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Supplemental Tables

Table S1 Homologs of NMD, EJC, CBC factors and other components related to these pathways.

The *N. crassa* homologs identified represent the best bidirectional hits for each organism as determined using BLASTP at the NCBI website.

Exceptions are indicated.

Protein Name	Organism	NCBI Reference Sequence ^a	Reciprocal BLAST ^b	Ref/Note
Upf1	<i>N. crassa</i>	XP_961233.1		NCU04242
	<i>S. pombe</i>	NP_593080.1	XP_961233.1	Upf1
	<i>S. cerevisiae</i>	NP_013797.1	XP_961233.1	NAM7
	<i>H. sapiens</i>	NP_001284478.1	XP_961233.1	regulator of nonsense transcripts 1 isoform 1
	<i>C. elegans</i>	NP_490829.1	XP_961233.1	SMG-2
Upf2	<i>N. crassa</i>	XP_961757.2		NCU05267
	<i>S. pombe</i>	NP_593784.1	XP_961757.2	Upf2
	<i>S. cerevisiae</i>	NP_011944.2	XP_961757.2	Nmd2p
	<i>H. sapiens</i>	NP_056357.1	XP_961757.2	regulator of nonsense transcripts 2
	<i>C. elegans</i>	NP_500974.2	XP_961757.2	SMG-3
Upf3	<i>N. crassa</i>	XP_956721.1		NCU03435
	<i>S. cerevisiae</i>	NP_011586.1	XP_956721.1	Upf3p
	<i>H. sapiens</i>	NP_075386.1	XP_956721.1	regulator of nonsense transcripts 3B isoform 2
	<i>C. elegans</i>	(NP_741600.1) c	XP_956721.1	SMG-4, isoform b
Xrn1	<i>N. crassa</i>	XP_960925.2		NCU06678
	<i>S. pombe</i>	NP_593482.1	XP_960925.2	exonuclease II Exo2
	<i>S. cerevisiae</i>	NP_011342.1	XP_960925.2	Xrn1p
	<i>H. sapiens</i>	NP_001269786.1	XP_960925.2	5'-3' exoribonuclease 1 isoform c
	<i>C. elegans</i>	NP_496945.3	XP_960925.2	XRN-1
Y14	<i>N. crassa</i>	XP_965326.1		NCU03226
	<i>S. pombe</i>	NP_594439.1	XP_965326.1	
	<i>S. cerevisiae</i>	not detected		
	<i>H. sapiens</i>	NP_005096.1	XP_965326.1	
	<i>C. elegans</i>	NP_497891.1	XP_965326.1	RNP-4
	<i>X. laevis</i>	NP_001079905.1	XP_965326.1	RNA-binding protein 8A-B

	<i>D. melanogaster</i>	NP_610454.2	XP_965326.1	tsunagi
	<i>A. thaliana</i>	NP_564591.1	XP_965326.1	
Mago	<i>N. crassa</i>	XP_957482.1		NCU04405
	<i>S. pombe</i>	NP_596666.1	XP_957482.1	mago nashi
	<i>S. cerevisiae</i>	not detected		
	<i>H. sapiens</i>	NP_060518.1	XP_957482.1	mago nashi
	<i>C. elegans</i>	NP_493025.1	XP_957482.1	MAG-1
	<i>X. laevis</i>	NP_00107972 4.1	XP_957482.1	mago nashi
	<i>D. melanogaster</i>	NP_476636.1	XP_957482.1	mago nashi
	<i>A.thaliana</i>	NP_171716.1	XP_957482.1	mago nashi
eIF4AIII	<i>N. crassa</i>	XP_961600.1		NCU01234
	<i>S. pombe</i>	NP_592863.1	XP_961600.1	
	<i>S. cerevisiae</i>	NP_010304.3	XP_961600.1	FAL1
	<i>H. sapiens</i>	NP_055555.1	XP_961600.1	eIF4AIII
	<i>C. elegans</i>	NP_490761.2	XP_961600.1	
	<i>X. laevis</i>	NP_00108420 0.1	XP_961600.1	eIF4A-III-B
	<i>D. melanogaster</i>	NP_649788.2	XP_961600.1	eIF4AIII
	<i>A.thaliana</i>	NP_188610.1	XP_961600.1	DEAD-box ATP-dependent RNA helicase 2
Btz ^d				
RNPS1	<i>N. crassa</i>	XP_958016.1		NCU09901
	<i>S. pombe</i>	NP_596549.2	XP_958016.1	RNA-binding protein (predicted)
	<i>S. cerevisiae</i>	NP_015147.1 ^e	XP_956595.1	Cbc2p
	<i>H. sapiens</i>	NP_00127355 6.1	XP_958016.1	RNA-binding protein with serine-rich domain 1 isoform c
	<i>C. elegans</i>	NP_497276.2	XP_958016.1	Protein RNP-5
CBP20	<i>N. crassa</i>	XP_956595.1		NCU00210
	<i>S. pombe</i>	NP_596414.1	XP_956595.1	nuclear cap-binding complex small subunit (predicted)
	<i>S. cerevisiae</i>	NP_015147.1	XP_956595.1	Cbc2p
	<i>H. sapiens</i>	NP_031388.2	XP_956595.1	nuclear cap-binding protein subunit 2 isoform 1
	<i>C. elegans</i>	NP_00125055 2.1	XP_956595.1	NCBP-2, isoform a
CBP80	<i>N. crassa</i>	XP_961147.1		NCU04187
	<i>S. pombe</i>	NP_594104.1	XP_961147.1	nuclear cap-binding complex large subunit (predicted)
	<i>S. cerevisiae</i>	NP_013844.2	XP_961147.1	Sto1p
	<i>H. sapiens</i>	NP_002477.1	XP_961147.1	nuclear cap-binding protein subunit 1
	<i>C. elegans</i>	NP_491850.2	XP_961147.1	NCBP-1
eRF1	<i>N. crassa</i>	XP_957296.1		NCU00410
	<i>S. pombe</i>	NP_594680.1	XP_957296.1	eRF1
	<i>S. cerevisiae</i>	NP_009701.3	XP_957296.1	eRF1
	<i>H. sapiens</i>	NP_004721.1	XP_957296.1	eukaryotic peptide chain release factor subunit 1 isoform 1
	<i>C. elegans</i>	NP_00102410 7.2	XP_957296.1	ETF-1

eIF4A ^f	<i>N. crassa</i>	XP_958421.2		NCU07420
	<i>S. pombe</i>	NP_594854.1	XP_958421.2	eIF4A
	<i>S. cerevisiae</i>	NP_012397.1	XP_958421.2	eIF4A
	<i>H. sapiens</i>	NP_001407.1	XP_958421.2	eIF4A-I isoform 1
	<i>C. elegans</i>	NP_001022623.1	XP_958421.2	INF-1, isoform a

^a. The *N. crassa* protein was used in BLAST and the entry represents the top hit

^b. The top hit identified in each organism was used to BLAST *N. crassa* proteins and the entry represents the top hit to evaluate best bidirectional hits

^c. *N. crassa* Upf3 did not give a significant hit when BLASTed against *C. elegans*, but *C. elegans* SMG4 identifies *N. crassa* NCU03435

^d. No Btz homolog was identified in *N. crassa*

^e. The protein identified as *N. crassa* RNPS1 has a best hit to *S. cerevisiae* CBP20 (which reciprocally hits *N. crassa* CBP20)

^f. eIF4A is distinct from eIF4AIII and the homologs are included here for reference