

>ENSG00000149187
UUGUG
|||||
UGUGUG
distance: 1

>ENSG00000149187
UUGUU
|||||
UGUGU
distance: 2

>ENSG00000149187
UGUU
|||||
UGUGU
distance: 1

>ENSG00000149187
UGUGUG
|||||
UGUGUG
distance: 0

>ENSG00000149187
UGUUU
|||||
UGUGU
distance: 1

>ENSG00000161547
UCCAGU
||||||
UCGAGAU
distance: 1

>ENSG00000161547
UGGAGU
||||||
UGGAGAU
distance: 1

>ENSG00000011304
UCUCU
|||||
UCUCU
distance: 0

>ENSG00000011304
CUCUCU
|||||
CUCUCU
distance: 0

>ENSG00000011304

CUCU

||||

CUCU

distance: 0

>ENSG00000197111

CCCUAA

|||||||

CCCUUAAA

distance: 1

>ENSG00000197111

CCCU

|||||

CCAUUC

distance: 1

>FBGN0264270 see Hennig,J., Militti,C., Popowicz,G.M., Wang,I.,
Sonntag,M., Geerlof,A., Gabel,F., Gebauer,F. and Sattler,M. (2014)
Structural basis for the assembly of the Sxl-Unr translation regulatory
complex. Nature, 515, 287-290. (see figure 2f)

GUGA

|||||||

UUUUUUU

distance: 6

>FBGN0264270

UGUUUUUUUU

|||||||

UUUUUUUU

distance: 0

>FBGN0264270 see Hennig,J., Militti,C., Popowicz,G.M., Wang,I.,
Sonntag,M., Geerlof,A., Gabel,F., Gebauer,F. and Sattler,M. (2014)
Structural basis for the assembly of the Sxl-Unr translation regulatory
complex. Nature, 515, 287-290.

GCACG

|||||||

UUUUUUU

distance: 7

>FBGN0264270

UUUUUUUGAGCA

|||||||

UUUUUUU

distance: 0

>ENSG00000063244

UUUUUUU

|||||||

UUUUUUC

distance: 1

>ENSG00000063244
UUUUU
|||||||
UUUUUCC
distance: 0

>ENSG00000234414
ACAAGAC
|||||
CACAA
distance: 1

>ENSG00000131914
AGGAGAU
|||||||
AGGAGAA
distance: 1

>ENSG00000138385
UUUU
|||||||
UGCUGUUUU
distance: 0

>ENSG00000138385
AUUU
|||||||
UGCUGUUUU
distance: 1

>ENSG00000138385
UGCUG
|||||||
UGCUGUUUU
distance: 0

>WBGENE00001595
CUAAC
|||||||
AUCUACUCAU
distance: 2

>WBGENE00001595
CUACUCAU
|||||||
AUCUACUCAU
distance: 0

>ENSG00000078328
UGCAUGU
|||||
UGCAUG
distance: 0

>YOR359W see Aviv,T., Lin,Z., Ben-Ari,G., Smibert,C.A. and Sicheri,F.
(2006) Sequence-specific recognition of RNA hairpins by the SAM domain of
Vtslp. Nat. Struct. Mol. Biol., 13, 168-176. (figure 3a)

UCUUUGA
|||||||
GCUGGUG
distance: 4

>YOR359W
CUGGCA
|||||||
GCUGGCC
distance: 1

>XB-GENE-6252591 see Lee,B.M., Xu,J., Clarkson,B.K., Martinez-
Yamout,M.A., Dyson,H.J., Case,D.A., Gottesfeld,J.M. and Wright,P.E.
(2006) Induced Fit and 'Lock and Key' Recognition of 5' S {RNA} by
Zinc Fingers of Transcription Factor {IIIA}. J. Mol. Biol., 357, 275-291.
(figure 1b left)

CCUGGUUAG
|||||||
GGGUGGG
distance: 5

>XB-GENE-6252591 see Lee,B.M., Xu,J., Clarkson,B.K., Martinez-
Yamout,M.A., Dyson,H.J., Case,D.A., Gottesfeld,J.M. and Wright,P.E.
(2006) Induced Fit and 'Lock and Key' Recognition of 5' S {RNA} by
Zinc Fingers of Transcription Factor {IIIA}. J. Mol. Biol., 357, 275-291.
(figure 1b right)

CCAUAC
|||||||
GGGUGGG
distance: 6

>ENSG00000147274
UCAAA
|||||
AUCAAA
distance: 0

>ENSG00000134644
UGUAAUAUU
|||||||
UGUAAAUA
distance: 1

>ENSG00000134644 see Gupta,Y.K., Nair,D.T., Wharton,R.P. and
Aggarwal,A.K. (2008) Structures of Human Pumilio with Noncognate {RNAs}
Reveal Molecular Mechanisms for Binding Promiscuity. Structure, 16, 549-
557.

UUUAAUGUU
|||||||
UGUAAAUA
distance: 4

>ENSG00000134644
UGUAUAUA
|||||||
UGUAUAUA
distance: 0

>ENSG00000134644
UGUAAAUA
|||||||
UGUAAAUA
distance: 0

>ENSG00000134644
UGUACAUA
|||||||
UGUACAUA
distance: 0

>ENSG00000134644
UGUACAUC
|||||||
UGUACAUA
distance: 1

>ENSG00000134644
UGUAGAUU
|||||||
UGUAAAUA
distance: 1

>ENSG00000134644
UGUCCAG
|||||||
UGUACAUA
distance: 2

>ENSG00000134644
UGUACAU
|||||||
UGUACAUA
distance: 0

>ENSG00000134644
UGUAUAU
|||||||
UGUAUAUA
distance: 0

>ENSG00000066044
AUUUU
|||||
AUUUA
distance: 1

>ENSG00000066044
UUUU
|||||
UUUUU
distance: 0

>ENSG00000066044
AUUU
|||||
AUUUA
distance: 0

>ENSG00000112531
ACUAAC
||||||
ACUAAC
distance: 0

>YGL014W
UGUAU
|||||||
UGUAUAUA
distance: 0

>YGL014W
UGUAUAUUA
|||||||
UGUAUAUUA
distance: 0

>YGL014W
UGUAUAUA
|||||||
UGUAUAUA
distance: 0

>ENSG00000070756
AAAAAAA
|||||||
AAAAAAA
distance: 0

>ENSG00000070756
AAAAAAA
|||||||
AAAAAAA
distance: 0

>ENSG00000077312
AUUGCACC
|||||||
AUUGCAC
distance: 0

>ENSG00000077312

AUUGCAC

|||||||

AUUGCAC

distance: 0

>ENSG00000102081 no reference

GCUGC

|||||||

GGACAGG

distance: 4

>YGL044C see Leeper,T.C., Qu,X., Lu,C., Moore,C. and Varani,G. (2010)
Novel Protein-Protein Contacts Facilitate mRNA 3'-Processing Signal
Recognition by Rna15 and Hrp1. J. Mol. Biol., 401, 334-349.

AAUAAU

|||||||

UGUUGU

distance: 4

>YGL044C see Leeper,T.C., Qu,X., Lu,C., Moore,C. and Varani,G. (2010)
Novel Protein-Protein Contacts Facilitate mRNA 3'-Processing Signal
Recognition by Rna15 and Hrp1. J. Mol. Biol., 401, 334-349.

UAUAUAUA

|||||||

UGUUGU

distance: 5

>ENSG00000162374

UAUUUAUUUA

|||||||

UUUUUUUU

distance: 1

>ENSG00000162374

AUUU

|||||||

UUUUUUU

distance: 1

>ENSG00000113742

CUUUA

|||||||

UUUUUUU

distance: 2

>ENSG00000055917

UGUACAUC

|||||||

UGUACAU

distance: 1

>ENSG00000055917
UGUAGUAU
|||||||
UGUAGUAU
distance: 0

>ENSG00000055917
UGUAAAUA
|||||||
UGUAAAUA
distance: 0

>YLL013C
UGUAUAUA
|||||||
CAUGUAUAUA
distance: 0

>YLL013C
UGUAAAUA
|||||||
CAUGUAAAUA
distance: 0

>YOL123W
UAUAUAU
|||||||
UAUAUAA
distance: 1

>ENSG00000139910
UCACC
|||||
AUCACC
distance: 0

>ENSG00000139910
CAGUCAC
|||||||
UCAGUCAC
distance: 1

>WBGENE00011279 see Kuwasako,K., Takahashi,M., Unzai,S., Tsuda,K.,
Yoshikawa,S., He,F., Kobayashi,N., Guntert,P., Shirouzu,M., Ito,T., et
al. (2014) RBFOX and SUP-12 sandwich a G base to cooperatively regulate
tissue-specific splicing. Nat. Struct. Mol. Biol., 21, 778-786. (results
and figure 1a)
GUGUGC
|||||||
AGCAUGC
distance: 3

>WBGENE00011279

UGCAUGG

|||||||

UGCAUGA

distance: 1

>ENSG00000104967 see Lewis,H.A., Musunuru,K., Jensen,K.B., Edo,C.,
Chen,H., Darnell,R.B. and Burley,S.K. (2000) Sequence-Specific {RNA}
Binding by a Nova {KH} Domain: Implications for Paraneoplastic Disease
and the Fragile X Syndrome. Cell, 100, 323-332. (figure 2 complex 1)
CCUAGAUCACC

|||||||

AACACC

distance: 5

>ENSG00000104967

GAUCACC

|||||||

AUCACC

distance: 0

>ENSG00000152518

UUUUUUUU

|||||||

UUUUUUUU

distance: 0

>ENSG00000120948

GUGAAUGA

|||||||

GAAUGA

distance: 0

>WBGENE00001402

UGUGUUAUC

|||||||

UGUGUUAUC

distance: 0

>WBGENE00001402

UGUGCCUUA

|||||||

UGUGCCAUU

distance: 1

>WBGENE00001402

UGUAA

|||||||

UGUAAAUC

distance: 0

>WBGENE00001402

UGUACCAUA

|||||

UGUACCAUA

distance: 0

>WBGENE00001402 see Qiu,C., Kershner,A., Wang,Y., Holley,C.P.,

Wilinski,D., Keles,S., Kimble,J., Wickens,M. and Hall,T.M.T. (2012)

Divergence of Pumilio/fem-3 mRNA binding factor (PUF) protein specificity through variations in an RNA-binding pocket. J. Biol. Chem., 287, 6949-6957. (see paragraph An Upstream C Is Required for Tight Binding by FBF)

CAUGUGC

|||||

UGUGUCAUC

distance: 5

>WBGENE00001402 see Wang,Y., Opperman,L., Wickens,M. and Hall,T.M.T.

(2009) Structural basis for specific recognition of multiple mRNA targets by a PUF regulatory protein. Proc. Natl. Acad. Sci. U. S. A., 106, 20186-20191. (figure 2a)

CUGUGC

|||||

UGUGCCAUA

distance: 1

>WBGENE00001402 see Wang,Y., Opperman,L., Wickens,M. and Hall,T.M.T.

(2009) Structural basis for specific recognition of multiple mRNA targets by a PUF regulatory protein. Proc. Natl. Acad. Sci. U. S. A., 106, 20186-20191. (figure 2b)

AUAC

|||||

UGUAAAUC

distance: 3

>WBGENE00001402

UGUGUCAUU

|||||

UGUGUCAUU

distance: 0

>WBGENE00001402

UGUGC

|||||

UGUGCCAUA

distance: 0

>WBGENE00001402

UGUACUAUA

|||||

UGUACUAUA

distance: 0

>ENSG00000048740
UGUU
||||
AUGUU
distance: 0

>ENSG00000168066
AUACUAACAA
|||||||
UAUACUAACAA
distance: 0

>ENSMUSG00000003410
AUUUUUUUU
|||||
UUUUUUU
distance: 1

>ENSG00000136527
AGAA
||||
AAGAA
distance: 0

>ENSG00000136527
AGAAC
|||||
AAGAAC
distance: 0

>ENSG00000136450
UGAAGGAC
|||||||
AGAAGGAC
distance: 1

>WBGENE00006321
GUGUGC
|||||||
AGUGUGA
distance: 1

>WBGENE00006321
GUGUG
|||||||
AGUGUGA
distance: 0

>YLR116W
AUACUAAC
|||||||
UACUAAC
distance: 0

```
>YLR116W
UACUAACA
|||||||
UACUAAC
distance: 0
```

```
>YLR116W
UACUAAC
|||||||
UACUAAC
distance: 0
```