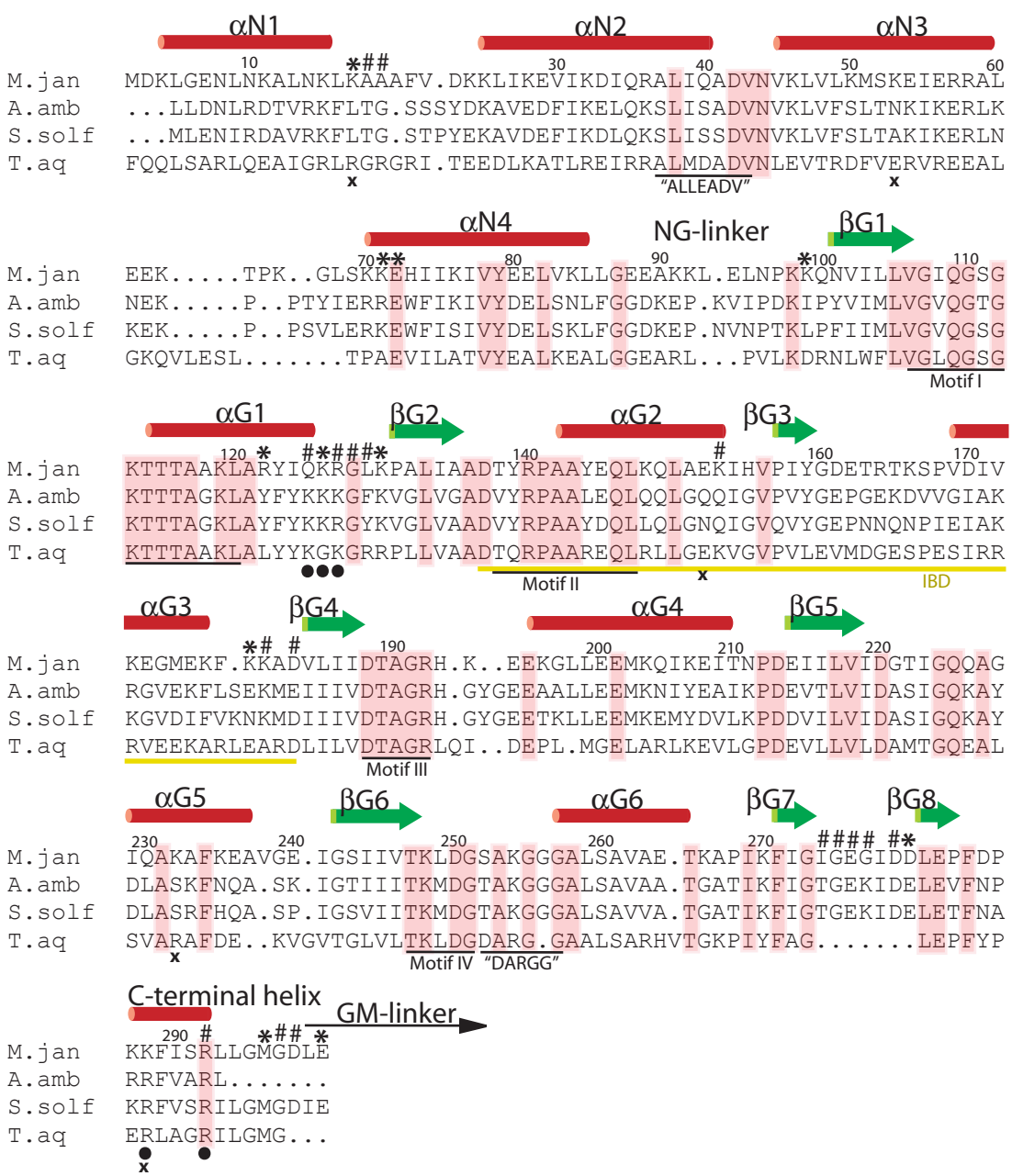
A


G213-R17
αN1
αN2
αN3
αN4
K71-G204,A203
E72-A203
C179-R292
αN5
βG8
βG7
αG6
βG6
αG5
βG5
αG4
βG1
K99 -C233'
αG1
R122-A186
K126-C187,-C188
K130-C233
βG4
βG2
αG2
βG3
αG3
K180-C188'
K181-A232'

B


αN1
αN2
αN3
M.jan MDKLGENLNKALNKLKAAAFV.DKKLIKEVIKDIQRALIQADVNVKLVLKMSKEIERRAL
A.amb ...LLDNLRDTVRKFLTG.SSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLK
S.solf ...MLENIRDAVRKFLTG.STPYEKAVDEFIKDLQKSLISSDVNVKLVFSLTAKIKERLN
T.aq FQQLSARLQEAIGRLRGRGRI.TEEDLKATLREIRRALMDADVNLEVTRDFVERVREEAL
"ALLEADV"
αN4
NG-linker
βG1
M.jan EEK.....TPK..GLSKKEHIIKIVYEELVKLLGEEAKKL.ELNPKKQNVILLVGIQGSG
A.amb NEK.....P..PTYIERREWFIKIVYDELSNLFGGDKEP.KVIPDKIPYVIMLVGVQGTG
S.solf KEK.....P..PSVLERKEWFISIVYDELSKLFGGDKEP.NVNPTKLPFIIMLVGVQGSG
T.aq GKQVLESL.....TPAEVILATVYEALKEALGGEARL...PVLKDRNLWFLVGLQGSG
Motif I
αG1
βG2
αG2
βG3
M.jan KTTTAAKLARYIQKRGLKPALIAADTYRPAAYEQLKQLAEKIHVPIYGDETRTKSPVDIV
A.amb KTTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQQLGQQIGVPVYGEPGEKDVVGIAK
S.solf KTTTAGKLAYFYKKRGYKVGLVAADVYRPAAYDQLLQLGNQIGVQVYGEPNNQNPIEIAK
T.aq KTTTAAKLALYYKGKGRRPLLVAADTQRPAAREQLRLLGEKVGVPVLEVMDGESPESIRR
Motif II
IBD
αG3
βG4
αG4
βG5
M.jan KEGMEKF.KKADVLIIDTAGRH.K..EEKGLLEEMKQIKEITNPDEIILVIDGTIGQQAG
A.amb RGVEKFLSEKMEIIIVDTAGRH.GYGEEAALLEEMKNIYEAIKPDEVTLVIDASIGQKAY
S.solf KGVDIFVKNKMDIIIVDTAGRH.GYGEETKLLEEMKEMYDVLKPDDVILVIDASIGQKAY
T.aq RVEEKARLEARDLILVDTAGRLQI..DEPL.MGELARLKEVLGPDEVLLVLDAMTGQEAL
Motif III
αG5
βG6
αG6
βG7
βG8
M.jan IQAKAFKEAVGE.IGSIIVTKLDGSAKGGGALSAVAE.TKAPIKFIGIGEGIDDLEPFDP
A.amb DLASKFNQA.SK.IGTIIITKMDGTAKGGGALSAVAA.TGATIKFIGTGEKIDELEVFNP
S.solf DLASRFHQA.SP.IGSVIITKMDGTAKGGGALSAVVA.TGATIKFIGTGEKIDELETFNA
T.aq SVARAFDE..KVGVTGLVLTKLDGDARG.GAALSARHVTGKPIYFAG.....LEPFYP
Motif IV "DARGG"
C-terminal helix
GM-linker
M.jan KKFISRLLGMGDLE
A.amb RRFVARL.....
S.solf KRFVSRILGMGDIE
T.aq ERLAGRILGMG...