

0.417,0.424,0.407,0.415,0.453,0.463,0.469,0.739,0.494,0.751,0.513,0.764,0.773,0.535,0.770,0.764,0.529,0.778,0.554,0.556,0.536,0.562,0.543,0.550,0.761,0.760,0.781,0.778,0.778,0.584,0.600,0.592,0.626,0.605,0.641,0.625,0.641,0.618,0.601,0.595,0.602,0.591,0.570,0.554,0.552,0.559,0.581,0.597,0.581,0.578,0.559,0.545,0.532,0.561,0.586,0.564,0.572,0.530,0.531,0.506,0.513,0.471,0.450,0.462,0.447,0.428,0.437,0.422,0.430,0.428,0.412,0.409,0.401,0.436,0.406,0.407,0.434,0.432,0.421,0.408,0.417,0.403,0.407,0.402,0.384,0.433,0.404,0.389,0.390,0.392,0.391,0.363,0.377,0.407,0.419,0.425,0.415,0.417,0.387,0.375,0.390,0.365,0.381,0.397,0.385,0.371,0.327,0.351,0.356,0.362,0.328,0.340,0.358,0.314,0.338,0.347,0.349,0.338,0.319,0.311,0.312,0.296,0.317,0.334,0.339,0.329,0.326,0.306,0.302,0.349,0.333,0.349,0.346,0.326,0.321,0.311,0.301,0.321,0.319,0.330,0.361,0.346,0.348,0.360,0.352,0.361,0.401,0.407,0.385,0.400,0.398,0.408,0.427,0.436,0.432,0.419,0.426,0.416,0.410,0.424,0.435,0.402,0.374,0.448,0.467,0.450,0.472,0.485,0.499,0.516,0.504,0.575,

>ORF1a Consensus sequence (1-845). Protein encoded sequence, where the lower (upper) case indicates the residue was predicted to interact (not to interact) with RNA/DNA/protein

MALPFDDTLKFGSAAARvkgrrldsvartKLDLLGDGPYFYDFGPLEVVDSSSKQLTVKMtSVQTVYVSSVV
EDNSYVITYKFVPGVNEWVETEPVLHKPTALVGVLWREYNRYKDKTESLSQELSQLRLEHSLLRHDYER
VRPQQPATPRCRLGFITKLLIGLLIGslMAHSTLAHKTPGTGLLGECLDIDVIDGKQVCVNFPLWNETET
NPTDGDKTTTISWDHEGLDLLVLIAPYLVSWPMIATMVGFFYVATAEQPAYMLVSLLLATYSKAQVL
ALAGLPFMDMPVVTLWVSMVLVHSYDAVLSLWVALLLaftlsagvfmpdvrySDLVRGQLVVFLVLFNYLVMMSL
pnwlvfslvgyrvlrvltflvaekvevrgpdGKvVETRRTSMPAWINKASNFLQTRFHQKIRTGISPTARVIPNGVIVV
ETQDGSSTGFRCRNYLVtAGHVVTGTETPKIQWAGVTAYSKVVHRVPDKDIAFLAIPQELQDLPSYRLA
KKVEDGPPVITSLEDSGALSVAVTEGVIVTDSITYAVQTRNGMSGSPVTNLDGRILAVHQTNTGFTGGA
VILTDEdFPQPKKSAREQQleARIKELEAAMNQSSNHEDIVELVRAAVAREFKVLRTELsattfiqakgknkhh
hrrrggKKRRRAVWSEEEYKELLEKGFSSQLRDMAEVLSHEEDPFGSDTESEGGFPEWSDVSDAESIERE
WFGQSWEDCKPVKEEPQDTLPVHLKEKYTLDAYVISKEELRSFAKEFKDYVDKVEALIDKTVQQGKWL
PSVNPTAIIIEELNDLWFGLNmLmwekGLVPFTqRkkikrkvqknskgapkrpLptP

Three non globular protein disordered regions and three putative disordered RNA-protein binding regions were identified within the nsp1a with DisoRDPbind webserver, respectively. Protein disordered regions were identified between residues 206-222 (consensus WNETETNPTDGDKTTTI), 691- 709 (consensus EDPFGSDTESEGGFPEWSD) and 832-845 (consensus SKGAPKRGPLPTP). Putative disordered RNA-protein binding regions were located within residues 316-392 (AAFTLSAGVFMPDVRYSDLVRGQLVVFLVLFNYLVMMSLPNWLVFSLVVG YRVLRVLTFLVAEKV EVRGPDPGKV), 633- 647 (SATTFIQAKGKNKK) and residues 807-813(MLMWEK).