

Sequence logo plot showing the conservation of amino acids across the 190 positions of the protein sequence. The x-axis represents positions 10 to 190. The y-axis lists 190 protein identifiers. Each position is represented by a stack of colored bars (A, T, C, G) indicating the frequency of each amino acid at that position. A vertical yellow bar highlights positions 250-260. A green box highlights positions 380-390.

	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790
800	
15231637.p	GKQSTLT	EARMKILVCTAACALAYLHB	E	KVVVRDIIKASNLIDDDFNAKISLDFGLAKLLEDSGES	HITTRVMGTFIVVAPEYANTCLLN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15228043.p	RQHGNLT	EARMKILVCTAACALAYLHB	E	KVVVRDIIKASNLIDDDFNAKISLDFGLAKLLEDSGES	HITTRVMGTFIVVAPEYANTCLLN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK065494.q	RQHGVES	EARMKVLVCTAACALAYLHB	E	KVVVRDIIKSSNLIDDEFNFKVSDFLAKLLEDSGES	HITTRVMGTFIVVAPEYANTCLLN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK103003.q	RQHGVLT	EARMKVLVCTAACALAYLHB	E	KVVVRDIIKSSNLIDDEFNFKVSDFLAKLLEDSGES	HITTRVMGTFIVVAPEYANTCLLN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK100061.q	SG-CILT	ENRMKILLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDEFNFKVSDFLAKLLEDSGES	YIINTTRVMGTYIVVAPEYANSCMLNN	EKSIDIYSFGVLLIESVTAIRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK073774.q	SGYSSLT	ENRMKILLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDEFNFKVSDFLAKLLEDSGES	YIINTTRVMGTYIVVAPEYANSCMLNN	EKSIDIYSFGVLLIESVTAIRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK100396.q	SIRGSLT	ENRMKILLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLEDSGES	HVTTRVMGTFIVVAPEYANTCLLN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
18405946.p	RQHGYL	EARMKVLIGTCAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLEDSGES	HVTTRVMGTFIVVAPEYANSCMLNN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15217511.p	KHGGLT	EARMKVLIGTCAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLEDSGES	HVTTRVMGTFIVVAPEYANSCMLNN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15238840.p	QNHSELT	EARVKILLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLEDSGES	FITTRVMGTFIVVAPEYANSCMLNN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
2233140.p	IHKGHLT	EARVKLVCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLEDSGSN	YVSTRVMGTFIVVAPEYANSCMLNN	EKSIDIYSFGVLLIEATGCRDPDVYDPRPANEVNLLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15223428.p	GDVSLET	DIRMNIIILCMAKCLAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGIILIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
30678150.p	GDVSLET	DIRMNIIILCMAKCLAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGIILIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15234142.p	GDKSLET	DIRMNIIILCMAKCLAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGIILIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
45370019.q	GEVSEL	EVRMNIILCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYASTGMLN	EKSIDIYSFGIILIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15235432.p	GFKSLET	EIRMRIVLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
AK069491.q	GFVSEL	DSRVKILCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
44990021.q	GFVSEL	DSRMNIVLCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYASTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
30690058.p	GFVSEL	DSRMKIACTGCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYASTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
62390013.q	GFVSEL	DSRMKIACTGCTAKALAYLHB	E	KVVVRDIIKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYASTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
48450017.q	DBISLET	DMRNIIIILCTAKALAYLHB	E	KIVVRDVKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15224589.p	GRNRLET	TRAMIIIILCTAKALAYLHB	E	KIVVRDVKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
28970005.q	ACECOM	PVRTRAIACMARECLAYLHB	E	KIVVRDVKSSNLIDDDFDKAVSDFLAKLLESES	YVTRTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15227189.p	DELAQALP	PLRTRAIACMARECLAYLHB	E	QSIIVHRDIIKASNLIDDEFNFKVSDFLAKFENGT	HMTTRVMGTFIVVAPEYACTGMLN	EKSIDIYSFGVLLIMEIIITGRNPDVYDPRPQECEVNLV	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
lir3_1RK	PRGPPEPF	QIOMAELADGMAYLN	E	AKVBRHDIIAANQCVADPFTVKEFIDGMDPTEKETDX	RKGCKLFLVPRMATESLKDQVFT	TSPDMSCFGVLLIEISLQKSVGFLVPRMATESLKDQVFT	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD	PEAKKRKMSQVYRMLLESDE											
15227459.p	LRSKKL	TRAPIDICLVARBLCYLN	E	REFVHCHNCNILLGEDLPKAKTIE	PLCA	ADPVEDBFCVTKVIALTICRVE	LACBQYQCLSNNECVLWVFDGGYCLDQPMCNCEVLD	LKMVYTRRRVEEDVSDRPEPPATAKRLALLVALRCVD											
lias_TGFBr	YVLT	TRAPIDICLVARBLCYLN	E	REFVHCHNCNILLGEDLPKAKTIE	PLCA	PEGVVSPWVREWIGGRCEVVDKCIJEGCFDVEELR	LIRISFCVQIDERLRSMGEVVRVLLRGLT												
2phb	VILSKP	TRAPIDICLVARBLCYLN	E	REFVHCHNCNILLGEDLPKAKTIE	PLCA	VKDLVSEFLWVOCRKYTRALAEHFFCGOY	VKDLVSEFLWVOCRKYTRALAEHFFCGOY												

	810	820	830	840	850	860
15231637.p					
15228043.p	HPPFERRNRNSRRTAISMEIVETTEESA	-DTSKGPGHSENTPKPEKTHV				
AK065494.q	HPFHKERRNRNSRKTAGMEIVETKDE	-SLGPGSSE--TKP				
AK103003.q	VPYREDRRNRNSRTGSMDIESIAEGSNSTEFANKWVEELEARHQTLGLSPETINRLSILSTHHHHH					
AK100061.q	VPSREDRSRNRGNTANADETSKTSSS	-EFTESGDRRSQGSARPPOP				
AK073774.q	NAYRQDQKRPSSQMGSVDVEQSQAEE	-EISNSADS				
AK100396.q	-PIPQEERRPRQRNHISNNSTEPLRKGSSSGKSDAPEENMRPFRYKNRSFPPK-					
AK100396.q	-PIPGRDPRRKHNRGGSTENDSDQRDNNSDTDKNSNDPDS-KPSSRASSKK-					
18405946.p	YPIFRED--RRRSTREGSMETNSDITDMSTPVSRSQSKRQ-					
15217511.p	YPVPREKSMQKLYKHKQEFNLQERRVRQEENSDTDRSPVRSRSQSKRL-					
15238840.p	YPIAEDRRR--RRSNGNTTRDSDPFRNSTDIDKSYEHDLK-EGG-					
22331140.p	YPVMPREERRR--RRRNQNAETH-RESTDTNKD-NDITTDAKI-					
15223428.p	LLYRDERRT--TRDHGSRERQETAVVAAGSESGESGRRIHHQQKQR-					
30678150.p						
15234142.p	LFYRDVSLI--IVLMNI					
45370019.p	LLCRDDKKP--GRDAPQTSDRHS	-SRDGGNFSKRENQRYR-				
15235432.p	LVEKDDRRNSGGGGGIEQGRS-RRKTNVNNESEDGESGNSVLIINNDQALELNKCN					
AK069491.q	FPYRDERGRARAPVQARADVKPAVIEAGDRESDSGNNSARQTEPFRWRNPES-					
4499021.q	FPPYREIIYLVHGS--SDSAGEPTQGQNKNICAEAGDGVRGRRGQHHHSQCQYAIQIARELEIGHT					
30690058.p	FPPFR-	PEHRNQERSK-				
62390013.q	FPPRTLRLWLAESKVFSDSPAEDPPDYEKL-					
48450017.q	LKFDRDELARLDLSPHASDSEYEL					
15224589.p	LLNNNNVNLKFDIQFLVLPQAK-					
28970005.q	ASGPLIIIPPERPLPVVANLAEIERSASSSS-GSGQLFSPSGFRSPTHINDEAALESPREE					
15227189.p	FT-VIAIPQPLVACREEIDRSVSSSSGSGKLTSPFTGYQAFASFGGDGFSGNTNTT					
1ir3_IRK	HPSFPEVSSFFHS--EENK-					
15227459.p	SVDPFFFFACARSPPTNSSESSSQSLYEP-					
1lias_TGFbR	LSQLSQQEGIKM					
2phk_PhK						