protein gene symbol residue (+/-)7 seq ACC# site group ID site ID unique MS peptides ambiguous MS pep ambiguous prot ambiguous ACC ambiguous modsite Channel 126: Normal Pool Channel 127: H2342 Channel 128: H2073 Channel 129: Lou-NH91 Channel 130: HCC15 Channel 131: H1703

G3BP-2 G3BP2 R468 AQKLGSGrGTGQMEG Q9UN86 6009010 6009003 LGSGrGTGQMEGR 2489.9270341 2652.245024 1093.110282 1079.5641 5390.519608 5350.43779

PROSER2 PROSER2 R378 GPALPSTrARQSFPG Q86WR7 27277412 27277413 SLCFRPGPALPSTr 1253.07028 393.51169 333.24256 273.786 747.74324 1399.7662

CDC42EP5 CDC42EP5 R38 RHTLHVGrGGDAFGD Q6NZY7 9479940 9479943 HTLHVGrGGDAFGDTSFLSR 1461.08699 453.81908 156.381732 255.876 295.016484 634.5217

CAPRIN1 CAPRIN1 R633 RGPANGFrGGYDGYR Q14444 6009594 6009595 ANGFrGGYDGYRPSFSNTPNSGYTQSQFSAPR; GPANGFrGGYDGYRPSFSNTPNSGYTQSQFSAPR 363.1190398 876.847686 335.071064 265.4846 707.880252 2361.742212

hnRNP A1 HNRNPA1 R336 KGGNFGGrSSGPYGG P09651 9300229 9300230 GGNFGGrSSGPYGGGGQYFAKPR; GGNFGGrSSGPYGGGGQYFAKPrNQGGYGGSSSSSSYGSGR GGNFGGrSSGPYGGGGQYFAK HNRNPA1; HNRNPA1L2 P09651; Q32P51 R336; R284 1582.121332 2073.13106 1793.62156 277.2831 1761.729 3663.4423

PSF SFPQ R242 HRGGGEPrGGRQHHP P23246 6009315 6009316 GGGEPrGGR 76.8391569 410.156175 396.099896 92.5419 555.787636 1087.7022

snRNP B1 SNRPB R108 AGGPGIGrAAGRGIP P14678 9291601 9291602 AGAAGGPGIGr; LAGAAGGPGIGr; VPLAGAAGGPGIGr 3972.7837963 610.7991318 704.2228088 546.7961 3103.687536 2847.14677

CCDC9 CCDC9 R107 GGRAGMGrASRSWEG Q9Y3X0 12190873 12190874 TPPQQGGrAGMGr

ZAP3 YLPM1 R636 PSTSLSPrQSGPQWK P49750 9300470 9300471 ASQFYITPSTSLSPr; GPASQFYITPSTSLSPr; WGMIPrGPASQFYITPSTSLSPr 3408.63622 1076.112609 707.484108 460.7881 1522.73836 1706.9749

RBM47 RBM47 R394 GNRAPGPrGSYLGGY A0AV96 9479268 9479271 APGPrGSYLGGYSAGRGIYSR; APGPrGSYLGGYSAGr; APGPrGSYLGGYSAGrGIYSR; GPrGSYLGGYSAGR; GPrGSYLGGYSAGRGIYSR; GPrGSYLGGYSAGr 550.49192 100.98088 126.18984 49.5776 779.0164 377.9429

HSPA9B HSPA9 R513 IGIPPAPrGVPQIEV P38646 27278414 27278415 LLGQFTLIGIPPAPr 1535.021301 962.954278 424.4029208 513.8211 554.322132 1788.20538

C8orf33 C8orf33 R27 PCASRGArLPGPVSS Q9H7E9 27277464 27277465 GArLPGPVSSAR 1005.19133 418.06765 458.80248 202.8196 495.49484 1365.0937

SMRT NCOR2 R1737 LNYAAGPrGIIDLSQ Q9Y618 27279736 27279737 ESSLALNYAAGPrGIIDLSQVPHLPVLVPPTPGTPATAMDR 47.0031188 16.3026006 7.9531492 26.15582 23.5873984 58.738412

KNOP1 KNOP1 R430 AMSWKYSrGAGLGFS Q1ED39 15380717 15380718 YSrGAGLGFSTAPNK 988.37365 656.40146 1189.76636 265.949 1057.9722 2707.0517

CHD-7 CHD7 R148 SSSMWGPrAVQVPDQ Q9P2D1 27277573 27277574 HGQSFVDSSSMWGPr 576.29583 256.68643 254.19876 109.785 758.62628 504.8891

TAGLN TAGLN R183 GLQMGSNrGASQAGM Q01995 8143883 8143886 HVIGLQMGSNrGASQAGMTGY 3719.426117 699.270429 324.67664 151.94581 403.936592 692.72596

C15orf52 C15orf52 R290 GPARAGSrRGPRSHQ Q6ZUT6 48897846 48899695 STLQDCSQLrGEGPArAGSr

HNRPUL2 HNRNPUL2 R695 RNFYDRYrGDYDRFY Q1KMD3 8093045 8093049 YrGDYDR 717.589543 1471.74742 597.587992 235.2451 776.031764 1383.15905

DDX17 DDX17 R100 DRGGFGArGGGGLPP Q92841 8144604 8152701 GGFGAr; GGFGArGGGGLPPK; GGFGArGGGGLPPKK 14323.441649 8417.50052 6963.654 2730.2872 7592.09792 21283.8251

PRRC2C PRRC2C R242 AALASQYrAMMPPYM Q9Y520 9483679 9483682 LNGQQAALASQYr 402.664768 366.842333 274.751884 30.25638 333.73754 654.1062

RBMX RBMX R298 SRSAPPTrGPPPSYG P38159 27279355 27279356 SAPPTrGPPPSYGGSSR 403.507885 376.08285 168.797728 103.7672 267.383796 621.2875

RBM3 RBM3 R47 DRETQRSrGFGFITF P98179 6009492 6009493 SrGFGFITFTNPEHASVAMR 524.26055 95.497688 150.10944 67.3363 184.254 415.2719

RBM27 RBM27 R943 LGILPVGrGKTMSSQ Q9P2N5 13247033 13247035 LGILPVGrGK 592.344401 308.404382 497.12964 283.7542 2186.37912 1652.7593

RBMXL1 RBMXL1 R125 GTRGPPSrGGHMDDG Q96E39 6010020 6010021 GPPSrGGHMDDGGYSMN; GPPSrGGHMDDGGYSMNFNMSSSR RBMXL1; RBMX Q96E39; P38159 R125; R125

WDR33 WDR33 R1030 KRFGHRLrEFEGRGG Q9C0J8 15494943 15494945 LrEFEGrGGPLPQEEK

TRA2B TRA2B R228 YYDRGYDrGYDDRDY P62995 40350966 40350967 GYDrGYDDRDYYSR 284.684851 285.75118 75.618176 75.6192 103.608312 461.3662

PITPNM1 PITPNM1 R1230 TPPTTLArGKARSIS O00562 41477402 41477403 EGPGTPPTTLAr; EGPGTPPTTLArGK 2109.03341 614.524625 1475.02216 111.5708 518.3794 1850.0464

RPS10 RPS10 R158 QFRGGFGrGRGQPPQ P46783 27281807 27281710 GGFGrGrGQPPQ

RBM15B RBM15B R95 SGAGGGGrGGKASGD Q8NDT2 40350454 40350455 SSGSGAGGGGrGGK 99.829774 233.52329 133.796 129.91 216.61448 629.0408

NCBP2 NCBP2 R146 RQDYDAGrGGYGKLA P52298 6009445 6009446 QDYDAGrGGYGK 426.39454 1208.67318 1449.84768 709.729 1173.66108 3381.0253

HNRPUL2 HNRNPUL2 R704 DYDRFYGrDYEYNRY Q1KMD3 41554256 41554257 FYGrDYEYNR 472.50918 363.80773 176.17424 97.5585 281.25016 545.2357

PSF SFPQ R706 EGPNKKPrF\_\_\_\_\_\_ P23246 27279167 27279168 EEYEGPNKKPr; EEYEGPNKKPrF 4719.5412 1250.659124 1297.01892 290.0359 1201.45088 2733.7041

KHDRBS1 KHDRBS1 R302 PPPPPVPrGRGVGPP Q07666 27279504 27279505 GAAPPPPPVPr; GrGAAPPPPPVPr 1713.48617 403.28431 369.136344 253.3224 721.460108 1436.5685

hnRNP A2/B1 HNRNPA2B1 R228 PGPGSNFrGGSDGYG P22626 6009297 6009298 FGPGPGSNFrGGSDGYGSGR; GGGGNFGPGPGSNFrGGSD; GGGGNFGPGPGSNFrGGSDGYGSGR; GGGGNFGPGPGSNFrGGSDGYGSGr; GGGGNFGPGPGSNFrGGSDGYGSGrGFGD; GGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGR; GGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGr; SGrGGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGR 4446.298879 2345.03698 1932.317048 786.4778 2836.289308 5164.82043

RBMXL1 RBMXL1 R372 SSSRGAPrGAGPGGS Q96E39 40350417 40350418 DSYSSSSrGAPrGAGPGGSr; GAPrGAGPGGSR DSYSSSSrGAPr RBMXL1; RBMX Q96E39; P38159 R372; R373 142.033793 72.240311 131.20688 26.9863 139.622712 527.2382

SON SON R950 RLGQDPYrLGHDPYR P18583 15380554 15380555 LGQDPYrLGHDPYR 281.930924 117.412009 70.807348 39.3358 125.113632 317.6024

TPR TPR R2163 PQVAGVPrFRFGPPE P12270 12205560 12205561 TDGFAEAIHSPQVAGVPr 1265.18271 518.30493 299.289996 302.256 567.05132 1090.2276

GATAD2B GATAD2B R286 PPKPGLVrTTTPNMN Q8WXI9 13247206 13247208 GPPKPGLVr 643.62397 432.76662 397.4572 124.632 505.64152 1073.8148

NEBL NEBL R795 DFEKTKGrGFTPVVD O76041 6009162 6009163 GrGFTPVVDD; GrGFTPVVDDPVTER 2731.69589 483.280655 108.51798 61.870372 784.615524 464.924323

Bcl-9 BCL9 R1254 QTLQYFPrGEVPGRK O00512 40351341 40351342 IIPSEKPSQTLQYFPrGEVPGR 1561.41249 1415.57988 840.0504 399.7478 3048.1696 5233.1049

hnRNP A3 HNRNPA3 R377 SGGYGSRrF\_\_\_\_\_\_ P51991 9483326 9483330 SSGSPYGGGYGSGGGSGGYGSrrF 1452.96844 308.408958 286.67126 79.8844 526.851148 557.1175

FOXK1 FOXK1 R191 LPKQCTFrFPSTAIK P85037 27278035 27278036 QCTFrFPSTAIK 1817.53121 537.966 854.99736 681.233 657.94668 2502.1148

KRT6B KRT6B R24 GFSANSArLPGVSRS P04259 41682275 41682276 GFSANSArLPGVSR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R24; R24; R24

HSPA2 HSPA2 R472 TGIPPAPrGVPQIEV P54652 40350978 40350979 DNNLLGKFDLTGIPPAPr 15120.380528 48829.37774 775.11828484 1743.7731 8533.088756 8508.68992

RBMXL1 RBMXL1 R368 DSYSSSSrGAPRGAG Q96E39 12197890 12197891 DSYSSSSrGAPrGAGPGGSr DSYSSSSr; DSYSSSSrGAPR; DSYSSSSrGAPr RBMXL1; RBMX Q96E39; P38159 R368; R369

KIF1C KIF1C R963 GGRGGGLrRPPARFV O43896 12197334 12197335 QEQLrLQGLQGSGGrGGGLr

DDX9 DHX9 R1227 GVSRGGFrGNSGGDY Q08211 12198277 12198278 AGYGAGVGGGYrGVSrGGFr

hnRNP A2/B1 HNRNPA2B1 R350 GSGGYGGrSRY\_\_\_\_ P22626 9300448 9300449 NMGGPYGGGNYGPGGSGGSGGYGGr 140.3595215 277.007588 150.538232 60.0049 210.19224 377.35387

DDX3 DDX3X R617 SSSFSSSrASSSRSG O00571 12205516 12205517 QSSGASSSSFSSSr; QSSGASSSSFSSSrASSSr 73.4467514 176.839377 195.780996 171.221 376.338836 283.52215

SART3 SART3 R918 TQLSLLPrALQRPSA Q15020 27279540 27279541 TQLSLLPr 957.80707 196.801176 287.361692 105.1312 834.28604 644.6118

KHDRBS1 KHDRBS1 R284 VPEPSRGrGVPVRGR Q07666 6009551 6009552 FLVPDMMDDICQEQFLELSYLNGVPEPSrGr; KFLVPDMMDDICQEQFLELSYLNGVPEPSrGr; YLNGVPEPSrGr 82.57315 8.7572771 10.9170344 7.61357 84.228596 54.291661

DERPC CHTF8 R172 LGAGPDPrGGGPMGP P0CG12 13247071 13372001 AGGLLGAGPDPr 1439.07918 433.024735 625.913684 248.9471 927.45444 1499.9657

hnRNP D0 HNRNPD R272 QQQQWGSrGGFAGRA Q14103 6009570 6009571 EQYQQQQQWGSr; EQYQQQQQWGSrGGFAG; EQYQQQQQWGSrGGFAGr; EQYQQQQQWGSrGGFAGrAr 2221.383934 1446.353909 580.332152 430.0413 1676.681388 4999.76254

NFI-C NFIC R451 PPPPGLPrLALPPAT P08651 27278820 27278821 MPSHCLSAQMLAPPPPGLPr 150.536419 35.242207 39.357228 34.5971 80.848884 171.7548

PNUTS PPP1R10 R726 PPPFRGArGGRSGGG Q96QC0 27279101 27279102 GGNEPPPPPPPFrGArGGr

TTDN1 MPLKIP R117 THPQGSPrTSTPFGS Q8TAP9 9300570 9300571 SPAGSQQQFGYSPGQQQTHPQGSPr 1082.9950791 208.939874 108.2644 61.12312 153.79346 520.25402

HNRNPA1L2 HNRNPA1L2 R196 ASSSQRGrRGSGNFG Q32P51 15379995 15379996 QEMASASSSQrGr HNRNPA1; HNRNPA1L2 P09651; Q32P51 R196; R196

RBM47 RBM47 R383 GSIRGRGrGAAGNRA A0AV96 27279331 27279332 GrGrGAAGNR

ZAP3 YLPM1 R589 GPRPKGPrFEGNRPD P49750 40350755 40350756 GPrFEGNrPDGPrPr

EIF4H iso2 EIF4H R146 RDDFLGGrGGSRPGD Q15056-2 6009618 40273030 1491.04428 542.89664 309.66086 377.8644 334.035692 2198.4343

SRRT SRRT R840 RGNYDAFrGQGGYPG Q9BXP5 15493061 15493063 GNYDAFrGQGGYPGKPR

HSP70 HSPA1B R469 SGIPPAPrGVPQIEV P0DMV8 2584352 2584968 DNNLLGRFELSGIPPAPr; DNNLLGRFELSGIPPAPrGVPQIEVT; FELSGIPPAPr; FELSGIPPAPrGVPQ; FELSGIPPAPrGVPQIEV; FELSGIPPAPrGVPQIEVT; FELSGIPPAPrGVPQIEVTF HSPA6; HSPA1B P17066; P0DMV8 R471; R469 62676.8022441 65816.8169659 37212.9350848 7703.712439 24871.4409756 50710.532181

FBP1 FUBP1 R363 PGGRGRGrGQGNWNM Q96AE4 6010005 6010006 GrGQGNWNMGPPGGLQEFNFIVPTGK; GrGrGQGNWNMGPPGGLQEFNFIVPTGK; SVQAGNPGGPGPGGrGrGr 271.793742 64.97205 45.00022 24.278 316.25596 203.42465

SAFB1 iso2 SAFB R751 LPPPPRGrRDWGDHG Q15424-2 40352103 40353228 MSEGrGLPPPPrGr SAFB; SAFB Q15424-3; Q15424-2 R820; R751 1812.940162 904.648888 777.920944 453.4375 1268.034388 3926.5945

PAI-RBP1 SERBP1 R195 RGKREFDrHSGSDRS Q8NC51 40350566 40350567 EFDrHSGSDR 156.972244 115.918803 76.840816 38.869 126.712632 434.5114

TRIP6 TRIP6 R238 SGPAGRGrGGEHGPQ Q15654 6009671 6009672 EEAAGVSGPAGrGr; EEAAGVSGPAGrGrGGEHGPQVPLSQPPEDELDR; SQREPGPGAKEEAAGVSGPAGrGr 234.165778 111.528703 36.64138 571.401 45.08032 219.1348

RBM16 SCAF8 R988 RPFLAPGrQSVDNVT Q9UPN6 40351445 40351446 GIPPPSVLDSALHPPPrGPFPPGDIFSQPErPFLAPGr

SRXN1 SRXN1 R11 RAGGTLGrAGAGRGA Q9BYN0 27279843 27279844 AGGTLGrAGAGrGAPEGPGPSGGAQGGSIHSGR

PABPN1 PABPN1 R269 PRARYRArTTNYNSS Q86U42 40350431 40350432 ArTTNYNSSr

SAFB1 iso3 SAFB R811 DKRMSEGrGLPPPPR Q15424-3 15494641 26358478 MSEGrGLPPPPrGr SAFB; SAFB Q15424-2; Q15424-3 R742; R811

ataxin-2 ATXN2 R640 NHRVSAGrGSISSGL Q99700 6010049 6010050 VSAGrGSISSGLEFVSHNPPSEAATPPVAR 535.438629 205.899837 185.584104 159.4461 328.278472 1141.7039

NICE-4 UBAP2L R174 GRGTERGrRGRGRGR Q14157 41682327 41682328 SGGPSGrGTErGr

CCT7 CCT7 R53 DKLIVDGrGKATISN Q99832 6010067 6010068 LIVDGrGK 919.075366 1151.31159 2696.64908 234.0873 1570.955672 6641.7951

E1B-AP5 HNRNPUL1 R661 NYRGGFNrSGGGGYS Q9BUJ2 15493497 15493499 GGFQNrGGGSGGGGNYrGGFNr

LSD1 KDM1A R838 GAMYTLPrQATPGVP O60341 48897893 48908204 IADQFLGAMYTLPr 312.842981 81.175809 71.973816 42.2285 104.407484 216.70255

Vimentin VIM R64 PGGVYATrSSAVRLR P08670 12195406 12195407 ASSPGGVYATr; SLYASSPGGVYATr; SLYASSPGGVYATrSSAVR; SLYASSPGGVYATrSSAVr; SSPGGVYATr; TYSLGSALRPSTSRSLYASSPGGVYATr; TYSLGSALRPSTSRSLYASSPGGVYATrSSAVR 10251.708742 673.2975249 2137.533576 1535.2971 3189.050192 6481.78226

CCT4 CCT4 R19 TAGAAGGrGKGAYQD P50991 15379637 15379638 SGATAGAAGGr; SGATAGAAGGrGK 796.3405307 2441.133409 4488.0374 105.85059 394.4635256 5864.2088

PCNXL3 PCNXL3 R274 SSRREQRrGAGGYQP Q9H6A9 27278967 27278968 rGAGGYQPLDRR 954.25022 99.854612 204.60744 102.063 419.9876 482.7286

NOL5A NOP56 R342 LFRALKTrGNTPKYG O00567 48885438 48889274 TrGNTPK 180.672987 158.19804 145.9728 46.7698 231.06288 568.0264

CCT7 CCT7 R539 AAGRGRGrGRPH\_\_\_ Q99832 12191628 12191629 STVDAPTAAGrGrGr; STVDAPTAAGrGrGrGrPH

GATAD2A GATAD2A R293 IIQQGLIrVANVPNT Q86YP4 13247219 13247221 IIQQGLIr; IIQQGLIrVANVPNTSLLVNIPQPTPASLK 1070.71393 599.9293157 354.545636 291.81937 591.3899368 1786.21818

Vimentin VIM R28 ASRPSSSrSYVTTST P08670 40350622 40350623 MFGGPGTASRPSSSrSYVTTSTR 348.290899 116.688 334.3071 118.5896 261.831412 1130.56224

FOXK1 FOXK1 R177 VDGAFQRrGAPALQL P85037 27278039 27278040 rGAPALQLPK 922.03441 166.76231 214.95028 115.744 274.58192 728.7228

EWS EWSR1 R471 RGMPPPLrGGPGGPG Q01844 6008935 6008936 EGrGMPPPLrGGPGGPGGPGGPMGr; GMPPPLrGGPGGPGGPGGPMGR; GMPPPLrGGPGGPGGPGGPMGr 1767.973603 769.958904 801.894236 395.4914 1267.901548 3521.5461

Zyxin ZYX R253 SLANTQPrGPPASSP Q15942 9483712 9483716 SLANTQPrGPPASSPAPAPK 1546.45458 0 23.912532 10.0003 27.181688 66.28784

PNUTS PPP1R10 R665 PGGPVGPrLLGPPPP Q96QC0 27279085 27279086 GMQHFPPGPGGPMPGPHGGPGGPVGPr 140.736739 65.132353 70.3483 20.3452 138.74892 160.85234

SNF8 SNF8 R4 \_\_\_\_MHRrGVGAGAI Q96H20 27279743 27279744 rGVGAGAIAK 1954.856882 2390.7884 665.303648 510.7854 1826.69924 3592.6161

ILF2 ILF2 R24 GGPGGGFrPFVPHIP Q12905 15380031 15380032 FGSrGGPGGGFrPFVPHIPFDFYLCEMAFPR

WDR33 WDR33 R1262 EDRGGKGrGGPGPAQ Q9C0J8 9291891 9291892 GrGGPGPAQR 195.2727238 255.036353 278.979168 125.9567 472.744268 1001.47543

SF1 iso5 SF1 R662 LPAAAMArAMRVRTF Q15637-5 27279576 27426006 SLPAAAMAr SF1; SF1 Q15637-5; Q15637-4 R662; R537

CMAS CMAS R16 ATSVSNPrGRPSRGR Q8NFW8 27277592 27277593 GAATSVSNPr; GAATSVSNPrGR 538.799932 355.861077 1012.80968 208.3231 572.462336 1793.4687

ZNF9 CNBP R27 PTGGGRGrGMRSRGR P62633 9479185 9479188 ECPTGGGrGr

PRRC2C PRRC2C R1190 QGYRGRGrGEYYSRG Q9Y520 12191661 12191664 GrGrGEYYSrGr

SPT5 SUPT5H R681 HPSAGGQrGGFGSPG O00267 15380589 15380590 ISSPMHPSAGGQrGGFGSPGGGSGGMSr

DATF1 DIDO1 R1882 QAPFLGSrGGAPFQF Q9BTC0 6010077 6010078 EFQDAPYNEVTGAPAQFEGTEQAPFLGSr 86.632744 60.640437 106.276556 20.43867 71.489076 257.48339

ZSWIM8 ZSWIM8 R1454 RAGGEAGrGMPEGRG A7E2V4 41398303 41398209 AGGEAGrGMPEGr

MSK2 RPS6KA4 R743 RSATASRrGSPAPAN O75676 41682338 41682339 rGSPAPANPGR 117.33458 87.784268 52.690576 59.4291 80.345568 291.0926

K19 KRT19 R51 GVSVSSArFVSSSSS P08727 6009239 6009240 APSIHGGSGGrGVSVSSAr; APSIHGGSGGrGVSVSSArFVSSSSSGAYGGGYGGVLTASDGLLAGNEK; FGPGVAFrAPSIHGGSGGrGVSVSSAr; FGPGVAFrAPSIHGGSGGrGVSVSSArFVSSSSSGAYGGGYGGVLTASDGLLAGNEK; GGSGGrGVSVSSAr; GSGGrGVSVSSAr; GVSVSSAr; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGrGVSVSSAr; RAPSIHGGSGGrGVSVSSAr; SIHGGSGGrGVSVSSAr; rAPSIHGGSGGrGVSVSSAr 2196.2608657 4064.239894 161.8171108 1762.81958 706.7738752 1284.746995

DATF1 DIDO1 R1835 PSYLGGPrGVAPSQF Q9BTC0 8143959 8143963 GPIPSLFSGQHGPPPYGDSrGPSPSYLGGPrGVAPSQFEEr; GPSPSYLGGPrGVAPSQFEER; SPSYLGGPrGVAPSQFEER 1572.198837 777.125635 1321.26092 273.529 1068.357008 3585.10177

LIX1L LIX1L R18 PGVGTSGrGTLRALR Q8IVB5 27278554 27278555 LQPGVGTSGrGTLR 288.918938 36.590411 172.81508 73.4012 75.687968 900.1924

DDX9 DHX9 R1174 YDNGSGYrRGGSSYS Q08211 27277725 27277726 YDNGSGYr 126.857049 185.54393 129.97928 47.0713 268.84848 360.0259

hnRNP D-like HNRPDL R336 AGGRGGTrGRGRGQG O14979 41477585 41477586 GAAAGGrGGTr

BAG3 BAG3 R261 DWEPRPLrAASPFRS O95817 27277274 27277275 IQGDDWEPRPLrAASPFR 963.69581 74.337692 134.11716 114.755 190.94848 342.0652

XRN2 XRN2 R936 QGYPREGrKYPLPPP Q9H0D6 40350324 40350325 QGYPREGr 218.598259 433.58601 259.758548 104.249 253.550396 796.789

STAU2 STAU2 R137 FRGMYNQrYHCPVPK Q9NUL3 27279855 27279856 ANYNFrGMYNQrYHCPVPK 980.185239 642.842772 1214.60232 153.379 811.446744 2672.4528

SNX3 SNX3 R43 PQTVGVGrGRFTTYE O60493 6009146 6009147 LITKPQNLNDAYGPPSNFLEIDVSNPQTVGVGr 8093.360165 4484.261067 2098.82772 1961.7722 2616.955872 11819.02426

eIF4G EIF4G1 R675 PSFANLGrTTLSTRG Q04637 12190745 12190746 LQGINCGPDFTPSFANLGr; LQGINCGPDFTPSFANLGrTTLSTR 552.985543 359.418059 358.945156 178.3785 213.2252888 1679.9269

EIF4B EIF4B R261 GRDRYDDrGSRDYDR P23588 40350360 40350361 YDDrGSR 87.227998 69.918134 73.7335 30.1792 209.633 140.32852

hnRNP 2H9 HNRNPH3 R138 SMYDRMRrGGDGYDG P31942 29428923 29540481 rGGDGYDGGYGGFDDYGGYNNYGYGNDGFDDR 139.849919 173.871412 32.961928 42.2392 264.102812 253.81903

FOXK2 FOXK2 R144 LPRVCTFrFPSTNIK Q01167 12205598 12205599 VCTFrFPSTNIK 1175.00141 458.47802 759.97988 449.64 835.78008 3240.6931

K18 KRT18 R45 GAGGSGSrISVSRST P05783 15380070 15380071 AGAGGSGSrISVSR; PVSSAASVYAGAGGSGSr; PVSSAASVYAGAGGSGSrISVSR; SLGSVQAPSYGARPVSSAASVYAGAGGSGSr; SLGSVQAPSYGARPVSSAASVYAGAGGSGSrISVSR 3518.4598812 3063.637434 3082.588912 1483.2837 7426.928928 2831.147142

DATF1 DIDO1 R1824 PPPYGDSrGPSPSYL Q9BTC0 27277660 27277661 GPIPSLFSGQHGPPPYGDSrGPSPSYLGGPrGVAPSQFEEr

LSM4 LSM4 R88 EEVVAKGrGRGGLQQ Q9Y4Z0 40724735 40725340 GrGrGGLQQQK

KRT6B KRT6B R16 RSHSSSRrGFSANSA P04259 41682273 41682274 rGFSANSAR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R16; R16; R16

FAM195A FAM195A R27 TQQQVEGrLGELLKC Q9BUT9 48897813 48897762 TGPTQQQVEGr 140.219959 37.320998 96.004148 31.7987 75.673372 142.34746

FBP3 FUBP3 R339 GLAAARGrGRGRGDW Q96I24 27277983 27277984 DGFGGLAAArGr

HuR ELAVL1 R217 PVHHQAQrFRFSPMG Q15717 9300340 9300341 FGGPVHHQAQr; FGGPVHHQAQrFR 2844.541183 919.610406 832.648592 402.6372 890.1182 2903.7937

PAI-RBP1 SERBP1 R201 DRHSGSDrSSFSHYS Q8NC51 27278931 27278932 HSGSDrSSFSHYSGLK 414.05243 268.89005 625.6172 57.9857 464.7596 751.3479

BYSL BYSL R8 MPKFKAArGVGGQEK Q13895 40350686 40350687 AArGVGGQEK 73.690595 391.08355 229.48556 177.863 419.76784 1355.7373

FAM50A FAM50A R13 GAASEAGrAMHLMKK Q14320 48897829 48899630 GAASEAGr 106.406597 228.70848 136.893396 112.1188 212.262412 843.1685

NUP107 NUP107 R60 PRTPSSFrQPFTPTS P57740 15380274 15380275 TPSSFrQPFTPTSR 614.08457 192.86982 180.74736 111.786 273.97348 543.8442

FMR1 FMR1 R546 RGQGGRGrGGGFKGN Q06787 41477456 41477457 GQGGrGrGGGFK

hnRNP L HNRNPL R46 GGGGGGGrYYGGGSE P14866 15379982 15379983 MAAAGGGGGGGrYYGGGSEGGR 117.197729 62.418356 188.301936 7.4185 473.961148 278.15027

hnRNP D-like HNRPDL R408 STYGKASrGGGNHQN O14979 6008909 6008910 ASrGGGNHQNNYQPY 409.204587 134.358367 120.755416 58.7994 159.54494 513.82161

SIRT7 SIRT7 R388 ILGGWFGrGCTKRTK Q9NRC8 27279656 27279657 GAPLSSAPILGGWFGrGCTK 361.484101 140.259977 194.98194 110.3456 223.163656 1005.6313

TFG TFG R400 TQPGPGYr\_\_\_\_\_\_\_ Q92734 9300581 9300582 NRPPFGQGYTQPGPGYr; NrPPFGQGYTQPGPGYr; TQPGPGYr 943.153167 413.510383 671.2616 220.9207 599.706672 1106.85913

AHNAK AHNAK R270 KGLDLGGrGGVQVPA Q09666 27277149 27277150 GLDLGGrGGVQVPAVDISSSLGGR 566.87895 70.764551 41.838716 39.6061 71.792148 256.6984

LSG1 LSG1 R5 \_\_\_MGRRrAPAGGSL Q9H089 12195765 12195766 rAPAGGSLGr

SAFB1 iso2 SAFB R742 DKRMSEGrGLPPPPR Q15424-2 15494641 40311320 MSEGrGLPPPPrGr SAFB; SAFB Q15424-2; Q15424-3 R742; R811

TAF15 TAF15 R467 GGGYGGDrGGGYGGD Q92804 6009931 6009932 GGGYGGDrGGGYGGDrGGGYGGDrGGYGGDr; SGGGYGGDrGGGYGGDrGGGYGGDR; SGGGYGGDrGGGYGGDrGGGYGGDr

DERPC CHTF8 R214 PGPNPNLrSGFLGTN P0CG12 40351035 40351036 GLGPGPNPNLr 1679.38826 36.445266 72.434972 37.5865 115.951116 230.7567

EIF4G2 EIF4G2 R360 EGPFMPPrMKMDRDP P78344 15379876 15379877 SDFFLEGPFMPPrMK 7704.05416 2196.51146 1913.5246 2487.926 2176.80808 4700.004

PSF SFPQ R695 PAGYGRGrEEYEGPN P23246 8093828 8093832 FGQGGAGPVGGQGPrGMGPGTPAGYGrGr 5701.680952 2812.493112 2938.18558 734.18771 2034.528404 12070.9543

HSPA6 HSPA6 R471 SGIPPAPrGVPQIEV P17066 9300428 9300429 DNNLLGRFELSGIPPAPr; DNNLLGRFELSGIPPAPrGVPQIEVT; FELSGIPPAPr; FELSGIPPAPrGVPQ; FELSGIPPAPrGVPQIEV; FELSGIPPAPrGVPQIEVT; FELSGIPPAPrGVPQIEVTF HSPA6; HSPA1B P17066; P0DMV8 R471; R469

ANKRD25 KANK2 R243 LGHPTAGrGRSELCL Q63ZY3 6009719 6009720 FLGHPTAGrGR 961.16933 20.650201 96.47758 40.2707 34.038692 409.6783

PNN PNN R56 GPGGGRGrGSLLLRR Q9H307 6010123 6010124 LLALSGPGGGrGr; LLALSGPGGGrGrGSLLLR; LLALSGPGGGrGrGSLLLr; RLLALSGPGGGrGr

LSM14B LSM14B R351 ETFGVSGrFLRGRSS Q9BX40 9483522 9483525 KLNTETFGVSGr 253.608509 470.3842 357.771 357.541 404.36824 1187.2048

NICE-4 UBAP2L R168 KSGGPSGrGTERGRR Q14157 15380250 15380251 SGGPSGrGTErGr 42.788108 121.027049 56.298356 40.5501 51.630316 368.1794

EIF4H EIF4H R174 GGSRPGDrRTGPPMG Q15056 27277842 27277843 DDFLGGRGGSRPGDrR; DDFLGGrGGSrPGDrR 1186.234357 898.283529 603.89798 710.6495 912.465332 3644.0809

K6a KRT6A R16 RSHSSSRrGFSANSA P02538 15560213 15561382 rGFSANSAR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R16; R16; R16 337.3623737 191.002383 85.8186144 1309.713 125.606124 487.230896

HSPB8 HSPB8 R71 LRSGMVPrGPTATAR Q9UJY1 13247329 13247331 SGMVPrGPTATAr

THOC4 ALYREF R71 GAAGGGGrNRPAPYS Q86V81 27279995 27279996 NrPAIArGAAGGGGr 97.58529 120.708016 75.281144 46.7257 139.730952 381.6712

THOC4 ALYREF R50 QAAARVNrGGGPIRN Q86V81 8094305 10339438 VNrGGGPIR 281.537916 161.799924 142.415984 91.8194 339.926572 1062.8208

DERPC CHTF8 R186 PGSGPNLrAGVLLTS P0CG12 13247073 13372000 GGGPMGPGSGPNLr 469.869136 169.776607 170.10568 69.2893 474.47824 684.2155

RBM3 RBM3 R145 RNQGGYDrYSGGNYR P98179 29429616 29429618 NQGGYDrYSGGNYR; NQGGYDrYSGGNYRDNYDN 1218.447296 313.909453 619.570588 294.1828 658.532488 1642.77983

hnRNP A1 HNRNPA1 R370 SSSYGSGrRF\_\_\_\_\_ P09651 12190734 12190735 NQGGYGGSSSSSSYGSGr; NQGGYGGSSSSSSYGSGrrF 279.863804 757.625011 747.933404 87.2479 788.340128 1089.0224

MPDZ MPDZ R1170 GISIVGGrGMGSRLS O75970 29429289 29429292 SLGISIVGGrGMGSR 948.34234 262.268006 434.0372 231.283 142.016128 1242.5244

SF3B2 SF3B2 R502 RNSVPVPrHWCFKRK Q13435 12191765 12191766 NSVPVPr; NSVPVPrHWCFK 1413.763659 2669.9387 197.1756488 776.925 1827.85544 2372.6478

ILF2 ILF2 R16 RGGRFGSrGGPGGGF Q12905 6009561 6009562 FGSrGGPGGGFR; FGSrGGPGGGFrPFVPHIPFDFYLCEMAFPR 464.687619 313.589562 96.6987092 195.2134 144.676864 689.09863

TCEAL5 TCEAL5 R185 PFAPRGQrGVRGVRG Q5H9L2 8093262 8093265 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R179; R179; R185

SEC16A SEC16A R1036 SAYAQNYrYPEPERP O15027 40351169 40351170 YRPYDGAASAYAQNYrYPEPERPSSR 404.397895 122.351372 157.770284 167.6779 160.022836 685.0895

CIRBP CIRBP R121 FSRGGGDrGYGGNRF Q14011 27277579 27277580 GGGDrGYGGNR 208.057542 72.69977 109.39962 41.4698 101.189804 343.8017

ADAR ADAR R26 GYEHRQLrYQQPGPG P55265 41554328 41554329 QLrYQQPGPGSSPSSFLLK 294.198069 269.31047 181.96504 62.9156 326.37148 351.4883

NICE-4 UBAP2L R172 PSGRGTErGRRGRGR Q14157 15380253 15380254 SGGPSGrGTErGr

K6a KRT6A R40 FSSVSVSrSRGSGGL P02538 15560212 15561380 SGFSSVSVSr 900.43173 189.844941 362.59088 977.707 212.63092 649.658

CSTF2 CSTF2 R303 QVPMQDPrAAMQRGS P33240 15493402 15493404 GQVPMQDPr 401.872053 103.14447 326.64638 163.5895 427.54226 948.7615

GATAD2A GATAD2A R273 PPLLLAPrASVPSVQ Q86YP4 27278092 27278093 QHSSTGPPPLLLAPr 1996.51254 395.899933 727.74112 218.114 1001.0724 1188.6722

TCEAL3 TCEAL3 R176 VQDPFAPrGQRGVRG Q969E4 29430018 29430020 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R176; R176; R182

BAT2 iso1 PRRC2A R1164 GGRVFTPrGVPSRRG P48634 27277309 27277310 VFTPrGVPSR 353.078132 460.97337 294.45784 99.6334 274.718204 1890.8714

LARP5 LARP4B R419 NPSKSHLrHAIPSAE Q92615 12205479 12205480 SHLrHAIPSAER; SHLrHAIPSAERGPGLLESPSIFNFTADR 1371.028824 572.761475 572.580044 237.3827 1237.82854 2305.083

EPPK1 EPPK1 R2603 REPGPAGrGDGDSGR P58107 41554392 41554393 EPGPAGrGDGDSGR; GPREPGPAGrGDGDSGR; REPGPAGrGDGDSGR EPPK1 P58107 R4739; R3137; R2603; R3671; R4205 558.249043 639.6633815 686.939044 152.54161 167.6112472 731.60723

K7 KRT7 R30 QVRLSSArPGGLGSS P08729 40350880 40350881 LSSArPGGLGSSSLYGLGASRPR; LSSArPGGLGSSSLYGLGASRPr

ZAP3 YLPM1 R566 LESPRGPrFDGPRRF P49750 27280375 27280376 SSYLESPrGPrFDGPr

EEFSEC EEFSEC R556 KKRARAGrGEATRQE P57772 8094630 8094633 AGrGEATR 176.0241362 123.283017 140.521388 76.6252 42.4273904 466.29809

K6c KRT6C R42 SISVSRSrGSGGLGG P48668 27278468 27278469 SrGSGGLGGACGGAGFGSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R42; R42; R42

G3BP-2 G3BP2 R457 DGRGPPPrGGMAQKL Q9UN86 6009006 6008999 GPPPrGGMAQK 139.653096 218.92585 52.735836 62.6532 106.261012 933.8943

hnRNP P2 FUS R371 IKVSFATrRADFNRG P35637 27278364 27278365 VSFATrR FUS; TAF15 P35637; Q92804 R371; R320 552.12839 429.57772 285.37732 123.165 555.30728 931.9508

SFRS5 SRSF5 R73 RVTIEHArARSRGGR Q13243 27279624 27279625 VTIEHAr 258.742176 348.84707 220.21656 91.7299 1062.28376 727.835

ITIH4 ITIH4 R56 AHTVVTSrVVNRANT Q14624 9483867 9483871 FAHTVVTSr 346.69239 209.26048 157.05592 135.215 277.59132 489.9575

SEPT9 SEPT9 R10 KSYSGGTrTSSGRLR Q9UHD8 27279569 27279570 SYSGGTr; SYSGGTrTSSGR 341.847418 158.260102 392.424536 260.0682 477.973736 1289.1477

CHTOP CHTOP R97 RPIGALArGAIGGRG Q9Y3Y2 40351258 40351259 LGRPIGALAr 412.40639 121.229537 78.828412 58.5846 181.5562 352.6314

BTF3 BTF3 R19 SRGRGRArGGCPGGE P20290 6009286 6009287 ArGGCPGGEATLSQPPPR; TGAPAQADSrGrGrAr 598.384985 613.627586 185.718024 132.7709 288.193428 1363.9828

ZAP3 YLPM1 R619 SKWGMIPrGPASQFY P49750 15380791 15380792 WGMIPrGPASQFYITPSTSLSPr

SDE2 SDE2 R203 PTKSQTDrGASAGKR Q6IQ49 27277437 27277438 SQTDrGASAGK 56.417064 446.35019 141.73448 56.6393 352.08668 337.5227

BLES03 C11orf68 R237 FQLGGSArGSRVLDR Q9H3H3 27277388 28801524 FQLGGSAr; FQLGGSArGSR 2152.83849 420.956107 482.177596 315.1686 564.58312 1739.7499

TCEAL6 TCEAL6 R179 PFAPRGQrGVRGVRG Q6IPX3 8093314 8093317 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R179; R179; R185

ANKRD25 KANK2 R117 QYGALETrGGFNPRV Q63ZY3 12205621 12205622 GFYPQYGALETr; HSAYSYCGrGFYPQYGALETr; HSAYSYCGrGFYPQYGALETrGGFNPr 6685.35956 125.20937 466.73538 638.524 898.49368 2248.02

TRA2B TRA2B R251 GGGGGGWrAAQDRDQ P62995 40350970 40350971 GYDDRDYYSRSYrGGGGGGGGWr

plakophilin 3 PKP3 R261 FQSSHRSrGVGGAVP Q9Y446 6010233 6010234 SrGVGGAVPGAVLEPVAR 839.570358 418.44231 390.44128 224.4473 364.454576 704.4118

AKAP8L AKAP8L R237 YGMFQGMrGGGAFPG Q9ULX6 12197918 12197919 LPSLFSQNIIPEYGMFQGMrGGGAFPGGSR 123.071476 68.291366 43.1679836 37.1674 51.0081328 274.1646

PROSER2 PROSER2 R320 PERVARGrGLPGPAE Q86WR7 6009797 6009798 GrGLPGPAESLR 1390.510473 1507.66759 154.6607856 381.2237 1441.62724 737.45935

hnRNP A1 HNRNPA1 R194 ASASSSQrGRSGSGN P09651 475948 67435 QEMASASSSQr; QEMASASSSQrGr HNRNPA1; HNRNPA1L2 P09651; Q32P51 R194; R194 366.281223 603.138965 465.371256 212.0523 711.78214 2794.00688

hnRNP P2 FUS R216 GQQDRGGrGRGGSGG P35637 1308910 1308821 GGrGrGGSGGGGGGGGGGYNR

K18 KRT18 R27 QAPSYGArPVSSAAS P05783 8094438 8094442 SLGSVQAPSYGArPVSSAASVYAGAGGSGSRISVSR

RBM7 RBM7 R201 PSSQRKVrMNSYPYL Q9Y580 27279337 27279338 VrMNSYPYLADR 506.21472 170.027 97.793592 61.5751 228.98664 592.8733

hnRNP A/B HNRNPAB R322 NYGKSQRrGGHQNNY Q99729 6008994 6008991 rGGHQNNYKPY 745.543194 589.144699 1129.771192 612.916 1965.4785 4564.2074

DDX3 DDX3X R93 SDRGSGSrGRFDDRG O00571 9479223 9479227 SSFFSDrGSGSrGR; SSFFSDrGSGSrGr

UBAP2 UBAP2 R166 QVDKPSDrGKRARGR Q5T6F2 9479263 9479266 EFRGEENGIDCNQVDKPSDrGK; GEENGIDCNQVDKPSDrGK 1043.847431 1231.16708 407.3524 662.2182 751.706136 5378.7915

WDR33 WDR33 R1067 EFSEGDGrGAARGPP Q9C0J8 29430144 29540315 EFSEGDGrGAAR 1439.695488 1331.972356 1494.24712 364.2943 980.798884 5458.6912

EIF4H EIF4H R19 YSSFGGGrGSRGSAG Q15056 6009606 6009607 AYSSFGGGr; AYSSFGGGrG; AYSSFGGGrGS; AYSSFGGGrGSR; AYSSFGGGrGSr; AYSSFGGGrGSrGSAGGHGSR; SSFGGGrGSR; SSFGGGrGSRGSAGGHGSR 9445.033983 4442.866428 4053.377224 3403.5741 4334.152968 19389.88941

API5 API5 R500 GNFNYEQrGAFRGSR Q9BZZ5 13246926 13246928 YSSNLGNFNYEQr 2343.816772 838.595901 579.654616 580.545 1579.512536 3208.316

C1orf106 C1orf106 R578 LKDSPAGrGLSKAAV Q3KP66 27277434 27277435 DSPAGrGLSK 809.53587 539.48323 443.2814 262.463 197.64624 456.1429

PABPN1 PABPN1 R291 FNSRPRGrVYRGRAR Q86U42 27278922 27278923 SrFYSGFNSrPrGr

C1orf106 C1orf106 R554 EEEGTPLrYQRLVPS Q3KP66 40350736 40350737 AAPGPAYEEEGTPLrYQR 380.402396 291.112679 668.16408 124.1493 156.537344 296.37616

RUFY1 RUFY1 R12 EGGCAAGrGRELEPE Q96T51 40350356 40350357 EGGCAAGr; EGGCAAGrGR 348.286114 56.7680971 823.487968 207.7679 234.38306 1464.65817

hnRNP A3 HNRNPA3 R226 GSGNFMGrGGNFGGG P51991 6009421 6009422 GGGSGNFMGrGGNFGGGGGNFGR 251.490987 100.582196 102.621408 54.5014 189.502 735.0156

CDK18 CDK18 R463 LAFQQPGrGKNRRQS Q07002 6009539 6009540 GLAFQQPGrGK 1458.20642 360.48012 463.80836 140.23 232.94724 609.4724

EWS EWSR1 R300 SMSGPDNrGRGRGGF Q01844 2159116 2159032 SMSGPDNr 553.61812 17.037592 36.03688 21.2097 62.803472 219.15021

EIF4H EIF4H R166 RDDFLGGrGGSRPGD Q15056 6009618 6009619 DDFLGGr; DDFLGGrGGSrPGDrR; GFRDDFLGGr 398.17899 381.93727 128.04736 64.4896 330.31568 790.7607

CCT7 CCT7 R535 DAPTAAGrGRGRGRP Q99832 12190687 12190688 STVDAPTAAGr; STVDAPTAAGrG; STVDAPTAAGrGR; STVDAPTAAGrGr; STVDAPTAAGrGrGR; STVDAPTAAGrGrGr; STVDAPTAAGrGrGrGrPH 908.852373 632.35315 559.14824 346.1986 2541.21608 3004.8373

SRm300 SRRM2 R2717 QQSSSSErGSRRGQR Q9UQ35 40350340 40350341 DQQSSSSErGSR 19.8753588 49.85552 40.371796 13.5499 54.94164 396.4257

EPRS EPRS R1152 NQWCNVVrWEFKHPQ P07814 27277862 27277863 LNQWCNVVrWEFK 744.6417 581.75832 332.93876 324.061 575.97128 1455.3894

SRm300 SRRM2 R2221 PVPLMSLrTAPAANL Q9UQ35 27279823 27279824 MSQVPAPVPLMSLr 1740.842015 523.782116 454.465828 231.1633 603.251532 1173.0713

PRRC2C PRRC2C R1198 GEYYSRGrSYRGSYG Q9Y520 27277339 27277340 GrGrGEYYSrGr

hnRNP K HNRNPK R316 LPPPPPPrGGDLMAY P61978 6009461 6009462 NLPLPPPPPPrGGDLMAYDR 7513.060885 5010.124405 4026.171376 1586.4959 4194.257196 8521.41145

TAF6 TAF6 R524 VQTLVSArAAAPPQP P49848 15494730 15494732 VPGSIALPVQTLVSAr

SCS-beta SUCLA2 R106 AQVLAGGrGKGTFES Q9P2R7 27279555 27279556 AQVLAGGrGK 1113.55882 1705.68541 618.42272 360.9 179.103744 2034.3408

WDR33 WDR33 R915 PLLGDGPrAPFNQEG Q9C0J8 40351107 40351108 TPLLGDGPrAPFNQEGQSTGPPPLIPGLGQQGAQGR 106.515376 55.592823 61.774692 16.85341 76.51502 194.47811

DCP2 DCP2 R319 KGKNQSMrGNGRKQY Q8IU60 41554361 41554362 NQSMrGNGR 6.8217831 47.999523 23.34362 5.57626 74.38548 143.77921

PRRC2C PRRC2C R2823 EVLQSTQrFFSEQQQ Q9Y520 9483861 9483864 AEVLQSTQrFFSEQQQSK 725.580174 260.087256 303.4466 212.654 235.201748 1623.3745

RABL6 RABL6 R508 IPASKPRrGTAPTRT Q3YEC7 40350352 40350353 rGTAPTR 40.087454 49.930881 45.502172 4.68354 46.534016 73.09607

RALY RALY R141 LSPVPVPrAVPVKRP Q9UKM9 27279241 27279242 LSPVPVPr 674.73285 317.46715 261.6028 135.248 388.5734 687.9415

DDX3 DDX3X R88 KSSFFSDrGSGSRGR O00571 8144615 8144619 SSFFSDrGSGSR; SSFFSDrGSGSRGR; SSFFSDrGSGSrGR; SSFFSDrGSGSrGr 950.5716396 1448.034731 1349.781416 959.8353 3078.27344 2695.98847

CSTF2 CSTF2 R344 VTGEVEPrGYLGPPH P33240 15493399 15493401 GGTLLSVTGEVEPr CSTF2; CSTF2T P33240; Q9H0L4 R344; R352 352.44396 110.458634 246.47604 52.0967 136.34058 335.4205

AKAP8L AKAP8L R171 YRDQFRMrGNDTFGP Q9ULX6 9291900 9291901 MrGNDTFGPR; MrGNDTFGPrAQGWAR 1826.451088 1600.304992 1253.858116 548.9152 1285.526464 3743.57775

PABP 4 PABPC4 R436 AQMRPNPrWQQGGRP Q13310 29427436 29427437 ALPANAILNQFQPAAGGYFVPAVPQAQGrPPYYTPNQLAQMrPNPr

TAB2 TAB2 R173 SLSQQTPrFNPIMVT Q9NYJ8 27279867 27279868 GTSSLSQQTPr 110.109868 79.363999 89.096976 87.5534 112.666032 323.6629

NARR NARR R42 RVIVGSArARPPPDG P0DI83 40350674 40350675 VIVGSAr 259.779883 155.30515 207.24988 139.771 235.22192 1698.2165

hnRNP 2H9 HNRNPH3 R129 GGYYGAGrGSMYDRM P31942 12191546 12191547 GGYYGAGrGSMYDR; LLGQRPGPYDRPIGGRGGYYGAGr 1251.790452 1041.131663 298.341892 365.3561 640.117092 3900.1951

LARP5 LARP4B R493 ESSPGLGrGRKNSFG Q92615 8094471 8094474 EAGPGRVEPGSLESSPGLGrGR 2467.2417 721.981832 647.09028 316.4212 2365.44908 2081.845

DATF1 DIDO1 R1845 APSQFEErKDPHGEK Q9BTC0 27277664 27277665 GPIPSLFSGQHGPPPYGDSrGPSPSYLGGPrGVAPSQFEEr

G3BP-1 G3BP1 R460 KPGFGVGrGLAPRQ\_ Q13283 476717 68278 GPPrGGMVQKPGFGVGr 280.85398 409.7951 161.03756 232.966 271.56104 1546.888

Vimentin VIM R45 YSLGSALrPSTSRSL P08670 40350646 40350647 SYVTTSTrTYSLGSALrPSTSR

SFRS9 SRSF9 R194 STSYGYSrSRSGSRG Q13242 40350846 40350847 STSYGYSr 322.64298 167.33288 204.67316 110.973 464.04784 757.781

SLTM SLTM R1017 ISGNSMPrGSGSGFK Q9NWH9 27279695 27279696 IVQISGNSMPrGSGSGFKPFK 661.91224 2059.44739 1741.26132 375.2089 2484.03584 3708.037

K7 KRT7 R64 GPVGAGIrEVTINQS P08729 40350892 40350893 SAYGGPVGAGIrEVTINQSLLAPLR; SAYGGPVGAGIrEVTINQSLLAPLRLDADPSLQR; VAVrSAYGGPVGAGIrEVTINQSLLAPLR 1514.721098 464.377199 305.785488 752.605 695.450364 538.35985

BTF3 BTF3 R15 AQADSRGrGRARGGC P20290 6009276 6009277 TGAPAQADSrGr; TGAPAQADSrGrGR; TGAPAQADSrGrGr; TGAPAQADSrGrGrAr

PNUTS PPP1R10 R705 PGPGPYHrGRGGRGG Q96QC0 12205705 12205706 GGPGPGPGPYHrGrGGr

BAG3 BAG3 R121 YPQPGMQrFRTEAAA O95817 27277278 27277279 QVHPFHVYPQPGMQr 1560.43635 476.598408 415.712852 312.5144 717.5 1392.1233

plakophilin 2 PKP2 R125 TYEGRWGrGTAQYSS Q99959 15380350 15380351 WGrGTAQYSSQK 905.010018 1101.33881 706.24572 424.568 443.76268 4664.6185

HRC1 RASSF7 R125 AALGCEPrKTLTPEP Q02833 48912712 48912658 AALGCEPrK 1293.59923 508.76397 310.27776 422.856 299.05728 844.1046

KIF1C KIF1C R958 GLQGSGGrGGGLRRP O43896 9479162 9479165 QEQLrLQGLQGSGGrGGGLr

RBMX RBMX R369 DSYSSSSrGAPRGGG P38159 12197764 12197765 DSYSSSSr; DSYSSSSrGAPR; DSYSSSSrGAPr RBMXL1; RBMX Q96E39; P38159 R368; R369

Trap150 THRAP3 R66 NRERNHPrVYQNRDF Q9Y2W1 27280139 27280140 NHPrVYQNR 532.5542948 317.119231 269.936592 121.78429 489.209376 1176.20781

SP3 SP3 R611 NCKEGGGrGTNLGKK Q02447 27279781 27279782 EGGGrGTNLGK 1157.305842 1391.88764 1525.62036 299.8053 569.50886 4270.9367

XRN2 XRN2 R946 PLPPPSGrYNWN\_\_\_ Q9H0D6 12190851 12190852 KYPLPPPSGrYNWN 6741.123631 5009.29572 3783.93688 1203.9966 3821.39762 11566.8656

PNUTS PPP1R10 R723 PPPPPPFrGARGGRS Q96QC0 27279089 27279090 GGNEPPPPPPPFrGArGGr

PSF SFPQ R25 RRGGGGGrGGLHDFR P23246 9480081 10340518 RGGGGGrGGLHDFR

SAFB2 SAFB2 R835 DKRLSEGrGLPPPPR Q14151 27279493 27279494 LSEGrGLPPPPR 1404.19972 1130.19764 830.6326 310.7668 732.63392 2892.8227

acinus ACIN1 R624 ARTHANPrGRPKMGS Q9UKV3 48897830 48899632 THANPr 54.240846 41.284386 38.229696 58.7993 51.601616 235.819

HNRPUL2 HNRNPUL2 R700 RYRGDYDrFYGRDYE Q1KMD3 40351083 40351084 GDYDrFYGR 727.74108 871.68653 285.414892 164.912 430.39176 1047.1762

PROSER2 PROSER2 R414 ITVQFAGrGSSEEAR Q86WR7 6009801 6009802 ADSLPRPQGITVQFAGrGSSEEAR; RADSLPRPQGITVQFAGrGSSEEAR 1605.318374 1356.78257 645.606248 652.9928 925.12318 3644.948

DATF1 DIDO1 R1799 PRGPPPArFGAQKGP Q9BTC0 48897886 48906272 EPGPHALGMSGLHGPNFPGPrGPAPPFPEENIASNDGPrGPPPAr

TAF15 TAF15 R185 GGSQGGGrGRGGYDK Q92804 8144237 8144240 GYGGSQGGGr; GYGGSQGGGrGR; GYGGSQGGGrGr; GYGGSQGGGrGrGGYDK; GYGGSQGGGrGrGGYDKDGR; GYGGSQGGGrGrGGYDKDGr 621.5691075 491.747971 728.256092 216.6292 913.915092 3925.0535

WIPF1 WIPF1 R134 PLLPPGGrSTSAKPF O43516 8143975 8143979 DNDSGGSrPPLLPPGGr

ZAP3 YLPM1 R594 GPRFEGNrPDGPRPR P49750 40560634 40560931 GPrFEGNrPDGPrPr

TAF15 TAF15 R483 GGGYGGDrGGYGGDR Q92804 6009941 6009942 GGGYGGDrGGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGGYGGDrGGYGGDR; GGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGYGGDR; GGGYGGDrGGYGGDrGGGYGGDR; GGGYGGDrGGYGGDrGGGYGGDrGGYGGDr GGYGGDrGGYGGDR TAF15 Q92804 R498; R483 1334.674308 417.499368 643.46328 184.7683 541.508812 5028.6303

THOC4 ALYREF R204 RGGMTRNrGAGGFGG Q86V81 6008982 6008983 NrGAGGFGGGGGTR 654.331205 172.703531 224.693952 80.9089 418.612788 763.1561

PABP 3 PABPC3 R475 PRVMSTQrVANTSTQ Q9H361 48990905 48990815 VMSTQr PABPC3; PABPC1 Q9H361; P11940 R475; R481

DDX3 DDX3X R95 RGSGSRGrFDDRGRS O00571 8144620 8144624 SSFFSDrGSGSrGr

hnRNP 2H9 HNRNPH3 R121 YDRPIGGrGGYYGAG P31942 6009354 6009355 LLGQRPGPYDRPIGGrGGYYGAGR 1374.640542 541.983585 363.904412 257.4609 2437.04164 1491.33909

hnRNP A1 HNRNPA1 R196 ASSSQRGrSGSGNFG P09651 8144208 8144211 QEMASASSSQrGr HNRNPA1; HNRNPA1L2 P09651; Q32P51 R196; R196 183.155445 111.763366 109.484808 51.191 191.971676 602.21199

COG5 COG5 R309 QPSQSAVrGGPGRST Q9UP83 27277598 27277599 VLTQPSQSAVrGGPGR 495.7579 194.1368 278.03528 116.864 238.73152 510.8829

DHX36 DHX36 R52 GGRGGRGrHPGHLKG Q9H2U1 15379772 15379773 GSGGGGGGGGGGrGGrGr

PABPN1 PABPN1 R238 ALDESLFrGRQIKVI Q86U42 6009768 6009769 TSLALDESLFr; TSLALDESLFrGR 11429.215259 2945.2777497 3089.393536 882.389 4976.860112 9094.4714

hnRNP A1 HNRNPA1 R352 GQYFAKPrNQGGYGG P09651 9300407 9300408 GGNFGGrSSGPYGGGGQYFAKPrNQGGYGGSSSSSSYGSGR; SSGPYGGGGQYFAKPr; SSGPYGGGGQYFAKPrNQGGYGGSSSSSSYGSGR 3576.306448 1877.42269 1725.3794 499.2946 2655.96852 2831.4311

QKI QKI R256 PTIMPLIrQIQTAVM Q96PU8 27279216 27279217 TPTPAGPTIMPLIr 880.860761 326.91087 233.101028 128.4938 310.263072 1119.065

ZNF9 CNBP R25 ECPTGGGrGRGMRSR P62633 9479181 9479184 ECPTGGGrGR; ECPTGGGrGr 219.5651161 229.861918 157.405104 165.5937 390.615364 1134.86784

CUL1 CUL1 R63 VHQSNQArGAGVPPS Q13616 12195711 12195712 YMELYTHVYNYCTSVHQSNQAr 751.872154 688.565163 281.685468 191.3653 340.033336 1814.0376

RBMX RBMX R164 SGGPPPKrSAPSGPV P38159 12190740 12190741 rSAPSGPVR; rSAPSGPVRSSSGMGGR; rSAPSGPVr; rSAPSGPVrSSSGMGGR 124.830442 195.866814 128.651984 51.2089 219.804608 409.88139

PSMF1 PSMF1 R231 PSSGLPNrLPPGAVP Q92530 27279175 27279176 ALIDPSSGLPNrLPPGAVPPGAR 4782.9584 1276.08481 1133.3104 578.6491 1483.608944 3694.4371

TAF15 TAF15 R505 RGGYGGDrGGYGGDR Q92804 12191833 12191834 GGGYGGDrGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGYGGDrGGYGGDr; GGYGGDrGGYGGDrGGYGGDrGGYGGDr

Trap150 THRAP3 R108 RGGYGNYrSNWQNYR Q9Y2W1 27280147 27280148 NrGFYPWGQYNrGGYGNYr

FLNB FLNB R262 KKARAYGrGIEPTGN O75369 48885440 48889282 AYGrGIEPTGNMVK 1426.48825 1362.82575 804.04452 358.728 358.416588 3033.9277

LIX1L LIX1L R22 TSGRGTLrALRPGVT Q8IVB5 41477387 41477388 LQPGVGTSGRGTLr 528.36289 146.31617 249.4322 103.15 250.44604 930.2074

K13 KRT13 R27 SCQLGGGrGVSTCST P13646 6009064 6009067 GGGFGGGSCQLGGGrGVSTCSTR; GGGrGVSTCSTR; LQSSSASYGGGFGGGSCQLGGGr; LQSSSASYGGGFGGGSCQLGGGrGVSTC; LQSSSASYGGGFGGGSCQLGGGrGVSTCSTR; LQSSSASYGGGFGGGSCQLGGGrGVSTCSTr; SYGGGFGGGSCQLGGGrGVSTCSTR 796.3728773 5924.811893 967.871212 58.075902 245.242672764 573.43185402

DERPC CHTF8 R225 LGTNPAPrSGVFPGP P0CG12 40351031 40351032 SGFLGTNPAPr 2234.313642 629.883826 529.639712 370.3464 1433.14024 2347.9389

FBP1 FUBP1 R361 PGPGGRGrGRGQGNW Q96AE4 6010000 6010001 GrGrGQGNWNMGPPGGLQEFNFIVPTGK; SVQAGNPGGPGPGGrGr; SVQAGNPGGPGPGGrGrGR; SVQAGNPGGPGPGGrGrGr

RPRC1 MAP7D1 R326 RNGRDQGrGCDPGRG Q3KQU3 41477601 41477602 DQGrGCDPGR 335.6883255 200.5599453 165.2924216 186.04199 182.7562044 2180.92463

PRRC2C PRRC2C R281 TNKGLRGrGPPPSWA Q9Y520 8144529 8152607 GLrGrGPPPSWASEPERPSILSASELK; GrGPPPSWASEPERPSILSASELK 531.149036 317.180578 296.18144 108.2939 201.088436 1506.0101

CDAN1 CDAN1 R134 PARERGGrGLEEGVS Q8IWY9 41398649 41398650 GGrGLEEGVSGESLPGAGGR 620.718175 301.3582 252.514964 158.5631 243.648568 1882.9594

snRNP D1 SNRPD1 R100 EAVAGRGrGRGRGRG P62314 40350409 40350410 EAVAGrGr; EAVAGrGrGr

PSMB2 PSMB2 R93 RNLADCLrSRTPYHV P49721 40724766 40726356 NLADCLr 1387.04071 489.90084 465.55304 347.726 817.10704 1253.7415

RBM3 RBM3 R131 GYGYGYGrSRDYNGR P98179 9300504 9300505 PGGYGYGYGr; YDSRPGGYGYGYGr; YYDSRPGGYGYGYGr; YYDSRPGGYGYGYGrS; YYDSrPGGYGYGYGr 15529.790551 2371.13718556 4053.887856 2100.1208 2744.338608 24760.25946

snRNP N SNRPN R108 AGGPGVGrAAGRGVP P63162 12195439 12195440 VPLAGAAGGPGVGr 1058.97473 373.870068 329.018004 326.6725 828.5526 1218.9977

FXR2 FXR2 R434 GSYGGRGrGRRTGGP P51116 12197365 12197366 TYGGSYGGrGr; TYGGSYGGrGrGr

hnRNP A1 HNRNPA1 R225 RGGNFSGrGGFGGSR P09651 9291710 9291711 GGGFGGNDNFGrGGNFSGrGGFGGSR; GGGFGGNDNFGrGGNFSGrGGFGGSr; GGNFSGrGGFGGSR; SGSGNFGGGrGGGFGGNDNFGrGGNFSGr; SGSGNFGGGrGGGFGGNDNFGrGGNFSGrGGFGGSr 944.446712 802.69189 631.653768 222.935 958.337444 3745.00122

SRm300 SRRM2 R2288 AVNLADPrTPTAPAV Q9UQ35 15380602 15380603 TAVAPSAVNLADPrTPTAPAVNLAGAR 418.17072 193.467703 148.833356 77.6811 218.28318 429.11951

HNRPUL2 HNRNPUL2 R671 QRRGYDNrAYGQQYW Q1KMD3 27278379 27278380 GYDNrAYGQQYWGQPGNrGGYr

PABP 1 PABPC1 R518 YKYAAGVrNPQQHLN P11940 29427420 29427421 YAAGVrNPQQHLNAQPQVTMQQPAVHVQGQEPLTASMLASAPPQEQK 85.546868 92.184521 78.507252 42.4727 90.767276 266.2802

SF2 SRSF1 R93 VEFPRSGrGTGRGGG Q07955 476743 68304 SGrGTGrGGGGGGGGGAPR; SGrGTGrGGGGGGGGGAPr; SGrGTGrGGGGGGGGGAPrGR; SGrGTGrGGGGGGGGGAPrGr

AKAP8 AKAP8 R233 ELNYVGGrGLGGPSP O43823 9483345 9483348 SDPFVPPAASSEPLSTPWNELNYVGGr 37.165733 23.372921 12.86996 6.61677 15.7988908 49.37617

DAZAP1 DAZAP1 R253 YGPPPAGrGAPPPPP Q96EP5 9483349 9483353 VVPNAANGWAGQPPPTWQQGYGPQGMWVPAGQAIGGYGPPPAGr 374.7349144 129.279865 130.962724 64.75541 201.191838 425.662771

PNN PNN R62 GRGSLLLrRGFSDSG Q9H307 6010129 6010130 LLALSGPGGGrGrGSLLLr

KHDRBS1 KHDRBS1 R331 TRGATVTrGVPPPPT Q07666 13247317 13247319 GAITrGATVTr; GAITrGATVTrGVPPPPTVR; GATVTr; GATVTrGVPPPPTVR; GATVTrGVPPPPTVr; GATVTrGVPPPPTVrGAPAPrAr; GTPVRGAITRGATVTr 646.651918 418.651948 551.551256 186.6476 1043.4418 2688.7023

KIAA1429 KIAA1429 R1723 YSRREGTrGSSWSAQ Q69YN4 6009729 6009730 EGTrGSSWSAQNTPR 129.135347 68.210714 120.63588 28.0106 96.683248 396.0807

MRE11A MRE11A R604 TGLETSTrSRNSKTA P49959 40350869 40350870 ADTGLETSTr 217.09864 220.77484 128.06472 124.117 400.00256 779.7851

TCEAL3 TCEAL3 R179 PFAPRGQrGVRGVRG Q969E4 29430026 29430028 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R179; R179; R185

THOC4 ALYREF R38 RAGSQGGrGGGAQAA Q86V81 8092929 8092932 AGSQGGrGGGAQAAAR 88.194568 145.046902 101.884228 72.6234 199.186856 945.0033

GRAMD1A GRAMD1A R116 DYSCALQrEILLQGR Q96CP6 48897894 48908210 LIVDYSCALQr GRAMD1A; GRAMD1B Q96CP6; Q3KR37 R116; R121 1013.64164 13.4192058 51.839192 33.2263 78.361332 147.35686

hnRNP 2H9 iso2 HNRNPH3 R129 GGYYGAGrGSYGGFD P31942-2 12191546 12191552 GGYYGAGrGSYGGFDDYGGYNNYGYGNDGFDDR; YGAGrGSYGGFDDYGGYNNYGYGNDGFDDR 632.7605845 792.555621 214.5827936 425.2779 1333.902692 4131.78394

Plectin-1 PLEC R4640 GSRAGSRrGSFDATG Q15149 27279026 27279027 rGSFDATGSGFSMTFSSSSYSSSGYGR 60.4111673 62.7665324 332.548656 10.1003 93.151098 160.36773

tensin 2 TNS2 R555 CGVASGGrGAGRETA Q63HR2 8094171 8094175 LLGGCGVASGGrGAGR 3037.34893 164.364343 540.70076 116.5923 412.74536 918.9328

CPSF6 CPSF6 R194 GPPGGSSrAAFPQGG Q16630 40350528 40350529 AGPPGGSSr 235.787574 347.471553 360.73274 104.9993 436.80088 1055.9875

albumin ALB R34 HKSEVAHrFKDLGEE P02768 41717813 41717753 HKSEVAHr 113.874068 184.74027 149.30964 203.995 336.95768 483.3243

PRX PRX R240 QVELVGPrLPGAEVG Q9BXM0 48897888 48906284 FTAPQVELVGPrLPGAEVGVPQVSAPK 678.59275 13.7753616 31.88412 22.4785 35.254588 88.94514

AKAP8 AKAP8 R188 GSLDGFMrGRGQGRF O43823 15493038 15493040 GSLDGFMr 2182.25348 857.13199 680.264992 502.5832 1459.56884 3591.6064

RPS10 RPS10 R153 SATEFQFrGGFGRGR P46783 15494626 15494628 KAEAGAGSATEFQFr 683.15445 183.51476 161.3922 122.976 503.8818 504.3141

CRMP-4 iso2 DPYSL3 R60 DALSVGQrGAKTPRS Q14195-2 15493389 15549478 TLDFDALSVGQrGAK 10590.76491 231.480106 2004.7638 16.71957 3186.38388 398.98859

PABP 1 PABPC1 R481 PRVMSTQrVANTSTQ P11940 26362108 26361883 VMSTQr PABPC3; PABPC1 Q9H361; P11940 R475; R481 291.270287 111.717749 70.166268 60.894 216.47344 404.8023

FAM120A FAM120A R884 PVPPSQGrGRGFAGV Q9NZB2 9291690 9291691 HFGPVPPSQGr; HFGPVPPSQGrGr; HFGPVPPSQGrGrGFAGVCGFGGPYGETVATGPYR 4125.918247 1687.747919 1297.05488 940.7323 3406.39644 5005.6326

FALZ BPTF R2155 TFTSFQPrTATVTIR Q12830 9300376 9300381 VLGIIPSSTGTSQQTFTSFQPr 796.639976 295.591296 321.435652 153.2936 419.414912 972.37192

TRA2B TRA2B R241 DYYSRSYrGGGGGGG P62995 6008927 6008928 GYDDRDYYSRSYrGGGGGGGGWr; SYrGGGGGGGGWR 1128.352445 544.866036 484.953336 278.4877 670.133356 2468.314

hnRNP A2/B1 HNRNPA2B1 R238 SDGYGSGrGFGDGYN P22626 6009303 6009304 GGGGNFGPGPGSNFrGGSDGYGSGr; GGGGNFGPGPGSNFrGGSDGYGSGrGFGD; GGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGr; GGSDGYGSGr; GGSDGYGSGrG; GGSDGYGSGrGFG; GGSDGYGSGrGFGD; GGSDGYGSGrGFGDG; GGSDGYGSGrGFGDGY; GGSDGYGSGrGFGDGYN; GGSDGYGSGrGFGDGYNG; GGSDGYGSGrGFGDGYNGY; GGSDGYGSGrGFGDGYNGYG; GGSDGYGSGrGFGDGYNGYGG; GGSDGYGSGrGFGDGYNGYGGG; GGSDGYGSGrGFGDGYNGYGGGPG; GGSDGYGSGrGFGDGYNGYGGGPGG; GGSDGYGSGrGFGDGYNGYGGGPGGG; GGSDGYGSGrGFGDGYNGYGGGPGGGN; GGSDGYGSGrGFGDGYNGYGGGPGGGNFGG; GGSDGYGSGrGFGDGYNGYGGGPGGGNFGGSPGYGGGR 11149.925336 5391.925539 4209.5396 1219.9185 1835.2885924 21686.332

eIF4G EIF4G1 R685 LSTRGPPrGGPGGEL Q04637 6009525 6009518 GPPrGGPGGELPR; GPPrGGPGGELPrGPAGLGPR 645.423768 626.90914 609.69684 312.3932 754.32784 1866.3235

hnRNP A0 HNRNPA0 R284 GGSSWGGrSNSGPYR Q13151 12205602 12205603 SGGGGGGGGSSWGGr 170.586207 352.47355 133.83692 70.424 202.5072 364.6489

ZNF9 iso2 CNBP R32 RGRGMRSrGRGFQFV P62633-2 12197173 15243312 SrGrGFQFVSSSLPDICYR

GSE1 GSE1 R232 YHTTDDLrMSSLPPL Q14687 15380082 15380083 SFRPYHTTDDLr 1998.62432 379.24315 342.41112 123.8159 472.42824 1087.5021

PATL1 PATL1 R385 NLNGAGDrGSHRSSH Q86TB9 7657603 7657534 NLNGAGDrGSHR 56.861431 184.27981 24.630616 72.5385 386.66936 348.9422

PLEKHA5 PLEKHA5 R424 WIKIQKGrGHEEETR Q9HAU0 27279030 27279031 GrGHEEETR 50.936963 15.453867 20.865356 13.0314 6.1114764 207.73899

LSM4 LSM4 R90 VVAKGRGrGGLQQQK Q9Y4Z0 40350694 40350695 GrGrGGLQQQK

CASKIN2 CASKIN2 R862 RSQSFALrARRKGPP Q8WXE0 27277498 27277499 SQSFALr 963.78194 206.30038 286.28748 126.575 339.19136 635.2186

ZAP3 YLPM1 R1563 KDHSSSRrGGFDRPS P49750 8144038 8144042 rGGFDRPSYDR 263.298772 208.89726 184.31112 68.6105 227.0334 624.4569

hnRNP A3 HNRNPA3 R214 MQSAGSQrGRGGGSG P51991 9300478 9300479 QEMQSAGSQr 1244.321067 324.400505 301.7261 178.6356 800.804128 1560.18453

PAI-RBP1 SERBP1 R181 GRGRGMGrGDGFDSR Q8NC51 6009853 6009854 GrGDGFDSR; GrGMGrGDGFDSR 2008.02844 83.777265 111.11392 127.1755 714.37088 452.26395

TAF15 TAF15 R512 RGGYGGDrGGYGGDR Q92804 12191836 12191837 GGGYGGDrGGYGGDrGGYGGDr; GGYGGDrGGYGGDrGGYGGDrGGYGGDr 1334.674308 417.499368 643.46328 184.7683 541.508812 5028.6303

UFM1 UFM1 R15 ITLTSDPrLPYKVLS P61960 27280230 27280231 ITLTSDPrLPYK 7173.65605 1307.399665 619.31986 1467.785 1020.656296 2093.02829

hnRNP H2 HNRNPH2 R224 RGYNSIGrGAGFERM P55795 12191568 12191569 GYNSIGrGAGFER HNRNPH1; HNRNPH2 P31943; P55795 R224; R224

TCEAL5 TCEAL5 R182 VQDPFAPrGQRGVRG Q5H9L2 8093258 8093261 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R176; R176; R182 3207.864 540.912944 925.013464 183.212222 1309.483584 3501.0692

snRNP D3 SNRPD3 R118 GRGRGMGrGNIFQKR P62318 40350468 40350469 GrGMGrGNIFQK

COPA COPA R965 LFLQTYArGRTTYQA P53621 12205574 12205575 QLFLQTYAr 2204.03161 1840.20122 2315.97404 266.6288 747.842132 2481.2308

hnRNP K HNRNPK R286 DYDDMSPrRGPPPPP P61978 13247128 13247130 DYDDMSPr 2505.509259 1814.252297 1446.313556 597.5497 1497.936312 3399.00601

eIF4G EIF4G1 R1042 PPGPPISrGLPLVDD Q04637 6009529 6009522 GGPPGPPISr; GGPPGPPISrGLPLVDDGGWNTVPISK; RGGPPGPPISrGLPLVDDGGWNTVPISK; rGGPPGPPISr; rGGPPGPPISrGLPLVDDGGWNTVPISK 3412.390531 2124.412719 1294.3864 990.0041 858.222004 6806.0565

EHM2 EPB41L4B R24 YARGAAGrGAAGLGD Q9H329 8143818 8143822 GAAGrGAAGLGDER 750.73779 466.73913 520.40444 90.4283 359.50604 931.0814

FBP3 FUBP3 R408 NLRRFTIrGVPQQIE Q96I24 9479611 9479614 FTIrGVPQQIEVAR 706.40955 171.39408 162.85044 101.709 187.20436 424.6789

neurogranin NRGN R68 PGGAGVArGGAGGGP Q92686 6009915 6009916 KGPGPGGPGGAGVArGGAGGGPSGD 376.14885 1.42225369 33.977116 15.0385 4.7304816 557.9593

ING5 ING5 R126 DFESSGGrGLKKGRG Q8WYH8 15380034 15380035 DKMEGSDFESSGGrGLK; FEADLKDKMEGSDFESSGGrGLK; MEGSDFESSGGrGLK 1438.547407 2012.34033 1209.39184 297.7426 1238.66084 7027.2981

PPP1R14A PPP1R14A R21 LQSPSRArGPGGSPG Q96A00 8143990 8143995 ArGPGGSPGGLQK 2725.27123 95.602364 217.90024 55.1251 242.98732 462.0792

hnRNP M HNRNPM R503 RMAAPIDrVGQTIER P52272 41477437 41477438 MAAPIDrVGQTIER 1031.96819 824.27488 373.97036 98.2497 228.957776 1389.3357

RBMX RBMX R172 SAPSGPVrSSSGMGG P38159 9300465 9300466 SAPSGPVr; SAPSGPVrSSSGMGGR; rSAPSGPVr; rSAPSGPVrSSSGMGGR 1113.2423082 1202.837064 689.9344624 418.39521 1459.9467452 2799.90845

82-FIP NUFIP2 R291 TGPGGTSrGKPAVGD Q7Z417 27277107 27277108 YETGPGGTSr 98.690306 101.681723 159.41688 40.4068 53.35002 770.6058

ZAK ZAK R693 ISLNSSPrGRYSGKS Q9NYL2 41477365 41477366 YGrGSISLNSSPrGr

CCDC9 CCDC9 R130 GGAGGRGrRGRGRGS Q9Y3X0 6010228 6010229 SWEGSPGEQPrGGGAGGrGr

HNRPUL2 HNRNPUL2 R747 YYGYQGYr\_\_\_\_\_\_\_ Q1KMD3 13247487 13247489 NYYGYQGYr 850.224958 677.51827 385.84088 195.0913 463.54108 1156.8011

ZO2 TJP2 R1176 QLSEHSKrGYYGQSA Q9UDY2 40712231 40720728 rGYYGQSAR 449.56989 238.252586 243.86212 94.9964 454.0668 542.9219

ZNF326 ZNF326 R235 NVTVAAArGIKRKMM Q5BKZ1 9300553 9300554 STNVTVAAAr; STNVTVAAArGIK 1249.624761 1995.67368 1577.388872 425.795 2451.5458 6444.2964

K19 KRT19 R7 \_MTSYSYrQSSATSS P08727 15380076 15380077 SYrQSSATSSFGGLGGGSVR; SYrQSSATSSFGGLGGGSVRFGPGVAFR; SYrQSSATSSFGGLGGGSVr; rQSSATSSFGGLGGGSVr 618.8281 183.2974 85.913276 120.017 122.071432 263.3109

BYSL BYSL R40 VREKRRGrGTGEAEE Q13895 6009779 6009780 GrGTGEAEEEYVGPR 565.565946 695.58489 503.967744 238.8394 608.4487084 2334.0492

hnRNP A2/B1 HNRNPA2B1 R266 SPGYGGGrGGYGGGG P22626 9300438 9300439 GFGDGYNGYGGGPGGGNFGGSPGYGGGr; GFGDGYNGYGGGPGGGNFGGSPGYGGGrG; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGG; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGGY; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGGYG; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGGYGG; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGGYGGGGPGYGNQGGGYG; GFGDGYNGYGGGPGGGNFGGSPGYGGGrGGYGGGGPGYGNQGGGYGG 992.2163878 728.5121415 756.481592 280.2488 2191.737984 3889.3598

Musashi-2 MSI2 R197 VMFPPGTrGRARGLP Q96DH6 27278723 27278724 EVMFPPGTrGr

PNUTS PPP1R10 R729 FRGARGGrSGGGPPN Q96QC0 27279109 27279110 GGNEPPPPPPPFrGArGGr

PABPN1 PABPN1 R287 FYSGFNSrPRGRVYR Q86U42 27278917 27278918 SrFYSGFNSrPrGr

K6a KRT6A R42 SVSVSRSrGSGGLGG P02538 15560216 15561392 SrGSGGLGGACGGAGFGSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R42; R42; R42 483.192171 225.504136 282.062428 816.299 290.81382 769.55516

DDX3 DDX3X R622 SSRASSSrSGGGGHG O00571 40350300 40350301 QSSGASSSSFSSSrASSSr

KHDRBS2 KHDRBS2 R348 YREHPYGrY\_\_\_\_\_\_ Q5VWX1 27278492 27278493 EHPYGrY KHDRBS1; KHDRBS2 Q07666; Q5VWX1 R442; R348

CCT7 CCT7 R541 GRGRGRGrPH\_\_\_\_\_ Q99832 12198329 12198330 STVDAPTAAGrGrGrGrPH

K18 KRT18 R14 STFSTNYrSLGSVQA P05783 40351071 40351072 STFSTNYr 396.369303 580.5943 622.71312 330.8938 1980.82152 80.318369

ZAP3 YLPM1 R571 GPRFDGPrRFEDLGS P49750 27280383 27280384 SSYLESPrGPrFDGPr

PABP 1 PABPC1 R436 AQLRPSPrWTAQGAR P11940 27278901 27278902 AAYYPPSQIAQLrPSPr; AVPNPVINPYQPAPPSGYFMAAIPQTQNrAAYYPPSQIAQLrPSPr 2783.445027 1729.11882 905.462012 520.8443 1815.2258 6133.5365

BCLAF1 iso3 BCLAF1 R794 FAGVSRPrGTFHDDR Q9NYF8-3 15568300 22599539 PrGTFHDDRDDGVDYWAK 1629.5477 1331.05687 647.43996 413.242 1461.855 1997.7846

CTAGE5 CTAGE5 R557 LLPGGGGrGSRGPGN O15320 6009110 6009111 LSPLLPGGGGrGSrGPGNPLDHQITNER

KRT6B KRT6B R42 SISVSRSrGSGGLGG P04259 27278516 27278517 SrGSGGLGGACGGAGFGSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R42; R42; R42

SF2 SRSF1 R109 GGGGGAPrGRYGPPS Q07955 9291750 9291751 GGGGGGGGGAPr; GGGGGGGGGAPrGR; GTGrGGGGGGGGGAPr; GTGrGGGGGGGGGAPrG; GTGrGGGGGGGGGAPrGR; GTGrGGGGGGGGGAPrGr; SGrGTGrGGGGGGGGGAPr; SGrGTGrGGGGGGGGGAPrGR; SGrGTGrGGGGGGGGGAPrGr 261.4658299 757.538639 634.48134 284.0751 1367.929904 3451.6192

CPSF6 CPSF6 R202 AAFPQGGrGRGRFPG Q16630 13246983 13246985 AAFPQGGrGr 214.152675 225.19068 171.2626 123.568 700.76052 702.6385

CCDC9 CCDC9 R121 GSPGEQPrGGGAGGR Q9Y3X0 6010218 6010219 SWEGSPGEQPrGGGAGGrGr

TAF15 TAF15 R528 GYGGDRSrGGYGGDR Q92804 8093781 8093784 SrGGYGGDRGGGSGYGGDR; SrGGYGGDrGGGSGYGGDR

SPT5 SUPT5H R696 GGSGGMSrGRGRRDN O00267 9483201 10339470 ISSPMHPSAGGQrGGFGSPGGGSGGMSr

FXR2 FXR2 R399 FRPPGSGrGSGGSDK P51116 7641400 7641303 QIGLGFRPPGSGrGSGGSDK 3674.132264 1901.59398 3128.41212 2169.388 3042.54112 8565.2989

NCL NCL R660 FGGRGGGrGGFGGRG P19338 9483618 10339590 GEGGFGGrGGGr 91.909323 114.308194 82.212992 71.1611 155.564824 813.5491

FXR2 FXR2 R436 YGGRGRGrRTGGPAY P51116 27278045 27278046 TYGGSYGGrGrGr

NFI-B NFIB R335 SPQDSSPrLSTFPQH O00712 27278813 27278814 KPEKPLFSSASPQDSSPr 1644.47371 213.668884 460.29048 254.995 114.319644 2785.507

RPS10 RPS10 R160 RGGFGRGrGQPPQ\_\_ P46783 26362109 26361885 GGFGrGrGQPPQ; GrGQPPQ 91.1612999 306.036445 98.88132 117.0812 414.82734 937.6479

EPPK1 EPPK1 R3671 REPGPAGrGDGDSGR P58107 41554396 41554397 EPGPAGrGDGDSGR; GPREPGPAGrGDGDSGR; REPGPAGrGDGDSGR EPPK1 P58107 R4739; R3137; R2603; R3671; R4205 558.249043 639.6633815 686.939044 152.54161 167.6112472 731.60723

FAM120C FAM120C R941 MPLPPQGrSRGFAGL Q9NX05 9300589 9300590 AMGSMPLPPQGr

KHDRBS1 KHDRBS1 R325 PVRGAITrGATVTRG Q07666 476704 68265 GAITrGATVTr; GAITrGATVTrGVPPPPTVR; GTPVRGAITrGATVTR; GTPVrGAITr

RBM10 RBM10 R902 RGSGLGArGSSYGVT P98175 6009484 6009489 GSGLGArGSSYGVTSTESYK 185.602175 190.905 208.23196 87.3714 242.6544 436.4618

hnRNP A2/B1 HNRNPA2B1 R325 SGNFGGSrNMGGPYG P22626 9300443 9300444 SGNFGGSr; SGNFGGSrNMGGPYGGGNYGPGGSGGSGGYGGR 1310.220725 1311.718265 740.953568 325.5923 951.57556 1976.19772

plakophilin 2 PKP2 R46 KLAGSSGrGGQTVKS Q99959 12197450 12197451 LAGSSGrGGQTVK 429.973082 946.00363 549.37084 306.343 814.15012 1525.7211

PABPN1 PABPN1 R259 PGISTTDrGFPRARY Q86U42 15380299 15380300 RTNRPGISTTDrGFPR 3037.169652 1838.382117 1029.742004 786.5431 1210.012664 4876.60168

BTF3 BTF3 R17 ADSRGRGrARGGCPG P20290 6009281 6009282 TGAPAQADSrGrGr; TGAPAQADSrGrGrAr

PPP1R13L PPP1R13L R200 PQAFFPErGPSPRPP Q8WUF5 29427444 29427445 GSPLAEGPQAFFPErGPSPrPPATAYDAPASAFGSSLLGSGGSAFAPPLR 87.5172034 130.8108373 45.674656 61.75614 15.0747652 111.745684

Vimentin VIM R69 ATRSSAVrLRSSVPG P08670 40350634 40350635 SLYASSPGGVYATrSSAVr 1180.132206 130.4644484 845.04884 327.4717 847.182672 2671.3764

TXLNG TXLNG R12 VEEAARGrGGGAEEA Q9NUQ3 6010153 6010154 GrGGGAEEATEAGR; GrGGGAEEATEAGrGGR 56.509893 32.138821 31.548452 17.0136 17.249356 373.6097

hnRNP A1 HNRNPA1 R232 RGGFGGSrGGGGYGG P09651 9479591 9479594 GGGFGGNDNFGrGGNFSGrGGFGGSr; SGSGNFGGGrGGGFGGNDNFGrGGNFSGrGGFGGSr 82.175676 43.262648 38.58074 16.6244 79.565256 189.94412

DDX5 DDX5 R20 DRGFGAPrFGGSRAG P17844 40350747 40350748 GFGAPrFGGSR 519.109338 403.584467 383.96848 154.6133 769.80616 1405.8382

K19 KRT19 R32 FGPGVAFrAPSIHGG P08727 6009227 6009228 FGPGVAFr; FGPGVAFrAPSIHGGSGGR; FGPGVAFrAPSIHGGSGGRGVSVSSAR; FGPGVAFrAPSIHGGSGGr; FGPGVAFrAPSIHGGSGGrGV; FGPGVAFrAPSIHGGSGGrGVSV; FGPGVAFrAPSIHGGSGGrGVSVS; FGPGVAFrAPSIHGGSGGrGVSVSSA; FGPGVAFrAPSIHGGSGGrGVSVSSAR; FGPGVAFrAPSIHGGSGGrGVSVSSAr; FGPGVAFrAPSIHGGSGGrGVSVSSArFVSSSSSGAYGGGYGGVLTASDGLLAGNEK; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGRGVSVSSAR; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGrGVSVSSAr; rAPSIHGGSGGRGVSVSSAR; rAPSIHGGSGGr; rAPSIHGGSGGrGVSVSSAR; rAPSIHGGSGGrGVSVSSAr 4564.542609 1974.16791 213.930318 1401.4348 1158.216052 822.34913

hnRNP A0 HNRNPA0 R189 GGGGGGSrSSRGGRG Q13151 9300522 9300523 EDIYSGGGGGGSr 621.372125 635.49772 271.625968 143.3942 451.83804 648.5149

EPPK1 EPPK1 R4205 REPGPAGrGDGDSGR P58107 41554398 41554399 EPGPAGrGDGDSGR; GPREPGPAGrGDGDSGR; REPGPAGrGDGDSGR EPPK1 P58107 R4739; R3137; R2603; R3671; R4205 558.249043 639.6633815 686.939044 152.54161 167.6112472 731.60723

PPP1R13L PPP1R13L R160 LGRAPSPrPGPGPLR Q8WUF5 27279133 27279134 APSPrPGPGPLrQQGPPTPFDFLGR

hnRNP A/B iso3 HNRNPAB R250 GGRGNRNrGNRGSGG Q99729-3 8093833 8093838 NrGNrGSGGGGGGGGQGSTNYGK

PNUTS PPP1R10 R693 PMRGGPMrGGPGPGP Q96QC0 6010035 6010036 GGPMrGGPGPGPGPYHR 217.182537 37.196159 43.542104 12.4497 58.072072 182.436

SF3B2 SF3B2 R222 VRTPLGPrVAAPVGP Q13435 9300525 9300526 MGTPVPRPPQDMGQIGVRTPLGPr; TPLGPr; TPLGPrVAAPVGPVGPTPTVLPMGAPVPRPR 513.118518 869.416405 394.694108 323.0399 1273.111992 2507.61985

Alix PDCD6IP R745 TPPTPAPrTMPPTKP Q8WUM4 15564601 15564707 EPSAPSIPTPAYQSSPAGGHAPTPPTPAPr 230.162966 60.50616 47.8950124 85.9528 52.7959952 205.67658

PABP 1 PABPC1 R432 PSQIAQLrPSPRWTA P11940 27278893 27278894 AAYYPPSQIAQLrPSPr; AVPNPVINPYQPAPPSGYFMAAIPQTQNrAAYYPPSQIAQLrPSPr

hnRNP A/B HNRNPAB R248 GSGGRGNrNRGNRGS Q99729 6009031 6009037 EVYQQQQYGSGGrGNr 75.2639349 77.927707 182.892932 82.7666 149.093548 545.61589

DDX9 DHX9 R1219 AGVGGGYrGVSRGGF Q08211 12191760 12191761 AGYGAGVGGGYrGVSrGGFr

Bcl-9L BCL9L R994 SPTGSPSrLKSPSMA Q86UU0 40350900 40350901 SPTGSPSrLK 540.33815 545.16605 343.97724 265.483 683.17972 1377.9875

ADO ADO R28 FRGSGGGrGASDRDA Q96SZ5 41477525 41477526 GSGGGrGASDR 85.902234 196.26607 0 116.499 47.584928 311.1969

NEK1 NEK1 R472 WKREIYGrGLPERGI Q96PY6 41477418 41477419 EIYGrGLPER 1171.82417 104.314925 218.7422 84.7076 163.091112 724.6449

Vimentin VIM R36 SYVTTSTrTYSLGSA P08670 15380758 15380759 SYVTTSTr; SYVTTSTrTY; SYVTTSTrTYSLGSALrPSTSR 1926.011307 287.931501 1187.99688 659.1617 1137.31048 2677.1172

SF1 iso4 SF1 R537 LPAAAMArAMRVRTF Q15637-4 27279576 27279577 SLPAAAMAr SF1; SF1 Q15637-5; Q15637-4 R662; R537 611.948227 703.386827 292.252624 208.6532 765.335848 1730.9616

PABPN1 PABPN1 R23 GRGSGPGrRRHLVPG Q86U42 41554405 41554406 MAAAAAAAAAAGAAGGrGSGPGr

SMARCA3 HLTF R27 GVHGNFPrLSYPTFF Q14527 27279702 27279703 GVHGNFPrLSYPTFFPR; YLQTVQYGVHGNFPr; YLQTVQYGVHGNFPrLSYPTFFPR 3468.133229 723.751743 695.626236 519.4756 767.560016 3356.6752

FMR1 FMR1 R544 GGRGQGGrGRGGGFK Q06787 41477452 41477453 GQGGrGrGGGFK

PITPNM1 PITPNM1 R1211 QSQLLRSrGPSQAER O00562 29429470 29429472 SrGPSQAER 62.291768 76.0188 109.756492 24.7372 60.654252 250.5758

E1B-AP5 HNRNPUL1 R181 PYEENRGrGYFEHRE Q9BUJ2 27277791 27277792 GrGYFEHR; GrGYFEHREDR 1410.409374 1343.57652 773.305788 133.68462 515.950396 1687.27057

Scribble SCRIB R1623 RPVRPGRrGLGPVPS Q14160 40351049 40351050 rGLGPVPS 430.06942 180.74628 168.76772 79.7453 248.71256 519.9863

K7 KRT7 R329 IDNIKNQrAKLEAAI P08729 41477565 41477566 NQrAKLEAAIAEAEER 274.892189 491.30653 1544.84656 250.513 1471.89672 1328.1557

KHDRBS1 KHDRBS1 R282 NGVPEPSrGRGVPVR Q07666 6009546 6009547 FLVPDMMDDICQEQFLELSYLNGVPEPSrGr; KFLVPDMMDDICQEQFLELSYLNGVPEPSrGr; YLNGVPEPSrGr

DDX17 DDX17 R684 QQFSGIGrSGQQPQP Q92841 9300548 9300549 SSQSSSQQFSGIGr 763.608483 969.902076 466.330148 210.478 271.932336 2050.9376

PAIP1 PAIP1 R17 GAGRGRSrGLGRGGG Q9H074 40350986 40350987 SrGLGrGGGGPEGGGFPNGAGPAER

DERPC CHTF8 R494 KSFVPFPrVGSLPGT P0CG12 40351039 40351040 SFVPFPr 1321.855612 818.04151 670.27332 285.3823 1858.34796 2689.0933

hnRNP P2 FUS R503 GGRGGGDrGGFGPGK P35637 8144214 8144217 GGGDrGGFGPGK 849.53209 399.71217 302.96176 122.548 713.97564 1372.6929

CD2BP2 CD2BP2 R181 ALRRLGArGGGKGRK O95400 27277558 27277559 LGArGGGK 100.976579 387.8017 360.49156 139.585 470.24704 1309.7097

OSBPL10 OSBPL10 R38 PSCSLAGrGVSSRSA Q9BXB5 6010084 6010085 ATSAGSSPSCSLAGrGVSSR 1301.50724 133.386539 676.3332 34.0104 141.110848 102.07768

ZAK ZAK R670 NTDTSSErGRYSDRS Q9NYL2 15380788 15380789 DSGFSSGNTDTSSErGR 153.4280583 666.31422 128.945244 91.0416 417.48824 1359.73102

EPB41L2 EPB41L2 R72 EKETSESrGISRFIP O43491 41477656 41477657 EKETSESrGISR 372.643997 90.079275 754.912 41.3507 100.834416 855.2711

K4 KRT4 R27 AIVGGGKrGAFSSVS P19013 40350487 40350488 rGAFSSVSMSGGAGR 479.55908 284.53139 53.485416 191.045 83.823188 262.6232

PRAS40 AKT1S1 R51 CAYAAHGrGALAEAA Q96B36 15380368 15380369 AAHGrGALAEAAR 246.776805 192.524618 130.795944 81.0985 148.222708 753.1097

K7 KRT7 R77 QSLLAPLrLDADPSL P08729 40350896 40350897 EVTINQSLLAPLrLDADPSLQR 1306.791794 641.229017 422.452996 1351.776 699.552496 771.3487

SRm300 SRRM2 R2384 GANLTSPrVPLSAYE Q9UQ35 13247493 13247495 MAPALSGANLTSPrVPLSAYER 1185.082448 585.414401 522.61722 267.0951 721.641 1919.4006

CGN CGN R188 SQLGGQArGRTGRRT Q9P2M7 15379651 15379652 FDSQLGGQAr; VASPGSTIDTAPLSSVDSLINKFDSQLGGQAr 506.549989 830.239553 123.514726 87.57942 187.4987564 461.95914

SSF1 PPAN R426 RKRWEMDrGRGRLCD Q9NQ55 27281810 27281720 WEMDrGR 101.744093 158.80007 116.214784 78.2649 250.59856 641.976

PRRC2C PRRC2C R2719 QSAPATVrMTQPFPT Q9Y520 27277315 27277316 QFQSAPATVr 674.653419 707.90863 241.93516 282.3839 737.26528 2757.3918

DDX3 DDX3X R632 GGGHGSSrGFGGGGY O00571 6009094 6009095 SGGGGHGSSrGFGGGGYGGFYNSDGYGGNYNSQGVDWWGN 38.157504 53.676623 47.143684 25.969 91.027216 119.24442

CSDA CSDA R326 GPNQPSVrRGYRRPY P16989 9300423 9300424 GPPRPRPAPAVGEAEDKENQQATSGPNQPSVr; PAPAVGEAEDKENQQATSGPNQPSVr 222.782263 236.655562 124.131068 140.3568 285.242084 1144.3121

WDR33 WDR33 R1257 PGGPSEDrGGKGRGG Q9C0J8 27280274 27280275 EMEAPGGPSEDrGGK 879.177717 1512.21213 1436.04276 373.6418 2221.60632 3981.277

Bcl-9L BCL9L R680 RVREELLrHQLLEKR Q86UU0 27277360 27277361 EELLrHQLLEK 979.184536 513.782984 506.980572 230.5043 848.183236 1660.3631

KHDRBS1 KHDRBS1 R310 GRGVGPPrGALVRGT Q07666 476771 68997 GrGVGPPrGALVR; GrGVGPPrGALVr; GrGVGPPrGALVrGTPVr

RBM3 RBM3 R99 GGFGAHGrGRSYSRG P98179 6009502 6009503 GGGFGAHGrGR 436.035039 40.6683277 227.033212 260.1025 355.990044 1513.5748

ZNF579 ZNF579 R92 AHLSRHLrGHGPQPP Q8NAF0 6009820 6009821 HLrGHGPQPPLR 1035.325027 494.718224 369.707736 210.5374 613.928096 2265.6196

RELB RELB R16 GPSVPTGrAMPSRRV Q01201 15380427 15380428 SGPASGPSVPTGr 367.59646 117.296322 151.319308 60.3386 186.120484 1531.0732

ASXL2 ASXL2 R639 HPSQVSPrARFPVSI Q76L83 41682282 41682283 ISPMPFHPSQVSPr 683.42879 136.549127 139.5744 61.6057 197.02796 368.5175

METT5D1 METTL15 R395 QDVQDNPrGRSAKLR A6NJ78 15494044 15494046 VLSPQDQDVQDNPrGR 528.488576 291.51694 489.73304 118.2116 320.81926 762.7858

CAPRIN1 CAPRIN1 R667 RDYSGYQrDGYQQNF Q14444 13246902 13246904 DYSGYQrDGYQQNFK 562.2694 710.14801 327.31536 383.843 931.70696 1539.7235

PEX6 PEX6 R161 RLAVTELrGRARLCP Q13608 40351127 40351128 LAVTELrGR 229.420653 279.28329 189.06776 22.7708 277.16164 525.6696

KHDRBS1 KHDRBS1 R346 VRGAPAPrARTAGIQ Q07666 27279508 27279509 GATVTrGVPPPPTVrGAPAPrAr

SHARP SPEN R3038 PGPSSFPrASHPSST Q96T58 40724736 40725343 LDAHSPRPSGPGPSSFPr

FAM120A FAM120A R886 PPSQGRGrGFAGVCG Q9NZB2 6010168 6010169 GrGFAGVCGFGGPYGETVATGPYR; HFGPVPPSQGrGr; HFGPVPPSQGrGrGFAGVCGFGGPYGETVATGPYR 485.400927 398.450624 231.174564 212.3252 1021.7938 1078.30141

ADAM9 ADAM9 R772 EVPIYANrFAVPTYA Q13443 27277129 27277130 EVPIYANrFAVPTYAAK 1420.72392 1050.07188 724.36956 1212.923 650.411044 3983.0526

MORF4L2 MORF4L2 R35 NMQRSKMrGASSGKK Q15014 27278700 27278701 MrGASSGK 324.318687 521.43091 488.94936 335.334 586.4968 1809.7021

ANKZF1 ANKZF1 R252 AQGLRDArGGPSHSA Q9H8Y5 27277223 27277224 DArGGPSHSAGANLR 59.330491 32.878989 54.905836 19.4248 68.944288 159.46498

PAPD4 PAPD4 R131 HYVPDIVrCVPPFRE Q6PIY7 27278949 27278950 YSMPPLFHTHYVPDIVr 710.11633 146.06449 126.77264 70.4466 170.12376 518.4798

ZAP3 YLPM1 R601 RPDGPRPrYEGHPAE P49750 40350759 40350760 GPrFEGNrPDGPrPr

LRRC40 LRRC40 R13 RIAGQDLrAGFKAGG Q9H9A6 40350856 40350857 IAGQDLr 255.283259 313.5561 149.93212 241.207 225.46064 653.8095

KIF1C KIF1C R948 WLKQEQLrLQGLQGS O43896 41398680 41398681 QEQLrLQGLQGSGGrGGGLr

TRIP6 TRIP6 R236 GVSGPAGrGRGGEHG Q15654 6009666 6009667 EEAAGVSGPAGr; EEAAGVSGPAGrGR; EEAAGVSGPAGrGr; EEAAGVSGPAGrGrGGEHGPQVPLSQPPEDELDR; EPGPGAKEEAAGVSGPAGr; SQREPGPGAKEEAAGVSGPAGr; SQREPGPGAKEEAAGVSGPAGrGR; SQREPGPGAKEEAAGVSGPAGrGr 5269.7633098 960.5790909 189.73905136 7666.8998 74.9542976 1689.094539

RBM33 RBM33 R1078 GVAGPMGrGRLMPNK Q96EV2 27279311 27279312 GrGVAGPMGr

XRN2 XRN2 R895 EPLLPWNrMLQTQNA Q9H0D6 15380779 15380780 GVGAEPLLPWNr; GVGAEPLLPWNrMLQTQN; GVGAEPLLPWNrMLQTQNAAFQPNQYQMLAGPGGYPPR 3460.8474604 1018.752449 688.7185804 513.36485 786.9930812 2442.22188

FOXRED1 FOXRED1 R12 VLPHGMGrGLLTRRP Q96CU9 27278043 27278044 VLPHGMGrGLLTR 222.092904 311.996828 146.438916 52.732 255.679116 435.54502

PPP1R12B PPP1R12B R853 TSDSYGDrASARARR O60237 48912709 48912642 LESGGSNPTTSDSYGDrASAR 1557.20169 0 12.71062 4.99058 16.2674388 47.48212

SFRS6 SRSF6 R85 DGYSYGSrSGGGGYS Q13247 40350380 40350381 DGYSYGSrSGGGGYSSR 172.229057 137.115979 107.330556 48.3367 120.238732 259.325

PABP 4 PABPC4 R419 AVPQAQGrPPYYTPN Q13310 29427424 29427425 ALPANAILNQFQPAAGGYFVPAVPQAQGrPPYYTPNQLAQMrPNPr

PAGE4 PAGE4 R12 VRSRSRGrGDGQEAP O60829 48885427 48889216 GrGDGQEAPDVVAFVAPGESQQEEPPTDNQDIEPGQER 50.4037226 123.585748 3.4247188 3.06961 8.0089728 40.75807

TSEN54 TSEN54 R316 DSRHTLLrAPAPELL Q7Z6J9 27280185 27280186 HTLLrAPAPELLPANVAGR 853.19102 197.77329 569.41792 138.362 456.97616 946.289

NARR NARR R125 RVIVGSPrARVADAD P0DI83 40350676 40350677 VIVGSPr 228.478646 116.396566 135.16744 111.856 183.02564 1080.9057

lamin A/C LMNA R644 FGDNLVTrSYLLGNS P02545 27278526 27278527 SVGGSGGGSFGDNLVTr; SVGGSGGGSFGDNLVTrSY 5450.43081 86.073273 390.701184 171.2598 1220.007316 1279.14822

KLHDC10 KLHDC10 R13 GWDRNRRrGGGAAGA Q6PID8 8093744 8093747 rGGGAAGAGGGGSGAGGGSGGSGGR; rGGGAAGAGGGGSGAGGGSGGSGGRGTGQLNR

ELMSAN1 ELMSAN1 R447 GDCGQVLrGGVIQST Q6PJG2 15379540 15379541 AVSTGDCGQVLrGGVIQSTR 390.2327 279.17175 155.71176 25.5243 197.6282 330.188

TAF15 TAF15 R562 GGGYGGDrGGGYGGD Q92804 6009955 6009956 GGDrGGGYGGDR; GGGYGGDr; GGGYGGDrGGGYGGD; GGGYGGDrGGGYGGDR; SGGGYGGDrGG; SGGGYGGDrGGG; SGGGYGGDrGGGY; SGGGYGGDrGGGYG; SGGGYGGDrGGGYGG; SGGGYGGDrGGGYGGD; SGGGYGGDrGGGYGGDR TAF15 Q92804 R475; R562; R459; R431; R450; R490

TTDN1 MPLKIP R126 STPFGSGrVREKRMS Q8TAP9 29430098 29430100 SPAGSQQQFGYSPGQQQTHPQGSPRTSTPFGSGr 16.4677689 38.98323 11.121002 7.3518 18.017696 94.21743

RPL23 RPL23 R4 \_\_\_\_MSKrGRGGSSG P62829 41717825 41718306 rGrGGSSGAK

NEBL iso2 NEBL R96 DFEESKGrGFSIVTD O76041-2 6008978 6008979 DFEESKGrGFSIVTDTPELQR; GrGFSIVTDTPELQR 26776.1901 699.8446312 514.5830864 276.519537 1162.6072012 1383.253442

PPP1R13L PPP1R13L R180 TPFDFLGrAGSPRGS Q8WUF5 15380365 15380366 QQGPPTPFDFLGr; QQGPPTPFDFLGrAGSPrGSPLAEGPQAFFPER 309.146728 371.06069 131.28872 133.057 110.22522 495.2751

ARHGAP17 ARHGAP17 R510 MDFQAHRrGGTLNRK Q68EM7 48912714 48912668 rGGTLNR 85.121003 39.267228 45.171588 32.4173 75.180716 120.90456

ZAK ZAK R683 RSRNKYGrGSISLNS Q9NYL2 8144726 8152707 YGrGSISLNSSPrGr

SMARCD2 SMARCD2 R529 LEQVLGIrLT\_\_\_\_\_ Q92925 27279706 27279707 RQELEQVLGIrLT 397.22199 114.90765 166.96352 148.588 376.26684 560.9608

hnRNP P2 FUS R242 SSGGYEPrGRGGGRG P35637 15379985 15379986 SSGGYEPr 1256.814702 665.949284 419.534656 269.2659 1023.375908 1910.61851

EIF4H EIF4H R22 FGGGRGSrGSAGGHG Q15056 6009612 6009613 AYSSFGGGrGSr; AYSSFGGGrGSrGSAGGHGSR

PEG10 PEG10 R598 LQVSYDCrAPNNFTI Q86TG7 29429423 29540148 LQVSYDCrAPNNFTIQNQYPR 101.343748 87.464234 295.25516 0 172.9626 52.60307

Vimentin VIM R12 SVSSSSYrRMFGGPG P08670 40350604 40350605 SVSSSSYr 750.849759 101.6497196 538.078904 245.5679 538.442996 1400.608

RBM33 RBM33 R1070 AIMHGRGrGVAGPMG Q96EV2 13247384 13247386 GrGVAGPMGr

hnRNP D0 HNRNPD R280 GGFAGRArGRGGGPS Q14103 6009584 6009585 EQYQQQQQWGSrGGFAGrAr; GGFAGrAr

SASH1 SASH1 R920 GSIAASGrGLSPPQC O94885 27279543 27279544 KLEGSIAASGrGLSPPQCLPR 1307.96061 249.10171 290.63492 61.4105 188.4524 662.1746

alphaSNBP(A) LSM14A R269 PGAPSAPrRGRGGHR Q8ND56 13247525 13247527 QVAPGAPSAPr 372.1135 187.13838 124.09672 96.8191 189.461 610.7167

K1 KRT1 R602 GGGSSGGrGSGGGSS P04264 48885407 48885331 GGSGGGGGGSSGGrGSGGGSSGGSIGGR 78.593625 14.2000287 6.6033472 15.3143 12.17003 47.44969

SMRT NCOR2 R1661 AAAYYLPrHLAPNPT Q9Y618 40351422 40351423 GIPLDAAAAYYLPr 1316.77139 99.101002 212.051036 188.9405 320.252148 415.71235

DDX3Y DDX3Y R615 SSGFGASrGSSSRSG O15523 40350542 40350543 QSSGSSSSGFGASrGSSSR 220.610192 385.32637 0 1.639807 0 1011.5515

USP54 USP54 R12 RNYFSGGrGSVQGMF Q70EL1 12197331 12197332 NYFSGGrGSVQGMFAPR 515.97293 182.05902 125.14576 66.3566 141.508548 350.9133

SSRP1 SSRP1 R645 EKKSTPSrGSSSKSS Q08945 27279848 27279849 STPSrGSSSK 107.080644 152.69969 126.13776 33.9557 152.11082 472.4844

Trap150 THRAP3 R101 YPWGQYNrGGYGNYR Q9Y2W1 12191875 12191876 NrGFYPWGQYNrGGYGNYr

FBL FBL R15 RGGGFGGrGGFGDRG P22087 12198037 12198038 GGGFGGrGGFGDR 376.74857 159.11181 119.959336 49.6528 208.60308 472.3625

TOMM70A TOMM70A R71 RRREARGrGDASGLK O94826 9300395 9300396 GrGDASGLKR 138.13019 125.786518 198.64552 49.2705 45.416684 676.8831

SF3B2 SF3B2 R884 KAQPQDSrGGSKKYK Q13435 27279591 27279592 AQPQDSr; AQPQDSrGGSKK; KAQPQDSrGGSK 364.095754 1603.49475 1009.396332 304.4303 1318.445528 2531.87726

RPS10 RPS10 R119 ERPARLTrGEADRDT P46783 6009395 6009396 LTrGEADRDTYR 1085.051704 390.300053 351.878644 133.0541 1226.98732 1393.616

snRNP N SNRPN R147 QVMTPQGrGTVAAAA P63162 9300495 9300496 GVGGPSQQVMTPQGr SNRPB; SNRPN P14678; P63162 R147; R147

SMG7 SMG7 R910 PEQDPVPrMPFEKSL Q92540 15494694 15494696 SPGVFRPEQDPVPrMPFEK 472.92707 513.74037 110.990168 141.293 422.956 748.2452

SFRS9 SRSF9 R98 GGRGGWPrGGRNGPP Q13242 15380505 15380506 TYGGrGGWPr; TYGGrGGWPrGGr

LSG1 LSG1 R14 PAGGSLGrALMRHQT Q9H089 12195664 12195665 APAGGSLGr; RAPAGGSLGr; rAPAGGSLGr 304.799077 262.480361 226.16484 203.5087 150.4126 1216.5919

BAT2 PRRC2A R1012 RVGPTSCrGRGRGEY P48634-2 41477002 41476911 VGPTSCr 262.740522 178.85868 85.312248 94.9992 185.525 568.7785

RNPC2 RBM39 R109 PKFNSAIrGKIGLPH Q14498 6009600 6009601 FNSAIrGK 1188.391754 1578.93593 1180.18488 369.4674 2509.35088 4329.0715

hnRNP A3 HNRNPA3 R354 KGGSFGGrSSGSPYG P51991 8144656 8144660 GGSFGGr; GGSFGGrSSGSPY; GGSFGGrSSGSPYGGGYGSGGGSGGYGSR; GGSFGGrSSGSPYGGGYGSGGGSGGYGSRR; GGSFGGrSSGSPYGGGYGSGGGSGGYGSRRF 3618.239636 1401.97629 1163.90616 328.0684 1580.303672 2960.20097

PROSER2 PROSER2 R252 PAQPKAPrFPSNIIV Q86WR7 40351011 40351012 APrFPSNIIVTNGAAR 378.97838 145.11926 88.822564 119.474 232.69468 389.3785

MTCH1 MTCH1 R29 AGAGAGArGGAAAGV Q9NZJ7 15380205 15380206 AGAGAGAGArGGAAAGVEAR; rGGAAAGVEAR 754.793237 723.986692 631.490708 174.7781 663.145972 1793.7999

RNF12 RLIM R360 TVTYESErGGFRRTF Q9NVW2 13247203 13247205 SQTPNNTVTYESErGGFR 533.169263 312.959647 215.52006 216.8528 381.492044 1561.6057

RBM3 RBM3 R105 GRGRSYSrGGGDQGY P98179 6008931 6008932 SYSrGGGDQGYGSGR 512.176192 76.829181 131.551352 125.8071 122.176884 1619.4898

CstF-64T CSTF2T R311 QVQMSDPrAPIPRGP Q9H0L4 15379702 15379703 GQVQMSDPrAPIPR 588.27428 134.512664 281.68336 66.205 189.13956 753.6594

PABP 4 PABPC4 R518 AVAAAAPrAVAPYKY Q13310 9483453 10340299 AAVAAAAPr 409.682449 811.69946 301.99208 189.4395 642.82096 2020.2671

HSC70 HSPA8 R469 TGIPPAPrGVPQIEV P11142 9300413 9300414 AMTKDNNLLGKFELTGIPPAPr; DNNLLGKFELTGIPPAPr; DNNLLGKFELTGIPPAPrG; DNNLLGKFELTGIPPAPrGVPQIEV; DNNLLGKFELTGIPPAPrGVPQIEVT; FELTGIPPAPr; FELTGIPPAPrGVPQIEVT 89699.9637391 34537.1877136 27496.0241324 24405.83967 36586.5205272 146568.28591

CIRBP CIRBP R154 QSGGYSDrSSGGSYR Q14011 40350661 40350662 SQSGGYSDrSSGGSYR 803.86724 110.526273 304.14844 51.7064 150.454584 271.9336

CTAGE5 CTAGE5 R560 GGGGRGSrGPGNPLD O15320 15493405 15493407 LSPLLPGGGGrGSrGPGNPLDHQITNER 3183.7476 1016.03359 623.65614 219.3411 422.538456 1443.7054

TSSC4 TSSC4 R139 SPVEGLGrAHRSPAS Q9Y5U2 12195535 12195536 SPVEGLGr 401.237243 641.38217 220.126412 428.29 302.066844 691.2581

ZNF326 ZNF326 R173 KPAPVGSrGRGTPAY Q5BKZ1 12195742 12195743 ENYSSYSSFSSPHMKPAPVGSr 488.048308 289.913052 213.574872 148.8311 416.126384 729.0011

KHDRBS1 KHDRBS1 R442 YREHPYGrY\_\_\_\_\_\_ Q07666 27279500 27279501 EHPYGrY KHDRBS1; KHDRBS2 Q07666; Q5VWX1 R442; R348 149.520404 192.49802 193.95336 57.4091 310.11908 631.2051

TAF15 TAF15 R431 GGGYGGDrSSGGGYS Q92804 12205698 12205699 SGGGYGGDrSSGGGYSGDR GGGYGGDr TAF15 Q92804 R562; R459; R431; R450 696.718649 354.744247 610.968584 115.934 350.706292 1959.9289

DATF1 DIDO1 R1793 IASNDGPrGPPPARF Q9BTC0 40351305 40351306 EPGPHALGMSGLHGPNFPGPrGPAPPFPEENIASNDGPrGPPPAr

TRIP6 TRIP6 R179 VKVAQPVrGCGPPRR Q15654 6009646 6009647 VAQPVrGCGPPR 537.934166 145.2722557 701.91254 716.3117 69.75822 357.3372

K4 KRT4 R56 SRSLYNLrGNKSISM P19013 40350491 40350492 SLYNLrGNK 4341.23591 5350.24633 45.954276 185.794 699.366684 783.59919

K7 KRT7 R46 LYGLGASrPRVAVRS P08729 27278470 27278471 LSSARPGGLGSSSLYGLGASrPR; LSSARPGGLGSSSLYGLGASrPr; PGGLGSSSLYGLGASrPr; PGGLGSSSLYGLGASrPrVAVr 1020.541291 697.72989 355.217592 632.5203 746.12128 422.98104

SRC-2 NCOA2 R1248 EILNQHLrQRQMHQQ Q15596 40724744 40725367 EILNQHLr 444.49141 111.679711 188.06088 82.5095 153.337376 442.3245

HSPB8 HSPB8 R78 RGPTATArFGVPAEG Q9UJY1 13247332 13247334 SGMVPrGPTATAr

hnRNP A3 HNRNPA3 R257 GGGGGGSrGSYGGGD P51991 6009439 6009440 GGNFGGGGGNFGrGGNFGGrGGYGGGGGGSr; GGNFGGRGGYGGGGGGSr 413.68877 310.14841 246.83192 105.352 397.02596 1459.0717

PRRC2C PRRC2C R747 MQSYMDPrMMSGRPA Q9Y520 12205510 12205513 WLMMQSYMDPr 491.221082 281.86158 227.499948 193.0627 236.53884 977.9301

hnRNP D0 iso3 HNRNPD R280 GGFAGRArGRGGDQQ Q14103-3 6009584 6009589 ArGrGGDQQSGYGK

AHDC1 AHDC1 R891 GLATFPSrGAKASPV Q5TGY3 15493033 15493035 GLATFPSrGAK 564.22487 503.63599 192.77164 129.693 679.22076 1103.5239

TAF9B TAF9B R128 CLTAPNYrLKSLIKK Q9HBM6 13247237 13247239 LPPDRYCLTAPNYrLK; YCLTAPNYrLK TAF9; TAF9B Q16594; Q9HBM6 R128; R128 1673.76748 1022.18974 1253.12788 388.9119 1152.8298 3202.0876

XRN2 XRN2 R883 FQQQRFDrGVGAEPL Q9H0D6 12197461 12197462 FDrGVGAEPLLPWNR 580.395299 575.79808 467.32128 278.0507 506.230444 1426.5244

RPS2 RPS2 R34 GGFGSGIrGRGRGRG P15880 12191522 12191523 GGFGSGIrGr

desmin DES R37 LSSPVFPrAGFGSKG P17661 8094042 8094045 RTFGGAPGFPLGSPLSSPVFPr; TFGGAPGFPLGSPLSSPVFPr 1731.80634 143.196768 147.039696 121.7294 252.650692 487.45763

PAI-RBP1 SERBP1 R188 RGDGFDSrGKREFDR Q8NC51 27278935 27278936 GDGFDSrGK 2061.33653 555.281727 466.597492 1484.686 4142.43664 1440.1128

SRm300 SRRM2 R2207 SAAGLAArMSQVPAP Q9UQ35 27279827 27279828 IALALTAISLGTARPPPSMSAAGLAAr; IALALTAISLGTArPPPSMSAAGLAAr 423.533429 149.599879 107.366764 155.6237 530.406668 430.56851

PAIP1 PAIP1 R21 GRSRGLGrGGGGPEG Q9H074 6010103 6010104 GLGrGGGGPEGGGFPNGAGPAER; SrGLGrGGGGPEGGGFPNGAGPAER 425.694973 155.202047 131.955468 85.07 1108.33332 482.62004

DHX36 DHX36 R50 GGGGRGGrGRHPGHL Q9H2U1 15379769 15379770 GSGGGGGGGGGGrGGrGr

PABP 1 PABPC1 R419 AIPQTQNrAAYYPPS P11940 9483274 9483278 AVPNPVINPYQPAPPSGYFMAAIPQTQNr; AVPNPVINPYQPAPPSGYFMAAIPQTQNrAAYYPPSQIAQLrPSPr 610.028485 239.9155902 152.5588988 91.92534 340.3787692 890.31206

TORC2 CRTC2 R161 AEKGQLFrLPSALNR Q53ET0 40351345 40351346 GQLFrLPSALNR 459.57692 151.30687 199.2494 37.7316 213.52144 222.71038

BAT2 iso1 PRRC2A R1066 EFRGDDGrGGGTGGP P48634 8093195 8113363 GDDGrGGGTGGPNHPPAPR 121.243925 82.874077 66.805 43.2716 109.6996 489.9

HNRPUL2 HNRNPUL2 R666 GYVGGQRrGYDNRAY Q1KMD3 27278375 27278376 rGYDNR 93.169373 252.683145 168.87808 64.5474 238.395976 423.86838

PLEKHA2 PLEKHA2 R333 GPNSILCrGRPPLEE Q9HB19 40351320 40351321 SISLTRPGSSSLSSGPNSILCr 1169.15095 241.154056 404.86992 264.667 371.779308 1474.0562

RAVER1 RAVER1 R534 RGWGGAGrSRRPAEG Q8IY67-2 40352104 40353239 GWGGAGr 665.23303 865.37022 856.2758 324.7367 277.70284 3911.6169

TAF15 TAF15 R490 RGGYGGDrGGGYGGD Q92804 6009946 6009947 GGGYGGDrGGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGYGGDrGGGYGGDR; GGGYGGDrGGYGGDrGGGYGGDrGGYGGDr GGDrGGGYGGDR TAF15 Q92804 R562; R475; R459; R490

ACF7 MACF1 R7361 GGQGNSRrGLNKPSK Q9UPN3 27277121 27277122 rGLNKPSK; rGLNKPSKIPTMSK 1297.1816 349.168248 459.3766 491.397 1389.15708 3338.3787

hnRNP D-like HNRPDL R25 APATLASrSLSHWRP O14979 9300384 9300385 LSHVPPPLFPSAPATLASr 2493.606731 1117.799254 892.959836 471.6508 1796.44616 3728.7761

DDX3 DDX3X R600 FSGGFGArDYRQSSG O00571 40350308 40350309 FSGGFGArDYR DDX3X; DDX3Y O00571; O15523 R600; R598 679.47319 281.96597 255.85292 165.276 535.59612 747.4172

EWS EWSR1 R464 GLPPREGrGMPPPLR Q01844 26362105 26361872 EGrGMPPPLrGGPGGPGGPGGPMGr

ZAK ZAK R695 LNSSPRGrYSGKSQH Q9NYL2 48897887 48906276 YGrGSISLNSSPrGr

RBM3 RBM3 R121 SGRYYDSrPGGYGYG P98179 9483266 9483269 SYSRGGGDQGYGSGrYYDSrPGGYGYGYGR; YYDSrPGGYGYGYGRSR; YYDSrPGGYGYGYGr

FBXL18 FBXL18 R446 PAMHAVPrGFGKKVR Q96ME1 40351047 40351048 ADRAPAQPAMHAVPrGFGK; APAQPAMHAVPrGFGK 990.825484 863.61847 366.466996 392.477 459.644768 2084.6487

PRMT7 PRMT7 R32 DYHQEIArSSYADML Q9NVM4 29429570 29429572 ANPTTGSVEWLEEDEHYDYHQEIAr 171.903996 83.020366 48.419768 40.0834 143.545264 229.39349

DDX42 DDX42 R814 RERYTENrGSSRHSH Q86XP3 27277695 27277696 YTENrGSSR 78.829047 141.265267 132.22616 64.0757 170.04176 421.9373

supervillin SVIL R1203 EAWKTRGrGAANDST O95425 6009166 6009167 GrGAANDSTQFTVAGR 609.423661 83.40189 200.776956 126.7663 186.549016 551.57864

THOC4 ALYREF R197 RPAQSVNrGGMTRNR Q86V81 6009774 6009775 RPAQSVNrGGMTR 612.91235027 510.264898 478.155036 231.17866 842.223804 2696.05333

SPATS2 SPATS2 R449 EVLPGNRrGGQGYRP Q86XZ4 15380578 15380579 rGGQGYRPQGQK 220.878152 405.797392 409.06608 194.2107 1166.48936 1672.2426

CPSF6 CPSF6 R204 FPQGGRGrGRFPGAV Q16630 13246986 13246988 AAFPQGGrGr

XRN2 XRN2 R851 NLYRPLLrGQAQIPK Q9H0D6 27280339 27280340 TLGHVMPrGSGTGIYSNAAPPPVTYQGNLYrPLLr

FMR1 FMR1 R477 GRGSRPYrNRGHGRR Q06787 27278017 27278018 SYVTDDGQGMGrGSrPYr

G3BP-2 G3BP2 R432 RDIRRNDrGPGGPRG Q9UN86 27278061 27278062 RNDrGPGGPR 53.4311602 216.340839 106.801696 80.0763 269.27734 504.33549

RFX5 RFX5 R354 SPPILAPrLSSGALK P48382 27279368 27279369 SLIPPIPVSPPILAPr 263.661475 143.294437 116.30394 108.41 169.427744 533.3838

K6c KRT6C R24 GFSANSArLPGVSRS P48668 41682271 41682272 GFSANSArLPGVSR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R24; R24; R24

RBM3 RBM3 R90 GKSARGTrGGGFGAH P98179 6009497 6009498 GTrGGGFGAHGRGR

BAD BAD R161 WWDRNLGrGSSAPSQ Q92934 6009960 6009961 NLGrGSSAPSQ 1213.599134 440.856845 155.930868 169.9284 143.7692388 1343.1816

SFRS2 SRSF2 R55 DRYTKESrGFAFVRF Q01130 40351138 40351139 ESrGFAFVR 281.137571 238.32237 143.1022 112.746 218.26104 533.8875

RBMX RBMX R101 RGPPPPPrSRGPPRG P38159 12205564 12205565 RGPPPPPrSR 108.503384 212.431362 106.572792 66.4118 231.813836 502.93433

TAF15 TAF15 R450 GGGYGGDrSGGGYGG Q92804 15558703 15559056 SGGGYGGDrSGGGYGGDR GGGYGGDr TAF15 Q92804 R562; R459; R431; R450 194.640402 140.4117 130.50008 41.0758 128.462348 432.9451

TAF15 TAF15 R195 GGYDKDGrGPMTGSS Q92804 27279893 27279894 GYGGSQGGGrGrGGYDKDGr

CSTF2 CSTF2 R475 RGPVPGPrGPIPSGM P33240 27277625 27277626 GPVPGPrGPIPSGMQGPSPINMGAVVPQGSR 224.818121 131.915498 66.984304 37.7492 318.80616 478.3908

FXR2 FXR2 R432 YGGSYGGrGRGRRTG P51116 12197360 12197361 TYGGSYGGrGr; TYGGSYGGrGrGr

OTUD4 OTUD4 R1050 YNQTYGSrKYKSDWG Q01804 40351091 40351092 QFYNQTYGSrK 1071.13501 854.44359 748.64504 558.105 1082.39344 1610.1794

LARP4 LARP4 R443 EQNGDYGrGRRTLFR Q71RC2 6009748 6009749 ETSTLQVEQNGDYGrGR 730.46753791 1052.293385 528.30634 201.016 541.82074 3154.80328

TIF1G TRIM33 R515 QINLAQLrLQHMQQQ Q9UPN9 9483740 9483743 TPGQINLAQLr; TPGQINLAQLrLQHMQQQVYAQK 1944.007373 1095.637829 846.064772 478.8517 1511.806284 2614.82515

DHX36 DHX36 R47 GGGGGGGrGGRGRHP Q9H2U1 15379766 15379767 GSGGGGGGGGGGrGGrGr

NFKBIL2 TONSL R797 AAYQAAIrGVGSAQS Q96HA7 15494321 15494323 AAYQAAIrGVGSAQSR 1129.18025 617.32814 589.73408 201.7544 807.49172 1377.562

HuR ELAVL1 R206 LYHSPARrFGGPVHH Q15717 12190764 12190765 rFGGPVHHQAQRFR

WDR32 DCAF10 R134 LKERSLGrGLFVDPA Q5QP82 15494940 15494942 SLGrGLFVDPAR; SLGrGLFVDPARDNFR 1469.55644 217.039394 542.50248 102.1194 193.5569 1254.742

DDX42 DDX42 R12 KGGPGTKrGFGFGGF Q86XP3 15379746 15379747 rGFGFGGFAISAGK 884.56786 645.66788 582.28044 303.0448 882.94484 2106.8161

FBP3 FUBP3 R337 FGGLAAArGRGRGRG Q96I24 12190820 12190821 DGFGGLAAAr; DGFGGLAAArGr 2208.26474 1063.21501 1208.24732 414.814 684.609472 3029.9648

K6a KRT6A R24 GFSANSArLPGVSRS P02538 15560215 15561388 GFSANSArLPGVSR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R24; R24; R24 1884.86892 418.47806 312.659056 977.606 421.448348 978.4775

hnRNP U HNRNPU R768 GRGSYSNrGNYNRGG Q00839 12197803 12197804 GSYSNrGNYNR 139.888199 182.50661 84.068032 63.2854 123.864608 649.7845

hnRNP H1 HNRNPH1 R233 AGFERMRrGAYGGGY P31943 6009378 6009379 rGAYGGGYGGYDDYN; rGAYGGGYGGYDDYNG; rGAYGGGYGGYDDYNGYNDGYGFGSDR; rGAYGGGYGGYDDYNGYNDGYGFGSDRFGR rGAYGGGYGGY; rGAYGGGYGGYDD; rGAYGGGYGGYDDY HNRNPH1; HNRNPH2 P31943; P55795 R233; R233 2619.4602698 1049.2974635 1555.123928 384.43565 1985.395316 3094.30454

VPS13C VPS13C R3519 DFGDSLArGGKGFLR Q709C8 6009743 6009744 DFGDSLArGGK 4477.72644 1727.15257 73.034388 359.66 897.21448 1936.0319

BAG4 BAG4 R108 NYWNSTArSRAPYPS O95429 9300403 9300404 AGGSHQEQPPYPSYNSNYWNSTAr 747.55736 251.792255 249.721492 125.98771 260.302932 1797.29222

EIF4H EIF4H R170 LGGRGGSrPGDRRTG Q15056 8094638 8094642 DDFLGGRGGSrPGDRR; DDFLGGrGGSrPGDrR 891.229218 416.483639 475.479364 410.1956 800.450708 2413.551

EIF4B EIF4B R268 RGSRDYDrGYDSRIG P23588 40350364 40350365 DYDrGYDSR 668.794665 431.940795 613.293584 91.0147 1139.6524 610.45703

MLL KMT2A R32 RGLGGAPrQRVPALL Q03164 41554142 41554143 GLGGAPr 734.93453 258.62837 238.20648 151.722 449.4994 1293.5453

CCDC9 CCDC9 R94 PGASKGGrTPPQQGG Q9Y3X0 27277530 27277531 GGrTPPQQGGr

K8 KRT8 R47 RVGSSNFrGGLGGGY P05787 15380079 15380080 VGSSNFr; VGSSNFrG; VGSSNFrGG; VGSSNFrGGL; VGSSNFrGGLG; VGSSNFrGGLGG; VGSSNFrGGLGGGY; VGSSNFrGGLGGGYGGASGMGGITAV; VGSSNFrGGLGGGYGGASGMGGITAVTVN; VGSSNFrGGLGGGYGGASGMGGITAVTVNQSLLSPLVLEVDPNIQAVR 7361.971001 4328.8544013 2734.835748 959.203 9533.003808 2598.835596

RPS29 RPS29 R12 QLYWSHPrKFGQGSR P62273 15380468 15380469 GHQQLYWSHPrK 527.374628 568.80252 724.6498 126.1481 629.61732 1731.0237

NFAT90 ILF3 R609 KRAPVPVrGGPKFAA Q12906 6008947 6008940 APVPVrGGPK; RAPVPVrGGPK 1664.050102 2635.786439 1104.245916 1017.3637 1848.650312 7828.0431

hnRNP D0 HNRNPD R278 SRGGFAGrARGRGGG Q14103 6009577 6009578 EQYQQQQQWGSrGGFAGr; EQYQQQQQWGSrGGFAGrAr; GGFAGr; GGFAGrAr 723.879266 602.790617 251.290588 182.5496 591.686744 2286.0068

TAF15 TAF15 R187 SQGGGRGrGGYDKDG Q92804 8144241 8144244 GYGGSQGGGRGrGGYDKDGR; GYGGSQGGGrGr; GYGGSQGGGrGrGGYDK; GYGGSQGGGrGrGGYDKDGR; GYGGSQGGGrGrGGYDKDGr; GrGGYDK; GrGGYDKDGR 536.498347 528.503118 585.57884 226.2085 1009.164488 2799.6221

JTV1 AIMP2 R26 ELPTCMYrLPNVHGR Q13155 13247174 13247176 VELPTCMYrLPNVHGR 1382.645528 848.672539 443.07432 376.5288 870.853776 1899.17187

KHDRBS1 KHDRBS1 R348 GAPAPRArTAGIQRI Q07666 27279516 27279517 GATVTrGVPPPPTVrGAPAPrAr

PNUTS PPP1R10 R710 YHRGRGGrGGNEPPP Q96QC0 27279105 27279106 GGPGPGPGPYHrGrGGr

AHNAK AHNAK R556 EGTLTGPrLGSPSGK Q09666 48897889 48906287 VDIETPNLEGTLTGPr 548.21745 142.720292 82.947692 125.146 157.488052 350.4096

PSF SFPQ R681 PVGGQGPrGMGPGTP P23246 6009327 6009328 FGQGGAGPVGGQGPr; FGQGGAGPVGGQGPrGMGPGTPA; FGQGGAGPVGGQGPrGMGPGTPAGY; FGQGGAGPVGGQGPrGMGPGTPAGYGR; FGQGGAGPVGGQGPrGMGPGTPAGYGRGR; FGQGGAGPVGGQGPrGMGPGTPAGYGr; FGQGGAGPVGGQGPrGMGPGTPAGYGrGREEYEGPNK; FGQGGAGPVGGQGPrGMGPGTPAGYGrGr 6552.246921 1566.040905 1541.548284 794.3873 3564.824048 4246.70896

Trap150 THRAP3 R91 YYFRGRNrGFYPWGQ Q9Y2W1 27280143 27280144 NrGFYPWGQYNrGGYGNYr

ASE-1 CD3EAP R162 NPPVTGPrSALAPNL O15446 29427311 29427312 FCAFGGNPPVTGPr 1408.146388 702.82927 864.05556 174.0495 948.02168 1337.3649

SON SON R964 RLTPDPYrMSPRPYR P18583 40350916 40350917 LTPDPYr 536.63775 295.12197 174.04764 148.784 498.52064 794.2199

snRNP D1 SNRPD1 R98 KREAVAGrGRGRGRG P62314 40350406 40350407 EAVAGr; EAVAGrGR; EAVAGrGr; EAVAGrGrGr 222.802679 136.567431 98.013196 36.79307 1761.856264 498.0742

RPL13 RPL13 R74 HTKVRAGrGFSLEEL P26373 27279434 27279435 AGrGFSLEELR 611.319797 386.87077 231.909636 204.046 55.143852 1425.3606

RTKN RTKN R14 RSRVTVArGSALEME Q9BST9 6010073 6010074 VTVArGSALEMEFK 1072.897485 903.527339 2580.55036 508.1819 811.036908 463.16227

XRN2 XRN2 R847 TYQGNLYrPLLRGQA Q9H0D6 27280331 27280332 TLGHVMPrGSGTGIYSNAAPPPVTYQGNLYrPLLr

PPP1R13L PPP1R13L R205 PERGPSPrPPATAYD Q8WUF5 29429548 29429550 GSPLAEGPQAFFPErGPSPrPPATAYDAPASAFGSSLLGSGGSAFAPPLR

HNRPUL2 HNRNPUL2 R693 GYRNFYDrYRGDYDR Q1KMD3 27278387 27278388 AYGQQYWGQPGNrGGYrNFYDr

SFRS9 SRSF9 R93 FPRTYGGrGGWPRGG Q13242 12197374 12197375 TYGGrGGWPR; TYGGrGGWPRGGR; TYGGrGGWPr; TYGGrGGWPrGGr 193.115263 211.211572 215.948976 134.8911 398.70368 987.1255

BLES03 iso3 C11orf68 R29 RQERSRArGWAGVER Q9H3H3-3 26362110 26361889 ArGWAGVER C11orf68; C11orf68 Q9H3H3-2; Q9H3H3-3 R29; R29

CCT7 CCT7 R537 PTAAGRGrGRGRPH\_ Q99832 12191625 12191626 STVDAPTAAGrGr; STVDAPTAAGrGrGR; STVDAPTAAGrGrGr; STVDAPTAAGrGrGrGrPH

ZGPAT ZGPAT R370 IHAVVLPrGKSLDQC Q8N5A5 27280405 27280406 VEPIHAVVLPr; VEPIHAVVLPrGK 1695.357081 1118.286598 892.35546 584.2257 941.38952 2717.6478

PRRC2C PRRC2C R1188 PDQGYRGrGRGEYYS Q9Y520 12191655 12191658 DWFPDQGYrGr; GrGrGEYYSrGr

CCDC9 CCDC9 R128 RGGGAGGrGRRGRGR Q9Y3X0 6010223 6010224 SWEGSPGEQPrGGGAGGrGr

SIPA1 SIPA1 R13 GGVGSPRrGMAPAST Q96FS4 27279648 27279649 rGMAPASTDDLFAR 809.44336 256.93525 131.0928 86.9835 362.40884 624.795

DDX3Y DDX3Y R598 FSGGFGArDYRQSSG O15523 40350562 40350563 FSGGFGArDYR DDX3X; DDX3Y O00571; O15523 R600; R598

HNRNPA1L2 HNRNPA1L2 R284 KGGNFGGrSSGPYGG Q32P51 9300235 9300236 GGNFGGrSSGPYGGGGQYFAK HNRNPA1; HNRNPA1L2 P09651; Q32P51 R336; R284

ZAP3 YLPM1 R563 SSYLESPrGPRFDGP P49750 27280359 27280360 SSYLESPrGPrFDGPr

PRPF6 PRPF6 R23 GYVPGLGrGATGFTT O94906 12192149 12192150 KKPFLGMPAPLGYVPGLGrGATGFTTR 359.772985 120.370107 91.015008 38.1411 1128.91204 290.02908

ADAR ADAR R91 RGRQVDIrGVPRGVH P55265 27277134 27277135 QVDIrGVPR 566.206498 615.7294 434.1488 227.0432 659.50796 899.231

ZNF828 CHAMP1 R398 KSGPPELrKTAPTLS Q96JM3 40712235 40720743 SGPPELrK 2375.00923 673.8446 1150.94444 193.4824 671.63904 1824.1346

TARDBP TARDBP R293 QGGFGNSrGGGAGLG Q13148 9300519 9300520 FGGNPGGFGNQGGFGNSr 1365.688126 993.16217 870.603876 340.8943 1617.262384 1952.77889

SRm300 SRRM2 R2194 AISLGTArPPPSMSA Q9UQ35 27279815 27279816 IALALTAISLGTArPPPSMSAAGLAAr

VPS13C VPS13C R3526 RGGKGFLrGVVGGVT Q709C8 15380767 15380768 GFLrGVVGGVTGIITKPVEGAK 3912.537552 2133.580163 130.1687892 462.9999 796.909292 2297.0537

ZDHHC5 ZDHHC5 R617 KPDGLRGrGVGSPEP Q9C0B5 27280398 27280399 GrGVGSPEPGPTAPYLGR 1074.428047 852.16846 407.941648 303.8984 1189.343908 1813.01709

DERPC CHTF8 R266 TGSGLNLrMAGPQGL P0CG12 9483240 9481651 AGGLLGTGSGLNLr 578.13965 269.43202 200.79072 86.9067 407.3432 1017.5752

C15orf52 C15orf52 R286 LRGEGPArAGSRRGP Q6ZUT6 48897845 48899689 STLQDCSQLrGEGPArAGSr

TAF15 TAF15 R475 GGGYGGDrGGGYGGD Q92804 6009936 6009937 GGGYGGDrGGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGGYGGDrGGYGGDR; GGGYGGDrGGGYGGDrGGYGGDr; SGGGYGGDrGGGYGGDrGGGYGGDr GGDrGGGYGGDR TAF15 Q92804 R562; R475; R459; R490

EIF4G2 EIF4G2 R23 SSGGGGSrGAPQHYP P78344 27277830 27277831 FSASSGGGGSrGAPQHYPK 319.59334 409.3947 182.11632 79.5334 148.442796 849.3026

GRAMD1B GRAMD1B R121 DYSCALQrDILLQGR Q3KR37 49251000 49250902 LIVDYSCALQr GRAMD1A; GRAMD1B Q96CP6; Q3KR37 R116; R121

BAT2 PRRC2A R232 LHHGHDPrGGLQPSG P48634-2 27277297 27277298 LHHGHDPr 62.3482948 149.181604 114.8709092 42.8657 145.465868 313.79521

KHDRBS1 KHDRBS1 R304 PPPVPRGrGVGPPRG Q07666 12197194 12197195 GrGVGPPrGALVR; GrGVGPPrGALVr; GrGVGPPrGALVrGTPVr

PABP 1 PABPC1 R385 LTNQYMQrMASVRAV P11940 13247326 13247328 QAHLTNQYMQr 262.777526 230.691175 212.413736 123.4167 281.287716 733.27381

EIF4G3 EIF4G3 R692 GRQTPGGrGVPLLNV O43432 13246977 13246979 QTPGGrGVPLLNVGSR 660.629222 484.210012 349.274768 604.72 1944.65296 875.61621

SRm300 SRRM2 R2342 SANLVGPrSAHATAP Q9UQ35 12194097 12194098 TPQAPASANLVGPr 1022.338218 743.816931 579.198172 289.433 999.549004 1776.49148

RBM3 RBM3 R116 DQGYGSGrYYDSRPG P98179 40351099 40351100 SYSRGGGDQGYGSGrYYDSrPGGYGYGYGR

hnRNP D-like HNRPDL R332 RGAAAGGrGGTRGRG O14979 41477581 41477582 GAAAGGrGGTr

PHIP PHIP R1804 LTFGTSSrGRVRKLT Q8WWQ0 40351402 40351403 QLLFEDTSLTFGTSSrGR 503.200808 300.57456 346.78088 102.9446 466.10604 671.0526

DDX5 DDX5 R478 LLQLVEDrGSGRSRG P17844 40350751 40350752 LLQLVEDrGSGR 171.576383 118.41401 69.411728 37.4094 107.909212 242.0589

ARHGEF17 ARHGEF17 R45 LRRRASCrPTTAARG Q96PE2 27277230 27277231 ASCrPTTAARGQPSR 146.75276 91.71019 58.577724 52.0852 67.114704 254.7273

ANKRD25 KANK2 R123 TRGGFNPrVERTLLD Q63ZY3 15379466 15379467 HSAYSYCGrGFYPQYGALETrGGFNPr

KHSRP KHSRP R442 KCGLVIGrGGENVKA Q92945 6009984 6009985 CGLVIGrGGENVK 1672.212674 1167.491039 1754.916696 434.657 1492.008368 3457.73605

hnRNP F HNRNPF R212 QRPGPYDrPGTARRY P52597 27278304 27278305 FMSVQRPGPYDrPGTAR 684.501268 661.914539 599.919688 153.1652 690.677144 1739.0921

K7 KRT7 R48 GLGASRPrVAVRSAY P08729 27278474 27278475 LSSARPGGLGSSSLYGLGASrPr; LSSArPGGLGSSSLYGLGASRPr; PGGLGSSSLYGLGASrPr; PGGLGSSSLYGLGASrPrVAVr 2640.0181291 3597.204468 1302.717836 2515.3261 5233.11208 1798.1142952

hnRNP U HNRNPU R727 RGGAPGNrGGYNRRG Q00839 12197791 12197792 GGAPGNrGGYNR 168.38734 215.04626 123.18966 67.1506 216.7916 627.4883

hnRNP A2/B1 HNRNPA2B1 R203 VQSSRSGrGGNFGFG P22626 476742 68303 SGrGGNFGFGD; SGrGGNFGFGDSR; SGrGGNFGFGDSr; SGrGGNFGFGDSrGG; SGrGGNFGFGDSrGGGG; SGrGGNFGFGDSrGGGGNFGPGPGSNF; SGrGGNFGFGDSrGGGGNFGPGPGSNFR; SGrGGNFGFGDSrGGGGNFGPGPGSNFRGGSDGYGSGR; SGrGGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGR 2674.144781 1922.7351 1367.167456 497.1005 1735.001264 3887.828

TAGLN TAGLN R197 MTGYGRPrQIIS\_\_\_ Q01995 41717819 41717776 GASQAGMTGYGRPr 3016.17052 81.9437476 132.985288 88.7043 191.987256 508.85246

RBM9 RBFOX2 R297 RTVYGAVrAVPPTAI O43251 40350988 40350989 TVYGAVr 538.549517 474.39535 388.570492 449.377 1297.54668 2064.8342

DDX3 DDX3X R99 SRGRFDDrGRSDYDG O00571 40350304 40350305 FDDrGR DDX3X; DDX3Y O00571; O15523 R99; R98 344.40835 405.376972 355.709376 244.9212 648.724468 1414.1642

QKI iso3 QKI R219 PTAQAAPrIITGPAP Q96PU8-3 27279220 34544017 SPTAQAAPr 163.177113 478.99995 147.80428 102.995 321.54824 573.7235

PRRC2C PRRC2C R279 SETNKGLrGRGPPPS Q9Y520 8144526 8152606 GLrGrGPPPSWASEPERPSILSASELK

DYN2 DNM2 R850 PPGVPSRrPPAAPSR P50570 27277775 27277776 rPPAAPSRPTIIrPAEPSLLD

IREB1 ACO1 R713 FNSYGSRrGNDAVMA P21399 40712213 40712157 rGNDAVMAR 129.949435 145.52395 84.928096 82.5592 177.29056 383.8815

Musashi-2 MSI2 R199 FPPGTRGrARGLPYT Q96DH6 27278720 27278721 EVMFPPGTrGr

BAG4 BAG4 R185 NSPTPVSrWIYPQQD O95429 13247228 13247230 SSGNSPTPVSr 151.168039 134.333056 171.669196 84.071 98.103488 1053.1792

NICE-4 UBAP2L R151 ASRGREFrGQENGLD Q14157 41477406 41477407 EFrGQENGLDGTK 328.05003 231.80729 399.20808 62.7118 196.98204 722.6393

YB-1 YBX1 R199 RFPPYYMrRPYGRRP P67809 9300499 9300500 FPPYYMr; RFPPYYMr 3727.7234665 3763.120075 3202.643108 1708.9219 6769.382408 10138.25188

PRRC2C PRRC2C R1186 WFPDQGYrGRGRGEY Q9Y520 13247522 13247524 DWFPDQGYrGr

CSTF2 CSTF2 R402 RGPPLDGrGGRDPRG P33240 27277637 27277638 GPPLDGrGGRDPR 1809.872658 995.14272 736.89976 287.8003 1400.12212 2042.1792

SRC-2 NCOA2 R489 PTSMLSPrHRMSPGV Q15596 48885439 48889275 MNSPSQSSPGMNPGQPTSMLSPr 40.545857 1.9005415 21.152044 1.48147 21.7956 26.79661

TRXR1 TXNRD1 R289 GQFIGPHrIKATNNK Q16881 48897892 48908201 VVYENAYGQFIGPHr 368.91712 65.780286 99.121136 64.3338 92.328064 206.21708

Mnk1 MKNK1 R455 RALAQAGrGEDRSPP Q9BUB5 27278697 27278698 ALAQAGrGEDR 147.296655 75.47111 69.840148 26.082 67.760044 192.3237

ZNF598 ZNF598 R324 RVARAGTrGAQQSRR Q86UK7 27280443 27280444 AGTrGAQQSR 47.4762277 125.115705 155.089032 37.6637 172.741364 484.21969

RBM3 RBM3 R138 RSRDYNGrNQGGYDR P98179 9300508 9300509 DYNGrNQGGYDR 401.784966 135.844995 219.7032 109.6081 235.385428 999.6283

DDX17 DDX17 R94 DRDRDRDrGGFGARG Q92841 27277686 27277687 DrGGFGAR 383.51775 515.174088 366.59422 199.9377 624.806052 1247.5545

hnRNP A2/B1 HNRNPA2B1 R213 NFGFGDSrGGGGNFG P22626 6009291 6009292 FGDSrGGGGNFGPGPGSNFR; FGFGDSrGGGGNFGPGPGSNFR; GDSrGGGGNFGPGPGSNFR; GFGDSrGGGGNFGPGPGSNFR; GGNFGFGDSr; GGNFGFGDSrG; GGNFGFGDSrGG; GGNFGFGDSrGGG; GGNFGFGDSrGGGG; GGNFGFGDSrGGGGN; GGNFGFGDSrGGGGNFG; GGNFGFGDSrGGGGNFGPG; GGNFGFGDSrGGGGNFGPGPG; GGNFGFGDSrGGGGNFGPGPGSN; GGNFGFGDSrGGGGNFGPGPGSNF; GGNFGFGDSrGGGGNFGPGPGSNFR; GGNFGFGDSrGGGGNFGPGPGSNFRGGSDGYGSGR; GGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGR; GGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGr; GNFGFGDSrGGGGNFGPGPGSNFR; NFGFGDSrGGGGNFGPGPGSNFR; SGrGGNFGFGDSr; SGrGGNFGFGDSrGG; SGrGGNFGFGDSrGGGG; SGrGGNFGFGDSrGGGGNFGPGPGSNF; SGrGGNFGFGDSrGGGGNFGPGPGSNFR; SGrGGNFGFGDSrGGGGNFGPGPGSNFRGGSDGYGSGR; SGrGGNFGFGDSrGGGGNFGPGPGSNFrGGSDGYGSGR 24654.086622 12527.0240095 10598.150172 3885.94612 16416.820168 29870.03399

ZNF511 iso2 ZNF511 R240 CFGQGAArGFKSNKK Q8NB15-2 15494957 29658011 IPSTICFGQGAArGFK 425.14406 210.80202 239.97596 83.8831 164.46412 774.6124

hnRNP 2H9 HNRNPH3 R301 GGYGSVGrMGMGNNY P31942 9300453 9300454 DGMDNQGGYGSVGr 77.742214 117.796536 40.301488 29.195 82.126444 357.0129

U2AF1 U2AF1 R211 SRSRDRGrGGGGGGG Q01081 40350312 40350313 DRGrGGGGGGGGGGGGR; GrGGGGGGGGGGGGR 6.03647528 230.497982 80.8863284 54.73974 204.213784 469.92358

snRNP D3 SNRPD3 R97 NQGSGAGrGKAAILK P62318 40350462 40350463 NQGSGAGrGK 158.649865 146.34477 54.204616 33.7659 923.89072 536.5785

TAFII31 TAF9 R128 CLTAPNYrLKSLQKK Q16594 13247080 13247082 LPPDRYCLTAPNYrLK; YCLTAPNYrLK TAF9; TAF9B Q16594; Q9HBM6 R128; R128

AHNAK2 AHNAK2 R327 RRKFLNLrFRTGSGQ Q8IVF2 48897874 48906225 FLNLrFR 20.0088284 0 29.387628 30.6654 8.5119772 212.50137

PUS7 PUS7 R450 CVEGQLLrGLSKYGM Q96PZ0 15494482 15494484 CVEGQLLrGLSK 762.70667 456.18716 792.1306 194.431 613.56336 1053.3471

DDX5 DDX5 R502 DRYSAGKrGGFNTFR P17844 6008922 6008923 rGGFNTFR 456.3788174 730.051608 595.158832 254.7211 1236.84126 3102.3849

SFRS9 SRSF9 R101 GGWPRGGrNGPPTRR Q13242 40350850 40350851 TYGGrGGWPrGGr

TRA2B TRA2B R238 DDRDYYSrSYRGGGG P62995 40350962 40350963 GYDDRDYYSr 818.2669 548.80826 353.32932 146.452 519.8144 985.1659

SAFB1 iso3 SAFB R820 LPPPPRGrRDWGDHG Q15424-3 40352103 40353229 MSEGrGLPPPPrGr SAFB; SAFB Q15424-3; Q15424-2 R820; R751

DSTYK DSTYK R29 GMIRELCrGFGRYRR Q6XUX3 27279636 27279637 ELCrGFGR 358.867025 306.201181 299.36824 140.4082 961.93708 927.2588

TAF15 TAF15 R206 TGSSGGDrGGFKNFG Q92804 6008986 6008987 GPMTGSSGGDrGGFK; MTGSSGGDrGGFK 2115.355033 812.417463 1010.7028084 383.0603 970.870816 8110.43917

K4 KRT4 R9 IARQQCVrGGPRGFS P19013 40350483 40350484 QQCVrGGPR 431.29119 396.71489 24.198352 36.1883 84.161192 213.87585

hnRNP A1 HNRNPA1 R218 GGNDNFGrGGNFSGR P09651 9479427 10339785 GGGFGGNDNFGrGGNFSGrGGFGGSR; GGGFGGNDNFGrGGNFSGrGGFGGSr; SGSGNFGGGrGGGFGGNDNFGrGGNFSGr; SGSGNFGGGrGGGFGGNDNFGrGGNFSGrGGFGGSr

NKX2-1 NKX2-1 R121 YGANPDPrFPAISRF P43699 41398763 41398764 NSASGPGWYGANPDPrFPAISR 1165.12517 498.443803 26.5398068 84.2836 96.221752 231.75743

AHNAK AHNAK R330 QTPKAGLrVSAPEVS Q09666 48885446 48895514 AGLrVSAPEVSVGHK 1420.27094 97.296199 86.153836 122.481 129.426996 331.6853

FMR1 FMR1 R474 QGMGRGSrPYRNRGH Q06787 8143878 8143882 SYVTDDGQGMGRGSrPYR; SYVTDDGQGMGrGSrPYr 213.27702 193.40607 69.781744 78.5843 71.658652 885.8956

PABPN1 PABPN1 R263 TTDRGFPrARYRART Q86U42 15380296 15380297 RTNRPGISTTDRGFPr 64.944572 114.607493 44.670504 33.5277 31.03946 177.03629

DBNL DBNL R282 SPQPGKLrSPFLQKQ Q9UJU6 48897891 48906293 LrSPFLQK 1388.16359 84.842329 61.566372 94.6719 158.915672 250.1664

K19 KRT19 R24 GLGGGSVrFGPGVAF P08727 6009221 6009222 QSSATSSFGGLGGGSVr; QSSATSSFGGLGGGSVrFGPGVAFR; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGRGVSVSSAR; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGrGVSVSSAr; SYrQSSATSSFGGLGGGSVr; rQSSATSSFGGLGGGSVr 7646.57036 3423.550845 529.9850644 2865.2378 1257.834572 2043.345001

PNUTS PPP1R10 R707 PGPYHRGrGGRGGNE Q96QC0 27279097 27279098 GGPGPGPGPYHrGrGGr

hnRNP A3 HNRNPA3 R246 RGGNFGGrGGYGGGG P51991 6009433 6009434 GGNFGGGGGNFGrGGNFGGrGGYGGGGGGSR; GGNFGGGGGNFGrGGNFGGrGGYGGGGGGSr; GGNFGGrGGYGGGGGGSR 216.797823 186.08447 137.43044 50.6004 219.68784 767.9516

TRIP6 TRIP6 R111 LAELNGGrGHASRRP Q15654 6009636 6009637 GGLRPGSLDAEIDLLSSTLAELNGGrGHASR 655.0223504 184.7505946 1477.983032 639.0147 110.1883364 393.07448431

hnRNP A1 HNRNPA1 R371 SSYGSGRrF\_\_\_\_\_\_ P09651 15379970 15379971 NQGGYGGSSSSSSYGSGrrF 206.670211 254.171918 260.596664 55.5369 362.08248 307.75817

RBM16 SCAF8 R981 DIFSQPErPFLAPGR Q9UPN6 40351441 40351442 GIPPPSVLDSALHPPPrGPFPPGDIFSQPErPFLAPGr

RBM16 SCAF8 R1120 PKGLHEErGRFRSGN Q9UPN6 9300593 9300594 GLHEErGR 293.04297 321.72426 280.340068 81.1735 511.440396 1055.1802

Musashi-1 MSI1 R197 MSPTGSArGRSRVMP O43347 8093735 8093738 EVMSPTGSArGr

TTDN1 MPLKIP R57 HTPPYGPrSRPYGSS Q8TAP9 27280193 27280194 DGYGSPHHTPPYGPr 626.044837 458.897725 347.504916 160.9132 454.428748 1443.9101

TAF15 TAF15 R320 IKVSFATrRPEFMRG Q92804 40724779 40726813 VSFATrR FUS; TAF15 P35637; Q92804 R371; R320

PSF SFPQ R693 GTPAGYGrGREEYEG P23246 6009333 6009334 FGQGGAGPVGGQGPrGMGPGTPAGYGr; FGQGGAGPVGGQGPrGMGPGTPAGYGrGREEYEGPNK; FGQGGAGPVGGQGPrGMGPGTPAGYGrGr; GMGPGTPAGYGr; GMGPGTPAGYGrG; GMGPGTPAGYGrGR 11080.644916 9001.908201 7760.676896 2445.3653 6897.893628 26793.7948

PABPN1 PABPN1 R289 SGFNSRPrGRVYRGR Q86U42 27278912 27278913 SrFYSGFNSrPrGr

E1B-AP5 HNRNPUL1 R645 NRGGFQNrGGGSGGG Q9BUJ2 12191850 12191851 GGFQNrGGGSGGGGNYrGGFNr

PAI-RBP1 SERBP1 R177 RGRGGRGrGMGRGDG Q8NC51 6009847 6009848 GrGMGrGDGFDSR

STAU2 STAU2 R131 YRANYNFrGMYNQRY Q9NUL3 15380634 15380635 ANYNFrGMYNQrYHCPVPK 471.86799 156.71227 227.13328 115.606 277.2584 529.805

PPP1R13L PPP1R13L R167 RPGPGPLrQQGPPTP Q8WUF5 12205681 12205682 APSPrPGPGPLrQQGPPTPFDFLGR

LARP LARP1 R334 SDGAGGArASFRGRG Q6PKG0 41554357 41554358 SDGAGGAr 40.842527 187.830071 110.719352 190.0926 243.704492 1152.4771

KIAA1429 KIAA1429 R1741 RGNYNESrGGQSNFN Q69YN4 12197863 12197864 GNYNESrGGQSNFNR 156.004398 98.543302 146.15136 21.0473 77.817836 471.3804

TFG TFG R385 PNPYARNrPPFGQGY Q92734 8094643 8094646 NrPPFGQGYTQPGPGYR; NrPPFGQGYTQPGPGYr 443.498363 304.139979 407.42556 105.7744 491.47848 688.5648

DERPC CHTF8 R387 SNPATFQrSAGLQGS P0CG12 29427810 29427812 GAGSSAFSQSSGTLASNPATFQr 142.418507 57.164679 60.149176 26.6797 124.216552 222.8861

CIRBP CIRBP R145 SRDYYSSrSQSGGYS Q14011 9483284 9483287 DYYSSrSQSGGYSDR 719.46303 393.135171 357.92972 114.4214 347.36184 812.3301

RBM47 RBM47 R332 SRYQKAArGGGAAEA A0AV96 27279328 27279329 AArGGGAAEAAQQPSYVYSCDPYTLAYYGYPYNALIGPNR 17.1287688 21.1139357 4.1029244 3.19588 39.195016 11.608238

KIN KIN R36 QMCQKQCrDENGFKC O60870 15380089 15380090 QCrDENGFK 918.74871 884.17186 686.93272 456.741 1450.3668 3438.6748

CTAGE5 CTAGE5 R751 PPAPFAMrNVYPPRG O15320 40351418 40351419 DYFPPGDFPGPPPAPFAMr 926.483503 262.829424 242.210688 134.9714 312.997608 900.7513

RBM16 SCAF8 R967 SALHPPPrGPFPPGD Q9UPN6 40351437 40351438 GIPPPSVLDSALHPPPrGPFPPGDIFSQPErPFLAPGr

RPS2 RPS2 R36 FGSGIRGrGRGRGRG P15880 27279451 27279452 GGFGSGIrGr

snRNP D3 SNRPD3 R114 VAARGRGrGMGRGNI P62318 40350465 40350466 GrGMGrGNIFQK

EPPK1 EPPK1 R4739 REPGPAGrGDGDSGR P58107 41554400 41554401 EPGPAGrGDGDSGR; GPREPGPAGrGDGDSGR; REPGPAGrGDGDSGR EPPK1 P58107 R4739; R3137; R2603; R3671; R4205 558.249043 639.6633815 686.939044 152.54161 167.6112472 731.60723

hnRNP A3 HNRNPA3 R239 GGGGNFGrGGNFGGR P51991 6009427 6009428 GGNFGGGGGNFGrGGNFGGrGGYGGGGGGSR; GGNFGGGGGNFGrGGNFGGrGGYGGGGGGSr

RBM47 RBM47 R405 LGGYSAGrGIYSRYH A0AV96 8144685 8144688 APGPrGSYLGGYSAGr; APGPrGSYLGGYSAGrGIYSR; GPrGSYLGGYSAGr; GSYLGGYSAGr; GSYLGGYSAGrGIY; GSYLGGYSAGrGIYSR 3686.7903754 3531.19195 1431.763644 557.17647 11153.79416 2949.5774609

tensin 2 TNS2 R816 CGSPGEGrGYPSPGA Q63HR2 29430051 29430054 HSCGSPGEGrGYPSPGAHSPR 671.137401 63.697634 88.684924 45.9436 119.632096 364.13807

E1B-AP5 HNRNPUL1 R656 SGGGGNYrGGFNRSG Q9BUJ2 12198334 12198335 GGFQNrGGGSGGGGNYrGGFNr

RBMX RBMX R125 GTRGPPSrGGHMDDG P38159 6009384 6009385 GPPSrGGHMDDGGYSMN; GPPSrGGHMDDGGYSMNFNMSSSR RBMXL1; RBMX Q96E39; P38159 R125; R125 3669.4203788 2970.6659983 2237.7755232 1280.29672 3264.8256048 7568.03109

ARID1A ARID1A R1276 GNVAMGPrQHYPYGG O14497 15493052 15493054 AAGPGLGNVAMGPr; AAGPGLGNVAMGPrQHYPYGGPYDR 1405.981016 793.324675 528.046064 321.6892 1160.783964 2120.3792

RBM47 RBM47 R381 KAGSIRGrGRGAAGN A0AV96 27279325 27279326 GrGrGAAGNR

THOC4 ALYREF R63 RNRPAIArGAAGGGG Q86V81 27279991 27279992 NrPAIArGAAGGGGr 120.596674 93.74937 74.987016 47.4126 108.825316 358.8322

THOC4 ALYREF R58 GGGPIRNrPAIARGA Q86V81 26362104 26361867 NrPAIArGAAGGGGr

K13 KRT13 R35 GVSTCSTrFVSGGSA P13646 15380061 15380062 LQSSSASYGGGFGGGSCQLGGGrGVSTCSTr

SF2 SRSF1 R97 RSGRGTGrGGGGGGG Q07955 1308911 1308823 GTGrGGGGGGGGGAPR; GTGrGGGGGGGGGAPRGR; GTGrGGGGGGGGGAPr; GTGrGGGGGGGGGAPrG; GTGrGGGGGGGGGAPrGR; GTGrGGGGGGGGGAPrGr; SGRGTGrGGGGGGGGGAPRGR; SGrGTGrGGGGGGGGGAPR; SGrGTGrGGGGGGGGGAPr; SGrGTGrGGGGGGGGGAPrGR; SGrGTGrGGGGGGGGGAPrGr 105.1913984 262.481362 245.436052 77.2832 408.137944 1173.87354

ZAP3 YLPM1 R599 GNRPDGPrPRYEGHP P49750 40350757 40350758 GPrFEGNrPDGPrPr

IRS2 IRS2 R412 LSGGCGGrGSKVALL Q9Y4H2 15380049 15380050 SHTLSGGCGGrGSK 346.587758 75.869365 287.9714 47.8387 699.48624 396.23779

snRNP A SNRPA R152 PPMTQAPrIMHHMPG P09012 13247225 13247227 AVQGGGATPVVGAVQGPVPGMPPMTQAPr; KAVQGGGATPVVGAVQGPVPGMPPMTQAPr 958.6943685 702.843713 666.333344 306.16824 864.510748 1729.96777

PNN PNN R54 LSGPGGGrGRGSLLL Q9H307 6010117 6010118 LLALSGPGGGr; LLALSGPGGGrGR; LLALSGPGGGrGr; LLALSGPGGGrGrGSLLLR; LLALSGPGGGrGrGSLLLr; RLLALSGPGGGrGr 2683.293382 1063.304528 881.136188 426.9818 2113.38108 3859.7657

PABP 4 PABPC4 R509 AVQNLAPrAAVAAAA Q13310 15494385 15494387 LAMDFGGAGAAQQGLTDSCQSGGVPTAVQNLAPr 280.4007448 317.2064181 159.862474 93.70283 479.8844344 841.16704

K7 KRT7 R20 RSAAFSGrGAQVRLS P08729 6008913 6008914 AAFSGrGAQVr; AFSGrGAQVR; SAAFSGr; SAAFSGrG; SAAFSGrGA; SAAFSGrGAQ; SAAFSGrGAQV; SAAFSGrGAQVR; SAAFSGrGAQVRLSSAR; SAAFSGrGAQVr; SAAFSGrGAQVrL; SAAFSGrGAQVrLS; SAAFSGrGAQVrLSSAR 18395.247607 9603.839817 936.1007132 2474.7971 8414.384572 3506.3625718

ZNF9 iso2 CNBP R34 RGMRSRGrGFQFVSS P62633-2 6009474 15297022 GrGFQFVSSSLPDICYR; SrGrGFQFVSSSLPDICYR 1111.607178 267.399132 332.610656 162.295 327.906684 2395.1418

FMR1 FMR1 R471 DDGQGMGrGSRPYRN Q06787 6009533 6009534 SYVTDDGQGMGrGSrPYr 2846.256446 2496.862797 1150.86694 1183.5059 1746.183932 9202.09691

eIF4G EIF4G1 R694 GPGGELPrGPAGLGP Q04637 27277823 27277824 GPPrGGPGGELPrGPAGLGPR 836.44671 285.87988 296.02644 143.679 309.1154 785.335

PABPN1 PABPN1 R17 AAGAAGGrGSGPGRR Q86U42 15380293 15380294 AAAAAAGAAGGrGSGPGR; AAAAGAAGGrGSGPGR; AAAGAAGGrGSGPGR; MAAAAAAAAAAGAAGGrGSGPGr 3444.99903 75.591516 149.50804 70.62356 427.94488 639.50603

hnRNP A1 HNRNPA1 R140 VIEIMTDrGSGKKRG P09651 15379973 15379974 DYFEQYGKIEVIEIMTDrGSGK; IEVIEIMTDrGSGK HNRNPA1; HNRNPA1L2 P09651; Q32P51 R140; R140 443.981648 769.60598 682.75516 157.8084 808.24448 1939.8154

SAFB1 SAFB R811 DKRMSEGrGLPPPPR Q15424 15494641 15494643 MSEGrGLPPPPR

RBMX RBMX R373 SSSRGAPrGGGRGGS P38159 40736006 40735919 DSYSSSSrGAPr RBMXL1; RBMX Q96E39; P38159 R372; R373

K7 KRT7 R25 SGRGAQVrLSSARPG P08729 8144028 8144031 AAFSGrGAQVr; GAQVrLSSAR; SAAFSGrGAQVr; SAAFSGrGAQVrL; SAAFSGrGAQVrLS; SAAFSGrGAQVrLSSAR 186.229648 170.97366 63.548884 73.5968 625.11224 174.69374

Vimentin VIM R71 RSSAVRLrSSVPGVR P08670 40350628 40350629 LrSSVPGVR 793.066219 162.3646024 401.048984 272.82 459.11964 1185.7236

ZSWIM8 ZSWIM8 R1460 GRGMPEGrGGPGTEP A7E2V4 48912719 48912687 AGGEAGrGMPEGr

hnRNP D0 HNRNPD R345 GYGKVSRrGGHQNSY Q14103 6008969 6008966 rGGHQNSYKPY 848.141569 464.51262 274.946812 125.1698 376.863308 1762.6901

PRRC2C PRRC2C R255 YMFQQYPrMTYPPLH Q9Y520 27277311 27277312 AMMPPYMFQQYPr 1988.726388 306.060755 255.889252 203.0752 575.486004 1219.49358

CFIM25 NUDT21 R15 RSQTGWPrGVTQFGN O43809 6009136 6009137 SQTGWPr; SQTGWPrGVTQF; SQTGWPrGVTQFGNK 10475.126772 5240.54388 4470.67492 1719.2146 6080.826932 14056.7122

TAF15 TAF15 R535 RGGYGGDrGGGSGYG Q92804 8093785 8093788 SrGGYGGDrGGGSGYGGDR

HNRNPA1L2 HNRNPA1L2 R194 ASASSSQrGRRGSGN Q32P51 9300542 9300543 QEMASASSSQr; QEMASASSSQrGr HNRNPA1; HNRNPA1L2 P09651; Q32P51 R194; R194

TFIP11 TFIP11 R166 KMGYVPGrGLGKNAQ Q9UBB9 27279970 27279971 MGYVPGrGLGK 1980.59444 1595.18645 1226.12936 365.6395 696.482416 5681.0989

HCFC1 HCFC1 R1253 SVGAGEPrMAPVCES P51610 12205569 12205570 SSVGAGEPr 263.019966 394.760366 413.112448 204.9873 617.52232 1576.3464

K8 KRT8 R18 KVSTSGPrAFSSRSY P05787 27278482 27278483 VSTSGPr; VSTSGPrAF; VSTSGPrAFSSR 1863.3974447 2685.246707 2776.81632 1155.0206 2716.975208 1287.249855

HCFC1 HCFC1 R855 TVPMGGVrLVTPVTV P51610 27278225 27278226 GAPGQPGTILrTVPMGGVr; TVPMGGVr 870.442859 863.33247 682.97712 328.513 1330.1548 2706.3111

PTPN23 PTPN23 R1595 FSLDSSLrGKQRMSK Q9H3S7 27279181 27279182 EEPPVPEAPSSGPPSSSLELLASLTPEAFSLDSSLrGK 37.4322575 20.6378887 27.376968 12.12696 29.017504 68.92502

PABP 4 PABPC4 R432 PNQLAQMrPNPRWQQ Q13310 29427432 29427433 ALPANAILNQFQPAAGGYFVPAVPQAQGrPPYYTPNQLAQMrPNPr

FBL FBL R78 GRGRGGKrGNQSGKN P22087 40724709 40724637 rGNQSGK 65.8545514 567.35107 88.933668 54.8724 90.01058 2660.3088

hnRNP A3 HNRNPA3 R376 GSGGYGSrRF\_\_\_\_\_ P51991 9483511 9483515 SSGSPYGGGYGSGGGSGGYGSrRF; SSGSPYGGGYGSGGGSGGYGSrrF 174.834649 741.97838 569.96228 91.6474 724.25844 1164.2186

ASPM ASPM R8 MANRRVGrGCWEVSP Q8IZT6 40351125 40351126 VGrGCWEVSPTER 472.610941 407.12958 346.94208 137.3068 328.188272 1254.2613

ataxin-2L ATXN2L R361 QRVREGPrGGVRCSS Q8WWM7 15493067 15493069 EGPrGGVR 27.654748 40.838941 89.78902 26.0617 97.135232 343.6292

SFRS2IP SCAF11 R1096 YKDQNENrWQNRKPL Q99590 40350715 40350716 DQNENrWQNR 98.50401 230.80629 80.248088 109.548 155.535632 581.6815

EIF4E2 EIF4E2 R241 FQNLWKPrLNVP\_\_\_ O60573 15379861 15379862 LLFQNLWKPr; LLFQNLWKPrLNVP 1568.095859 1377.512136 2312.3179 1531.4936 3184.47246 5196.40909

K8 KRT8 R32 YTSGPGSrISSSSFS P05787 12075405 12075406 AFSSrSYTSGPGSrISSSSFSR; SYTSGPGSr; SYTSGPGSrISSSSFSR; SYTSGPGSrISSSSFSr 612.175355 1284.906766 943.753708 319.8263 1890.305 312.998122

MAST2 MAST2 R1004 PAMETRGrGTSQLAE Q6P0Q8 8094079 8094082 GrGTSQLAEGATAK 428.71686 197.80761 236.08608 118.238 168.51 492.5312

RBMX RBMX R258 SRDDYPSrGYSDRDG P38159 40724778 40726807 DDYPSrGYSDR 154.094545 288.65122 112.536944 72.5785 230.24288 319.2354

FOXK1 FOXK1 R161 QEPHFYLrCLGKNGV P85037 27278031 27278032 HLQLSFQEPHFYLr 177.460019 46.378904 92.205656 48.7548 107.475432 213.23254

hnRNP 2H9 HNRNPH3 R343 GMSGGGWrGMY\_\_\_\_ P31942 6009368 6009369 GGGGSGGYYGQGGMSGGGWrGMY 387.9164729 184.758717 74.576204 77.11574 1803.68676 308.79662

SART3 SART3 R906 LPQTYGArGKGRTQL Q15020 2584350 2584965 KAPGGPMLLPQTYGAr; KAPGGPMLLPQTYGArGK 3626.958544 3679.900224 3482.734928 1436.2935 4104.33944 14079.5765

QKI QKI R227 ATAQAAPrIITGPAP Q96PU8 27279220 27279221 SPALAFSLAATAQAAPr 841.942123 672.445631 300.47618 186.8918 501.839508 1151.64519

SRXN1 SRXN1 R16 LGRAGAGrGAPEGPG Q9BYN0 6010088 6010089 AGAGrGAPEGPGPSGGAQGGSIHSGR; AGGTLGrAGAGrGAPEGPGPSGGAQGGSIHSGR 461.7683543 317.9290972 405.719816 87.94953 1189.832136 792.405338

RPL23 RPL23 R6 \_\_MSKRGrGGSSGAK P62829 13247143 13247145 GrGGSSGAK; rGrGGSSGAK 186.8463388 866.13813 304.172372 301.043 454.250644 4881.5959

hnRNP 2H9 HNRNPH3 R323 DGLGGYGrGGGGSGG P31942 6009361 6009362 GLGGYGrGGGGSGGYYGQGGMSGGGWR; MGMGNNYSGGYGTPDGLGGYGr; MGMGNNYSGGYGTPDGLGGYGrG; MGMGNNYSGGYGTPDGLGGYGrGG; MGMGNNYSGGYGTPDGLGGYGrGGG; MGMGNNYSGGYGTPDGLGGYGrGGGG; MGMGNNYSGGYGTPDGLGGYGrGGGGSG; MGMGNNYSGGYGTPDGLGGYGrGGGGSGG; MGMGNNYSGGYGTPDGLGGYGrGGGGSGGYYGQGGMSGGGWR; SGGYGTPDGLGGYGrGGGGSGGYYGQGGMSGGGWR 2251.6878494 1024.587564 432.4262168 380.12354 1181.045836 3584.59255

UFL1 UFL1 R433 TEGSGSMrGGGGGNA O94874 15493867 15493869 ATEGSGSMrGGGGGNAR 379.777156 358.058987 515.59448 129.8514 844.380896 964.20048

SRm300 SRRM2 R2370 PASLTSArMAPALSG Q9UQ35 40350348 40350349 TAAALAPASLTSAr 622.369 111.607925 95.615408 55.6631 169.02004 324.9049

EPPK1 EPPK1 R3137 REPGPAGrGDGDSGR P58107 41554394 41554395 EPGPAGrGDGDSGR; GPREPGPAGrGDGDSGR; REPGPAGrGDGDSGR EPPK1 P58107 R4739; R3137; R2603; R3671; R4205 558.249043 639.6633815 686.939044 152.54161 167.6112472 731.60723

CETN2 CETN2 R16 NMASSSQrKRMSPKP P41208 48897895 48908214 ANMASSSQr 18.8243176 22.657635 7.09714 5.70463 31.402884 68.90363

EIF4B EIF4B R297 DYRGGGDrYEDRYDR P23588 40724722 40724692 RDDDYRGGGDrYEDR 292.9312881 374.578061 429.056492 115.68274 642.429492 632.15868

VIPAS39 VIPAS39 R114 YSLSSFFrGRTRPGS Q9H9C1 27278003 27278004 NSFSSYAQLPKPTSTYSLSSFFrGR 245.139378 304.27111 531.25816 44.6705 147.535056 462.6197

ARHGAP21 ARHGAP21 R574 DNRRMSGrGVGSVSQ Q5T5U3 6009703 6009704 MSGrGVGSVSQFK 2987.55622 1272.86445 922.80304 681.561 687.71924 2021.3366

TRIP6 TRIP6 R205 PHFPLPGrGEVWGPG Q15654 6009656 6009657 GASQASGPLPGPHFPLPGrGEVWGPGYR 4774.249062 785.111327 1301.374048 1718.9862 701.074006 1934.68985

NCL NCL R656 GEGGFGGrGGGRGGF P19338 9479025 10339588 GEGGFGGrGGGr 87.963612 73.050549 59.542072 39.8229 120.776652 606.0615

hnRNP D0 iso3 HNRNPD R282 FAGRARGrGGDQQSG Q14103-3 9291843 9291844 ArGrGGDQQSGYGK; GrGGDQQSGYGK 357.872383 1172.9861 265.254848 219.7982 523.080132 4076.9248

NICE-4 iso2 UBAP2L R969 SHGYNTGrKYPPPYK Q14157-1 27278832 27278833 QHGVNVSVNASATPFQQPSGYGSHGYNTGrK 97.452267 40.959633 73.084484 39.5191 47.05734 116.25258

eIF4G EIF4G1 R110 YYIPGQGrSTYVVPT Q04637 15379864 15379865 MIPSQISYPASQGAYYIPGQGr; VQSAAPARPGPAAHVYPAGSQVMMIPSQISYPASQGAYYIPGQGr; VQSAAPArPGPAAHVYPAGSQVMMIPSQISYPASQGAYYIPGQGr 444.5927244 243.993464 175.9064 93.92761 78.82243768 807.61717

G3BP-1 G3BP1 R447 GGMRGPPrGGMVQKP Q13283 476716 68277 GPPrGGMVQKPGFGVGr

HNRPUL2 HNRNPUL2 R716 NRYRDYYrQYNRDWQ Q1KMD3 40724718 40724679 DYYrQYNR 278.081232 331.63416 115.623304 106.104 175.5456 736.5129

DERPC CHTF8 R146 PGPLSNPrLGGLPGP P0CG12 41398713 41398714 TGALPGPGPLSNPr 229.864382 117.384124 101.670452 39.6039 235.01692 358.2112

CDC42EP1 CDC42EP1 R53 RHTMHVGrGGDVFGD Q00587 6009512 6009513 HTMHVGrGGDVFGDTSFLSNHGGSSGSTHR 1260.361663 242.020207 275.279132 299.675 240.972908 1847.3071

BTBD1 BTBD1 R79 RFVLGKGrGAAAAGG Q9H0C5 27277406 27277407 GrGAAAAGGPQR 260.389492 149.306443 118.693048 73.9238 124.719212 736.828

XRN2 XRN2 R824 TLGHVMPrGSGTGIY Q9H0D6 13247051 13247053 TLGHVMPr; TLGHVMPrGSGTGIYSNAAPPPVTYQGNLYrPLLr 240.993654 244.231273 181.95574 111.7035 321.265504 813.9884

DDX17 DDX17 R81 LYPFGTMrGGGFGDR Q92841 8093088 8113357 APLPDLYPFGTMr; MrGGGFGDR 2018.817977 1308.476884 573.054716 568.0215 740.430972 3671.5452

BTF3 BTF3 R13 APAQADSrGRGRARG P20290 6009271 6009272 RTGAPAQADSr; TGAPAQADSr; TGAPAQADSrGR; TGAPAQADSrGr; TGAPAQADSrGrGR; TGAPAQADSrGrGr; TGAPAQADSrGrGrAr 277.5811357 655.889663 214.251416 348.0563 1456.694904 1072.34372

TPR TPR R2111 TRRQSVGrGLQLTPG P12270 6009257 6009258 QSVGrGLQLTPGIGGMQQHFFDDEDR; QSVGrGLQLTPGIGGMQQHFFDDEDRTVPSTPTLVVPHR 1591.745881 1036.770306 631.469008 520.3845 1133.539628 2200.59906

VHL VHL R79 SQVIFCNrSPRVVLP P40337 40351142 40351143 EPSQVIFCNrSPR 586.50702 238.11359 165.5896 174.397 397.42284 919.1927

C6orf132 C6orf132 R1127 LSLEGAArGAAEAKH Q5T0Z8 40712229 40720719 LSLEGAAr; LSLEGAArGAAEAK 2314.55235 2757.96521 318.5498 464.467 795.51152 1583.3683

TCEAL6 TCEAL6 R176 VQDPFAPrGQRGVRG Q6IPX3 8093310 8093313 DVQDPFAPrGQr TCEAL6; TCEAL3; TCEAL5 Q6IPX3; Q969E4; Q5H9L2 R176; R176; R182

PABPN1 PABPN1 R279 NYNSSRSrFYSGFNS Q86U42 9300345 9300346 SrFYSGFNSR; SrFYSGFNSrPrGr 786.523529 822.27145 553.531412 203.5458 446.759944 1568.9542

FKBP15 FKBP15 R520 RQHNTEIrMAVSKVA Q5T1M5 48912704 48912621 QHNTEIrMAVSK 1513.53059 123.074094 170.18008 91.7145 208.56372 483.1886

RBM27 RBM27 R455 PPPLLAArLVPPRNL Q9P2N5 13247036 13247038 LQLGTPPPLLAAr 900.57528 397.649824 497.500152 278.5532 858.990836 2231.989

DDX9 DHX9 R1223 GGYRGVSrGGFRGNS Q08211 12198272 12198273 AGYGAGVGGGYrGVSrGGFr

ARHGAP23 ARHGAP23 R1335 PDGEGAGrGGPRAPE Q9P227 40350384 40350385 GRPDGEGAGrGGPR 266.946218 187.310838 95.854604 160.9138 200.141008 1000.38017

hnRNP A/B iso3 HNRNPAB R253 GNRNRGNrGSGGGGG Q99729-3 6010059 6010060 GNrGSGGGGGGGGQGSTNYGK; NrGNrGSGGGGGGGGQGSTNYGK 171.4277928 428.187331 825.23736 389.9962 905.479424 1660.7265

DDX9 DHX9 R1235 GNSGGDYrGPSGGYR Q08211 15493456 15493458 GNSGGDYrGPSGGYR 283.992302 155.24652 101.89762 49.4306 104.98952 478.1056

KHDRBS1 KHDRBS1 R315 PPRGALVrGTPVRGA Q07666 476772 68999 GrGVGPPrGALVr; GrGVGPPrGALVrGTPVr

HCFC1 HCFC1 R847 GQPGTILrTVPMGGV P51610 13247531 13247533 GAPGQPGTILr; GAPGQPGTILrTVPMGGVr 2318.38673 744.648333 929.82888 337.2721 1044.537156 2292.7297

hnRNP K HNRNPK R377 DYSYAGGrGSYGDLG P61978 29428940 29428943 AYEPQGGSGYDYSYAGGrGSYGDLGGPIITTQVTIPK 366.362249 132.166177 100.61484 32.8176 100.786528 167.19827

SFRS2IP SCAF11 R969 YSPRWKGrWANDGWR Q99590 48885422 48885397 GrWANDGWR 764.668201 469.83794 343.390968 173.8994 767.40356 1073.8148

K18 KRT18 R55 VSRSTSFrGGMGSGG P05783 6009189 6009190 STSFrGGMGSGGLATGIAGGLAGMGGIQNEK; STSFrGGMGSGGLATGIAGGLAGMGGIQNEKETMQSLNDR 1462.3954642 3401.677422 2528.143496 609.9024 6873.99768 436.6339412

K6c KRT6C R16 RSHSSSRrGFSANSA P48668 41682269 41682270 rGFSANSAR; rGFSANSArLPGVSR KRT6C; KRT6B; KRT6A P48668; P04259; P02538 R16; R16; R16

ETFA ETFA R223 KVVVSGGrGLKSGEN P13804 27277869 27277870 VVVSGGrGLK 1344.41912 1147.82668 741.43196 317.687 410.780312 2867.2927

K8 KRT8 R40 ISSSSFSrVGSSNFR P05787 27278478 27278479 ISSSSFSr; SYTSGPGSrISSSSFSr 745.713221 567.80152 633.26304 432.173 1134.67828 723.71731

TRIM24 TRIM24 R469 QISLAQLrLQHMQQQ O15164 12205544 12205545 FPTQISLAQLr 775.650414 861.24896 316.516572 266.8875 579.518108 1284.6259

PPP1R13L PPP1R13L R185 LGRAGSPrGSPLAEG Q8WUF5 27279129 27279130 AGSPrGSPLAEGPQAFFPER; AGSPrGSPLAEGPQAFFPERGPSPRPPATAYDAPASAFGSSLLGSGGSAFAPPLR; QQGPPTPFDFLGrAGSPrGSPLAEGPQAFFPER 540.63163 366.11861 116.091776 137.918 167.19144 624.3212

Hrs HGS R557 QKQTVQMrAQMPAFP O14964 41717814 41717758 QTVQMr 861.940871 745.384068 669.56838 1065.7415 1162.194528 2411.38739

hnRNP H2 HNRNPH2 R233 AGFERMRrGAYGGGY P55795 6009450 6009451 rGAYGGGYGGYDDYG; rGAYGGGYGGYDDYGGY; rGAYGGGYGGYDDYGGYNDGYGFGSDR; rGAYGGGYGGYDDYGGYNDGYGFGSDRFGR rGAYGGGYGGY; rGAYGGGYGGYDD; rGAYGGGYGGYDDY HNRNPH1; HNRNPH2 P31943; P55795 R233; R233 5041.2929259 1422.68555 1038.8196968 501.01021 1459.49668 6767.18029

CCDC117 CCDC117 R60 SPAGSAArGRVSVHC Q8IWD4 12197407 12197408 AVPSSPAGSAAr 581.610689 644.63828 265.635032 138.7009 415.134184 1412.0942

SF3B2 SF3B2 R515 RKYLQGKrGIEKPPF Q13435 27279594 27279595 rGIEKPPFELPDFIKR 545.520624 388.540152 1787.79356 15.6377 731.89756 1914.0646

DYN2 DNM2 R862 PSRPTIIrPAEPSLL P50570 26362100 26361855 rPPAAPSRPTIIrPAEPSLLD

QKI QKI R242 VLPPAALrTPTPAGP Q96PU8 13247320 13247322 IITGPAPVLPPAALr; IITGPAPVLPPAALrTPTPAGPTIMPL 4522.497771 1691.993732 1295.520132 777.14904 1881.34568 5722.92992

BXDC2 BRIX1 R9 AATKRKRrGGFAVQA Q8TDN6 6009883 6009884 rGGFAVQAK 1733.68844 1038.90358 1743.69048 220.3781 1788.00508 3186.5143

hnRNP H1 HNRNPH1 R224 RGYNSIGrGAGFERM P31943 12191555 12191556 GYNSIGrGAGFER HNRNPH1; HNRNPH2 P31943; P55795 R224; R224 739.234969 284.260691 254.37732 97.673 2852.28636 612.38305

STAU STAU1 R108 STYNYNMrGGAYPPR O95793 9480132 9480135 MQSTYNYNMrGGAYPPR 357.151124 395.658406 233.135996 159.2341 256.996856 1461.9927

HNRNPA1L2 HNRNPA1L2 R140 VIEIMTDrGSGKKRG Q32P51 15379993 15379994 DYFEQYGKIEVIEIMTDrGSGK; IEVIEIMTDrGSGK HNRNPA1; HNRNPA1L2 P09651; Q32P51 R140; R140

EWS EWSR1 R486 GPGGPMGrMGGRGGD Q01844 9300511 9300512 EGrGMPPPLrGGPGGPGGPGGPMGr; GMPPPLrGGPGGPGGPGGPMGr 184.605619 59.075874 70.643048 37.995 123.591548 421.2174

IRS2 IRS2 R429 GGALQHSrSMSMPVA Q9Y4H2 27278446 27278447 VALLPAGGALQHSr 1159.83615 86.430201 147.99152 69.0365 226.99404 601.5029

CSTF2 CSTF2 R468 EARGMDTrGPVPGPR P33240 15379705 15379706 GMDTrGPVPGPR 113.845677 78.079144 40.462812 25.5642 170.40256 268.2053

FBP1 FUBP1 R359 GGPGPGGrGRGRGQG Q96AE4 6009995 6009996 SVQAGNPGGPGPGGr; SVQAGNPGGPGPGGrGr; SVQAGNPGGPGPGGrGrGR; SVQAGNPGGPGPGGrGrGr 563.113155 344.247189 179.890892 130.1195 1117.25328 1033.89646

E1B-AP5 HNRNPUL1 R685 DNNNSNNrGSYNRAP Q9BUJ2 15379844 15379845 DNNNSNNrGSY; DNNNSNNrGSYNR 117.9640308 568.270703 396.439532 59.71521 787.168184 784.58865

RBMXL1 RBMXL1 R380 GAGPGGSrSDRGGGR Q96E39 40724782 40726820 DSYSSSSrGAPrGAGPGGSr

CRIP1 CRIP1 R68 FGPKGFGrGGAESHT P50238 6009410 6009411 FGrGGAESHTFK; GFGrGGAESHTFK 31730.350058 177.6342139 19785.283636 84.10961 5554.622436 1720.2479125

PDLIM7 PDLIM7 R103 APAADPPrYTFAPSV Q9NR12 40351316 40351317 ASAPAADPPrYTFAPSVSLNK 3161.85782 119.17191 884.11876 807.589 379.581444 908.3528

LARP LARP1 R285 PRHIPANrGEIKGSE Q6PKG0 48885441 48889285 HIPANrGEIK 389.194674 1079.58279 627.19324 680.349 791.4886 5867.576

WDR33 WDR33 R1144 DASEEAArGRDLRGR Q9C0J8 8144677 8144680 GRDGFPGPEDFGPEENFDASEEAArGR 2347.994396 1808.662284 2256.193764 640.964 2870.123 7792.9221

TAF15 iso2 TAF15 R464 GGGYGGDrGGGYGGD Q92804-2 6009931 40298079 1160.88885 22.97285276 124.0217 12.1475 37.789618 626.1543

HNRPUL2 HNRNPUL2 R738 QDRDRYYrNYYGYQG Q1KMD3 15379997 15379998 YYrNYYGYQGYR 578.983405 972.0997 507.868412 166.3474 573.0611 1139.26751

HCFC1 HCFC1 R1219 APLSSKVrLSSPSIK P51610 27278229 27278230 VrLSSPSIK 1065.05487 1033.00054 1067.12788 380.381 1639.46208 3579.0898

TXLNG TXLNG R24 EEATEAGrGGRRRSP Q9NUQ3 6010158 6010159 GRGGGAEEATEAGrGGR; GrGGGAEEATEAGrGGR 176.1340955 214.634563 214.975824 139.7486 340.078436 1696.2431

DATF1 DIDO1 R1775 GPNFPGPrGPAPPFP Q9BTC0 40351301 40351302 EPGPHALGMSGLHGPNFPGPrGPAPPFPEENIASNDGPRGPPPAR; EPGPHALGMSGLHGPNFPGPrGPAPPFPEENIASNDGPrGPPPAr

hnRNP P2 FUS R514 GPGKMDSrGEHRQDR P35637 27278360 27278361 MDSrGEHR 359.20886221 2039.078327 841.891924 403.89596 1515.581236 2822.41717

TAF15 TAF15 R519 RGGYGGDrGGYGGDR Q92804 12191839 12191840 GGYGGDrGGYGGDrGGYGGDrGGYGGDr

53BP1 TP53BP1 R1338 GKGAGPLrGKTSGTE Q12888 48885445 48895505 GAGPLrGK 343.31737 514.85434 259.57168 184.558 454.65064 1973.952

BLES03 iso2 C11orf68 R29 RQERSRArGWAGVER Q9H3H3-2 26362110 28801505 ArGWAGVER C11orf68; C11orf68 Q9H3H3-2; Q9H3H3-3 R29; R29 1356.47094 506.470536 537.181888 600.592 629.265376 2691.322

snRNP B1 SNRPB R147 QVMTPQGrGTVAAAA P14678 9300308 9300309 GVGGPSQQVMTPQGr SNRPB; SNRPN P14678; P63162 R147; R147 353.284844 230.9439275 122.5690772 92.02399 1299.10468 680.10563

hnRNP A2/B1 HNRNPA2B1 R352 GGYGGRSrY\_\_\_\_\_\_ P22626 9483261 9483265 NMGGPYGGGNYGPGGSGGSGGYGGRSr 600.680509 635.518455 471.972892 99.1737 381.221444 902.9133

FAM120A FAM120A R873 YPASAYPrHFGPVPP Q9NZB2 27277922 27277923 QSHTLPFPPPPALPFYPASAYPr 665.624124 139.069645 152.015072 151.7202 187.265204 329.79861

SF2 SRSF1 R111 GGGAPRGrYGPPSRR Q07955 15494655 15494657 GTGrGGGGGGGGGAPrGr; SGrGTGrGGGGGGGGGAPrGr

PRRC2C PRRC2C R1196 GRGEYYSrGRSYRGS Q9Y520 12191667 12191670 GrGrGEYYSrGr

TAF15 TAF15 R459 GGGYGGDrGGGYGGD Q92804 51357302 6009927 SGGGYGGDrGGGYGGDrGGGYGGDR; SGGGYGGDrGGGYGGDrGGGYGGDr GGDrGGGYGGDR; GGGYGGDr; GGGYGGDrGGGYGGD; GGGYGGDrGGGYGGDR; SGGGYGGDrGG; SGGGYGGDrGGG; SGGGYGGDrGGGY; SGGGYGGDrGGGYG; SGGGYGGDrGGGYGG; SGGGYGGDrGGGYGGD; SGGGYGGDrGGGYGGDR TAF15 Q92804 R475; R562; R459; R431; R450; R490 2020.837566 1142.290578 2249.718608 324.64855 2203.367224 9216.90408

hnRNP A3 HNRNPA3 R286 GGPGYSSrGGYGGGG P51991 9300483 9300484 GSYGGGDGGYNGFGGDGGNYGGGPGYSSr 204.609152 133.826121 108.94454 70.3672 294.615996 602.50593

K7 KRT7 R52 SRPRVAVrSAYGGPV P08729 40350888 40350889 PGGLGSSSLYGLGASrPrVAVr; VAVrSAYGGPVGAGIR; VAVrSAYGGPVGAGIrEVTINQSLLAPLR 982.554452 519.95372 307.373556 361.849 801.01372 812.62174

RAD54L2 RAD54L2 R1433 YPAGGLLrSQVPPFD Q9Y4B4 40712216 40712169 GMSIYPGYMSPHAGYPAGGLLr 130.175606 56.438954 50.615808 30.5532 66.453456 163.27884

MYPN MYPN R810 SGNQFQPrCVSPIPV Q86TC9 41477329 41477330 GNQFQPr; SPGGLSIQNEPLPPGPTEPTPPPFTFSIPSGNQFQPr 588.9805141 120.2879249 108.8482168 79.28397 125.91170192 3291.40166

K8 KRT8 R23 GPRAFSSrSYTSGPG P05787 12075400 12075401 AFSSrSYTSGPGSR; AFSSrSYTSGPGSrISSSSFSR 1081.075688 1094.18023 941.5754 270.1488 891.04316 769.93328

SON SON R929 RLAQDPYrLGHDPYR P18583 40350920 40350921 LAQDPYrLGHDPYR 440.07007 172.10336 141.89072 68.4656 253.13072 526.9829

WDR33 WDR33 R782 PLMGLNPrGMQGPPG Q9C0J8 27280270 27280271 GMQGPPHPHGIQGGPGSQGIQGPVSQGPLMGLNPr 64.775183 66.056133 60.090152 23.8561 68.2363 181.87756

KHDRBS1 KHDRBS1 R340 VPPPPTVrGAPAPRA Q07666 476724 68285 GATVTrGVPPPPTVr; GATVTrGVPPPPTVrGAPAPrAr; GVPPPPTVr 1554.58908 661.865633 764.482816 464.5115 1687.01224 3683.5742

liprin beta 1 PPFIBP1 R527 KVRSSFGrGFFKIKS Q86W92 6009785 6009786 SSFGrGFFK 2067.0243 107.330366 628.78664 104.769 282.24974 4648.5668

PABPN1 PABPN1 R277 TTNYNSSrSRFYSGF Q86U42 15380290 15380291 ArTTNYNSSr 142.410213 203.74497 26.158544 50.1354 66.84722 235.3199

CCDC9 CCDC9 R102 TPPQQGGrAGMGRAS Q9Y3X0 12190869 12190870 GGrTPPQQGGr; TPPQQGGr; TPPQQGGrAGMGr 356.525246 114.144173 173.91806 39.8335 259.956072 764.75

FAM120A FAM120A R986 GPARGRPrGVISTPV Q9NZB2 27277934 27277935 PrGVISTPVIR 1038.956204 619.958482 779.93768 368.152 970.22236 1397.1212

FRMD8 FRMD8 R219 LFAALRGrGARAGPG Q9BZ67 40724713 40724650 GQSLFAALRGr 258.193815 130.943813 934.32512 40.4323 511.147 667.1886

FAM103A1 FAM103A1 R112 GHYGYNQrPPYGYY\_ Q9BTL3 27277906 27277907 QEPYYPQQYGHYGYNQrPPYGYY 38.40441 66.315249 65.20416 45.5213 58.03304 293.0683

NUP153 NUP153 R1465 SGTSFSGrKIKTAVR P49790 27278873 27278874 NVFSSSGTSFSGrK 482.71718 535.55931 467.08568 116.277 810.98656 1006.6502

FAM195A FAM195A R65 PLSSPGPrLVFNRVN Q9BUT9 27277966 27277967 AQPFAQPPGPWPLSSPGPr; AQPFAQPPGPWPLSSPGPrLVFNR 1410.303785 700.273288 623.071852 409.5115 926.169828 2293.5485

EIF4H EIF4H R136 RKGGPDDrGMGSSRE Q15056 29428723 29428725 GGPDDrGMGSSR; KGGPDDrGMGSSR 151.9232077 767.024687 296.946148 184.5399 931.707616 685.06466

RENT1 UPF1 R1019 ANGPAAGrGTPKGKT Q92900 27279365 27279366 NLVMPPMPPPGYFGQANGPAAGrGTPK 579.00414 401.26515 110.613704 181.4061 448.16116 976.1108

SAFB1 iso3 SAFB R818 RGLPPPPrGRRDWGD Q15424-3 15494644 26358483 MSEGrGLPPPPrGr SAFB; SAFB Q15424-2; Q15424-3 R749; R818

ZC3H7A ZC3H7A R334 GTLPIGArYAPPPSF Q8IWR0 27280395 27280396 GPLQTASVSPSMPFSASLLGTLPIGAr 90.599828 36.27624 20.7315228 24.33438 42.580796 99.81287

G3BP-1 G3BP1 R435 LRGPGGPrGGLGGGM Q13283 6008955 6008956 GPGGPrGGLGGGMR 959.674177 1282.340631 603.555864 685.6029 801.58772 5716.5189

YB-1 YBX1 R142 GSKYAADrNHYRRYP P67809 40350596 40350597 YAADrNHYR 189.966733 150.71199 130.19256 61.7019 201.94304 416.8934

YB-1 YBX1 R242 QNMYRGYrPRFRRGP P67809 41398909 41398910 QNMYRGYrPR 437.69033 222.10474 188.13528 94.7766 323.06196 486.5742

BAZ2B BAZ2B R1021 LMKAMEArKKAEEKE Q9UIF8 48990903 48990812 AMEAr

DDX3Y DDX3Y R98 SRGRFDDrGRSDYDG O15523 40350538 40350539 FDDrGR DDX3X; DDX3Y O00571; O15523 R99; R98

POP1 POP1 R30 SSGFVADrGVKHHSG Q99575 48897890 48906291 NQPTNVTLSSGFVADrGVK 203.233943 173.15298 175.73776 41.1074 176.18848 252.5676

hnRNP F HNRNPF R218 DRPGTARrYIGIVKQ P52597 40351177 40351178 rYIGIVK 553.596428 501.409623 569.561884 122.7155 666.381856 1492.6126

GATAD2A GATAD2A R539 RGSATTPrGVLHTFS Q86YP4 27278084 27278085 GSATTPrGVLHTFSPSPK 448.99569 318.65405 260.99148 145.921 271.0018 920.0575

HCFC1 HCFC1 R524 TSLPAGVrMVVPTQS P51610 9300473 9300474 APVTVTSLPAGVr; VTVTSLPAGVr 2993.73206 763.467991 1357.584116 265.3864 1961.197772 1988.47098

HNRPUL2 HNRNPUL2 R720 DYYRQYNrDWQSYYY Q1KMD3 27278383 27278384 QYNrDWQSYYYHHPQDR; QYNrDWQSYYYHHPQDRDR 2078.679603 1457.203033 793.181376 424.1984 1062.96436 2143.59356

KHSRP KHSRP R415 PGGRGRGrGQGNWGP Q92945 6009978 6009979 GrGQGNWGPPGGEMTFSIPTHK; GrGrGQGNWGPPGGEMTFSIPTHK; SGPPGPPGGPGMPPGGrGrGr 326.57944 115.789674 116.609104 99.6331 648.88896 350.405

AKAP8L AKAP8L R208 WEDPMGArGQCMSGA Q9ULX6 6010187 6010188 MWEDPMGArGQCMSGASR 298.31285 345.857512 295.514816 86.062 263.2815 876.9992

MTMR14 MTMR14 R638 GLLEQFArGVGLRSI Q8NCE2 15380208 15380209 AVAPSPSGAIGGLLEQFAr 1117.252521 325.753285 225.349416 170.6083 316.995764 1106.38671

REXO2 REXO2 R12 SLGSRLLrGVGGSHG Q9Y3B8 6010213 6010214 LLrGVGGSHGR 251.669627 231.101585 115.17492 88.1294 910.49028 454.54831

AKAP8L AKAP8L R179 GNDTFGPrAQGWARD Q9ULX6 27278214 27278215 GNDTFGPrAQGWAR; MrGNDTFGPrAQGWAR 428.96887 251.30105 217.86676 91.5962 208.75888 791.361

eIF4G EIF4G1 R73 VQSAAPArPGPAAHV Q04637 29427350 29427351 VQSAAPArPGPAAHVYPAGSQVMMIPSQISYPASQGAYYIPGQGr

hnRNP P2 FUS R218 QDRGGRGrGGSGGGG P35637 9291610 9291611 GGrGrGGSGGGGGGGGGGYNR; GrGGSGGGGGGGGGGYNR 59.336233 50.475997 34.353952 25.0722 64.507596 173.87471

snRNP D1 SNRPD1 R102 VAGRGRGrGRGRGRG P62314 40350412 40350413 EAVAGrGrGr

SFRS5 SRSF5 R88 GRGRYSDrFSSRRPR Q13243 12190751 12190752 YSDrFSSR 381.1704523 943.6856 622.317808 145.0024 776.70236 2415.5865

RPL4 RPL4 R80 VARIPRVrGGGTHRS P36578 41477527 41477528 VrGGGTHR 18.4403692 71.39132 40.48538 17.1309 102.588888 206.7631

NSAP1 SYNCRIP R526 GRAGYSQrGGPGSAR O60506 12191709 12191710 AGYSQrGGPGSAR 109.488775 100.175647 88.44114 41.16 158.91026 434.1848

hnRNP A1 HNRNPA1 R206 SGNFGGGrGGGFGGN P09651 6008918 6008919 SGSGNFGGGrGGGFGGNDNFGR; SGSGNFGGGrGGGFGGNDNFGrGGNFSGr; SGSGNFGGGrGGGFGGNDNFGrGGNFSGrGGFGGSr 1355.986379 697.91722 596.035512 233.8356 1017.484864 3631.9254

PABP 1 PABPC1 R493 STQTMGPrPAAAAAA P11940 27278897 27278898 VMSTQRVANTSTQTMGPrPAAAAAAATPAVR

SAFB1 iso2 SAFB R749 RGLPPPPrGRRDWGD Q15424-2 15494644 40311298 MSEGrGLPPPPrGr SAFB; SAFB Q15424-2; Q15424-3 R749; R818 1720.628261 649.467676 570.550412 244.1022 800.175844 2833.0135

TRIP6 TRIP6 R186 RGCGPPRrGASQASG Q15654 6009651 6009652 rGASQASGPLPGPHFPLPGR; rGASQASGPLPGPHFPLPGRGEVWGPGYR 546.910826 122.783089 188.570024 157.0471 121.195508 337.52776

HNRPUL2 HNRNPUL2 R684 YWGQPGNrGGYRNFY Q1KMD3 6009676 6009677 AYGQQYWGQPGNrGGYrNFYDr; GYDNrAYGQQYWGQPGNrGGYr 525.321225 314.479594 227.93246 174.6903 327.745308 1302.513

INA INA R39 AGGAGGFrSQSLSRS Q16352 41477422 41477423 LSGAGGAGGFrSQSLSR 537.53733 158.66994 83.498996 118.951 194.40396 1156.0697

C15orf52 C15orf52 R280 LQDCSQLrGEGPARA Q6ZUT6 48897844 48899685 STLQDCSQLrGEGPArAGSr

TFPT TFPT R68 DEEEEAArGRRRRQR P0C1Z6 8143915 8143920 ERDEEEEAArGR 238.0972297 269.464338 283.87692 80.32716 521.194624 1102.21497

NCL NCL R694 RGGFRGGrGGGGDHK P19338 15494306 15494308 GGrGGGGDHKPQGK 78.619145 182.70681 130.68608 91.3916 299.11796 1685.4124

Cortactin CTTN R119 CSQVDSVrGFGGKFG Q14247 8093109 8093112 HCSQVDSVrGFGGK 1068.71061 446.09136 425.12036 280.698 1242.79528 1136.6462

MRCKB CDC42BPB R671 LKVKQGGrGAGATLE Q9Y5S2 6010248 6010249 QGGrGAGATLEHQQEISK 1155.99539 482.28466 541.1236 39.5809 158.643104 628.3991

CPT2 CPT2 R51 HYQDSLPrLPIPKLE P23786 41398787 41398788 SIVPTMHYQDSLPrLPIPK 460.49245 163.36749 197.26416 129.857 262.54268 481.4705

KHDRBS1 KHDRBS1 R320 LVRGTPVrGAITRGA Q07666 476773 69001 GTPVrGAITR; GTPVrGAITr; GrGVGPPrGALVrGTPVr 459.32172 258.534276 298.271336 133.2674 604.769844 1876.9771

WDR33 WDR33 R1035 RLREFEGrGGPLPQE Q9C0J8 6010093 6010094 EFEGrGGPLPQEEK; LREFEGrGGPLPQEEK; LrEFEGrGGPLPQEEK 2718.59456 2594.65492 3022.73436 655.5358 1714.482404 10391.5403

WIPF1 WIPF1 R125 DNDSGGSrPPLLPPG O43516 29430146 29430148 DNDSGGSrPPLLPPGGr

TNRC15 GIGYF2 R149 EVEGVFGrGGGREMH Q6Y7W6-3 6009736 6009740 SFDEVEGVFGr; SFDEVEGVFGrGGGR 5014.722427 1425.443448 1448.427508 1553.7908 2946.05992 4428.8777

KHDRBS1 KHDRBS1 R291 RGVPVRGrGAAPPPP Q07666 27279496 27279497 GrGAAPPPPPVPr

EIF4G2 EIF4G2 R460 QSKDMPPrFSKKGQL P78344 40724724 40724699 DMPPrFSK 1913.92344 459.00426 561.64932 613.659 726.233 1374.5605

FBS1 FBRS R408 AHPLLYSrLAPPPPP Q9HAH7 27277989 27277990 LYGLEPAHPLLYSr 391.21841 113.110712 143.66516 63.1286 185.86448 364.6328

WDR33 WDR33 R1071 GDGRGAArGPPGAWE Q9C0J8 40351103 40351104 EFSEGDGRGAArGPPGAWEGR 340.49422 401.08926 330.54556 74.6957 322.02056 1192.4994

K7 KRT7 R13 SSPVFTSrSAAFSGR P08729 40350884 40350885 SSPVFTSr 4278.92883 164.130538 283.725888 292.194 279.604092 594.52033

TCERG1 TCERG1 R20 RFNPGELrMAQQQAL O14776 9483526 9483529 FNPGELr 951.935237 817.389573 1225.98676 435.8983 2416.34976 4351.2159

POM121 POM121 R223 DCGTLPNrFVITPRR Q96HA1 29427440 29427441 DCGTLPNrFVITPR 424.37208 148.19805 142.66944 122.835 283.59536 454.7882

RAI1 RAI1 R249 PTAQPHDrPLTASSS Q7Z5J4 48885418 48885380 SCTAPTAQPHDrPLTASSSLAPGQR 139.518159 35.501323 37.867492 10.5914 67.45156 144.0536

hnRNP A/B HNRNPAB R245 QQYGSGGrGNRNRGN Q99729 6009023 6009029 EVYQQQQYGSGGr; EVYQQQQYGSGGrG; EVYQQQQYGSGGrGN; EVYQQQQYGSGGrGNR; EVYQQQQYGSGGrGNRNR; EVYQQQQYGSGGrGNr; YQQQQYGSGGrGNR 3669.4514813 1169.752441 2133.071064 1015.6369 1932.306548 6837.21

AVL9 AVL9 R588 HSVQNSErGKKIGNV Q8NBF6 6009829 6009830 FSHSVQNSErGK 721.228057 347.365304 725.15076 349.712 871.26312 1140.2135

HNRPUL2 HNRNPUL2 R656 RNRQNRSrGQGYVGG Q1KMD3 6008974 6008975 SrGQGYVGGQR 241.849212 187.95777 115.717792 67.1681 254.141124 513.56217

KHSRP KHSRP R411 PGMPPGGrGRGRGQG Q92945 6009966 6009967 SGPPGPPGGPGMPPGGr; SGPPGPPGGPGMPPGGrGRGR; SGPPGPPGGPGMPPGGrGr; SGPPGPPGGPGMPPGGrGrGr 2571.22294 645.044972 617.43072 495.0817 1709.970928 2019.74569

hnRNP A3 HNRNPA3 R216 SAGSQRGrGGGSGNF P51991 6009415 6009416 GrGGGSGNFMGR 169.671953 81.22257 54.187008 30.1945 86.070316 328.0283

WDR36 WDR36 R800 TIPGLVPrYAAPEQN Q8NI36 13247417 13247419 SAPFFIPTIPGLVPr; SAPFFIPTIPGLVPrYAAPEQNNDPQQSK 899.723231 221.2385604 348.569332 405.3052 523.918008 1438.01244

HNRPUL2 HNRNPUL2 R688 PGNRGGYrNFYDRYR Q1KMD3 6009682 6009683 AYGQQYWGQPGNrGGYrNFYDr; GYDNrAYGQQYWGQPGNrGGYr

TIF1G TRIM33 R591 AFQAHQMrLAQNAAR Q9UPN9 12195769 12195770 GNMNCGAFQAHQMr 88.513887 56.462692 50.113112 22.0487 93.17742 131.2288

CDK16 CDK16 R19 SMTLRGGrGIDKTNG Q00536 41477665 41477666 GGrGIDK 77.318901 641.90269 325.58556 153.182 56.42338 803.344

Musashi-1 MSI1 R199 PTGSARGrSRVMPYG O43347 27278716 27278717 EVMSPTGSArGr

HSP27 HSPB1 R12 RVPFSLLrGPSWDPF P04792 15380009 15380010 RVPFSLLrGPSWDPFR; SLLrGPSWDPFR; rGPSWDPFR 5830.645634 259.2256238 426.519204 882.2248 425.646748 2083.74388

TAF15 TAF15 R498 GGGYGGDrGGYGGDR Q92804 6009950 6009951 GGGYGGDrGGYGGDrGGGYGGDrGGYGGDr; GGGYGGDrGGYGGDrGGYGGDr; GGYGGDrGGYGGDrGGYGGDrGGYGGDr GGYGGDrGGYGGDR TAF15 Q92804 R498; R483 1334.674308 417.499368 643.46328 184.7683 541.508812 5028.6303

ARHGAP23 ARHGAP23 R180 EPYSGEArSIPEPPP Q9P227 40350390 40350391 GNEPYSGEAr 473.966372 464.79862 108.505456 352.633 92.118636 191.55343

eIF4G EIF4G1 R1032 AKGSDKRrGGPPGPP Q04637 9479233 9481615 rGGPPGPPISr; rGGPPGPPISrGLPLVDDGGWNTVPISK

ANKRD25 KANK2 R105 SAYSYCGrGFYPQYG Q63ZY3 6009713 6009714 HSAYSYCGr; HSAYSYCGrGFYPQYGALETR; HSAYSYCGrGFYPQYGALETRGGFNPR; HSAYSYCGrGFYPQYGALETr; HSAYSYCGrGFYPQYGALETrGGFNPr; SYCGrGFYPQYGALETR 8627.5145 128.3218079 449.836288 402.315 408.498088 2123.0127

NARR NARR R71 RVIFGTPrARVILGS P0DI83 41477480 41477481 VIFGTPr 363.17512 160.12568 192.3674 165.19 243.1792 1691.2843

TAGLN2 TAGLN2 R196 MTGYGMPrQIL\_\_\_\_ P37802 9300460 9300461 GASQAGMTGYGMPr; GASQAGMTGYGMPrQ; GASQAGMTGYGMPrQIL 11474.820137 1800.163222 3697.4764168 1231.2031 2446.6122372 4722.538411

CstF-64T CSTF2T R352 VTGEVEPrGYLGPPH Q9H0L4 15493396 15493398 GGTLLSVTGEVEPr CSTF2; CSTF2T P33240; Q9H0L4 R344; R352

PEG10 PEG10 R611 TIQNQYPrLSIPNLE Q86TG7 29429427 29540149 APNNFTIQNQYPr 1880.41887 318.89715 490.04676 191.1329 524.93284 1175.7002

KHSRP KHSRP R413 MPPGGRGrGRGQGNW Q92945 6009972 6009973 GrGrGQGNWGPPGGEMTFSIPTHK; SGPPGPPGGPGMPPGGrGr; SGPPGPPGGPGMPPGGrGrGr

PSPC1 PSPC1 R507 GGPGGFGrGSQGGNF Q8WXF1 6009888 6009889 TGSETPQAPMSGVGPVSGGPGGFGr; TGSETPQAPMSGVGPVSGGPGGFGrGSQGGNFEGPNK 1878.837906 3402.530703 1272.69508 348.9259 1386.977192 1608.41507

DNCLI2 DYNC1LI2 R397 GSPRTQGrGGPASVP O43237 6009114 6009115 TQGrGGPASVPSSSPGTSVK 3703.75907 775.22016 660.70796 373.4714 416.512276 1803.7152

FAM120B FAM120B R885 RTGSGYSrSSQGQPW Q96EK7 27277950 27277951 TGSGYSr 151.68769 168.35819 200.77336 104.683 71.487764 655.0584

NCL NCL R561 RLELQGPrGSPNARS P19338 27278748 27278749 LELQGPrGSPNAR 1315.24976 509.18725 643.00076 216.968 1151.06844 1799.4947

UBE2M UBE2M R169 QNVQRSMrGGYIGST P61081 6009456 6009457 SMrGGYIGSTYFER 714.842315 564.834842 335.723924 172.78 758.488028 1054.5454

K19 KRT19 R43 IHGGSGGrGVSVSSA P08727 6009233 6009234 APSIHGGSGGr; APSIHGGSGGrGV; APSIHGGSGGrGVS; APSIHGGSGGrGVSV; APSIHGGSGGrGVSVS; APSIHGGSGGrGVSVSS; APSIHGGSGGrGVSVSSA; APSIHGGSGGrGVSVSSAR; APSIHGGSGGrGVSVSSAr; APSIHGGSGGrGVSVSSArFVSSSSSGAYGGGYGGVLTASDGLLAGNEK; FGPGVAFRAPSIHGGSGGrGVSVSSAR; FGPGVAFrAPSIHGGSGGr; FGPGVAFrAPSIHGGSGGrGV; FGPGVAFrAPSIHGGSGGrGVSV; FGPGVAFrAPSIHGGSGGrGVSVS; FGPGVAFrAPSIHGGSGGrGVSVSSA; FGPGVAFrAPSIHGGSGGrGVSVSSAR; FGPGVAFrAPSIHGGSGGrGVSVSSAr; FGPGVAFrAPSIHGGSGGrGVSVSSArFVSSSSSGAYGGGYGGVLTASDGLLAGNEK; GGSGGrGVSVSSAR; GGSGGrGVSVSSAr; GGrGVSVSSAR; GSGGrGVSVSSAr; IHGGSGGrGVSVSSAR; QSSATSSFGGLGGGSVrFGPGVAFrAPSIHGGSGGrGVSVSSAr; RAPSIHGGSGGrGVSVSSAR; RAPSIHGGSGGrGVSVSSAr; SGGrGVSVSSAR; SIHGGSGGr; SIHGGSGGrGVSVSSAR; SIHGGSGGrGVSVSSAr; rAPSIHGGSGGr; rAPSIHGGSGGrGVSVSSAR; rAPSIHGGSGGrGVSVSSAr; rGVSVSSAR 21848.5072696 17654.627705 2176.40077708 4794.08803 5314.62041456 9773.2335379