

(A)

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SP|Q06787|FMR1_HUMAN RLRVNPKNPKATKDTFHKIKLDVPEDLRQMCakeAAHKDFKKAVGAFSVTYDPENYQLVI 170
SP|P51114|FXR1_HUMAN RLRFPVNQNKTVKKNTEFFKCTVDVPEDLREACANENAHKDFKKAVGACRIFYHPETTQLMI 170
SP|P51116|FXR2_HUMAN RLRFPVNPPLATKGSFFKVTMAVPEDLREACSNENVHKEFKKALGANCIFLNITNSELFI 180
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SP|Q06787|FMR1_HUMAN QG-----MGRGSRPYRNRGHRGRRGPGYTS--GTNSEASNAsetESDHRDELSDWslAPTE 519
SP|P51114|FXR1_HUMAN -----YSGRGRGRRGPNYTSgyGTNSELSNPsetESERKDELSDWslAGED 428
SP|P51116|FXR2_HUMAN SSSSLHATRtyGGSyGGRGRGRRT--GGPAYGpSSDvStasetESEKREEPNR---AGPG 469
* .**:* ** * .*: * .*****:*** * . *

SP|Q06787|FMR1_HUMAN EERESFLRRGDGRRRGGGGRGQGGRGRGGGfKGNDD-----HSRT-DNRPRNPRE--- 568
SP|P51114|FXR1_HUMAN DRDSRHQRDSRRRPGGRGRSVSGGRGRGGP-----RGGKSSISSVLKDPDSNPYSLLD 481
SP|P51116|FXR2_HUMAN DRDPPT-----RGEESRRRPTGGRGRGPPAPRPTsRYNSSISSVLKDPDSNPYSLLD 523
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