

Supplemental materials: Results for DisoRDPbind webserver.

Further information regarding results formatting and interpretations can be found at:

<http://biomine.cs.vcu.edu>. The annotations are encoded as follows: "1" denotes residues annotated with the particular type of binding, "0" denotes residues with annotations that include other types of disordered or ordered residues, and "x" denotes the residues that lack annotations

RNA-binding residues:

[illegible]

RNA-binding propensity:

0.092,0.058,0.052,0.058,0.057,0.051,0.052,0.058,0.060,0.062,0.071,0.061,0.068,0.068,0.075,0.072,0.073,0.085,0.073,0.077,0.077,0.086,0.091,0.087,0.082,0.079,0.069,0.072,0.073,0.083,0.065,0.071,0.073,0.072,0.055,0.053,0.055,0.053,0.043,0.042,0.053,0.064,0.058,0.054,0.057,0.064,0.066,0.064,0.053,0.044,0.038,0.046,0.043,0.039,0.044,0.042,0.060,0.058,0.058,0.064,0.066,0.065,0.080,0.094,0.096,0.077,0.096,0.085,0.092,0.092,0.072,0.066,0.056,0.051,0.055,0.052,0.047,0.043,0.048,0.055,0.072,0.091,0.081,0.073,0.059,0.081,0.079,0.081,0.085,0.113,0.111,0.102,0.098,0.117,0.095,0.096,0.091,0.109,0.112,0.108,0.089,0.099,0.110,0.119,0.102,0.087,0.081,0.106,0.106,0.077,0.068,0.063,0.063,0.065,0.064,0.080,0.069,0.057,0.052,0.047,0.056,0.044,0.045,0.045,0.044,0.065,0.058,0.065,0.074,0.073,0.054,0.046,0.048,0.045,0.039,0.031,0.030,0.031,0.030,0.032,0.026,0.023,0.021,0.022,0.018,0.019,0.016,0.019,0.020,0.017,0.018,0.014,0.012,0.014,0.011,0.010,0.010,0.011,0.012,0.018,0.021,0.020,0.020,0.014,0.019,0.023,0.024,0.023,0.022,0.018,0.016,0.021,0.020,0.021,0.021,0.022,0.029,0.027,0.032,0.031,0.029,0.022,0.024,0.020,0.019,0.022,0.019,0.018,0.016,0.018,0.018,0.014,0.012,0.010,0.011,0.011,0.013,0.013,0.010,0.012,0.015,0.019,0.019,0.017,0.021,0.020,0.027,0.030,0.028,0.037,0.029,0.027,0.024,0.024,0.020,0.024,0.019,0.021,0.025,0.025,0.017,0.017,0.020,0.020,0.019,0.018,0.015,0.016,0.013,0.011,0.011,0.010,0.012,0.008,0.007,0.008,0.009,0.011,0.016,0.016,0.020,0.024,0.027,0.026,0.022,0.020,0.022,0.027,0.032,0.032,0.042,0.034,0.035,0.047,0.046,0.047,0.046,0.041,0.049,0.044,0.046,0.042,0.039,0.034,0.040,0.052,0.041,0.039,0.044,0.051,0.040,0.046,0.049,0.056,0.041,0.044,0.049,0.043,0.048,0.052,0.053,0.047,0.052,0.058,0.079,0.075,0.080,0.084,0.095,0.095,0.096,0.097,0.072,0.071,0.074,0.070,0.069,0.085,0.089,0.111,0.099,0.108,0.112,0.137,0.135,0.109,0.096,0.103,0.115,0.128,0.126,0.117,0.139,0.138,0.145,0.150,0.158,0.185,0.228,0.238,0.216,0.251,0.248,0.214,0.223,0.262,0.243,0.227,0.199,0.253,0.249,0.231,0.258,0.282,0.270,0.245,0.240,0.263,0.244,0.227,0.235,0.238,0.261,0.266,0.265,0.305,0.318,0.354,0.283,0.325,0.353,0.357,0.335,0.333,0.352,0.397,0.415,0.428,0.448,0.470,0.475,0.488,0.498,0.482,0.500,0.550,0.523,0.454,0.468,0.414,0.396,0.380,0.328,0.314,0.336,0.343,0.343,0.319,0.333,0.279,0.245,0.263,0.263,0.297,0.230,0.263,0.267,0.174,0.155,0.149,0.130,0.155,0.144,0.134,0.135,0.119,0.101,0.072,0.071,0.077,0.081,0.067,0.056,0.066,0.070,0.079,0.065,0.071,0.073,0.074,0.058,0.061,0.050,0.045,0.038,0.045,0.032,0.032,0.033,0.035,0.031,0.033,0.041,0.038,0.047,0.056,0.049,0.056,0.060,0.037,0.041,0.049,0.041,0.042,0.040,0.046,0.038,0.032,0.037,0.049,0.044,0.062,0.081,0.085,0.102,0.091,0.084,0.099,

0.094,0.102,0.115,0.120,0.123,0.127,0.135,0.137,0.173,0.177,0.183,0.182,0.180,0.174,0.191,0.227,0.236,0.252,0.25
2,0.302,0.252,0.349,0.333,0.320,0.317,0.321,0.309,0.305,0.294,0.223,0.184,0.160,0.148,0.123,0.131,0.119,0.118,0.
096,0.092,0.097,0.074,0.079,0.066,0.073,0.092,0.089,0.087,0.086,0.084,0.110,0.128,0.147,0.172,0.179,0.207,0.195,
0.203,0.183,0.221,0.231,0.241,0.249,0.239,0.190,0.175,0.121,0.132,0.118,0.124,0.118,0.084,0.101,0.087,0.083,0.07
9,0.083,0.088,0.074,0.067,0.045,0.043,0.033,0.031,0.025,0.029,0.031,0.037,0.037,0.053,0.051,0.051,0.058,0.046,0.
056,0.057,0.060,0.059,0.039,0.049,0.049,0.064,0.054,0.070,0.065,0.101,0.102,0.126,0.120,0.091,0.077,0.080,0.089,
0.085,0.069,0.069,0.071,0.069,0.069,0.105,0.100,0.100,0.121,0.149,0.143,0.159,0.134,0.149,0.116,0.109,0.109,0.10
8,0.108,0.107,0.105,0.125,0.122,0.111,0.115,0.110,0.101,0.106,0.133,0.129,0.122,0.125,0.104,0.097,0.086,0.112,0.

Protein-binding residues:

[illegible]

0.391,0.372,0.356,0.358,0.398,0.423,0.415,0.371,0.326,0.278,0.293,0.267,0.262,0.256,0.250,0.263,0.264,0.283,0.310,0.318,0.314,0.293,0.301,0.325,0.356,0.388,0.399,0.390,0.388,0.405,0.409,0.426,0.420,0.413,0.424,0.415,0.427,0.451,0.428,0.452,0.441,0.444,0.462,0.486,0.466,0.439,0.449,0.449,0.458,0.449,0.418,0.448,0.438,0.448,0.466,0.454,0.428,0.388,0.377,0.383,0.382,0.401,0.387,0.392,0.399,0.369,0.391,0.380,0.392,0.379,0.364,0.383,0.392,0.434,0.453,0.433,0.450,0.479,0.478,0.474,0.460,0.428,0.416,0.435,0.401,0.407,0.403,0.405,0.407,0.416,0.393,0.403,0.410,0.426,0.419,0.423,0.426,0.423,0.425,0.388,0.415,0.390,0.396,0.392,0.361,0.359,0.347,0.361,0.336,0.343,0.371,0.350,0.358,0.378,0.372,0.429,0.422,0.425,0.412,0.427,0.444,0.440,0.494,0.481,0.468,0.451,0.433,0.429,0.444,0.462,0.480,0.489,0.478,0.487,0.503,0.494,0.493,0.488,0.482,0.457,0.471,0.484,0.462,0.457,0.435,0.420,0.450,0.439,0.404,0.408,0.406,0.401,0.380,0.354,0.351,0.364,0.345,0.344,0.348,0.349,0.365,0.338,0.320,0.316,0.326,0.321,0.315,0.312,0.324,0.333,0.315,0.330,0.300,0.293,0.293,0.317,0.322,0.328,0.344,0.350,0.341,0.370,0.384,0.394,0.389,0.400,0.441,0.442,0.463,0.471,0.482,0.477,0.488,0.462,0.475,0.487,0.487,0.483,0.510,0.503,0.503,0.507,0.502,0.476,0.497,0.485,0.455,0.472,0.472,0.526,0.524,0.508,0.508,0.504,0.477,0.484,0.486,0.493,0.483,0.424,0.394,0.376,0.374,0.362,0.340,0.348,0.357,0.362,0.340,0.333,0.317,0.303,0.286,0.277,0.283,0.323,0.347,0.367,0.397,0.395,0.350,0.343,0.320,0.332,0.341,0.349,0.358,0.336,0.330,0.320,0.338,0.329,0.324,0.295,0.285,0.272,0.310,0.306,0.318,0.303,0.317,0.331,0.333,0.299,0.307,0.323,0.321,0.320,0.320,0.301,0.284,0.294,0.298,0.314,0.317,0.322,0.299,0.283,0.262,0.258,0.260,0.264,0.255,0.245,0.264,0.309,0.313,0.332,0.335,0.318,0.309,0.308,0.316,0.271,0.281,0.295,0.306,0.313,0.300,0.276,0.284,0.285,0.285,0.290,0.271,0.304,0.287,0.286,0.286,0.312,0.283,0.297,0.292,0.292,0.297,0.297,0.309,0.301,0.297,0.294,0.282,0.277,0.302,0.305,0.296,0.282,0.299,0.267,0.287,0.286,0.259,0.284,0.292,0.308,0.326,0.302,0.301,0.278,0.266,0.265,0.259,0.273,0.263,0.309,0.272,0.258,0.285,0.285,0.278,0.262,0.254,0.281,0.298,0.293,0.288,0.257,0.274,0.274,0.291,0.275,0.300,0.299,0.299,0.302,0.321,0.310,0.279,0.292,0.292,0.289,0.292,0.315,0.313,0.314,0.299,0.311,0.279,0.286,0.288,0.282,0.288,0.270,0.269,0.287,0.278,0.267,0.249,0.266,0.262,0.252,0.266,0.269,0.320,0.305,0.322,0.349,0.351,0.358,0.385,0.418,0.400,0.419,0.431,0.427,0.424,0.428,0.429,0.463,0.460,0.495,0.499,0.501,0.484,0.469,0.470,0.483,0.447,0.441,0.410,0.404,0.417,0.413,0.443,0.454,0.423,0.407,0.404,0.371,0.386,0.396,0.389,0.371,0.354,0.356,0.401,0.391,0.361,0.368,0.371,0.365,0.378,0.405,0.382,0.373,0.365,0.377,0.405,0.393,0.399,0.409,0.410,0.465,0.469,0.463,0.467,0.431,0.399,0.389,0.402,0.412,0.405,0.403,0.388,0.395,0.405,0.397,0.403,0.385,0.383,0.364,0.350,0.348,0.360,0.327,0.320,0.321,0.339,0.375,0.420,0.410,0.441,0.446,0.443,0.491,0.475,0.473,0.486,0.493,0.500,0.521,0.516,0.486,0.494,0.506,0.508,0.522,0.493,0.488,0.498,0.487,0.483,0.518,0.529,0.549,0.556,0.523,0.528,0.526,0.535,0.527,0.491,0.475,0.482,0.478,0.471,0.468,0.443,0.443,0.415,0.411,0.418,0.444,0.451,0.468,0.488,0.475,0.491,0.475,0.472,0.489,0.486,0.465,0.477,0.472,0.505,0.520,0.516,0.477,0.500,0.508,0.516,0.505,0.514,0.502,0.505,0.512,0.500,0.537,0.577,0.548,0.561,0.552,0.531,0.535,0.526,0.531,0.519,0.505,0.510,0.470,0.468,0.442,0.441,0.456,0.459,0.476,0.479,0.506,0.491,0.494,0.500,0.494,0.516,0.521,0.531,0.556,0.589,0.600,0.593,0.602,0.801,0.780,0.780,0.569,0.571,0.585,0.548,0.553,0.550,0.776,0.791,0.591,0.612,0.801,0.809,0.626,0.634,0.615,0.795,0.798,0.777,0.769,0.791,0.793,0.585,0.552,0.767,0.526,0.517,0.752,0.749,0.730,0.727,0.717,0.727,0.728,0.423,0.712,0.408,0.402,0.396,0.426,0.415,0.401,0.694,0.371,0.684,0.669,0.652,0.653,0.317,0.357,0.683,0.361,0.362,0.366,0.360,0.358,0.363,0.353,0.351,0.321,0.304,0.657,0.327,0.661,0.325,0.330,0.667,0.676,0.343,0.372,0.375,0.371,0.676,0.677,0.317,0.668,0.376,0.389,0.393,0.393,0.408,0.423,0.704,0.384,0.688,0.381,0.684,0.363,0.700,0.695

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

MALPFDDTLKFGSAAARvkgrldsvartKLKDLLGDGPYFYDFGPLEVVDSSSKQLTVKMtSVQTVYVSSVV
EDNSYVITYKFVPGVNEWVETEPVLHKPTALVGVLWREYNRYKDKTESLSQELSQRLEHSLLRHDYER
VRPQQPATPRCRLGFITKLLIGLLIGsIMAHSTLAHKTPGTGLLGECLDTDVIDGKQVCVNFLPWNETET
NPTDGDKTTTISWDHEGLDLLVLIAPYLVSWPMIATMVGFFYVATAEQPAYMLVSLLLATYSKAQVL
ALAGLPFMDMPSVVTLWVSMVLVHSYDAVLSLWVALLLaftlsagvfmpdvrysdlvrgqlvvflvlfnylvvmmsl
pnwlvfslvgyrvlrvltflvaekvevrgpdGKvVETRSTMPAWINKASNFLQTRFHQKIRTGISPTARVIPNGVIVV
ETQDGSGTGFRCRNYLVtAGHVVTGTETPKIQWAGVTAYSKVVHRVPDKDIAFLAIPQELQDLPSYRLA
KKVEDGPVVITSLEDSGALSVAVTEGVIVTDSITYAVQTRNGMSGSPVTNLDGRILAVHQTNTGFTGGA
VILTDEdFPQPKKSAREQQleARIKELEAAMNQSSNHEDIVELVRAAVAREFKVLRTELsattfiqak**gknk**kh
hrrrggKKRRRAVW**SEEEY**KELLEKGFSSKQLRDMAEVLRSHEEDPFGSDTESEGGFPEWSDVSDAESIERE
WFGQSWEDCKPVKEEPQDTLPVHLKEKYTLDAYVISKEELRSFAKEFKDYVDKVEALIDKTVQQGKWL
PSVNPTAIIIEELNDLWFGLNmLmwekGLVPFTqRkkikrvqknskgapkrpLptP

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 (AAFTLSAGVFMPDVRYSDLVRGQLVVFLVLFNYLVVMMSLPNWLVSFLVVGyrvlrvltflvaekv EVRGPdGKV), 633- 647 (SATTFIQAK**GKNKK**) and residues 807-813(MLMWEK).