

Online Resource 5.

a) Divergent V-IgSF domains of Elephant shark B7H6 genes

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AAVX01166257.1 DALEMTIFKQLEVFQGDVVLDCCKVTGYTPAVLNLSFVAVEWRFVS----TQQLVYSFN 56
AAVX01015110.1 S...VL.HSPMKGQVNET.K.E...S...SSPQ.Q.KT.G.Q.I.T.----.RKE...YI 56
AAVX01166967.1 .V.NVLMDSGPVR.AVNK.TL.K.Q.P..ESRTID.AS.S...Y.SKPPDV.RK...K.V 60
AAVX01076204.1 -.AR..LRTSPA.CLVNE..S.Q.EIADL.GIT.DKNHLG.L.S.TD-----DIFKYI 52

AAVX01166257.1 GGFIDALRPGATVTIENLKRGDASLHLPKQIEEEGEYKCIYVYVTP-SKAEKSSSVRVL 114
AAVX01015110.1 ..KAS.S.N...ISED..RT....Y..NI...D..D.T.V.I...-E.V..T.TLQ.S 114
AAVX01166967.1 NSAHTPH.K..KISDDK..K.I...F.LS.GFQD..Q.E.V.FI...-DSGRGNAEMF.G 118
AAVX01076204.1 N.ALFK.GK.VELLESSLK.NM..L.KN.TMKQM...T.F.P.NEQ.TGTVRLE.- 110
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b) Divergent V-IgSF domains of Elephant shark NKp30 genes

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AAVX01127481 ----VVQSPSRVEAAEGERVSLSCITYTGDVGSIGGYQWLKHS--PHGVPVSNDETEGYRG 54
AAVX01545093.1 -----.....A.....--..... 53
AAVX01630919 -----.....H.....--..... 53
AAVX01169427 -----.T..SLN.T..QT.L.N..FD.PS--TN..FS.VRDLGGERERE...T.GP.E. 52
AAVX01221896 DPPG.T.W.PAIQ.LS.QT.T.N.SFAAR---.VTVKT...DG-----AALDLSSPR.S. 52

AAVX01127481 RVHRKHGRSFIETRDASIAISDVRQSDSGVYYCAIDLMDVVRGYGSGTTTLT----- 105
AAVX01545093.1 .....QN..G.....N.....EA----- 94
AAVX01630919 .....D..N..G.....T.....I.----- 84
AAVX01169427 ..ISRSSAE.KTLK...S.R.LTGR...L...RVE.VSQTESV.P..R.QVV--- 105
AAVX01221896 ..AQADAQT.RARG..T.HL.NLSVC...R.V.RVQPL.SAAAL.R..QV.VTRES 108
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Figure legend:

Deduced amino acid alignment of V domains screened from E-shark genome using ClustalW2. Gaps and Identical aa residues are indicated with dashes and dots, respectively. Canonical amino acids characteristic for IgSF domains are highlighted in grey. a) B7H6, b) NKp30.