

Supplemental Material

Supplemental Figure S1. Protein Sequence alignment of human EXOSC2 and EXOSC3. Protein Sequence alignment of the human RNA exosome cap subunits EXOSC2 and EXOSC3, *S. cerevisiae* Rrp4 and Rrp40, including other EXOSC2/Rrp4 and EXOSC3/Rrp40 orthologs. Conserved EXOSC2 amino acids substituted in patients with SHRF (DI DONATO *et al.* 2016) and EXOSC3 amino acids substituted in patients with PCH1b disease (WAN *et al.* 2012) are highlighted in green. Identical residues (in red) and similar residues (in blue) are indicated. The different species aligned are as follows: Hs: *Homo sapiens*, Mm: *Mus musculus*, Dr: *Danio rerio*, Dm: *Drosophila melanogaster*, Ce: *Caenorhabditis elegans*, Sc: *Saccharomyces cerevisiae*, Sp: *Schizosaccharomyces pombe*, Cn: *Cryptococcus neoformans*, At: *Arabidopsis thaliana*, Os: *Oryza sativa*, Ss: *Sulfolobus solfataricus* (archaea).

Supplemental Figure S2. Modeling of the human EXOSC2-EXOSC4 and yeast Rrp4-Rrp41 interface show structural conservation. (A) Zoomed-in representations of the interface between the RNA exosome cap subunit EXOSC2 (teal blue) and core subunit EXOSC4 (light gray). EXOSC2 G30 facilitates a β turn that positions EXOSC2 Asp31 (D31) near an arginine in EXOSC4, R232. Structural modeling shows a salt bridge that forms between EXOSC2 D31 and EXOSC4 R232, represented by the red dashed lines. (B) Zoomed-in representation of the interface between the yeast RNA exosome cap subunit Rrp4 (teal blue) and core subunit Rrp41 (light gray). Rrp4 G58, which corresponds to EXOSC2 G30, facilitates a β turn that positions Rrp4 Glu59 (E59) near an arginine in the EXOSC4 yeast ortholog, Rrp41 (R233). Structural modeling shows salt bridge forms between Rrp4 E59 and Rrp41 R233, represented by the red dashed lines. Structural modeling in (A) was performed with the human RNA exosome structure (PDB 6D6R) (WEICK *et al.* 2018) and in (B) with the yeast RNA exosome structure (PDB 6FSZ) (SCHULLER *et al.* 2018) using PyMOL (PYMOL).

Supplemental Figure S3. Volcano plot of autophagy transcripts differentially expressed in the *rrp4-G226D* RNA-Seq. A total of 18 autophagy transcripts show ± 1.5 -fold change (p -value adjusted < 0.05) in *rrp4-G226D* cells compared to *RRP4* cells. Of those, 2 transcripts are increased 1.5-2 fold (*NFT1* and *SNO4* (blue)) and 16 transcripts are decreased 1.5-2-fold (*TEF4*, *RPL14A*, *RAS2*, *EGD1* *SEC4*, *TPS1*, *TMA19*, *PEP4*, *SEC14*, *MSS51*, *RPL15B*, *CAP1*, *FRQ1*, *PNP1* (blue)) with two transcripts decreased > 2 -fold (*ASC1* and *SOD1* (orange)).

Table S1. Yeast Strains and Plasmids used in this study.

Table S2. DNA Oligonucleotides employed for RT-qPCR

Table S3. Summary of *in silico* predictions for pathogenic amino acid substitutions in EXOSC2 and Rrp4.

Strain/Plasmid	Description	Source
<i>rrp4Δ</i> (yAV1103)	MATa his3Δ1 leu2Δ0 ura3Δ0 lys2Δ0 rrp4Δ::NEO [RRP4,URA3]	(SCHAEFFER <i>et al.</i> 2009)
<i>rrp40Δ</i> (yAV1107)	MATa his3Δ1 leu2Δ0 ura3Δ0 rrp40Δ::NEO [RRP40,URA3]	(SCHAEFFER <i>et al.</i> 2009)
<i>rrp4Δ mpp6Δ</i> (ACY2471)	<i>MATα, ura3Δ0, leu2Δ0, his3Δ1, lys2Δ0, rrp4Δ::NEO, mpp6Δ::natMX4, [RRP4, URA3]</i>	This study
<i>rrp4Δ rrp47Δ</i> (ACY2474)	<i>MATα, ura3Δ0, leu2Δ0, his3Δ1, lys2Δ0, rrp4Δ::NEO, rrp47Δ::natMX4, [RRP4, URA3]</i>	This study
<i>rrp4Δ rrp6Δ</i> (ACY2478)	<i>MATα, ura3Δ0, leu2Δ0, his3Δ1, lys2Δ0, rrp4Δ::NEO, rrp6Δ::natMX4, [RRP4, URA3]</i>	This study
<i>rrp40Δ mpp6Δ</i> (ACY2638)	<i>MATa; ura3Δ0, leu2Δ0, his3Δ1, rrp40Δ::NEO, mpp6Δ::natMX4, [RRP40, URA3]</i>	This study
<i>rrp40Δ rrp47Δ</i> (ACY2462)	<i>MATa; ura3Δ0, leu2Δ0, his3Δ1, rrp40Δ::NEO, rrp47Δ::natMX4, [RRP40, URA3]</i>	This study
<i>rrp40Δ rrp6Δ</i> (ACY2466)	<i>MATa; ura3Δ0, leu2Δ0, his3Δ1, rrp40Δ::NEO, rrp6Δ::natMX4, [RRP40, URA3]</i>	This study (SIKORSKI AND HIETER 1989)
pRS315	CEN61 LEU2, amp ^R	(FASKEN <i>et al.</i> 2017)
pAC3161	RRP40-2xMyc in pRS315, CEN6, LEU2, amp ^R	(FASKEN <i>et al.</i> 2017)
pAC3162	rrp40-G8A-2xMyc in pRS315, CEN6, LEU2, amp ^R	(FASKEN <i>et al.</i> 2017)
pAC3259	rrp40-W195R-2xMyc in pRS315, CEN6, LEU2, amp ^R	(FASKEN <i>et al.</i> 2017)
pAC3652	RRP40-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study
pAC3655	rrp40-W195R-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study
pAC3474	RRP4-2xMyc in pRS315, CEN6, LEU2, amp ^R	This study
pAC3476	rrp4-G58V-2xMyc in pRS315, CEN6, LEU2, amp ^R	This study
pAC3477	rrp4-G226D-2xMyc in pRS315, CEN6, LEU2, amp ^R	This study
pAC3656	RRP4-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study
pAC3659	rrp4-G226D-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study
pAC3669	RRP4-2xMyc-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study
pAC3672	rrp4-G226D-2xMyc-Native 3'UTR in pRS315, CEN6, LEU2, amp ^R	This study

Description	Sequence (5'-3')	Name
<i>pre-U4 snRNA</i> Fwd	ATCCTTATGCACGGGAAATACG	AC5723
<i>pre-U4 snRNA</i> Rev	AAAGAATGAATATCGGTAATG	AC5722
<i>pre-U6 snRNA</i> Fwd	GAAGTATCGTGACTIONTGTACATTTG	AC7748
<i>pre-U6 snRNA</i> Rev	TCTTCTATGTTCAACCGATAGC	AC7749
<i>U14 snoRNA (snR128)</i> Fwd	GATCACGGTGATGAAAGACTGG	AC5397
<i>U14 snoRNA (snR128)</i> Rev	CTACAGTATACGATCACTCAGACATCCTA	AC5398
<i>snR44 snoRNA</i> Fwd	GCATTTCCACATGGGATTAATA	AC6272
<i>snR44 snoRNA</i> Rev	ATGGTGTGATCGGGCAGTAT	AC6270
<i>TLC1 ncRNA</i> Fwd	AAGGCAAGGGTGTCTTTCT	AC6420
<i>TLC1 ncRNA</i> Rev	TTCCGCTTGAAAATAATGC	AC6421
<i>RPS3 mRNA</i> Fwd	TCCAACCAAGACCGAAGTTATC	AC9226
<i>RPS3 mRNA</i> Rev	GTACCTGGAGCGTACTTGAATC	AC9227
<i>RPL15A mRNA</i> Fwd	CCAGACAAGGCTAGAAGATTGG	AC9309
<i>RPL15A mRNA</i> Rev	CCGTAAGTAGCACCCCTTTGG	AC9308
<i>INO1 mRNA</i> Fwd	TTGGACTGCAAATACTGAGAGG	AC9303
<i>INO1 mRNA</i> Rev	AAGATCGTGGAAGGAGCAATC	AC9302
<i>PTH4 mRNA</i> Fwd	ACTGTGCTTGGATTCCCTCAG	AC9248
<i>PTH4 mRNA</i> Rev	CTATAGAATCGCTGCCCTTAGC	AC9249
<i>HXK2 mRNA</i> Fwd	TACTGGTGTCAATGGTGCTTAC	AC9307
<i>HXK2 mRNA</i> Rev	TTGGAGCAGATGGTGGAAATG	AC9306
<i>TDH1 mRNA</i> Fwd	GGTAGATACAAGGGTACTGTTTCC	AC9230
<i>TDH1 mRNA</i> Rev	TGAGCGGTGTCCAATTCC	AC9232
<i>CUT501</i> Fwd	GGTTCAACGTTGCAGGATCT	AC9254
<i>CUT501</i> Rev	GCTAGCACCTGTTGCTGTAAT	AC9255
<i>CUT770</i> Fwd	AAACAACCCGCTAGTGTGAC	AC9262
<i>CUT770</i> Rev	AGAGCAACTCACTGCAAAGG	AC9263
<i>CUT896</i> Fwd	ATCAGCAGGTGTCATGTTACAG	AC9256
<i>CUT896</i> Rev	CCCAGAGGCAAAGATGTAAAGT	AC9257
<i>NRD1 mRNA</i> Fwd	CAAGCAGAGGTCGAAACAAATC	AC9244
<i>NRD1 mRNA</i> Rev	GCTGGATCTGTGGAAGTCAA	AC9245
<i>NAB3 mRNA</i> Fwd	ACAGTTCGGTAGGCTCAGATAG	AC9246
<i>NAB3 mRNA</i> Rev	GGCGAAGTTCGACCTCTTTATC	AC9247
<i>ALG9 mRNA</i> Fwd	CACGGATAGTGGCTTTGGTGAACAATTAC	AC5067
<i>ALG9 mRNA</i> Rev	TATGATTATCTGGCAGCAGGAAAGAACTTGGG	AC5068

Exosomopathy amino acid substitution	<i>Hs</i> EXOSC2		<i>Sc</i> Rrp4	
	G30V	G198D	G58V	G226D
Missense 3D* (Phyre2)	Neutral	Damaging	Neutral	Damaging
PolyPhen-2** (HumDiv)	Possibly Damaging (Score: 1.000)	Probably Damaging (Score: 1.000)	Probably Damaging (Score: 1.000)	Probably Damaging (Score: 1.000)
Provean†	Deleterious (-7.938)	Deleterious (-6.35)	Deleterious (-8.981)	Deleterious (-6.517)
SNAP2‡	Effect (Score: 91)	Effect (Score: 94)	Effect (Score: 63)	Effect (Score: 92)

***Missense 3D** part of tool suite **Phyre2 (Protein Homology/analogy Recognition Engine)** v2.0; predicts structural changes introduced by an amino acid substitution through three-dimensional protein modeling.

****PolyPhen-2 (Polymorphism Phenotyping)** v2 HumDiv trained model; Naïve Bayes posterior probability that mutation is damaging and qualitative classification as benign, possibly damaging, or probably damaging based on 5%/10% false positive rate (FPR) thresholds (FPR, the chance the mutation is classified as damaging when it is non-damaging).

†**PROVEAN (Protein Variation Effect Analyzer)** v1.1; delta alignment scores equal to or below predefined threshold (-2.5), protein variant predicted to have "deleterious" effect on function.

‡**SNAP2** predicted score for functional effects of mutations; scores range from -100 strong neutral prediction to +100 strong effect prediction.

Supplemental Figure S1

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HsEXOSC2 -----MAMMRLPVARK--PL-SERLGR--DTKKHLVVTITTD-----TGFMRGHGTYMGEEK-----LTASVAGSVERVNKL-----ICVKAL
MmRrp4 -----MAEMRLPKARK--PL-SESLGR--DSKKHLVPCDITTD-----TGFMRGHGTYMGEEK-----LTASVAGSVERVNKL-----ICVKAL
DrRrp4 -----MAEMRLPAVHK--HV-SLKTGSSREKHLVPCDITSD-----TGFMRGHGTYMDEDR-----LTASVAGQVERVNKL-----ICVKPL
DmRrp4 -----MSTNAIDLALD--RVDWRDLAQTTEQPRVVTGCVLMPDE-----AGFMRGHGTYFVEDEN-----IKSSVAGVIQKVNKL-----ISVRPL
CeRrp4 -----MSFEVTGFP-----LVSFMMMLMSSEARNDIDETKIVIPGHSVCDAP-----QQFMRGHGTYVRDGE-----IVSSLSGVVQLNKL-----LMVKTI
ScRrp4 MSEVITITKRNQAFQNSNLSYNNITGIS--DDNEDEEDIY--MHDVNSAKSESSESDIVTGGVLTDD-----PIWMRGHGTYFLDNM-----TYSSVAGTVSRVNKL-----LSVPL
SpRrp4 -----MVTLLKPEEFVVSSEADIVNDVMTMEDEIMEDEQMGVLVDGELEEFDKSIHQNLVTGGVLTDD-----PQFMRGHGTYFEDGG-----IYASVAGSQRVNKL-----ISVKPL
CnRrp4 -----MFSVKAV--APSISQAFTEIVPSTHRK--HQALDAMDLDDEFGGAGPSKRSIVSGCVITSS-----KEYMRGHGTYVEESN-----VVSSVAGTIERVNKL-----ISVRPL
AtRrp4 -----MVMRKLQLPLSQTQ--KVRFERAIE--RLQSLSS--SANSASVITDSTIPVNH-----SDSIIIGYISVGGT-----RLATQGAFFH-----NDDGKVMWLV
OsRrp4 -----MRDLQLSLNQTQ--RVRLEAALH--ELQTVAP--AAAVTADTIPVND-----DNI LKHGTSDDQGE-----VVATLGVVERVNKL-----VYVRTL
HsEXSOC3 -----MAEPASVAEESLAGSRAARTVILGQVVLLEELLPQEDAEPPGGAVERPLSLNARACSRVVCVCGPLRRCGDR-----LVHTKCGRLRHKPEPS--GGGGVYVWDS
MmRrp40 -----MAEVLGAGSEVAVGARARVHVILGQVVLGCEELVLPDHEVDVGLGGAGQPLRLNAGARPRLRVCGPLRRCGDR-----LIVTKCGRLRHKPEPS--GGGGVYVWDS
DrRrp40 -----MDSVVHTSLLERIGDVLVPGDILVFSFPE-----AGDANPKADRLICGGLRRSGAE-----LRVCRAGLRRHKPFN-----MYWVNC
DmRrp40 -----MSATSIIVMPCERAA-----TEELAKSKRVLGGLRRLDDT-----VVASAGAPLRRHKPEG-----TFVDN
CeRrp40 -----MTVVLGPDVINEPSS-----MTPVLGPDVINEPSS-----TPVKLGPGLIYCDNTQF-----IRPVNTGVHVSAGK--KSGVQATVYIDY
ScRrp40 -----MSTFIFGDSFPVDP-----MSTFIFGDSFPVDP-----MSTFIFGDSFPVDP-----IRPVNTGVHVSAGK--KSGVQATVYIDY
SpRrp40 -----MAVVEEKLGLSYFPCERIPDSIIIS-----QDGSIRLGPGLVQKQKRD-----EIVVSKAGRLH-Q-----TGKNAMLIDY
CnRrp40 -----MPTLLGLDCTVPIPS-----MPTLLGLDCTVPIPS-----TSKAVVLGPGISQSTPTLQASSSTASGSSAQIATRLGLMHS--SGKG--KERSQKLIWEG
AtRrp40 -----MAAKVSVSTSLNLIQVVDVLDLNSM-----NNQTIKLGSLQLDQND-----ISAMRCKLISYKFN-----KYMLES
OsRrp40 -----MESKPPSALVDNHVVDVLDLDAEM-----TNQTIKLGAGLRQDCDT-----IQATSRKLRLSKFS-----KYMVES
SsRrp4 -----MMSQSQKIVLQPRSIIVGPELLAEGE-----FQIPWSPYILKINSK-----YYSVTGGLDFVDKDTQ-----FEVIFL
consensus -----gg 1 g g 1
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HsEXOSC2 KT-RYIGVEGDIIVGRITTEVQQRKWKVETNSR-LDSVLLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-GQCVLVQ--VSPSLVK-----RQKTHFHDLP-----CGASVILNNGFIWIY
MmRrp4 KT-RYNGVEGDIIVGRITTEVQQRKWKVETNSR-LDSVLLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-GQCVLVQ--VSPSLVK-----RQKTHFHDLP-----CGASVILNNGFIWIY
DrRrp4 KT-RYNGVEGDIIVGRITTEVQQRKWKVETNSR-LDSVLLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-GQCVLVQ--VSPSLVK-----RQKTHFHDLP-----CGASVILNNGFIWIY
DmRrp4 KS-RYVGEIGDIIIVARVEVQQRKWRVDTNSR-LDSVLLSSNLPGLGELRRSRAEDEMQRRLYLDGDLISAEVQAVFSDGAVSL-----YTRSLKYGKL-SQCVLVK--VPPALVK-----RRKMHFHDLP-----CGASVILNNGFIWIY
CeRrp4 KQ-RYAGEVGDVIVARVEVQQRKWKVDTNSR-LHANLPLGSLVLPFGDPRRVDDEDEKMSFLEKNGELICAEVQVQGHQDTLML-----HTRNNKYGKL-QQGLIK--VPPALVK-----RQKTHFHDLP-----YGMVILGNGSIVWY
ScRrp4 KG-RYAPETGDHVVGRITAEVGNKRWKVDIGGK-QHAVMLGSLVNLPGGILRRKSEDELMQMSRFLKNGELICAEVQVQGHQDTLML-----HTRSLKYGKL-RNGMPCQ--VPPALVK-----RQKTHFHDLP-----GNITVVLGNGYIWLIR
SpRrp4 RS-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
CnRrp4 RS-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
AtRrp4 RA-RYKFEVGDIVGRITAEVQQRKWKVETNSR-LDSVLLSSNLPGLGELRRSRAEDEMQRRLYLDGDLISAEVQAVFSDGAVSL-----YTRSLKYGKL-SQCVLVK--VPPALVK-----RRKMHFHDLP-----CGASVILNNGFIWIY
OsRrp4 RA-RYKFEVGDIVGRITAEVQQRKWKVETNSR-LDSVLLSSNLPGLGELRRSRAEDEMQRRLYLDGDLISAEVQAVFSDGAVSL-----YTRSLKYGKL-SQCVLVK--VPPALVK-----RRKMHFHDLP-----CGASVILNNGFIWIY
HsEXSOC3 QQR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
MmRrp40 QQR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
DrRrp40 QQR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
DmRrp40 YQR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
SpRrp40 RTR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
CnRrp40 NSKR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
AtRrp40 SHKR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
OsRrp40 SQKR-RYVPEIGDILIGKIAEVQQRKWKVDIGAK-QNAVMLSSNLPGLGELRRSRAEDELAMRGLQEGDLISAEVQAVFSDGAVSL-----HTRSLKYGKL-RNGVFLK--VPPALVK-----RQKTHFHDLP-----GGVDIILSNGYIWWY
SsRrp4 EGSFYYPKINDIVIGLVEDVETIYVGVVDIKAP-YKAVLPAS-----NLLGRSINVGEDLRLRYLDGDIYIARINENFORSIDPVL-----SVKGDLRV-SNGIVID-IMPVYPRVIRGNKSMYETLAL---SKSGCSIFVANNRITWAT
consensus xY d v i g v f v d l l a r g l i g m r G i G i i v g N G i W
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HsEXOSC2 PTPHKE-----EE-AGGFIANL-EPV-SLADREVISRLNRCIISLVTQRMLYDTSILCYEASLPHQIKDI-----LKPEIME-EIVMETRQRL-----LEQEG--
MmRrp4 PTPHKD-----ED-AGGFIANL-EPV-ALSDEVISRLNRCVVLVQRMFLDFTSILCYEASLASHQIKDI-----LKPEIME-EIVMETRQRL-----LEQEG--
DrRrp4 PTPALQE-----EQ-AGGFYSM-EPV-SLDRVYSRLNRCLLALANQKVLFDFTSILCYEASLPHQIKDI-----LKPEIME-EIVMETRQRL-----MEHEG--
DmRrp4 PTKQEE-----EGGEGFQAQNLNEHV-PRADREVIARLRNRSIALAKKLMIVDTSIQAYAEESLRVEAHEL-----LQONAIY-DIQGQOARL-----RDADE--
CeRrp4 PSLPETTLE-----EDGS--HVH-EFQVPPDVRVTVMRIAACVRLRDSYISIVLNSLTCYMSQPYEKELAEQDTSRSLAYL-----IAARLQELQ-----QK--
SpRrp4 KTSQMDLARDTPSANSSSIKSTG PTGAVSLNFSITRLEEESWQIYSDENDPISGNIRQAIARVANCYKGLASRSLPTQASITNFYESSLVF--SNLQDL--TPVKNM-DIAMEAMQ-----MRGNGN-
CnRrp4 KHNNQH-----SSVITRLEEESWQIYSDENDPISGNIRQAIARVANCYKGLASRSLPTQASITNFYESSLVF--SNLQDL--TPVKNM-DIAMEAMQ-----MRGNGN-
AtRrp4 NGTSQARRE-----GGEGFDEGVSNQNDIE-PPQGREASIVLANIKALASEGVLPTETLIGESYAWAEKNVPSGSGFPDSETERKMLNEIVGLELEFA-----
OsRrp4 EHVVGENANMME-----NKL-----N-LSAEVENFTPETRKICRLANAVRSLALGFTLVELIETAEASVSNIEIN-----NMLGAEFYVQTAERVKRRADLRKKSAR
HsEXSOC3 AKTIQQTLLANLLEACEHMTSDQRKQ-----IFSRLAES-----
MmRrp40 AKTIQQTLLANLLEACEHMTTEQRKQ-----IFSRLAES-----
DrRrp40 ARTVQHTLLANLLEACEHMTSQRHT-----LFRVADGGI-----
DmRrp40 AHSKKTVALANALSAEQSCAEIDK-----LVQNNYTRVSD-----
CeRrp40 ASTSDDIKIHDIINKSEFITDEDELIT-----LVQNNYTRVSD-----
SpRrp40 CEELSNTLACRYTIRMECCQKNDTAAFKD-----IAKRQFKEILLTVKEE-----
CnRrp40 SENLSTTVLICTAIRNCEPMSDEQIKY-----CKDLIKL-----
AtRrp40 AETVGETLAKRLIESVDDHIIFVEEKA-----IHEKLERELS-----
OsRrp40 ATAPRIVITIVANAIMNSESLSGTOQRIL-----MVEKLAISD-----
SsRrp40 APSNSNIVVSNAIKESSELGGIQRG-----MVESLERLS-----
consensus -----RKI-----ENESH-----IKGLDRIKQFTIEEKLGRNASSGETKTNS-----
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