

Bichir HoxA cluster sequence reveals surprising trends in ray-finned fish genomic evolution

Chi-hua Chiu, Ken Dewar, Günter P. Wagner, Kazuhiko Takahashi, Frank Ruddle, Christina Ledje, Peter Bartsch, Jean-Luc Scemama, Edmund Stellwag, Claudia Fried, Sonja J. Prohaska, Peter F. Stadler, Chris T. Amemiya

Supplement 2: Protein Alignments

Sequences for the Hox proteins of human (Hs), shark (Hf), bichir (Ps), zebrafish (Dr), pufferfish (Tr) and striped bass (Ms) have been extracted from the complete Hox cluster sequences. The coelacanth (*Latimeria menandoensis*) sequence (Lm) is unpublished data from C. Amemiya. The mouse (Mm) hoxc6 sequence is XM181367.

HoxA2

Full alignment:

Hs A2	MNYEFEREIGFINSQPSLAECITSFP-PVADTFQSSSIKTSTLSHSTLIPPPFEQTIPSL
Hf A2	MNYEFEREIGFINSQPSLAECITSFP-PVGDTFQSSSIKNSTLSHSTVIPPPFEQTIPSL
Ps A2	MNYEFERESGFINSQPSLAECITSFP-PVGDTFQSSSIKNSTLSHSTLIPPPFEQTIPSL
Dr A2b	MNYEFERETGFINSQPSLAECITSFP-PVGDAFQSSSIKSSTLSHSTLIPPPFEQTIPSL
Tr A2a	MNYEFERESGFINSQPSLAECITSFP-PVADSFQSSSIKSSTLSRPTLIPPPFEQTIPSL
Tr A2b	MNYEFGRESGFINSQPSLAECITSLSNPVGDAFQSSSIKSSALSPSTLIPPPFEQTVIGL
Hs A2	NPGSHPRHGAGRPKPSPAGSRGSPVPAGALQPPEYPMKEKKAAKKTALLPAAAAATA
Hf A2	NPSSHPRQS---RPKQSPNGT--SPLPAATL-PPEYPMKEKKNSKKN-HLPASS-----
Ps A2	NPGSHPRHN---RPKQSPNGN--SPLPAASL-PPEYPMKEKKASKKN-HLPTATSTATA
Dr A2b	NPGSHPRHS---RPKQNPNGS--CPLPAASL-PPEYPMKEKKASKKN---QT-TSTAAT
Tr A2a	NPGSHPRHG---RPRHSPDGC--SPLPTASL-PPEYPMREKKASKRN-HLPNSTTTTIS
Tr A2b	NPGTHPRHS---RSKQSLRGC--SPLQAASL-PPEYPMKEKKSIKRS---QTASAAAAA
Hs A2	AATGPA--CLSHK
Hf A2	---GPAASCLSQK
Ps A2	TATGQL--CFPPK
Dr A2b	TDPGPL--YFSPQ
Tr A2a	--NGPV--CFSPK
Tr A2b	PDASPL--CFSPQ

Characters for McClade analysis only:

Hs A2	MNYEFEREIGFINSQPSLAECITSFPVADTFQSSSIKTSTLSHSTLIPPPFEQTIPSLNP
Hf A2	MNYEFEREIGFINSQPSLAECITSFPVGDTFQSSSIKNSTLSHSTVIPPPFEQTIPSLNP
Ps A2	MNYEFERESGFINSQPSLAECITSFPVGDTFQSSSIKNSTLSHSTLIPPPFEQTIPSLNP
Dr A2b	MNYEFERETGFINSQPSLAECITSFPVGDAFQSSSIKSSTLSHSTLIPPPFEQTIPSLNP
Tr A2a	MNYEFERESGFINSQPSLAECITSFPVADSFQSSSIKSSTLSRPTLIPPPFEQTIPSLNP
Tr A2b	MNYEFGRESGFINSQPSLAECITSLPVGDAFQSSSIKSSALSPSTLIPPPFEQTVIGLNP
Hs A2	GSHPRHGRPKPSPAGSSPVPAGALPPEYPMKEKKAAKKTCLSHK
Hf A2	SSHPRQSRPKQSPNGTSPLPAATLPPEYPMKEKKNSKKNCLSQK
Ps A2	GSHPRHNRPKQSPNGNSPLPAASLPPEYPMKEKKASKKNCFPPK
Dr A2b	GSHPRHSRPKQNPNGSCPLPAASLPPEYPMKEKKASKKNYFSPQ
Tr A2a	GSHPRHGRPRHSPDGCSPPTASLPPEYPMREKKASKRNCFSKP
Tr A2b	GTHPRHSRSKQSLRGCSPLQAASLPPEYPMKEKKSIKRSCFSQP

HoxA6

Full alignment:

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Hs A6      MSSYFVNPTFPGLPSGQDSFLGQLPLYQAGYDALRPFASYGASSLPDKTYTSPCFYQQ
Mm A6      MSSYFVNPTFPGLPSGQDSFLGQLPLYPAGYDALRPFASYGASSLPDKTYTSPCFYQQ
Hf A6      MSSYFVNPTFPVSLPSGQDSFLGQIPLYTTGYDALRHFPASYGAATLQDKSYSSPCYYQQ
Ps A6      MNSYFVNNVFPITLSSGQDSFLGQIPLYTNGYDPLKHFPSYGPVTIQDKTTPSPCYQQ
Lm A6      MSSYFVNSTFPSNPPSSQDSFLGQIPLYTAGYDALRHFQASYGATTLQDKTYSSSCFYQQ
Mm C6      MNSYFTNP SLCHLAGGQD-VLPNVALNSTAYDPVRHF-STYGAAVAQNRIYSTPFYSPQ

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Hs A6      SNSVLACNRASYEYGASCFYSDKDLSGASPSGSGKQRGPGDYLHFSPEQQYKPDSSSGQG
Mm A6      SNSVLACNRASYEYGASCFYSDKDLSGASPSGNNKQRGPGDYLHFSPEQQYKPDGS-VQG
Hf A6      SNSVIACNRASYDYGASCFYPEKDLASVSPSGSGKHRAQDDFFSS--DQHYKPDCA--QN
Ps A6      STTVFNS-RVQCDYGPTCFYPEKETSSALPTGSIKERACSEHVQCNADLQYKSYCA--EK
Lm A6      SNSVFACNRTPYECGASCLYPEKDTDVSSPS-SSKQRAHGDYLHFSTDQQHKSECV--QN
Mm C6      ENVVFSSSRGPYDYGNSFYQEKDMLS-----NCRQNTLGHNTQTSIAQDFSSEQG-----

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Hs A6      KALHDEGADRKY
Mm A6      KALHEEGTDRKY
Hf A6      KILSEEGNDRKY
Ps A6      KILNNELLERRH
Lm A6      KILNEEVNDRRY
Mm C6      RTAPQ---DQKA

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Characters for McClade analysis only:

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Hs A6      MSSYFVNPTFPGLPSGQDLGQLPLYQAGYDALRPFASYGASSLPDKTYTSPCFYQQSNS
Mm A6      MSSYFVNPTFPGLPSGQDLGQLPLYPAGYDALRPFASYGASSLPDKTYTSPCFYQQSNS
Hf A6      MSSYFVNPTFPVSLPSGQDLGQIPLYTTGYDALRHFPASYGAATLQDKSYSSPCYYQQSNS
Ps A6      MNSYFVNNVFPITLSSGQDLGQIPLYTNGYDPLKHFSSYGPVTIQDKTTPSPCYQQSTT
Lc A6      MSSYFVNSTFPSNPPSSQDLGQIPLYTAGYDALRHFASYGATTLQDKTYSSSCFYQQSNS
Mm C6      MNSYFTNP SLCHLAGGQDLNVALNSTAYDPVRHFSTYGAAVAQNRIYSTPFYSPQENV

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Hs A6      VLACRASYEYGASCFYSDKDEQQYKPDDRKY
Mm A6      VLACRASYEYGASCFYSDKDEQQYKPDDRKY
Hf A6      VIACRASDYGASCFYPEKDDQHYKPDDRKY
Ps A6      VFNSRVQCDYGPTCFYPEKEDLQYKSYERRH
Lc A6      VFACRTPYECGASCLYPEKDDQHKSEDRRY
Mm C6      VFSSRGPYDYGNSFYQEKDAQDFSSEDQKA

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HoxA10

Full alignment:

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Hs A10      PGAHGYGPSPIDLWLDAPRSCRMEPPDGPPPPPQQQPPPPPQPPQPAPQATSCSF
Hf A10      SG-----MEVWSDPPRSCRMEQP-----ATQQVATCSF
Ps A10      PG-----MEVWLDPPRPCRMDQP-----ASQQVAPCSF
Ms A10a     SS-----MEMWMDAQRSCRMDQEH-----PVGPPQVAPCSF
Dr A10b     QG-----METWLETSSRSRIEQP-----NSQITPRSF
Tr A10a     SS-----MEMWMDTQRSCRMDQEH-----PVGSQVAPCSF
Tr A10b     QG-----METWLEASRPCRVDQP-----RGQHMAQCSF

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Characters for McClade analysis only:

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Hs A10      PGIDLWLDAPRSCRMEPQATSCSF
Hf A10      SGMEVWSDPPRSCRMEQQVATCSF
Ps A10      PGMEVWLDPPRPCRMDQQVAPCSF
Ms A10a     SSMEMWMDAQRSCRMDQQVAPCSF
Dr A10b     QGMETWLETSSRSRIEQQITPRSF
Tr A10a     SSMEMWMDTQRSCRMDQQVAPCSF
Tr A10b     QGMETWLEASRPCRVDQHMAQCSF

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HoxA11

Full alignment:

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Dr A11a      YYVP-GADFSTLPSFLSQSPSTRPVITYSYA-SNLPQVQHVREVTFRDY-AIDPSTKWPH
Tr A11a      YYVSAGADFGSLPSF-----STRPMTYSYS-SNLPQVQPVREVTFRDYAAIDASGKWPH
Dr A11b      YYVS-GTDFSSLPPFLPQTPSSCPMTYSYSTSSLPQVQSVREVSRDY-AIDTSSKWHS
Tr A11b      YYVS-GADFGSLPHYLTQNQSTCPMTYPYQSTALPQVPSVRDVAFRDY-GIDTSNKWHH
Ps A11       YYVS-APDFSSLPSFLPQTPSSRPMTYSYS-SNLPQVQPVREVTFRDY-AIDTSSKWHH
Lc A11       YYVS-GPDFSSLPSFLPQTPSSRPMTYSYS-SNLPQVQPVREVTFRDY-AIDTSNKWHP
Hf A11       YYVS-GPDFSSLPSFLPQTPASRPMTYSYS-SNIPQVQPVREVTFRDY-AIDPSNKWHH

Dr A11a      -RGPLAHCY-PSEDSVHRECLP--AVTTVGEMFPKNNAS-----AYYHS-----TSNTT
Tr A11a      -RGNLPQCYTSAEDMVHRDCLSA-QTAVVGDMFGKNSP--AAAAAYHHHHHHHTSASS
Dr A11b      -RGNLPHCY-ATEDMVHRECLS--NPGTLGDMLSKNNS-----VLYH-----SNSS
Tr A11b      SRGSLSHCY--TEDIVHRDGWTS-PTPRGGEILVKGSSSGGGGGGGHP-----GSSN
Ps A11       -RSNLSHCY-SAEDIMHRDCLTT-APSNMGEMYAKNNS-----TVYH-----ASSN
Lc A11       -RSNLPHCY-STEEILHRDCLATTASSIGEIFGKGNA-----NVYH-----PGSS
Hf A11       -RGNLPHCY-SAEELMHRECLPAST---MGEMLMKNSA-----SVYH-----PSSN

Dr A11a      SASNFYGNVGRNGVLPQAFDQFFDTAYGGSDSVVDNDY--AARDKMHSSK-QSTPAPAP
Tr A11a      AATNFYGNVGRNGVLPQAFDQFYDTAYGNASESSSTNG--FSGDKTPTKQ-PSSAPEDA
Dr A11b      HTSNVYGSVGRNGVLPQAFDQFFETAYGNVENQPT-----HPVDRATSKA-PPPAESGS
Tr A11b      HTPGFYGSVGRNGVLPQAFDQFFDTAYGSSEGSATPTAHAADADRQAAKTSPASQAQS
Ps A11       PSSNFYSSVGRNGVLPQAFDQFFETAYGNGENPSPD----FSGDKNSSKL-PAAAMPNS
Lc A11       TSSNFYNTVGRNGVLPQAFDQFFETAYGTTENHSSD----YSADKNSDKI-PSAATSRs
Hf A11       ASSSFYNPVGRNGVLPQGFDQFFETAYGSSENQSE----YCGEKSPDKV-PSAATSSS

Dr A11a      E--QQPEGKER-PETSSPESSSGNNEEKTSGANSGRFRKKRCPYTKFQIRELEREFFF
Tr A11a      QACRDTEAKEPREESSPELSSGNTEEKSS-STNGQRTRKKRCPYKYQIRELEREFFF
Dr A11b      DSCRGTDETERCEETSSPEPSSGNNEEDKFSGSSNGQKTRKKRCPYTKYQIRELEREFFF
Tr A11b      DS-----AESFSPKSSSGHSEEKQSRGSGQRARKKRCPYTKYQIRELEREFFF
Ps A11       ETCRMTEEKERREENSSPESSSGNNEEKSH-SSSGQRTRKKRCPYTKYQIRELEREFFF
Lc A11       ETCRETDEKERREESSPESSSGNNEEKSS-SSSGQRTRKKRCPYTKYQIRELEREFFF
Hf A11       ETSRVSVEKETSPGSSPESSSGNNEEKGS-NSSGQRTRKKRCPYTKYQIRELEREFFF

Dr A11a      SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK
Tr A11a      SVYINKEKRMQLSRMLNLTDRQVKIWFQNRMMKEKK
Dr A11b      SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK
Tr A11b      SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK
Ps A11       SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK
Lc A11       SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK
Hf A11       SVYINKEKRLQLSRMLNLTDRQVKIWFQNRMMKEKK

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Characters for McClade analysis only:

Dr A11a	YYVPGADFSTLPSFSTRPVTYSYNLPQVQHVREVTFRDYAIDPSTKWPHRGPLAHCYED
Tr A11a	YYVSGADFSGLPSPFSTRPMTYSYNLPQVQPVREVTFRDYAIDASGKWPHRGNLPQCYED
Dr A11b	YYVSGTDFSSLPFPFSSCPMTYSYSLPQVQSVREVSVFRDYAIDTSSKWHSRGNLPHCYED
Tr A11b	YYVSGADFSGLPHYSTCPMTYPYALPQVPSVRDVAFRDYGIDTSNKWHHRGSLSHCYED
Ps A11	YYVSAPDFSSLPSPFSSRPMTYSYNLPQVQPVREVTFRDYAIDTSSKWHHRSNLSHCYED
Lc A11	YYVSGPDFSSLPSPFSSRPMTYSYNLPQVQPVREVTFRDYAIDTSNKWHPRSNLSHCYEE
Hf A11	YYVSGPDFSSLPSPFASRPMTYSYNIPQVQPVREVTFRDYAIDPSNKWHHRGNLSHCYEE
Dr A11a	SVHRECLGEMFPKNNAAYYHSNTTSASNIFYGNVGRNGVLPQAQFDQFFDTAYGETSSPES
Tr A11a	MVHRDCLGDMFGKNSPAAYHSASSAATNFYGNVGRNGVLPQAQFDQFYDTAYGESSSPES
Dr A11b	MVHRECLGDMLSKNNSVLYHSNSSHTSNVYGSVGRNGVLPQAQFDQFFETAYGETSSPEP
Tr A11b	IVHRDQGWGEILVKGSSGGHPGSSNHTPGFYGSVGRNGVLPQAQFDQFFDTAYGESFSPKS
Ps A11	IMHRDCLGEMYAKNNSTVYHASSNPSSNFYSSVGRNGVLPQAQFDQFFETAYGENSSPES
Lc A11	ILHRDCLGEIFGKGNANVYHPGSSTSSNFYNTVGRNGVLPQAQFDQFFETAYGESSSPES
Hf A11	LMHRECLGEMLMKNSASVYHPSSNASSSFYNPVGRNGVLPQGFQFFETAYGGSSSPES
Dr A11a	SSGNNEEKTSANSGPRFRKKRCPTYKFQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Tr A11a	SSGNTEEKSSSTNGQRTRKKRCPYKYQIRELEREFFFSVYINKEKRMQLSRMLNLTD
Dr A11b	SSGNNEEDKFSSNGQKTRKKRCPTYKYQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Tr A11b	SSGHSEKQSGSGGQRARKKRCPTYKYQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Ps A11	SSGNNEEKSHSSSGQRTRKKRCPTYKYQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Lc A11	SSGNNEEKSSSSSGQRTRKKRCPTYKYQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Hf A11	SSGNNEEKGSNSSGQRTRKKRCPTYKYQIRELEREFFFSVYINKEKRLQLSRMLNLTD
Dr A11a	QVKIWFQNRRMKEKK
Tr A11a	QVKIWFQNRRMKEKK
Dr A11b	QVKIWFQNRRMKEKK
Tr A11b	QVKIWFQNRRMKEKK
Ps A11	QVKIWFQNRRMKEKK
Lc A11	QVKIWFQNRRMKEKK
Hf A11	QVKIWFQNRRMKEKK

HoxA13

Full alignment:

Dr A13a	P-VMFLYDNGGGGLDDTSKNMEGFTGGNFSPSPCRNLMSHPASLAPSATYPSSEVAAAAA
Tr A13a	PSVMFLYDNGGGSDEVSKNMEGFAGGNFAANQCRNLMGHPASLAPSTAYSSCDVPTSAI
Dr A13b	P-VMFLYDN--GLDDMSKNMEGFVGGNFAANQCRNLIAHPSTLAPSTTYTSSEVPVSGM
Tr A13b	P-VMFLYEN--GLDERNKNMEGFTGSNFPANQCRNLLAHPTSLAPNTTYTSNDVPISGI
Ps A13	P-VMFLYDN--GLDEVNKNMDGFAGGNFAANQCRNLMAHPASLAPSTAYTSSEVSASGI
Lc A13	P-VMFLYDN--GLDEVNKNMEGFPGGNFAANQCRNLMAHPASLAPSTAYTSSEVPASGI
Hf A13	T-VMFVYDN--SLDEINKNMDGFGSGNFTANQCRNLMAHPASLAPSSAYTSSEVPASGI
Dr A13a	GDSGKQCSPCSAVQGSASASISYGYFGGGGYPCRMSSHHSAGGGGVKTC-AQSPASGSP
Tr A13a	GEPVKQCSPCSAAQNSSSASLPYGYFGSG-YYPECRMSSHSS----IKSCSAQPP---SA
Dr A13b	GEPVKQCSPCSAVQNTPSASLPYGYFGGS-YYPECRMP-----KSC-TQP----TT
Tr A13b	GEPGKQCSPCPATQSSPNASLPYGYFGSS-YYPECRVSHGS-----VKAC-AQP----SG
Ps A13	AEPVKQCSPCSAAQSSSSASLPYGYFGSG-YYPECRMAHQSS----IRSC-AQP----SA
Lc A13	AEPVKQCSPCSAAQSSSSASLPYGYFGSS-YYPECRMTHHNA----IKSC-AQP----ST
Hf A13	AEPVKQCSPCPAAQTSSSAAALPYGYFGSS-YYPECRMSSHSS----IKSC-AQP----ST
Dr A13a	----YGEKYMDTSASTGEDYTSSRAKEFALYSSYASSPYQPVPVSYLDVPVQAIISGPSE
Tr A13a	----YGEKYMDTSAT-SDDFT-SRAKEFAFYPTYPSGPYQPVPVSYLDVPVVPTISAPSE
Dr A13b	----YGEKYMDTSVS-GEEFP-SRAKEFAFYQGYSSGPYQPVPVSYLDVPVVPALSAPSE
Tr A13b	----YGDKYMDSPVS-GEEFS-SRAKEYAFYQGYSSAPYQ--PSYLDVPVVPALSAPSE
Ps A13	----YAEKYMDTSVS-GEEFT-SRAKELAFYQGYTTSPYQHVPSYLDVPVVPTISGPGE
Lc A13	----FAEKYMDTSVS-GEEFT-SRAKEFAFYQGYAAGPYQPVPVSYLDVPVVPTIGGPGE
Hf A13	LSGYPADKYMDTSA--GEEFT-SRAKEFAFYQGY-AGPYQPMPSYLDVPVVPTISAPGE
Dr A13a	PRHESLLPMESYQPWAITTSGWNGQVYCTKEQQQTGNVWKSSIPESVS-HGGADGSSFR
Tr A13a	ARHESLLSMESYQPWTLAPNGWNSQVYCAKEQPQAGHMWKSSVSDATS-HTGGDSGSYR
Dr A13b	PRHESLLPVETYQPWAIT-NGWSSPVYCPKDQTSSTLWKSSIQDTVS---GTDGASVR
Tr A13b	TRHEPLLMEPYQPWTIT-NGWSGQVYCTKEQPQSNPLWKSSLQVFISDISGGDSG-VR
Ps A13	PRHDTLLPMESYQPWAIT-NGWNGQVYCSKEQTQPSHLWKSTMQEVVT-HP-GDANSFR
Lc A13	PRHEPLLPMETYQPWAIT-NGWNGQVYCSKEQAQPNHLWKSTLPDVVS-HP-SDANSFR
Hf A13	PRHDTLLPMESYQPWAIT-NGWNGQVCCSKEQPQATHLWKSSLPDVVS-HP-SDASSFR
Dr A13a	RGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISAQTNLSEQRVTI
Tr A13a	RGRKKRVPYTKVQLKELEREYAANKFITKDKRRRISAQTNLSEQRVTI
Dr A13b	RGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISAHTNLTERQVTI
Tr A13b	RGRKKRVPYTKVQLKELEREYAANKFITKDKRRRISAQTNLTERQVTI
Ps A13	RGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISATTNLSEQRVTI
Lc A13	RGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISATTNLSEQRVTI
Hf A13	RGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISASTNLSEQRVTI

Characters for McClade analysis only:

Dr A13a	PVMFLYDNGLDDTSKNMEGFTGGNFSPSPCRNLM SHPASLAP SATYPSSEVAAAAAGDS
Tr A13a	PVMFLYDNGSDEVSKNMEGFAGGNFAANQCRNLMGHPASLAPSTAYSSCDVPTSAIGEP
Dr A13b	PVMFLYDNGLDDMSKNMEGFVGGNFAANQCRNLIAHPSTLAPSTTTYTSSEVPVSGMGEP
Tr A13b	PVMFLYENGLDERNKNMEGFTGSNFPANQCRNLLAHPTSLAPNTTYTSNDVPISGIGEP
Ps A13	PVMFLYDNGLDEVNKNMMDGFAGGNFAANQCRNLMAHPASLAPSTAYTSSEVSASGIAEP
Lc A13	PVMFLYDNGLDEVNKNMEGFPGGNFAANQCRNLMAHPASLAPSTAYTSSEVPASGIAEP
Hf A13	TVMFVYDNSLDEINKNMDGFGSGGNFTANQCRNLMAHPASLAPSSAYTSSEVPASGIAEP
Dr A13a	GKQCSPCSAVQGSASASISYGYFGGGYYPCRM SKTCAQSSPGEKYMDTSAGEDYTSRAK
Tr A13a	VKQCSPCSAAQNSSSASLPYGYFGSGYYPCRM SKSQAQPSAGEKYMDTSASDDFTSRAK
Dr A13b	VKQCSPCSAVQNTPSASLPYGYFGSGYYPCRM PKSCTQPTTGEKYMDTSVGEEFPSRAK
Tr A13b	GKQCSPCPATQSSPNASLPYGYFGSSYYPCRVSKACAQPSGGDKYMDSPVGEEFSSRAK
Ps A13	VKQCSPCSAAQSSSSASLPYGYFGSGYYPCRM ARSQAQPSAAEKYMDTSVGEEFTSRAK
Lc A13	VKQCSPCSAAQSSSSASLPYGYFGSSYYPCRM TKSCAQPSAEKYMDTSVGEEFTSRAK
Hf A13	VKQCSPCPAAQTSSSAALPYGYFGSSYYPCRM SKSQAQPSADKYMDTSAGEEFTSRAK
Dr A13a	EFALYSSYSSPYQPSYLDVPVVQAISGPSEPRHESLLPMESYQPWAISGWNGQVYCTKE
Tr A13a	EFAFYPTYSGPYQPSYLDVPVVPTISAPSEARHESLLSMESYQPWTNGWNSQVYCAKE
Dr A13b	EFAFYQGYSGPYQPSYLDVPVVPAL SAPSEPRHESLLPVETYQPWAINGWSSPVYCPKD
Tr A13b	EYAFYQGYSA PYQPSYLDVPVVPAL SAPSETRHEPLLPMEPYQPWTINGWSGQVYCTKE
Ps A13	ELAFYQGYTSPYQPSYLDVPVVPTISGPGEPRHDTLLPMESYQPWAINGWNGQVYCSKE
Lc A13	EFAFYQGYAGPYQPSYLDVPVVPTIGGPGEPRHEPLLPMEYQPWAINGWNGQVYCSKE
Hf A13	EFAFYQGYAGPYQPSYLDVPVVPTISAPGEPRHDTLLPMESYQPWAINGWNGQVCCSKE
Dr A13a	QQQTGNVWKSSIPESVSFRGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISAQTN
Tr A13a	QPQAGHMWKSSVSDATSYRRGRKKRVPYTKVQLKELEREYAANKFITKDKRRRISAQTN
Dr A13b	QTQSSTLWKSSIQDTVSVRRGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISAHTN
Tr A13b	QPQSNPLWKSSLQVFISVRRGRKKRVPYTKVQLKELEREYAANKFITKDKRRRISAQTN
Ps A13	QTQPSHLWKSTMQEVVTFRRGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISATTN
Lc A13	QAQPNHLWKSTLPDVVSFRGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISATTN
Hf A13	QPQATHLWKSSLPDVVSFRGRKKRVPYTKVQLKELEREYATNKFITKDKRRRISASTN
Dr A13a	LSERQVTI
Tr A13a	LSERQVTI
Dr A13b	LTERQVTI
Tr A13b	LTERQVTI
Ps A13	LSERQVTI
Lc A13	LSERQVTI
Hf A13	LSERQVTI