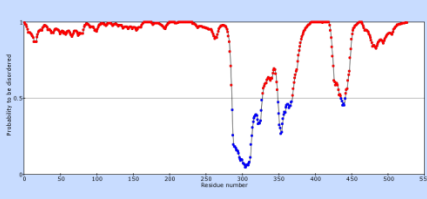
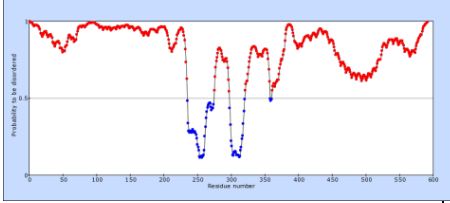


	Protein name, Length, Function, Number of protein partners (BioGrid)	Amino acid sequence and repeats identified by UniProt and the T-reks program	Prion domain, Neurodegenerative disease	Profile of probability to be ordered or disordered by using IsUnstruct program
1.	<p>RNA-binding protein FUS, 1-526, DNA binding nucleotide binding RNA binding</p> <p>298</p>	<p>>sp P35637 FUS_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1</p> <p>MASNDYTQQATQSYGAYPTQPGQGYSSQSSQPFYQOQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSTGGYGSSQSSQSSYGQSSYPGYGQQPAPSSTSGSYGSSSQSSSYGQPQSGSYSQQFSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSRGGGGGGGGNYGQDQSSMSSGGGSGGGYGQQDQSGGGGSGGGYGQQDRGGRGRGGSQGGGGGGGYNRSSGGYEPFRGRGGRRGGRGGMGGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIITNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRRGGNGRGGRRGGPMGRGGYGGGGSGGGRRGGFPSRGGGGQQRAGDWKCPNPTCENMNF'SWRNECNQCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSRGEHRQDRRERPY</p> <p><u>UniProt</u> Zinc finger 422-453 285-371 RRM 1-165 Q/G/S/Y-rich 166-267 Gly-rich 371-526 RGG</p> <p><u>T-reks</u> Length: 8 residues - nb: 5 from 36 to 76 - Psim:0.74 region Length:41 QSY--SGYS- QSTDTSGYG- QSSY-SSYG- QSQN-TGYGT QSTP-QGYG- ***** Length: 8 residues - nb: 2 from 74 to 87 - Psim:0.75 region Length:14 GYGSTG--</p>	<p>N-terminal, 1-237 ALS, FTLD</p>	

```

GYGSSQSS
*****
Length: 8 residues - nb: 3 from 81 to
107 - Psim:0.7 region Length:27
YGSSQSSQSS
YG-QQSSYPG
YG--QQPAPS
*****
Length: 8 residues - nb: 5 from 112
to 147 - Psim:0.7111111111111111 region
Length:36
SYGSSSQSS
SYGQPQSG-
SYSQQP---
SYGGQQQ--
SYGQQQ---
*****
Length: 8 residues - nb: 3 from 132
to 152 - Psim:0.7916666666666666 region
Length:21
QQPSYGG-
QQQSYG--
QQQSYNPP
*****
Length: 10 residues - nb: 9 from 20
to 109 - Psim:0.7142857142857143 region
Length:90
QPGQGYS-QQSS-----
---QPYG--QSSYSG-----
-----Y--SQSTDTSGY----
-----G--QSSYSSY-----
-----G--QSQNTGYG-T--
-----QSTPQGYGSTGG
-----YGSSQSSQSS-----
-----YG-QQSSYPG-----
-----YG-QQPAPSSST-----
*****
Length: 11 residues - nb: 7 from 91
to 166 - Psim:0.7142857142857143 region
Length:76
---YGQ-Q---S-S-Y-PG---
---YGQ-QPAPS-S-T-SG--S
---YGS-S---S-Q-S-SS---
---YGQPQ---S-GS-YS--Q-
QPSYGG-Q----Q-QS--Y---
----GQ-Q---Q-S-YNPPQGY

```

		<p>----GQ-Q---N-Q-YNSSSG- *****</p> <p>Length: 13 residues - nb: 2 from 189 to 216 - Psim:0.8333333333333334 region Length:28 GSGGGYGNQDQSGGG GSGG-YGQQDR-GGR</p>		
2.	<p>TATA-binding protein-associated factor 2N, 1-592 DNA binding poly(A) RNA binding 53</p>	<p>>tr Q86X94 Q86X94_HUMAN TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa OS=Homo sapiens GN=TAF15 PE=2 SV=2 MSDSGSYGQSGGEEQQSYSTYGNPGSQGYGQASQSYSGYG QTTDSSYGQNYSGYSSYGQSQSGYSQSYGGYENQKQSSY SQQPYNNQGGQQNMESSGSQGGRAPSYDQPDYGGQDSYD QQSGYDQHQGSYDEQSNYDQQHDSYSQNNQSYHSQRENY SHHTQDDRRRDVSRYGEDNRGYGGSQGGRRGRGGYDKDGR GPMTGSSGGDRGGFKNFGGHRDYGPRTDADSESDNSDNN TIFVQGLGEGVSTDQVGEFFKQIGI IKTNKKTKGKPMINL YTDKDTGKPKGEATVSFDDPPSAKAAIDWFDGKEFHGNI IKVSFATRRPEFMRGGGSGGGRRGRGGYRGRGGFQGRGG DPKSGDWVCPNPSCGNMNFARRNSCNQCNEPRPEDSRPS GGDFRGRGYGGERGYRGRGGRGGDRGGYGGDRSGGGYGG DRSSGGGYSGDRSGGGYGGDRSGGGYGGDRGGYGGDRG GGYGGDRGGYGGDRGGYGGDRGGYGGDRGGYGGDRGG YGGDRGGYGGDRGGYGGDRSRGGYGGDRGGGSGYGGDRS GGYGGDRSGGGYGGDRGGYGGDRGGYGGKMGGRNDYRN DQRNRPY</p> <p>UniProt 407-575 21 X approximate tandem repeats of D-R-[S,G](0,3)-G-G-Y-G-G 354-385 Zinc finger 234-320 RRM 407-575 - 21 repeats 1-208 Q/G/S/Y-rich 320-590 - RGG-rich 576-592 - NLS</p> <p>T-reks Length: 7 residues - nb: 4 from 116 to 141 - Psim:0.75 region Length:26 YDQQ-SG- YDQH-QGS YDEQ-SN- YDQQHDS-</p>	<p>N-terminal, 1-152 ALS, FTLD</p>	

Length: 7 residues - nb: 4 from 331
to 356 - Psim:0.71875 region Length:26
GGGR-RGR
GG-Y-RGR
GG-F-QGR
GG-DPKSG

Length: 7 residues - nb: 11 from 454
to 534 - Psim:0.9090909090909091 region
Length:81

-GY-GGDRGG
-GY-GGDRGG
-GY-GGDRGG
-GY-GGDRG-
-GY-GGDRGG
-GY-GGDRG-
-GY-GGDRG-
-GY-GGDRG-
-GY-GGDRG-
-GY-GGDRG-
-GY-GGDRS-
RGGYGGD---

Length: 7 residues - nb: 14 from 466
to 567 - Psim:0.8333333333333334 region
Length:102

DRG-G-GYGG--
DRG-G-GYGG--
DRG-G--YGG--
DRG-G-GYGG--
DRG-G--YGG--
DRG-G--YGG--
DRG-G--YGG--
DRG-G--YGG--
DRSRRG-GY----
G-G-DRG-GG--
S-G----YGGDR
S-G-G--YGGDR
S-G-G-GYGG--
DRG-G-GYG---

Length: 7 residues - nb: 14 from 479

```
to 578 - Psim:0.8441558441558441 region
Length:100
--YGGDR-GG-
--YGGDR-GGG
--YGGDR-GG-
--YGGDR-GG-
--YGGDR-GG-
--YGGDR-GG-
--YGGDR-SR-
GGYGGDR----
G--GGS--GY-
G--G-DRSGG-
--YGGDRSGG-
G-YGGDR-GG-
G-YGGDR-G--
G-YGG-K-MG-
*****

Length: 7 residues - nb: 5 from 490
to 525 - Psim:0.975 region Length:36
RGGGYGGD
RGG-YGGD
RGG-YGGD
RGG-YGGD
RGG-YGGD
*****

Length: 7 residues - nb: 4 from 503
to 530 - Psim:0.90625 region Length:28
GDRG-GYG
GDRG-GYG
GDRG-GYG
GDRSRG-G
*****

Length: 7 residues - nb: 3 from 514
to 534 - Psim:0.7777777777777778 region
Length:21
-GY-GGDRG
-GY-GGDRS
RGGYGGD--
*****

Length: 7 residues - nb: 6 from 536
to 578 - Psim:0.7592592592592593 region
Length:43
```

G-GGS--GY
 G-G-DRSGG
 -YGGDRSGG
 GYGGDR-GG
 GYGGDR-G-
 GYGG-K-MG

Length: 7 residues - nb: 3 from 557
 to 578 - Psim:0.875 region Length:22
 GYGGDRGG
 GYGGDRG-
 GYGGKMG-

Length: 8 residues - nb: 7 from 7 to
 63 - Psim:0.7428571428571429 region
 Length:57
 YGQ-S-G-GEQ----
 --Q-SYS-T-----
 YGN-PGSQG-----
 YGQASQS---Y--SG
 YGQ-TTD-S-S----
 YGQ-NYS-G-YSS--
 YGQ-SQS-G-Y----

Length: 8 residues - nb: 4 from 39 to
 72 - Psim:0.65 region Length:34
 GQT-TD-SSY
 GQNYSGYSSY
 GQSQSGYS--
 -QSYGGYEN-

Length: 8 residues - nb: 3 from 338
 to 357 - Psim:0.6666666666666666 region
 Length:20
 GGY-RG-R
 GGF-QG-R
 GGDPKSGD

Length: 8 residues - nb: 20 from 413
 to 575 - Psim:0.9125 region Length:163
 GDR--GG--YG-

GDRS-GG-GYG-
GDRSSGG-GYS-
GDRS-GG-GYG-
GDRS-GG-GYG-
GDR--GG-GYG-
GDR--GG-GYG-
GDR--GG-GYG-
GDR--GG--YG-
GDR--GG-GYG-
GDR--GG--YG-
GDR--GG--YG-
GDR--GG--YG-
GDR--GG--YG-
GDRS-RG-GYG-
GDRG-GGSGYG-
GDRS-GG--YG-
GDRS-GG-GYG-
GDR--GG-GYG-
GDR--GG--YGG

Length: 8 residues - nb: 19 from 423
to 576 - Psim:0.8866396761133604 region
Length:154

--SGG-GYGGDRS
--SGG-GYSG--D
-RSGG-GYGG---
DRSGG-GYGG---
DR-GG-GYGG---
DR-GG-GYGG---
DR-GG-GYGG---
DR-GG--YGG---
DR-GG-GYGG---
DR-GG--YGG---
DR-GG--YGG---
DR-GG--YGG---
DR-GG--YGG---
DRSRG-GYGG---
DRGGGSGYGG---
DRSGG--YGG---
DRSGG-GYGG---
DR-GG-GYGG---
DR-GG--YGG--K

Length: 8 residues - nb: 17 from 439

to 575 - Psim:0.9321266968325792 region
Length:137
GDRSG-GG--YG-
GDRSG-GG--YG-
GDR-G-GG--YG-
GDR-G-GG--YG-
GDR-G-GG--YG-
GDR-G-G---YG-
GDR-G-GG--YG-
GDR-G-G---YG-
GDR-G-G---YG-
GDR-G-G---YG-
GDR-G-G---YG-
GDR-SRGG--YG-
GDR-G-GSGYG-
GDR-S-GG--YG-
GDRSG-GG--YG-
GDR-G-GG--YG-
GDR-G-G---YGG

Length: 8 residues - nb: 16 from 455
to 580 - Psim:0.921875 region
Length:126
YGGDR-G-GG--
YGGDR-G-GG--
YGGDR-G-GG--
YGGDR-G-G---
YGGDR-G-GG--
YGGDR-G-G---
YGGDR-G-G---
YGGDR-G-G---
YGGDR-G-G---
YGGDR-SRGG--
YGGDR-G-GSG
YGGDR-S-GG--
YGGDRSG-GG--
YGGDR-G-GG--
YGGDR-G-G---
YGGKM-G-GR--

Length: 8 residues - nb: 14 from 467
to 575 - Psim:0.8428571428571429 region
Length:109
--RG-G-GYG-GD--


```
--RG-G-GYG-GD--  
--RG-G--YG-GD--  
--RG-G-GYG-GD--  
--RG-G--YG-GD--  
--RG-G--YG-GD--  
--RG-G--YG-GD--  
--RG-G--YG-GD--  
--RG-G--YG-GDRS  
--RG-G--YG-GD--  
--RG-G-GSGYG---  
GDRS-G-GYG-----  
GDRS-GGG-YG----  
GDRG-G-GYG-----  
--GDRG-GYG-G---  
*****
```

Length: 8 residues - nb: 12 from 481
to 575 - Psim:0.9166666666666666 region

Length:95

```
GDR-G-G---YG-  
GDR-G-GG--YG-  
GDR-G-G---YG-  
GDR-G-G---YG-  
GDR-G-G---YG-  
GDR-G-G---YG-  
GDR-SRGG--YG-  
GDR-G-GSGYG-  
GDR-S-GG--YG-  
GDRSG-GG--YG-  
GDR-G-GG--YG-  
GDR-G-G---YGG  
*****
```

Length: 8 residues - nb: 11 from 493
to 579 - Psim:0.9015151515151515 region

Length:87

```
GYGGDR-G-----  
GYGGDR-G-----  
GYGGDR-G-----  
GYGGDR-G-----  
GYGGDR-SRG--  
GYGGDR-G-GGS  
GYGGDR-S-G--  
GYGGDRSG-G--  
GYGGDR-G-G--  
GYGGDR-G-----  
GYGGKM-G-G--
```

```
*****
Length: 8 residues - nb: 9 from 504
to 576 - Psim:0.9074074074074074 region
Length:73
DR--GG--YGG-
DR--GG--YGG-
DR--GG--YGG-
DRSRGG--YGG-
DRG-GGSGYGG-
DRS-GG--YGG-
DRS-GG-GYGG-
DRG-GG--YGG-
DR--GG--YGGK
*****

Length: 8 residues - nb: 8 from 515
to 580 - Psim:0.8375 region Length:66
YGGDR-GG--
YGGDRSRG-G
YGGDRGGGSG
YGGDRSGG--
YGGDRSGG-G
YGGDR-GG-G
YGGDR-GG--
YGG-KMGG-R
*****

Length: 8 residues - nb: 6 from 525
to 576 - Psim:0.8787878787878788 region
Length:52
DRSRG-GYGG-
DRGGGSGYGG-
DRSGG--YGG-
DRSGG-GYGG-
DR-GG-GYGG-
DR-GG--YGGK
*****

Length: 8 residues - nb: 5 from 540
to 579 - Psim:0.8888888888888888 region
Length:40
GYGGDR-SG
GYGGDRSGG
GYGGDR-GG
GYGGDR-G-
```

GYGKMG-GG

Length: 8 residues - nb: 3 from 552
to 576 - Psim:0.9 region Length:25
DRSGGGYGG-
DR-GGGYGG-
DR-GG-YGGK

Length: 9 residues - nb: 5 from 20 to
66 - Psim:0.7 region Length:47
YG--NP-G-SQG
YGQASQS-YS-G
YGQ-T-TD-S-S
YGQ-NYSGYS-S
YGQ-SQSGYSQS

Length: 9 residues - nb: 4 from 38 to
75 - Psim:0.65909090909091 region
Length:38
YGQT-TD-S-S
YGQNYSGYS-S
YGQSQSGYSQS
YG-GYENQK-Q

Length: 9 residues - nb: 3 from 52 to
77 - Psim:0.6666666666666666 region
Length:26
GYSSYGQSQS
GYS---QSYG
GYENQKS-S

Length: 9 residues - nb: 20 from 413
to 576 - Psim:0.9041666666666667 region
Length:164
GDR--G-G--YG
GDRS-G-G-GYG
GDRSSG-G-GYS
GDRS-G-G-GYG
GDRS-G-G-GYG
GDR--G-G-GYG
GDR--G-G-GYG

GDR--G-G-GYG
 GDR--G-G--YG
 GDR--G-G-GYG
 GDR--G-G--YG
 GDR--G-G--YG
 GDR--G-G--YG
 GDR--G-G--YG
 GDRS-R-G-GYG
 GDRG-G-GSGYG
 GDRS-G-G--YG
 GDRS-G-G-GYG
 GDR--G-G-GYG
 GDRG-GYG-GK-

 Length: 9 residues - nb: 3 from 423
 to 450 - Psim:0.9333333333333333 region
 Length:28
 SGGGYGGDRS
 SGGGYSGDR-
 SGGGYGGDR-

 Length: 9 residues - nb: 17 from 439
 to 576 - Psim:0.9327731092436975 region
 Length:138
 GDRSG-GG--YG--
 GDRSG-GG--YG--
 GDR-G-GG--YG--
 GDR-G-GG--YG--
 GDR-G-GG--YG--
 GDR-G-G---YG--
 GDR-G-GG--YG--
 GDR-G-G---YG--
 GDR-G-G---YG--
 GDR-G-G---YG--
 GDR-G-G---YG--
 GDR-SRGG--YG--
 GDR-G-GGSGYG--
 GDR-S-GG--YG--
 GDRSG-GG--YG--
 GDR-G-GG--YG--
 GDR-G-G---YGGK

 Length: 9 residues - nb: 16 from 455

GDR-G-GGSGYG--
GDR-S-GG--YG--
GDRSG-GG--YG--
GDR-G-GG--YG--
GDR-G-G---YGGK

Length: 9 residues - nb: 11 from 493
to 580 - Psim:0.8939393939393939 region
Length:88
GYGGDR-G----
GYGGDR-G----
GYGGDR-G----
GYGGDR-G----
GYGGDR-SRG--
GYGGDR-G-GGS
GYGGDR-S-G--
GYGGDRSG-G--
GYGGDR-G-G--
GYGGDR-G----
GYGGKM-G-G-R

Length: 9 residues - nb: 9 from 504
to 577 - Psim:0.905982905982906 region
Length:74
DR--GG--YGG--
DR--GG--YGG--
DR--GG--YGG--
DRSRGG--YGG--
DRG-GGSGYGG--
DRS-GG--YGG--
DRS-GG-GYGG--
DRG-GG--YGG--
DR--GG--YGGKM

Length: 9 residues - nb: 8 from 515
to 581 - Psim:0.825 region Length:67
YGGDR-GG--
YGGDRSRG-G
YGGDRGGGSG
YGGDRSGG--
YGGDRSGG-G
YGGDR-GG-G
YGGDR-GG--

YGG-KMGGRN

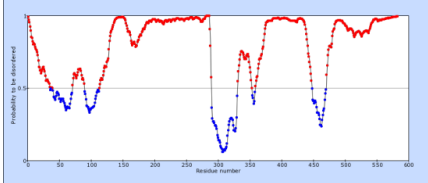
Length: 9 residues - nb: 3 from 528
to 552 - Psim:0.777777777777778 region
Length:25
-RG-G---YGGD
-RG-GSGYGG-
DRSG---GYGGD

Length: 9 residues - nb: 5 from 541
to 581 - Psim:0.86 region Length:41
YGGDR-SG-G
YGGDRSGG-G
YGGDR-GG-G
YGGDR-GG--
YGGKM-GGRN

Length: 9 residues - nb: 3 from 557
to 580 - Psim:0.8518518518518519 region
Length:24
GYGGDRGG-
GYGGDRG--
GYGKMGGR

Length: 11 residues - nb: 3 from 44
to 75 - Psim:0.6944444444444444 region
Length:32
SSYGQNYSGY--
SSYGQSQSGY-S
QSYG-GYENQKQ

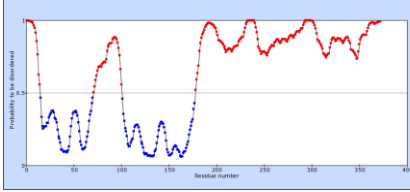
Length: 11 residues - nb: 5 from 417
to 464 - Psim:0.9166666666666666 region
Length:48
GYGGDRS-GG--
GYGGDRSSGG--
GYSGDRS-GG--
GYGGDRS-GG--
GYGGDRG-GGYG

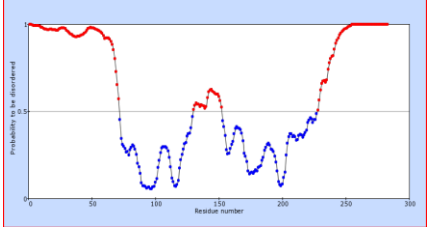
		<p>Length: 11 residues - nb: 3 from 431 to 460 - Psim:0.8888888888888888 region Length:30 RSSGGGYSGD-- RS-GGGYGGD-- RS-GGGYGGDRG *****</p> <p>Length: 11 residues - nb: 5 from 519 to 567 - Psim:0.8153846153846154 region Length:49 RGGYGGDRS---- RGGYGGDRGGG-- -SGYGGDRSG--- -G-YGGDRSGG-- -G-YGGDRGGGYG *****</p> <p>Length: 13 residues - nb: 4 from 27 to 74 - Psim:0.6666666666666666 region Length:48 GY-GQ--A-SQ--S-YS- GYGQTTDSSYGQ-N--YS GY-S---SYGQ--S-QS- GY-SQ--SYGG-YENQK- *****</p> <p>Length: 13 residues - nb: 3 from 46 to 79 - Psim:0.6888888888888889 region Length:34 YG--QNYSG--YS-S YG--QSQSG--YSQS YGGYENQKQSS-YS- *****</p>		
3.	<p>RNA-binding protein EWS, 1-656 identical protein binding poly(A) RNA binding zinc ion binding</p>	<p>>sp Q01844 EWS_HUMAN RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 MASTDYSTYSQAAQQGYSAYTAQPTQGYAQTTQAYGQQ SYGTYGQPTDVSYTQAQTTATYGQTAYATSYGQPPTGYT TPTAPQAYSQPVQGGYGTGAYDTTTATVTTTQASYAAQSA YGTQPAYPAYGQQPAATAPTRPDGNKPTETSQPQSSTG GYNQPSLGYGQSNYSYPQVPGSYPMQPVTAPPSYPPTSY SSTQPTSYDQSYSQQNTYGQPSYGQQSSYGQQSSYGQ QPPTSYPPQTGSYSQAPSQYSQQSSSYGQSSFRQDHPS SMGVYGQESGGHSGPGENRSMSGPDNRGRGRGGFDRGGM SRGGRGGGRGGMGSAGERGGFNKPGGPMDEGPDLDLGPP</p>	<p>N-terminal, 1-280 ALS, FTLD, Ewing sarcoma (ES)</p>	

<p>210</p>	<p>VDPDESDNSAIYVQGLNDSVTLDDLADFFKQCGVVKMN KRTGQPMIHIYLDKETGKPKGDATVSYEDPPTAKAAVEW FDGKDFQGSKLKVS LARKKPPMNSMRGGLPPREGRGMPP PLRGGPGGPGGPGGPMGRMGGRGGDRGGFPPRGPRGSRG NPSGGNVQHRAGDWQCPNPGCGNQNFARTECNQCKAP KPEGFLPPPPFPFPPGGDRGRGGPGMRGGRGGLMDRGGPG GMFRGGRGGDRGGFRGGRGMDRGGFGGGRRGGPGGPPGP LMEQMGGRRGGRGGPGKMDKGEHRQERRDRPY UniProt 8-285; 31 approximate tandem repeats – UniProt 518-549 Zinc finger 1-285 Q/P/T/-rich 361-447 RRM 639-656 NLS 300-340 RGG-rich 454-513 RGG 559-640 RGG</p> <p><u>T-reks</u> Length: 7 residues - nb: 6 from 207 to 245 - Psim:0.7291666666666666 region Length:39 SYSQQNT- -YGQPSS- -YGQQSS- -YGQQSS- -YGQQPPT SYPPQTG- ***** Length: 7 residues - nb: 3 from 247 to 267 - Psim:0.7619047619047619 region Length:21 YSQAPSQ YSQQSSS YGQQSSF *****</p>		
<p>4.</p>	<p>Heterogeneous nuclear ribonucleoprotein D-like, 1-420 DNA binding nucleotide binding</p> <p>>sp O14979 HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 MEVPPRLSHVPPPLFSPAPATLASRSLSHWRPRPPRQLA PLLPSLAPSSARQGARRAQRHVTAQQPSRLAGGAAIKGG RRRRPDLFRRHFKSSSIQRSAAAAA TRTARQHPPADSS VTMEDMNEYSNIEEFAEGSKINASKNQDDGKMFIGGLS WDTSKKDLTEYLSRFGVVDCTIKTDPVTGRSRGFGFVL FKDAASVDKVLLELKEHKLDGKLLIDPKRAKALKGKEPPKK</p>	<p>C-terminal, 316-420</p>	

<p>poly(A) RNA binding single-stranded DNA binding 94</p>	<p>VFVGGLS PDTSEEQIKEYFGAFGEIENIELPMDTKTNER RGFCFITYTDEEPVKKLLESRYHQIGSGKCEIKVAQPKE VYR QQQQQK GGRGAAA GGRGGTRGRGRG QGQNWQGFN NYYDQGYGNYSAYGGDQNYSGYGGYDYGNYGNYGYG QGYADYSGQQSTYKASRGGGNHQNNYQPY <u>UniProt</u> Contains 2 RRM (RNA recognition motif) domains 148-230 RRM1 233-312 RRM2 79-82 Poly-Arg 316-321 Poly-Gln 323-411 Gly-rich 353-396 Tyr-rich</p> <p><u>T-reks</u> >sp O14979 HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 Length: 4 residues - nb: 6 from 373 to 395 - Psim:0.7 region Length:23 GYG-- GYDYT GYNY- G-NY- GYGQ- GYAD- *****</p> <p>Length: 6 residues - nb: 4 from 323 to 347 - Psim:0.65625 region Length:25 GGRG-AAA GGRG-GT- RGRGRG-- QGQN-WN- *****</p> <p>Length: 7 residues - nb: 2 from 323 to 336 - Psim:0.7857142857142857 region Length:14 GGRGAAA GGRGGTR *****</p>		
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<p>5. Heterogeneous nuclear ribonucleoprotein D0, 1-355 nucleotide binding RNA binding 169</p>	<p>>sp Q14103 HNRPD_HUMAN Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 MSEEQFGGDG AAAAA TAAVGG SAGEQEGAMVAATQGAAA AAGSGAGTGGGTASGGTEGGSAESEGA KIDASKNEEDEG HSNSSPRHSEAATAQREEWKMF IGGLSWDTTKKDLKDYF SKFGEVVDCTLKLDPITGRSRGFGFVLFKESESVDKVM D QKEHKLNGKVIDPKRAKAMKTKEPVKKIFVGG LSPDTPE EKIREYFGGFGEVESIELPMDNKTNRRGFCFITFKEEE PVKKIMEKKYHNVGLSKCEIKVAMSKEQY QQQQWGSRG GFAGRARGRGGGPSQNWNOGYSNYWNOGYGNYGNSQGY GGYGGYDYTGYNYYGYGDY SNQQSGY GKVSRRGGHQ NS YKPY UniProt Contains 2 RRM (RNA recognition motif) domains 97-179 RRM1 182-261 RRM2 11-45 Ala-rich 270-347 Gly rich 294-332 Tyr-rich <u>T-reks</u> Length: 10 residues - nb: 3 from 290 to 317 - Psim:0.7666666666666667 region Length:28 WNQYSNY-- WNQYGN YGY NSQYGGYGG</p>	<p>C-terminal, 262-355</p>	
<p>6. HNRNPA2B1 protein, nucleic acid binding 153</p>	<p>>sp P22626 ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2, C-terminal, 235-327, IBMPFD MEKTLETVPLERKKREKEQFRKLF IGGLSFETTEESLRNYEQWG KLTDCVVMRDPASKRSRGFGFVTFSSMAEVDAAAMAARPHSID GRVVEPKRAVAREESGKPGAHVTVKKLFVGGIKEDTEEHLRDY FEYEGKIDTIEITDRQSGKKRGFGFVTFDDHDPVDKIVLQKYHTI NGHNAEVRKALSRQEMQEVQSSRSRGGNFGFGDS RGGGGN FGPGGSNFRGGSDGYGSGRFGDGYNGYGGPGGGNFGGS PGYGGGRGGYGGGGPGYGNQGGGYGGYDNYGGNYGSG NYNDFGNYNQQPSNYGPMKSGNF GGSRNMGGPYGGNYGP GGSGGSGGYGGRSRY</p>	<p>C-terminal, IBMPFD</p>	

<p>7. Heterogeneous nuclear ribonucleoprotein A1, 1-372 nucleotide binding RNA binding single-stranded RNA binding</p> <p>308</p>	<pre>>sp P09651 ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 MSKSESPKEPEQLRKLFIGGLSFETTDESLRSHFEQWGT LTDCVVMRDPNPKRSRGGFVVTYATVEEVDAAMNARPHK VDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTE EHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFVTFDDH DSVDKIVIQKYHTVNGHNCEVRKALSKQEMASASSSQRG RSGSGNFGGGRGGGFGGNDNFGRGGNFSGRGGFGGSRGG GGYGGSGDGYNGFGNDGGYGGGGPYSGGSRGYGSGGQG YGNQGSYGGSSTYDSYNNGGGGGFGGSGSNFGGGGSY NDFGNYNQSSNFGPMKGGNFGGRSSGPYGGGGQYFAKP RNQGGYGGSSSSSYGSRRF</pre> <p>UniProt</p> <p>Contains 2 RRM (RNA recognition motif) domains</p> <p>14-97 RRM1</p> <p>105-184 RRM2</p> <p>218-240 RNA-binding RGG-box</p> <p>4-94 Globular A domain</p> <p>95-185 Globular B domain</p> <p>195-372 Gly-rich</p> <p><u>T-reks</u></p> <p>Length: 6 residues - nb: 3 from 217 to 235 - Psim:0.7619047619047619 region</p> <p>Length:19</p> <p>GRGGNFS</p> <p>GRGG-FG</p> <p>GSRG-GG</p> <p>*****</p> <p>Length: 6 residues - nb: 5 from 252 to 285 - Psim:0.7142857142857143 region</p> <p>Length:34</p> <p>GYGGGGP</p> <p>GYSGGSR</p> <p>GYGSGGQ</p> <p>GYGNQGS</p> <p>YGGS-</p> <p>*****</p> <p>Length: 6 residues - nb: 3 from 267 to 286 - Psim:0.7142857142857143 region</p> <p>Length:20</p> <p>YSGGGQG</p> <p>YGNQGS</p>	<p>C-terminal, 186-372 IBMPFD3, ALS</p>	
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		<p>YGGSGS- ***** Length: 7 residues - nb: 2 from 216 to 229 - Psim:0.7857142857142857 region Length:14 FGRGGNF SGRGGFG *****</p>		
<p>8. Heterogeneous nuclear ribonucleoprotein A/B, nucleic acid binding 60</p>		<p>>tr D6RD18 D6RD18_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1 MSEAGEEQPMETTGATENGHEAVPEGESPAGAGTGAAAAG AGGATAAPPSGNQNGAEGDQINASKNEEDAGKMFVGGLS WDTSKKDLKDYFTKFGEVVDCTIKMDPNTGRSRGFGFIL FKDAASVEKVLDQKEHRLDGRVIDPKKAMAMKKDPVKKI FVGGLNPEATEEKIREYFGEFGEIEAIELPMDPKLNKRR GFVFITFKEEEPVKKVLEKFHTVSGSKCEIKVAQPKEV YQQQYGSGGRGNRNRGNRGSGGGGGQGSTNYGKSQRR GGHQNNYKPY T-teks Length: 4 residues - nb: 4 from 31 to 45 - Psim:0.75 region Length:15 GAGT GAAA GAG- GATA ***** Length: 4 residues - nb: 4 from 245 to 260 - Psim:0.7 region Length:16 RGNRN RGN-- RGS-G GGG-G ***** Length: 5 residues - nb: 3 from 143 to 158 - Psim:0.6666666666666666 region Length:16 KKAMAM KKD-PV KKI-FV</p>	<p>C-terminal 235-327</p>	

<p>9. Heterogeneous nuclear ribonucleoprotein A3, nucleotide binding RNA binding 1-378 80</p>	<p>>sp P51991 ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 MEVKPPPGRPQPDSEGGGRRRRRRGEEGHDPKEPEQLRKLFI GGLSFETDDSLREHFKEKWGLTLDCCVVMRDPQTKRSRGGF GFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSV KPGAHLTVKKIFVGGIKEDTTEENLRDYFEKYGKIETIE VMEDRQSGKKRGFAFVTFDDHDTVDKIVVQKYHTINGHN CEVKKALSKEQEMQSAGSQRGRGGGSGNFMGRGGNFGGGG GNFGRGGNFGGRGGYGGGGGSRGSYGGGDGGYNGFGGD GGNYGGGPGYSSRGGYGGGGPGYGNQGGYGGGGYDGY NEGGNFGGGNYGGGGYNDFGNYSGQQQSNYGPMMKGSF GGRSSGSPYGGGYGSGGGSGGYGSRRF</p> <p>Contains 2 RRM (RNA recognition motif) domains 35-118 RRM1 126-205 RRM2 211-378 Gly-rich</p> <p><u>T-reks</u> Length: 6 residues - nb: 8 from 221 to 272 - Psim:0.6607142857142857 region Length:52 GNFMGRG GNFGGGG GNFGRG- GNFGGR- GGYGGG GGRGSY GG-GDGG YN-GFGG ***** Length: 6 residues - nb: 4 from 288 to 313 - Psim:0.8125 region Length:26 GYGG-GGP GYGNQGG- GYGG-GG- GYDG-YN- ***** Length: 6 residues - nb: 4 from 316 to 338 - Psim:0.7083333333333334 region Length:23 GNFGG-</p>	<p>C-terminal 207-378 C9orf72 ALS/FTLD</p>	
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GNYGGG
 GNYNDF
 GNYSGQ

Length: 7 residues - nb: 7 from 221
 to 267 - Psim:0.7142857142857143 region
 Length:47
 GNFMRGRG-
 GNFGGGG-
 GNFRGR--
 GNFGGRG-
 G-YGGGG-
 GGSRGSY-
 GG-GDGGY

Length: 7 residues - nb: 5 from 233
 to 267 - Psim:0.7 region Length:35
 GGGNFG-R
 GG-NFGGR
 GG-YGGGG
 GG-SRGSY
 GG-GDGGY

Length: 7 residues - nb: 10 from 288
 to 355 - Psim:0.7583333333333333 region
 Length:68
 G-YG-G-G--GP
 G-YG-NQG--G-
 G-YG-G-G--G-
 G-YD-GYN--E-
 G-GNFG-G--G-
 N-YG-G-G--G-
 N-YN-D-F--G-
 N-YS-G-QQOS-
 N-YG-PMK--G-
 GSFG-G-R--S-

Length: 7 residues - nb: 3 from 321
 to 339 - Psim:0.7142857142857143 region
 Length:19
 GNYGGG-
 GNYNDF-

GNYSGQQ

 Length: 8 residues - nb: 5 from 211
 to 248 - Psim:0.76 region Length:38
 G--SQRGRGG
 GSGNFMGR--
 G-GNFGG-GG
 G--NFG-RG-
 G--NFGGRGG

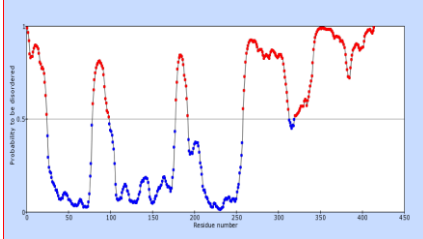
 Length: 8 residues - nb: 3 from 228
 to 248 - Psim:0.875 region Length:21
 GNFGG-GG
 GNFG-RG-
 GNFGGRGG

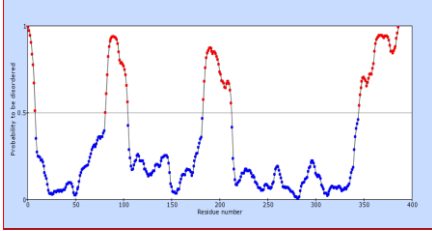
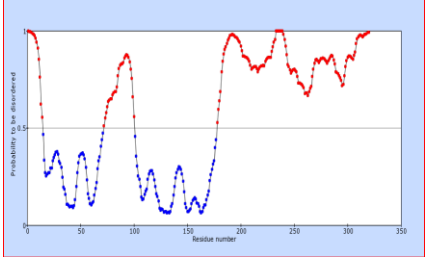
 Length: 8 residues - nb: 4 from 288
 to 315 - Psim:0.75 region Length:28
 GYGG-GGP
 GYGNQGG-
 GYGG-GG-
 GYDGYNEG

 Length: 8 residues - nb: 3 from 349
 to 372 - Psim:0.6666666666666666 region
 Length:24
 GSFGRSS
 GSPYGGGY
 GSGGSGG

 Length: 9 residues - nb: 3 from 211
 to 236 - Psim:0.696969696969697 region
 Length:26
 GS-QR-GRGG-
 GSGNFMGRG--
 GN-FG-GGGGN

 Length: 9 residues - nb: 2 from 228
 to 243 - Psim:0.8333333333333334 region
 Length:16

		<p>GNFG-GGG- GNFGRGGNF *****</p> <p>Length: 9 residues - nb: 3 from 288 to 310 - Psim:0.8 region Length:23 GYGG-GG--P GYGNQGG--- GYGG-GGGYD *****</p> <p>Length: 9 residues - nb: 3 from 349 to 373 - Psim:0.7037037037037037 region Length:25 GSFGGRSS- GSPYG-GGY GSGGSGGY *****</p>		
10	<p>TAR DNA-binding protein 43, 1-414 double-stranded DNA binding mRNA 3'-UTR binding poly(A) RNA binding sequence-specific DNA binding transcription factor activity RNA polymerase II distal enhancer sequence-specific DNA binding</p>	<p>>sp Q13148 TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 MSEYIRVTEDEENDEPIEIPSEDDGTVLLSTVTAQFPGAC GLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTE QDLKEYFSTFGEVLMVQVKDLKTGHSKGFGFVRFTEYE TQVKVMSQRHMDGRWCCKLPNSKQSQDEPLRSRKVFV GRCTEDMTEDELREFFSQYGDVMDVFIKPPFAFAFVTF ADDQIAQSLCGEDLIKGISVHISNAEPKHNSNRQLERS GRFGGNPGGF^{FGNQGG}FGNSRGGGAGLGN^{NN}QGSNMGGGMN FGA^FSINPAM^MAAA^QAA^LQSSW^{MM}GMLAS^{QQ}NQSGPSG NN^QN^QGN^MQ^REP^NQ^AF^GSG^NNS^{YS}GS^{NS}GAA^IGW^{GS}ASN ^{AG}SG^{SG}F^{NG}GFG^{SS}MDSK^{SS}GWGM UniProt Contains 2 RRM (RNA recognition motif) domains. 104-200 RRM1 191-262 RRM2 274-413 Gly-rich <u>T-reks</u> Length: 8 residues - nb: 3 from 276 to 296 - Psim:0.8148148148148148 region Length:21 ^{FGGN}-^{PGG}- ^{FG}-^N-^{QGG}-</p>	<p>C-terminal, 277-414 ALS, FTLD</p>	

	transcription factor activity involved in positive regulation of transcription 286	<p>FG-NSRGGG *****</p> <p>Length: 8 residues - nb: 4 from 368 to 399 - Psim:0.65 region Length:32</p> <p>GSGNNSY-S- GSNSGAAIGW GSAS--N-A- GSGSGFN-G-</p>		
11	cytotoxic granule-associated RNA binding protein, 1-386 AU-rich element binding poly(A) binding 21	<p>>sp P31483 TIA1_HUMAN Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=1 SV=3</p> <p>MEDEMPKTLYVGNLSRDVTEALILQLFSQIGPCKNCKMI MDTAGNDPYCFVEFHEHRHAAAALAAMNGRKIMGKEVKV NWAATTPSSQKKDTSSSTVVSTQRSQDHFHVFVGDLSPEI TTEDIKAAFAPFGRISDARVVKDMATGKSKGYGFVSFFN KWDAENAIQQMGQWLGGRQIRTNWATRKPPAPKSTYES NTKQLSYDEVVNQSSPSNCTVYCGGVTSGLTEQLMRQTE SPFGGIMEIRVFPKGYSFVRFNSHESAAHAIVSVNGTT IEGHVVKCYWGKETLDMINPVQQNQIGYPOPYGQWGQW YGNAQQIGQYMPNGWQVPAYGMYGQAWNQQGFNOTQSSA PWMGPNYGVQPPQGQNGSMLPNQPSGYRVAGYETQ</p> <p>UniProt Contains 3 RRM (RNA recognition motif) domains. 7-83 RRM1 106-184 RRM2 214-286 RRM3</p>	C-terminal, 292-386, Welander distal myopathy	
12	Heterogeneous nuclear ribonucleoprotein A1-like 2, 2-320 nucleotide binding 12	<p>>sp Q32P51 RA1L2_HUMAN Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2</p> <p>MSKSASPKEPEQLRKLFIGLSFETTDESLRSHFEQWGT LTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAMNTTPHK VDGRVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTE EHHLRDYFEQYGKIEVIEIMTDRGSGKRGFAFVTFDDH DSVDKIVIQKYHTVKGHNCEVRKALPKQEMASASSSQRG RRGSGNFGGGRGDGFGGNDNFGRGGNFSGRGGFGGSCGG GGYGGSGDGYNGFGNDGSNFGGGGSYNDFGNYNQSSNF GPMKGGNFGRSSGPYGGGGQYFAKPQNQGGYGVSSSS SYGSGRRF</p> <p>UniProt Contains 2 RRM (RNA recognition motif) domains</p>	C-terminal, 198-320	

14-97 RMM1
105-184 RMM2
4-94 Globular Domain A
95-185 Globular Domain B
218-240 RNA-binding RGG-box
195-317 Gly-rich

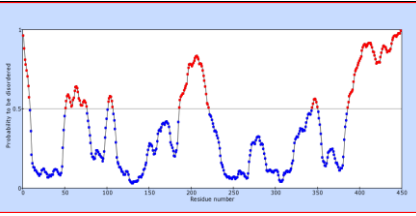
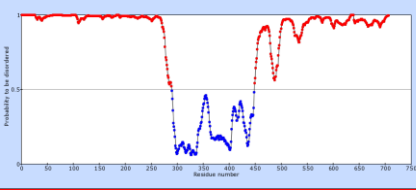
T-reks

>sp|Q32P51|RA1L2_HUMAN Heterogeneous
nuclear ribonucleoprotein A1-like 2
OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2
Length: 6 residues - nb: 5 from 217
to 248 - Psim:0.7777777777777778 region
Length:32
GR-GGNFS-
GR-GG-FG-
GSCGG--G-
GY-GG-SGD
GY-NG-FG-

Length: 7 residues - nb: 4 from 202
to 229 - Psim:0.7222222222222222 region
Length:28
FGGGRGDG-
FG-G-NDN-
FGRG-GNF-
SGRG-G-FG

Length: 7 residues - nb: 5 from 215
to 249 - Psim:0.6666666666666666 region
Length:35
NF-GR-GG-
NFSGR-GG-
-FGGSCGGG
GYGGS-GD-
GYNGF-GN-

Length: 8 residues - nb: 2 from 195
to 212 - Psim:0.85 region Length:18
GRRGSGNFGG
GR-GDG-FGG

<p>13</p>	<p>Heterogeneous nuclear ribonucleoprotein H, 1-449 nucleotide binding poly(U) RNA binding</p> <p>145</p>	<p>*****</p> <p>>sp P31943 HNRH1_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 MMLGTEGGEGFVVKVRGLPWSCSADEVQRFSDCKIQNG AQQIRFIYTREGRPSGEAFVELESEDEVKLALKKDRETM GHRYVEVFKSNVEMDWVLKHTGPNSPDTANDGFVRLRG LPFGCSKEEIVQFFSGLIIVPNGITLPVDFQGRSTGEAF VQFASQEI AEKALKKHKERIGHRYIEIFKSSRAEVRTHY DPPRKLAMQRPGPYDRPGAGRGYNSIGRGAGFERMRRG AYGGGYGGYDDYNGYNDGYGFGSDRFGRDLNYCFSGMSD HRYGDGGSTFQSTTGHCVMRGLPYRATENDIYNFFSPL NPVRVHIEIGPDGRVTGEADVEFATHEDAVAAMSKDKAN MQHRYVELFLNSTAGASGGAYEHRYVELFLNSTAGASGG AYG SQMMGGMGLSNQSSYGGPASQQLS GGYGGGYGGQSS MSGYDQVLQENSSDFQSNIA</p> <p>UniProt</p> <p>Contains 3 RRM (RNA recognition motif) domains</p> <p>11-90 RMM1 111-188 RMM2 289-364 RMM3 234-249 repeat 1-1 354-372 repeat 2-1 374-392 repeat 2-2 418-433 repeat 1-2</p> <p><u>T-reks</u> Length: 20 residues - nb: 3 from 354 to 413 - Psim:0.7 region Length:60 HRYVELFLNSTAGASGGAYE HRYVELFLNSTAGASGGAYG SQMMGGMGLSNQSSYGGPAS</p>	<p>C-terminal, 382-449</p>	
<p>14</p>	<p>Splicing factor, proline- and glutamine-rich, 1-707 core promoter binding nucleotide binding transcription</p>	<p>>sp P23246 SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 MSRDRFRSRGGGGGFHRRGGGGRGGLHDFRSPPPGMG LNQNRGPMGPGPGQSGPKPPIPPPPPHQQQQQPPPOQPP PQQPPPHQPPPHQPHQQQQPPPPQDSSKPVVAQGGPGP APGVGSAPPASSAPPATPPTSGAPPGSGPGPTPTPPPA VTSAPPGAPPPTPPSSGVPTTPPQAGGPPPPAAVPGPG PGPKQGGPGGPKGGKMPGGPKGGPGLSTPGGHPKPP HRGGGEPRGGRQHHPYHQHHQGGPPGGPGRSEEKIS DSEGFKANLSLLRRPGEKTYTQRCLFVGNLPADITEDE FKRLFAYGEPGEVFINKGKGFIFIKLESRALAEIAKAE LDDTPMRGRQLRVRFATHAAALSVRNLSPVVSNELLEEA</p>	<p>N-terminal, 41-104</p>	

<p>regulatory region DNA binding transcription regulatory region sequence-specific DNA binding 136</p>	<p>FSQFGPIERAVVIVDDRGRSTGKGI VEFASKPAARKAFE RCSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEKLAQKNP MYQKERETPPRFAQHGTFEYEYSQRWKS LDEMEKQQREQ VEKNMKDAKDKLESEMEDAYHEHQANLLRQDLMR RQEEL RRMEELHNQEMQKRKEMQLRQEEERRRRREEEMMI RQREM EEQMRRQREEESYSRMGYMDPRERDMRMGGGGAMNMGDPY GSGGQKFPPLGGGGIGYEANPGVPPATMSGSM MG S DMRTERFGQGGAGPVGGQGPRGMGP GTPAGYGRGREEYE GPNKKPRF <u>UniProt</u> Contains 2 RRM (RNA recognition motif) domains. 297-369 RRM1 371-452 RRM2 10-266 Gln/Glu/Pro-rich</p> <p><u>T-reks</u> Length: 5 residues - nb: 4 from 69 to 89 - Psim:0.9166666666666666 region Length:21 QQQPPP QQ-PPP QQ-PPP HQ-PPP *****</p> <p>Length: 5 residues - nb: 4 from 81 to 102 - Psim:0.75 region Length:22 QPPPH- QPPPHP QPHQQQ QPPP-P *****</p> <p>Length: 5 residues - nb: 3 from 132 to 146 - Psim:0.7222222222222222 region Length:15 PPAT-- PPTSGA PPGSG- *****</p> <p>Length: 5 residues - nb: 4 from 161 to 177 - Psim:0.65 region Length:17 PPGA-</p>		
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	<p>PPPT- PPSSG VPTT- *****</p> <p>Length: 5 residues - nb: 4 from 205 to 223 - Psim:0.75 region Length:19 GG-PK- GG-KMP GG-PKP GGGPG- *****</p> <p>Length: 5 residues - nb: 5 from 218 to 242 - Psim:0.6571428571428571 region Length:25 -PGGG-- -PGLST- -PGGHP- KPP-HR- -GGGEPR *****</p> <p>Length: 5 residues - nb: 3 from 541 to 556 - Psim:0.6666666666666666 region Length:16 RRQEEL RRMEE- LHNQE- *****</p> <p>Length: 5 residues - nb: 3 from 670 to 685 - Psim:0.7777777777777778 region Length:16 GGAGPV GGQGP- RGMGP- *****</p> <p>Length: 6 residues - nb: 6 from 69 to 103 - Psim:0.6944444444444444 region Length:35 QQQPPP QQPPP- QQPPPH QPPPHP</p>		
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QPHQQQ
QPPPPP

Length: 6 residues - nb: 4 from 81 to 103 - Psim:0.75 region Length:23
QPPPH-
QPPPHP
QPHQQQ
QPPPPP

Length: 6 residues - nb: 3 from 123 to 141 - Psim:0.7083333333333334 region
Length:19
SAPPAS-S
SAPPAT--
--PPTSGA

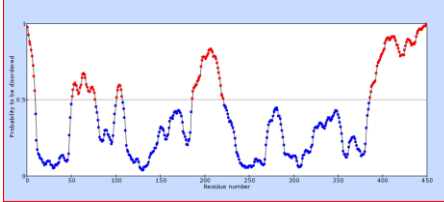
Length: 6 residues - nb: 3 from 209 to 224 - Psim:0.7222222222222222 region
Length:16
GG-KMP
GG-PKP
GGPGL

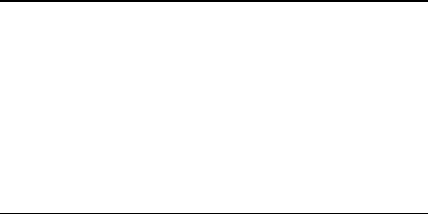
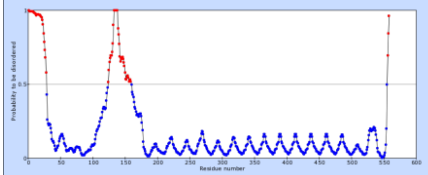
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Length:20
APGVGS-
APPASSS
APPATPP

Length: 8 residues - nb: 3 from 117 to 140 - Psim:0.6666666666666666 region
Length:24
PA-PGVGSAP
PA--S-SSAP
PATPPT-SG-

Length: 8 residues - nb: 3 from 198 to 223 - Psim:0.7777777777777778 region

		<p>Length:26 PKQGP G P G G PKGGKMPGG PKP G G G P G - *****</p> <p>Length: 8 residues - nb: 3 from 574 to 600 - Psim:0.7333333333333333 region Length:27 RE-EEMMIRQ REMEEQMRRQ RE-ESYS-RM *****</p>		
15	<p>Heterogeneous nuclear ribonucleoprotein A0, 1-305 AU-rich element binding poly(A) RNA binding RNA binding 89</p>	<p>>sp Q13151 ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 MENSQ LCKLFIGGLNVQTSSEGLRGHFEAFGTLTDCVVV VNPQTKRSRCFGFVTYSNVEEADAAMAASPHAVDGN TVE LKRAVSREDSARPGAHAKVKKL FVGG LKGDVAEGDLIEH FSQFGTVEKAEI IADKQSGKKRFGFVYFQNHDAADKAA VVKFHP IQGHRVEVKKAVPKEDIYSGGGGGSRSSRGGR GGRGRGGGRDQNGLSKGGGGYNSYGGYGGGGGGYNAY GGGGGSSYGGSDYGNFGGFGSYSQHSSYGPMKSGGG GGGGSSWGGRSNSGYPYRGQYGGGGYGGSSF</p> <p>UniProt Contains 2 RRM (RNA recognition motif) domains. 7-86 RRM1 98-175 RRM2 191-305 Gly-rich</p> <p><u>T-reks</u> Length: 6 residues - nb: 11 from 239 to 305 - Psim:0.6636363636363637 region Length:67 --GG-SS-Y- --GG-SDYG- -NGF-GGFG- SYSQ-HQ-S- SYGP-MK--- -SGG-GG-GG --GG-SS-W- --GGRSN-S- --GPYRG-G- -YGG-GG-G-</p>	<p>C-terminal, 206-305</p>	

		-YGG-SS-F-		
16	<p>Heterogeneous nuclear ribonucleoprotein H2, 1-449 nucleotide binding RNA binding 62</p>	<p>>sp P55795 HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 MMLSTEGREGFVVKVRGLPWSCSADEVMRFFSDCKIQNG TSGIRFIYTREGRPSGEAFVELESEEEVKKLALKKDRETM GHRYVEVFKSNVEMDWVLKHTGPNSPDTANDGFVRLRG LPFGCSKEEIVQFFSGLEIVPNGMTLPVDFQGRSTGEAF VQFASQEI AEKALKKKHKERIGHRYIEIFKSSRAEVRTHY DPPRKLAMQRPGPYDRPGAGRGYNSIGRGAGFERMRRG AYGGGYGGYDDYGGYNDGYGFGSDRFGRDLNYCFSGMSD HRYGDGSSSFQSTTGHCVHMRGLPYRATENDIYNFFSPL NPMRVHIEIGPDGRVTGEADVEFATHEDAVAAMAKDKAN MQHRYVELFLNSTAGTSGGAYDHSYVELFLNSTAGASGG AYGSMGGMGLSNQSSYGGPASQQLSGGYGGYGGQSS MSGYDQVLQENSDDYQSNLA UniProt Contains 3 RRM (RNA recognition motif) domains 11-90 RRM1 111-188 RRM2 289-364 RRM3</p> <p><u>T-reks</u> Length: 5 residues - nb: 4 from 236 to 254 - Psim:0.7083333333333334 region Length:19 YGGG-- YGGYDD YGGYN- -DGYG- *****</p> Length: 6 residues - nb: 3 from 240 to 258 - Psim:0.7619047619047619 region Length:19 YGGYDD- YGGYNDG YFGSD- ***** Length: 9 residues - nb: 2 from 235 to 252 - Psim:0.7083333333333334 region Length:18	<p>C-terminal, 382-449</p>	

		<p>AYGGGYGGYDD- -----YGGYNDG ***** Length: 20 residues - nb: 2 from 356 to 395 - Psim:0.9 region Length:40 YVELFLNSTAGTSSGGAYDHS YVELFLNSTAGASGGAYGSQ</p>		
17	Deleted in azoospermia protein 2, 1-558 nucleotide binding 1	<p>>sp Q13117 DAZ2_HUMAN Deleted in azoospermia protein 2 OS=Homo sapiens GN=DAZ2 PE=1 SV=3 MSAANPETPNSTISREASTQSSSAAASQGWWLPEGKIVP NTVFGGIDARMDETEIGSCFGRYGSVKEVKIITNRTGV SKGYGFVSVFVNDVDVQKIVGSQIHFGKKLKLGPAIRKQ KLCARHVQPRPLVVNPPPPQFQNVWRNPNTETYLQPOI TPNPVTQHVQAYSAYPHSPGQVITGCQLLVYNYQEYPTY PDSAFQVTTGYQLPVYNYQPFPAIPRSPPFQVTAGYQLPV YNYQAFPAYPNSPFQVATGYQFPVYNYQFPFAYPSSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQFPVYNYQAF PAYPNSPFVQVTTGYQLPVYNYQAFPAYPNSPFVQVTTGYQ LPVYNYQAFPAYPSSPFQVTTGYQLPVYNYQAFPAYPSS PFQVTTGYQLPVYNYQAFPAYPSSPFQVTTGYQLPVYNY QAFPAYPSSPFQVTTGYQLPVYNYQAFPAYPSSPFQVTT GYQLPVYNYQAFPAYPSSPFQVTTGYQLPVYNYQAFPAY PNSAVQVTTGYQFHVYNYQMPPQCPVGEQRRNLWTEAYK WWYLVCLIQRRD UniProt The DAZ-like repeats are essential and mediate the interaction with DAZAP1 and DAZAP2. Contains 15 DAZ-like domains [AYPHSPGQVITGCQLLVYNYQ] Contains 1 RRM (RNA recognition motif) domain 40-115 RRM1</p> <p>MSAANPETPNSTISREASTQSSSAAASQGWWLPEGKIVP NTVFGGIDARMDETEIGSCFGRYGSVKEVKIITNRTGV SKGYGFVSVFVNDVDVQKIVGSQIHFGKKLKLGPAIRKQ KLCARHVQPRPLVVNPPPPQFQNVWRNPNTETYLQPOI TPNPVTQHVQAYSAYPHSPGQVITGCQLLVYNYQEYPTY PDSAFQVTTGYQLPVYNYQPFPAIPRSPPFQVTAGYQLPV YNYQAFPAYPNSPFQVATGYQFPVYNYQFPFAYPSSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQFPVYNYQAF PAYPNSPFVQVTTGYQLPVYNYQAFPAYPNSPFVQVTTGYQ LPVYNYQAFPAYPSSPFQVTTGYQLPVYNYQAFPAYPSS PFQVTTGYQLPVYNYQAFPAYPSSPFQVTTGYQLPVYNY QAFPAYPSSPFQVTTGYQLPVYNYQAFPAYPSSPFQVTT</p>	C-terminal, 211-410	

		<p>GYQLPVYNYQAFPAYPSSPFQVTTGYQLPVYNYQAFPAY PNSAVQVTTGYQFHVYNYQMPPQCPVGEQRRNLWTEAYK WWYLVCLIQRD</p> <p>T-reks Length: 21 residues - nb: 15 from 177 to 533 - Psim:0.902777777777778 region Length:357 QVITGCQLLVYNYQEYPTYPSAF QVTTGYQLPVYNYQFPAYPRSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQFPAYPSSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPNSAV QVTTGYQFHVYNYQ-MP--PQCPV</p>		
18	<p>RNA binding motif protein 14, 1-669 ligand- dependent nuclear receptor transcription coactivator activity nucleotide binding protein binding, bridging RNA polymerase II</p>	<p>>sp Q96PK6 RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 MKIFVGNVDGADTTPEELAALFAPYGTVMSCAVMKQFAF VHMRENAGALRAIEALHGHELRLPGRALVVEMSRPRPLNT WKIFVGNVSAACTSQELRSLFERRGRVIECDVVKDYAFV HMEKEADAKAAIAQLNGKEVKGKRINVELSTKGQKKGPG LAVQSGDKTKKPGAGDTAFPGTGGFSATFDYQQAAGNST GGFDGQARQPTPPFFGRDRSPLRRSPPRASYVAPLTAQP ATYRAQPSVSLGAA YRAQPSASLGVGYRTQPMTAQAASY RAQPSVSLGAPYRGQLASPSSQSAASLGPYGAQPSA SALSSYGGQAAAASSLNS YGAQSSLAS YGNQPSYGAQ AASSYGVRAAASSYNTQGAASSLGSYGAQAASYGAQSAA SSLAYGAQAASYNAPSA SYNAPSA YAAQQAASYSQF AAYVAQPATAAAYASQPAAYAAQATTPMAGSYGAQPVVQ TQLNSYGAQASMLSGSYGAQSAAAAATGSYGAAAAAYGAQ PSATLAAPYRTQSSASLAASYAAQHPQAAAASYRGQPGN AYDGAGQPSAAYLSMSQGANANANSTPPPYERTRLSPPR ASYDDPYKKAVAMSKRYGSDRRLAELSDYRRLSESQLSF RRSPTKSSLDYRRLPDAHSDYARYSGSYNDYLRAAQMHS GYQRRM UniProt</p>	<p>Middle , 264-576</p>	

<p>transcription cofactor activity 95</p>	<p>Contains 2 RRM (RNA recognition motif) domains 1-73 RRM1 79-149 RRM2 224-569 Ala-rich</p> <p><u>T-reks</u> Length: 8 residues - nb: 3 from 346 to 371 - Psim:0.777777777777778 region Length:26 SSYGAQAA- SSYGVRAAA SSYNTQGAA ***** Length: 8 residues - nb: 5 from 378 to 416 - Psim:0.7 region Length:39 ---GAQAAS--Y ---GAQSAASS- LAYGAQAA---- -SYNAQPSA--- -SYNAQSAP--- ***** Length: 8 residues - nb: 3 from 397 to 418 - Psim:0.75 region Length:22 -AQAASYN AQPSASYN -AQSAPYA ***** Length: 8 residues - nb: 4 from 422 to 454 - Psim:0.725 region Length:33 AASYSSQP-- -AAYVAQPAT AAAYASQP-- -AAYAAQAT- ***** Length: 8 residues - nb: 2 from 436 to 453 - Psim:0.7727272727272727 region Length:18 PATAAAYASQ- P---AAYAAQA ***** Length: 8 residues - nb: 2 from 604 to 619 - Psim:0.8333333333333334 region Length:16 SD-RRLAEL</p>		
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SDYRRLSE-
*****
Length: 9 residues - nb: 5 from 346
to 389 - Psim:0.7333333333333333 region
Length:44
---SSYGAQAA-
---SSYGVRAAA
---SSYNTQGAA
SSLGSYGAQ---
--AASYGAQSA-
*****
Length: 9 residues - nb: 5 from 346
to 389 - Psim:0.7333333333333333 region
Length:44
---SSYGAQAA-
---SSYGVRAAA
---SSYNTQGAA
SSLGSYGAQ---
--AASYGAQSA-
*****
Length: 9 residues - nb: 6 from 362
to 416 - Psim:0.7307692307692307 region
Length:55
AS---SYNTQGA-
ASSLGSYGAQA--
A----SYGAQSA-
ASSL-AYGAQA--
A----SYNAQPS-
A----SYNAQSAP
*****
Length: 9 residues - nb: 3 from 378
to 404 - Psim:0.7272727272727273 region
Length:27
GAQAASY----
GAQSAASSLAY
GAQAASYNA--
*****
Length: 9 residues - nb: 3 from 397
to 418 - Psim:0.75 region Length:22
-AQAASYN
AQPSASYN
-AQSAPYA
*****
Length: 9 residues - nb: 4 from 422
to 455 - Psim:0.7 region Length:34
AASYSSQP--

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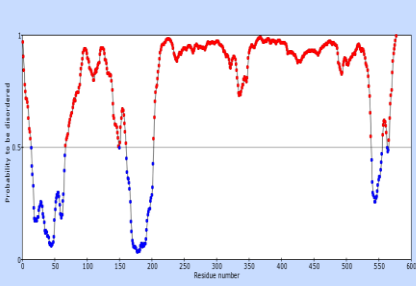
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AAAYASQP--
-AAYAAQATT
*****
Length: 9 residues - nb: 2 from 436
to 454 - Psim:0.75 region Length:19
PATAAAYASQ
PAAAYAAQAT-
*****
Length: 10 residues - nb: 4 from 237
to 284 - Psim:0.7708333333333334 region
Length:48
YRAQPSVSLGAA
YRAQPSASLGVG
YRTQPMTAQAAS
YRAQPSVSLGAP
*****
Length: 10 residues - nb: 4 from 346
to 381 - Psim:0.7 region Length:36
SSYGAQAA--
SSYGVRAAAA-
SSYNTQGAA-
SSLGSYGAQA
*****
Length: 10 residues - nb: 2 from 348
to 365 - Psim:0.75 region Length:18
YGAQAASS--
YGVRAAASSY
*****
Length: 10 residues - nb: 2 from 363
to 381 - Psim:0.7 region Length:19
SSYNTQGAA-
SSLGSYGAQA
*****
Length: 10 residues - nb: 2 from 384
to 404 - Psim:0.7272727272727273 region
Length:21
YGAQSAASSLA
YGAQAASYN-
*****
Length: 10 residues - nb: 3 from 430
to 456 - Psim:0.7575757575757576 region
Length:27
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AAAYASQP---
-AAYAAQATTP

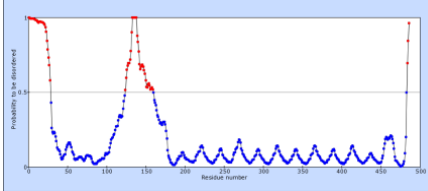
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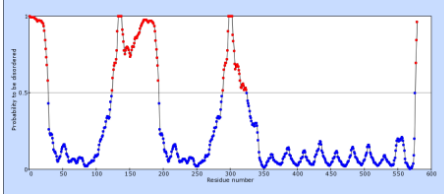
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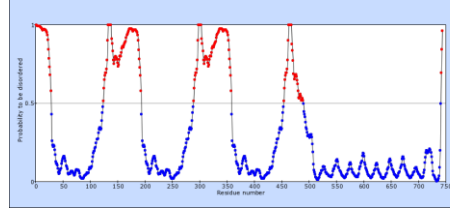
*****
Length: 10 residues - nb: 2 from 474
to 497 - Psim:0.75 region Length:24
YGAQASMGLSGS
YGAQSAAAATGS
*****
Length: 11 residues - nb: 4 from 237
to 284 - Psim:0.7708333333333334 region
Length:48
YRAQPSVSLGAA
YRAQPSASLGVG
YRTQPMTAQAAS
YRAQPSVSLGAP
*****
Length: 11 residues - nb: 2 from 331
to 351 - Psim:0.7272727272727273 region
Length:21
YGAQGSSLAS-
YGNQPSSYGAQ
*****
Length: 11 residues - nb: 4 from 353
to 392 - Psim:0.7166666666666667 region
Length:40
---ASSYGVRAA---
---ASSYNTQGA---
ASSLGSYGAQA----
----ASYGAQSAASS
*****
Length: 11 residues - nb: 2 from 384
to 405 - Psim:0.7272727272727273 region
Length:22
YGAQSAASSLA
YGAQAASYNAQ
*****
Length: 11 residues - nb: 3 from 473
to 507 - Psim:0.7222222222222222 region
Length:35
SYGAQASMGLSG
SYGAQSAAAATG
SYGAAAAYGAQ-
*****
Length: 12 residues - nb: 4 from 237
to 284 - Psim:0.7708333333333334 region
Length:48
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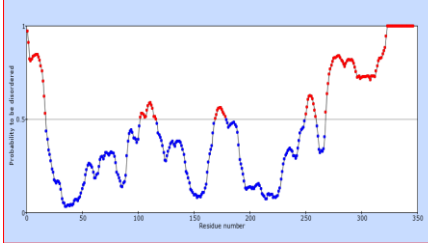
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		<p>YRTQPMTAQAAS YRAQPSVSLGAP ***** Length: 12 residues - nb: 2 from 305 to 330 - Psim:0.7692307692307693 region Length:26 YGGAQPSASALSS YGGQAAAASSLNS ***** Length: 12 residues - nb: 3 from 473 to 508 - Psim:0.7222222222222222 region Length:36 SYGAQASMGLSG SYGAQSAAAATG SYGAAAAYGAQP</p>		
19	<p>Cleavage stimulation factor 64 kDa subunit, 1-577 nucleotide binding RNA binding 54</p>	<p>sp P33240 CSTF2_HUMAN Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1 MAGLTVRDPVDRSLRSVVFVGNIPYEATEEQLKDIFSEV GPVVSFRLVYDRETGKPKGYGFCEYQDQETALSAMRNLN GREFSGRALRVDNAASEKNKEELKSLGTGAPVIESPYGE TISPEDAPESISKAVASLPPEQMFELMKQMKLCVQNSPQ EARNMLLQNPQLAYALLQAQVVMRIVDPEIALKILHRQT NIPTLIAGNPQPVHGAGPGSGSNVSMNQNPQAQASL GGMHVNGAPPLMQASMQGGVPAPGQMPAAVTGPGPGSLA PGGGMQAQVGMFPGSPVSMERGOVPMQDPRAAMQRGSLP ANVPTPRGLLGDAPNDPRGGTLLSVTGEVEPRGYLGPPH QGPPMHHVPGHESRGGPPHELRRGGPLPEPRPLMAEPRGP MLDQRGPPLDGRGGRDPRGIDARGMEARAMEARGLDARG LEARAMEARAMEARAMEARAMEARAMEVRGMEARGMDTR GPVPGPRGPIPSGMQGPSPINMGAVVPQGSRQVPVMQGT GMOGASIQGGSQPGGFSPGQNVTPQDHEKAALIMQVLQ LTADQIAMLPPPEQRQSILILKEQIQKSTGAP UniProt Contains 1 RRM (RNA recognition motif) domain 16-94 RRM 198-409 Gly/Pro-rich 470-526 Gly/Pro-rich 12 X 5 AA tandem repeats of M-E-A-R-[AG] <u>T-reks</u> Length: 5 residues - nb: 9 from 416 to 460 - Psim:0.8444444444444444 region Length:45</p>	Middle, 203-288	

		<p>EARAM EARGL DARGL EARAM EARAM EARAM EARAM EARAM EVRGM Length: 6 residues - nb: 6 from 435 to 465 - Psim:0.8888888888888888 region Length:31 MEARA- MEARA- MEARA- MEARA- MEVRG- MEARGM ***** Length: 6 residues - nb: 4 from 443 to 464 - Psim:0.7857142857142857 region Length:22 RAMEA-- RAMEA-- RAMEVR- -GMEARG *****</p>		
20	Deleted in azoospermia protein 3, 1-486 nucleotide binding 1	<p>>sp Q9NR90 DAZ3_HUMAN Deleted in azoospermia protein 3 OS=Homo sapiens GN=DAZ3 PE=1 SV=1 MSAANPETPNSTISREASTQSSSAAASQGWWLPEGKIVP NTVFGGIDARMDETEIGSCFGRYGSVKEVKIITNRTGV SKGYGFVSFVNDVDVQKIVGSOIHFHGKKLKLGP AIRKQ KLCARHVQPRPLVWNPPPPQFQNVWRNPNTETYLQPOI TPNPVTQHVQAYSAYPHSPGQVITGCQLLVYNYQEYPTY PDSAFQVTTGYQLPVYNYQFPAYPRSPFQVITAGYQLPV YNYQAFPAYPNSPFQVATGYQFPVYNYQFPAYPSSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQFPVYNYQAF PAYPNSPVQVTTGYQLPVYNYQAFPAYPNSPFQVATGYQ FPVYNYQAFPAYPNSPVQVTTGYQLPVYNYQAFPAYPNS PFQVATGYQFPVYNYQAFPAYPNSPVQVTTGYQLPVYNY QAFPAYPNSAVQVTTGYQFHVYNYQMPPOCPVGEQRRNL WTEAYKWWYLVCLIQRRD UniProt: 12 DAZ-like domains AYPHSPGQVITGCQLLVYNYQ</p>	C-terminal, 211-410	

		<p>1 RRM (RNA recognition motif) domain</p> <p>T-reks Length: 21 residues - nb: 12 from 177 to 461 - Psim:0.875 region Length:285 QVITGCQLLVYNYQEYPTYPDSAF QVTTGYQLPVYNYQFPAYPRSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQFPAYPSSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPNSAV QVTTGYQFHVYNYQ-MP--PQCPV</p>		
21	Deleted in azoospermia protein 4, nucleotide binding 1-579 1	>sp Q86SG3 DAZ4_HUMAN Deleted in azoospermia protein 4 OS=Homo sapiens GN=DAZ4 PE=1 SV=2 MSAANPETPNSTISREASTQSSSAAASQGWVLPPEGKIVP NTVFGGIDARMDETEIGSCFGRYGSVKEVKIITNRTGV SKGYGFVSFVNDVDVQKIVGSQIHFGKCLKLGP AIRKQ KLCARHVQPRPLVVNPPPPQFQNVWRNPNTETYLQPQI TPNPVTQHVQSAANPETPNSTISREASTQSSSAAASQGW VLPPEGKIVPNTVFGGIDARMDETEIGSCFGRYGSVKEV KIITNRTGVSKGYGFVSFVNDVDVQKIVGSQIHFGKCLKL KLGPAIRKQKLCARHVQPRPLVVNPPPPQFQNVWRNP TETYLQPQITPNPVTQHVQAYSAYPHSPGQVITGCQLLV YNYQEYPTYPDSAFQVTTGYQLPVYNYQFPAYPRSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQFPVYNYQPF PAYPSSPFQVATGYQLPVYNYQAFPAYPNSPFQVATGYQ FPVYNYQAFPAYPNSPVQVTTGYQLPVYNYQAFPAYPSS PFQVTTGYQLPVYNYQAFPAYPNSAVQVTTGYQFHVYNY QMPFPQCPVGEQRRNLWTEAYKWWYLVLCLIQRD UniProt 2 RRM (RNA recognition motif) domains 40-115 RRM1 205-280 RRM2 UniProt 9 DAZ-like domains AYPHSPGQVITGCQLLVYNYQ 335-355; 359- MSAANPETPNSTISREASTQSSSAAASQGWVLPPEGKIVP NTVFGGIDARMDETEIGSCFGRYGSVKEVKIITNRTGV SKGYGFVSFVNDVDVQKIVGSQIHFGKCLKLGP AIRKQ	C-terminal, 211-382	

		<p> KLCARHVQPRPLVVNPPPPQFQNVWRNPNTETYLQPOI TPNPVTQHVQSAANPETPNSTISREASTQSSSAAASQGW VLPEGKIVPNTVFVGGIDARMDETEIGSCFGRYGSVKEV KIITNRTGVSKGYGFVSFVNDVDVQKIVGSQIHFHGKKL KLGPAIRKQKLCARHVQPRPLVVNPPPPQFQNVWRNP TETYLQPOITPNPVTQHVQAYSAYPHSPGQVITGCQLLV YNYQEYPTYPDSAFQVTTGYQLPVYNYQFPAYPRSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQFPVYNYQFPAYPSSPFQ VTAGYQLPVYNYQAFPAYPNSPFQVATGYQ FPVYNYQAFPAYPNSPVQVTTGYQLPVYNYQAFPAYPSS PFQVTTGYQLPVYNYQAFPAYPNSAVQVTTGYQFHVYNY QMPPQCFVGEQRRNLWTEAYKWWYLLVCLIQRRD </p> <p>T-reks</p> <p>Length: 21 residues - nb: 9 from 342 to 554 - Psim:0.8564814814814815 region Length:213</p> <p> QVITGCQLLVYNYQEYPTYPSAF QVTTGYQLPVYNYQFPAYPRSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQFPAYPSSPF QVTAGYQLPVYNYQAFPAYPNSPF QVATGYQFPVYNYQAFPAYPNSPV QVTTGYQLPVYNYQAFPAYPSSPF QVTTGYQLPVYNYQAFPAYPNSAV QVTTGYQFHVYNYQ-MP--PQCFV </p>	
22	Deleted in azoospermia protein 1, 1-744 nucleotide binding translation activator activity 11	>sp Q9NQZ3 DAZ1_HUMAN Deleted in azoospermia protein 1 OS=Homo sapiens GN=DAZ1 PE=1 SV=2 MSA ANPETPNSTISREASTQSSSAAASQGW VLPEGKIVP NTV FVGGIDARMD ETEIGSCFGRYGSVKEV KIITNRTGV SKGYGFV SFVNDVDVQKIVGSQIHFHGKKL KLGPAIRKQ KLCARHVQPRPLVVN PPPPQ FQNVWRNPNTETYLQPOI TPNPVTQHVQSA ANPETPNSTISREASTQSSSAAASQGW VLPEGKIVPNTV FVGGIDARMD ETEIGSCFGRYGSVKEV KIITNRTGVSKGYGFV SFVNDVDVQKIVGSQIHFHGKKL KLGPAIRKQKLCARHVQPRPLVVN PPPPQ FQNVWRNP TETYLQPOITPNPVTQHVQSA ANPETPNSTISREASTQ SSAAASQGW VLPEGKIVPNTV FVGGIDARMD ETEIGSCF GRYGSVKEV KIITNRTGVSKGYGFV SFVNDVDVQKIVGS QIHFHGKKL KLGPAIRKQKLCARHVQPRPLVVN PPPPQ FQNVWRNPNTETYLQPOITPNPVTQHVQAY SAYPHSPGQ VITGCQLLV YNYQEYPTYPSAFQVTTGYQLP VYNYQFP PAYPRSPFQ VTAGYQLP VYNYQAF PAYPNSPFQ VATGYQ	C-terminal, 541-716 

		<p>FFVYNYQFFPAYPSSPFQVVTAGYQLFVYNYQAFPAYPNS PFQVATGYQFFVYNYQAFPAYPNSPVQVTTGYQLFVYNY QAFPAYPSSPFQVTTGYQLFVYNYQAFPAYPNSAVQVTT GYQFHVYNYQMPPQCPVGEQRRNLWTEAYKWWYLVCLIQ RRD</p> <p><u>UniProt</u> 9 DAZ-like domains. AYPHSPGQVITGCQLLVYNYQ 500-520; 524-544 3 RRM (RNA recognition motif) domains 40-115 RRM1 205-280 RRM2 370-445 RRM3</p> <p><u>T-reks</u> Length: 24 residues - nb: 9 from 516 to 731 - Psim:0.8240740740740741 region Length:216 VYNYQEYPTYPDSAFQVTTGYQLP VYNYQFFPAYPRSPFQVVTAGYQLP VYNYQAFPAYPNSPFQVATGYQFF VYNYQFFPAYPSSPFQVVTAGYQLP VYNYQAFPAYPNSPFQVATGYQFF VYNYQAFPAYPNSPVQVTTGYQLP VYNYQAFPAYPSSPFQVTTGYQLP VYNYQAFPAYPNSAVQVTTGYQFH VYNYQMPPQCPVGEQRRNLWTEAY</p>		
23	<p>Heterogeneous nuclear ribonucleoprotein H3, 1-346 nucleotide binding RNA binding 68</p>	<p>>sp P31942 HNRH3_HUMAN Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 MDWVMKHNGPNDASDGTVRLRGLPFGCSKEEIVQFFQGL EIVPNGITLTMDYQGRSTGEAFVQFASKEIAENALGKHK ERIGHRYIEIFRSSRSEIKGFYDPPRLLGQRPGPYDRP I GGRRGYYGAGRGSMDRMRRGGDGYDGGYGGFDDYGGY NNYGYGNDGFDDRMRDGRGMGGHGYGGAGDASSGFHGGH FVHMRGLPFRATENDIANFFSPLNPIRVHIDIGADGRAT GEADVEFVTHEDAVAAMSKDKNNMQHRYIELFLNSTPGG GSGMGGSGMGGYGRDGMDNQGGYGSVGRMGMGNNYSSGGY GTPDGLGGYGRGGGGSGGYYGQGGMSSGGWRRGMY</p> <p><u>UniProt</u> Contains 2 RRM (RNA recognition motif) domains 16-93 RRM1 195-270 RRM2 108-344 Gly-rich</p>	<p>C-terminal, 268-346</p>	

T-reks

Length: 3 residues - nb: 8 from 319
to 341 - Psim:0.71875 region Length:23

GGY-

GR--

GG--

GGs-

GGY-

YGQ-

GGMS

GGG-

Length: 5 residues - nb: 5 from 139
to 164 - Psim:0.65 region Length:26

-G-GDGYD

-GGY-GG-

FD-DYG--

-G-Y-NNY

-G-Y-GND

Length: 5 residues - nb: 3 from 272
to 287 - Psim:0.8333333333333334 region

Length:16

GGGSGM

GG-SGM

GG-YGR

Length: 6 residues - nb: 3 from 147
to 164 - Psim:0.75 region Length:18

YG--GFDD

YGGY--NN

YG-YG-ND

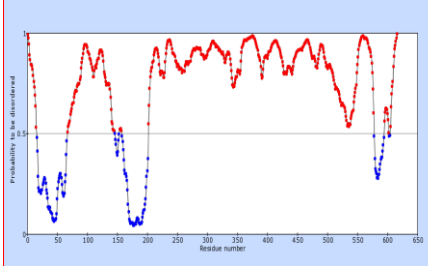
Length: 6 residues - nb: 3 from 272
to 288 - Psim:0.8095238095238095 region

Length:17

GGGSGM-

GG-SGM-

GG-YGRD

		<p>Length: 8 residues - nb: 2 from 146 to 162 - Psim:0.7222222222222222 region Length:17 GYGGFDDYG GYNNYG-YG *****</p> <p>Length: 9 residues - nb: 2 from 281 to 297 - Psim:0.7727272727272727 region Length:17 GM--GGYGRD GMDNQGGYG--</p>		
24	<p>Cleavage stimulation factor subunit 2 tau variant, 1-616 nucleotide binding 8</p>	<p>>sp Q9H0L4 CSTFT_HUMAN Cleavage stimulation factor subunit 2 tau variant OS=Homo sapiens GN=CSTF2T PE=1 SV=1 MSSLAVRDPAMDRSLRSVVFVGNIPYEATEEQLKDIFSEV GSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAMRNLN GREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGD PIDPEDAPESITRAVASLPPEQMFMKQMKLCVQNSHQ EARNMLLQNPQLAYALLQAQVVMRIMDPEIALKILHRKI HVTPLIIPGKSQSVSVSGPVPGLCPGPNVLLNQNP PAPQPQHLARRPVKDI PPLMQTPIQGGIPAPGPIPAAVP GAGPGSLTPGGAMQPQLGMPGVGPVPLERGVQMSDRA PIPRGPVTPGGLPPRGLLDAPNDPRGGTLLSVTGEVEP RGLYLGPPHQGPPMHASGHDTRGPSSHEMRGGPLGDPRL LIGEPKPMIDQRLPMDGRGRDRSRAMETRAMETEVL TRVMERRGMETCAMETRGMEARGMDARGLEMVGPVSSR GPMTGGIQQGPGPINIGAGGPPQGPVPGISGVGNPGAG MQGTGIQGTGMQAGIQGGGMQAGIQGVSIQGGGIQGG GIQGASKQGGSQPSSFSFGQSQVTPQDQEKAALIMQVLQ LTADQIAMLPPPEQRQSILILKEQIQKSTGAS UniProt 9 X 5 AA tandem repeats of M-E-T-R-[AG] 9 X 5 AA tandem repeats of G-[AT]-G-[MI]-Q GPMTGGIQQGPGPINIGAGGPPQGPVPGISGVGNPGAG MQGTGIQGTGMQAGIQGGGMQAGIQGVSIQGGGIQGG GIQGASKQGGSQPSSFSFGQSQVTPQDQEKAALIMQVLQ LTADQIAMLPPPEQRQSILILKEQIQKSTGAS 16-94 RRM</p> <p><u>T-reks</u> Length: 4 residues - nb: 10 from 509 to 557 - Psim:0.74 region Length:49</p>	<p>C-terminal, 476-568 infertility phenotyp e</p>	

		<p>QGTGI QGTGM QGAGI QGGGM QGAGI QGVSI QGGGI QGGGI QGASK QGS-</p>		
25	<p>CUGBP Elav-like family member 4, BRE binding nucleotide binding translation repressor activity, nucleic acid binding 1-486 2</p>	<p>>sp Q9BZC1 CELF4_HUMAN CUGBP Elav-like family member 4 OS=Homo sapiens GN=CELF4 PE=1 SV=1 MYIKMATLANGQADNASLSTNGLGSSPGSAGHMNGLSHS PGNPSTIPMKDHDAIKLFIGQIPRNLDEKDLKPLFEEFG KIYELTVLKDRFTGMHKGCAFLTYCERESALKAQSALHE OKTLPGMNRPIQVKPADSESRGGSSCLRQPPSQDRKLFV GMLNKQSEDDVRRRLF EAFGNIEECTILRGPDGNSKGC FVKYSSHAEAQAAINALHGSQTMPGASSSLVVKFADTDK ERTMRRMQMAGQMGMFNPMAIPFGAYGAYAQALMQQA ALMASVAQGGYLNMAAFAAAQMQQMAALNMNGLAAAPM TPTSGGSTPPGITAPAVPSIPSEIGVNGFTGLPPQANGQ PAAEAVFANGIHPYPAQSPTAADPLQQAYAGVQQYAGPA AYPAAYGQISQAFPPPPMIPQQQREGPEGCNLFYHLP QEFGDAELMQMFLPFGFVSDNPASAQTAIQAMNGFQIG MKRLKVQLKRPKDANRPY UniProt Contains 3 RRM (RNA recognition motif) domains RRM 1 54-135 RRM2 152-232 RRM3 404-479 260-310 Ala-rich <u>T-reks</u> Length: 7 residues - nb: 2 from 377 to 390 - Psim:0.75 region Length:14 QQAYAGV- -QQYAGPA</p>	<p>Middle, 241-305</p>	

789-835 Coiled coil

113-263-Glu-rich

306-659 Pro-rich

605-641 His-rich

T-reks

>sp|Q96EV2|RBM33_HUMAN RNA-binding
protein 33 OS=Homo sapiens GN=RBM33
PE=1 SV=3

Length: 4 residues - nb: 13 from 581
to 633 - Psim:0.7692307692307693 region

Length:53

-P-LH--P

-P--L-PP

-P--H-QP

QP-----Q-

QP--Q-Q-

QP-----PP

-Q--H-QP

-P--H-QP

-P--H-QP

-PPQH-Q-

-P--PPQH

-P--P-QH

-P--P-QH

Length: 4 residues - nb: 10 from 595
to 633 - Psim:0.7571428571428571 region

Length:39

-Q--QP-

-QQ-QP-

-PP-QH-

-QP-PH-

-QP-PH-

QPP-P--

----QHQ

-PPPQH-

-PP-QH-

-PP-QH-

Length: 4 residues - nb: 7 from 607
to 634 - Psim:0.6785714285714286 region

Length:28

PPHQ
PPHQ
PPPQ
HQPP
PQHP
PQHP
PQHQ

Length: 4 residues - nb: 4 from 624
to 639 - Psim:0.6875 region Length:16

QHPP
QHPP
QHQH
HHHH

Length: 5 residues - nb: 3 from 367
to 382 - Psim:0.6666666666666666 region

Length:16

TPR-MMM
TPP-PV-
TPQQP--

Length: 5 residues - nb: 7 from 596
to 629 - Psim:0.7857142857142857 region

Length:34

QP--QQ
QPPPQH
QPP--H
QPP--H
QPPPQH
QPPPQ-
HPP-QH

Length: 5 residues - nb: 5 from 606
to 629 - Psim:0.8 region Length:24

QPP--H
QPP--H
QPPPQH
QPPPQ-
HPP-QH

Length: 5 residues - nb: 3 from 614
to 629 - Psim:0.8333333333333334 region

Length:16

QPPPQH

QPPPQ-

HPP-QH

Length: 5 residues - nb: 4 from 624
to 641 - Psim:0.65 region Length:18

QHPP-

QHPP-

QHQQH

HHHHH

Length: 6 residues - nb: 6 from 597
to 631 - Psim:0.7222222222222222 region

Length:35

-PQ-QQ-PP

-P--QHQP

HQP-PH-Q-

-PPPQH-Q-

-PPPQH---

-PP-QH-PP

Length: 6 residues - nb: 3 from 615
to 631 - Psim:0.8095238095238095 region

Length:17

PPPQHQ-

PPPQH--

PP-QHPP

Length: 6 residues - nb: 3 from 1006
to 1024 - Psim:0.6666666666666666
region Length:19

QPQRL-P

QPPEVGP

QPARK-V

28 DAZ associated protein 1, 1-407, nucleotide binding RNA binding 21

```
>sp|Q96EP5|DAZP1_HUMAN DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1 PE=1 SV=1
MNNNGADEIGKLFVGGLDWSTTQETLRSYFSQYGEVVDV
VIMKDKTTNQSRGFGFVKFKDPNCVGTVLASRPHTLDGR
NIDPKPCTPRGMQPERTRPKEGWQKGRSDNSKSNKIFV
GGIPHNCGETELREYFKKFGVVTEVVMIIYDAEKQRPRGF
GFITFEDEQSVDDQAVNMHFHDIMGKKVEVKRAEPRDSKS
QAPGQPGASQWGSRVVFNAAANGWAGQPPPTWQQGYGPQG
MWPVAGQAIIGGYGPPPAGRGAPPPPPPTTSYIVSTPPGG
FPPQGFPPQGYGAPPQFSFGYGGPPPPPDQFAPPGVPPP
LATPGAAPLAFPPPPSQAAPDMSKPPTAQPDPFYGOYAG
YGDLSGFQGFSDPSQQPPSYGGPSVPGSGGPPAGGSG
FGRGQNHNVQGFHPYRR
```

UniProt

Contains 2 RRM (RNA recognition motif) domains
 10-97 RRM1
 113-190 RRM2
 222-385 Pro-rich

T-reks

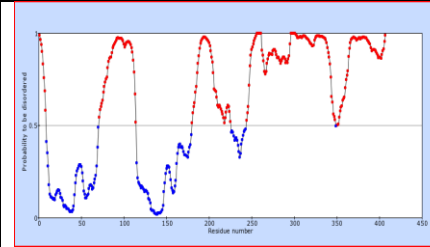
```
Length: 5 residues - nb: 3 from 300 to 314 - Psim:0.7142857142857143 region
Length:15
-PPDQFA
-PPG--V
PPPP--A
*****

Length: 6 residues - nb: 3 from 270 to 286 - Psim:0.75 region Length:17
-PPGGF--
PPPQGF--
--PQGYGA
*****

Length: 7 residues - nb: 2 from 374 to 388 - Psim:0.75 region Length:15
GGPSVPGS
GGPPAGG-
*****

Length: 8 residues - nb: 2 from 281 to 295 - Psim:0.75 region Length:15
PQ---GYGAP
PQFSFGYG--
```

C-terminal, 346-407



<p>29 Paraspeckle component 1, 1-523 core promoter binding poly(A) RNA binding 18</p>	<pre>>sp Q8WXF1 PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1 MMLRGNLQVRIEKNPARLRALESVAGESEPAAMAL ALAGEPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGKTY TQRCRLFVGNLPTDITEEDFKRLFERYGEPSEVFINRDR GFGFIRLESRTLAEIAKAELDGTILKSRPLRIRFATHGA ALTVKNLSPVVSNELLEQAFSQFGPVEKAVVVVDDRGRA TGKGFVEFAAKPPARKALERCQDGAFLLLTTTPRPVIVEP MEQFDDDEDGLPEKLMQKTQQYHKEREQPPRFAQPGTFEF EYASRWKALDEMEKQQREQVDRNIREAKEKLEAEMEAAAR HEHQMLMRQDLMRROEELRRLEELRNQELQKRKQIQLR EEEEHRRREEEMIRHREQEELRRQEGFKPNYEMENREQE MRMGDMGPRGAINMGDAFSPAPAGNQGPPPMGMNMR ATIPGPPMGPGPAMGPEGAANMGTMPMPDNGAVHNDRFP QGPPSQMGSPMGSRTGSETPOAPMSGVGPVSGGPGGFGR GSQGGNFEGPNKRRRY UniProt Contains 2 RRM (RNA recognition motif) domains 82-154 – RRM1 156-237 – RRM2 283-377- Coiled coil 394-516 - Gly-rich T-reks Length: 5 residues - nb: 3 from 399 to 413 - Psim:0.6666666666666666 region Length:15 L-MRQD L-MRRQ EELRR- ***** Length: 5 residues - nb: 3 from 410 to 425 - Psim:0.6666666666666666 region Length:16 ELRRLE ELRN-Q ELQK-R ***** Length: 5 residues - nb: 5 from 556 to 578 - Psim:0.6571428571428571 region Length:23 -GS-PM- -GS-RT-</pre>	<p>C-terminal, 414-523</p>	
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		<pre> -GS-ETP -QA-PM- SGVGP-V ***** Length: 6 residues - nb: 3 from 399 to 415 - Psim:0.6666666666666666 region Length:17 -LMRQD LMRRQE ELRRLE ***** Length: 8 residues - nb: 2 from 406 to 419 - Psim:0.8125 region Length:14 RRQEEL-- RRLEELRN ***** </pre>		
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Inclusion body myopathy with early-onset Paget disease with or without frontotemporal dementia 3 (IBMPFD3)

Amyotrophic lateral sclerosis (ALS)