Supplemental data

Experimental procedures

Oligonucleotides and plasmids

The open reading frames (ORF) of SART3, DDX30, DHX36, DDX47, RHA, HuR, hnRNP-C, RBM4, Matrin3, UPF1/RENT1, hnRNP-F, PABP-C1, ZBP1 and ZBP3 were cloned from HeLa Marathon cDNA library (Clontech Inc.). All cDNAs were PCR-amplified using primers that introduce Not1 restriction sites at the 5' end and BamH1 or EcoR1 restriction sites at the 3' end of the ORF. Restricted cDNAs were subsequently ligated into pIRES-VP5 (Meister et al., 2004). For expression of recombinant proteins N-terminal fragments of Ago1, Ago2 or full length TRBP were cloned into pGEX-6P1 (Amersham) using EcoR1 and Xho1 restriction sites. The construction of the human FLAG/HA-Ago1 and FLAG/HA-Ago2 was reported earlier (Meister et al., 2004). miRNA reporter plasmids which express the firefly luciferase orf fused to a regulatory 3'UTR sequence and renilla luciferase as a transfection control were generated from pMIR-REPORT (Ambion) as follows: The renilla luciferase gene including a SV40 promoter and a poly(A) site was PCR-cloned from pRL-SV40 (Promega) into the SspI site of the pMIR-REPORT plasmid. Furthermore, the CMV promoter of the firefly luciferase was replaced by a HSV-TK promoter using PCR amplification from pRL-TK (Promega). A 3'UTR fragment from the KRAS mRNA was PCR-amplified from a published construct (Johnson et al., 2005) and inserted into the SacI and NaeI restriction sites of the reporter plasmid. Alternatively, the HMGA2 3'UTR sequence was PCR amplified from HEK 293 cDNA using oligonucleotides 5' CGCTGAGCTCTACTAATAGTTTGTTGATCTG and 5' CGCTGCCGGCGACCAAACTTTATTACTCATT and cloned into the described reporter construct via the SacI and NaeI restriction sites. The SERBP1, DNAJB11 and Raver2 reporter constructs have been reported before (Beitzinger et al., 2007). Further, the following DNA oligonucleotides containing a sequence perfectly complementary to miR-21 were annealed, digested with SacI and NaeI and inserted into the SacI and NaeI restriction sites of the

reporter plasmid: 5’ CGCTGAGCTCATCGCCACCTTGTTTAAGCCTCAACATCAGTCTGATAAGCTAATT AGACCTACGCACTCCAGGCCGGCTCGC, 5’ GCGAGCCGGCCTGGAGTGCGTAGGTCTAATTAGCTTATCAGACTGATGTTGAGGC TTAAACAAGGTGGCGATGAGCTCAGCG. The construct carrying a mutated miR-21 binding site was cloned using the following DNA oligonucleotides: 5’ CGCTGAGCTCATCGCCACCTTGTTTAAGCCTCAACATCAGCACCATTCTATAATTA GACCTACGCACTCCAGGCCGGCTCGC, 5’ GCGAGCCGGCCTGGAGTGCGTAGGTCTAATTATAGAATGGTGCTGATGTTGAGGC TTAAACAAGGTGGCGATGAGCTCAGCG.

The following oligonucleotides were used for detection of KRAS mRNA by qRT-PCR: ODN1, 5’ TTTTAGGACTCTTCTTCCATATTA; ODN2, 5’ TGGGGCATGTGGAAGGTAGGGAGG. For qPCR validation of siRNA knock downs, the following primers were used: 5’ CTTGAGGTGGGATGTGTGTG, 5’ GCAGGAGAGGAAAGGAAAGG (RBM4); 5’ AAGTGATGGAGGGTGCTGAC, 5’ TGCGTCGGTAATTGAAGTTG (YB1); 5’ AGTTGTTGTCCCTCGTGACC, 5’ AGCCTTCTGTTGTTGGTGCT (ZBP3); 5’ CACCTCAAAGCGAGCACATA, 5’ CAATAGCAGTGACCCCAGGT (FMRp); 5’ TGGTATCGTGGAAGGACTCATGAC, 5’ ATGCCAGTGAGCTTCCCGTTCAGC (GAPDH).

The following siRNAs were used for knock down experiments: RBM4#1: UUACGGCUUUGUGCACAUAUT, UAUGUGCACAAAGCCGUAAUT; RBM4#2: GGAGCUUCGAGCCAAGUUUUT, AAACUUGGCUCGAAGCUCCUT; YB1#1: AACCUUCGUUGCGAUGACCUT, GGUCAUCGCAACGAAGGUUUT; YB1#2: GCAGACCGUAACCAUUAUAUT, UAUAAUGGUUACGGUCUGCUT; YB1#3: AGAAGGUCAUCGCAACGAAUT, UUCGUUGCGAUGACCUUCUUT; ZBP3#1: UCCAGAACGCACUAUUACAUT, UGUAAUAGUGCGUUCUGGAUT; FMRp#1:

GGCAGCUUGCCUCGAGAUUUT, AAUCUCGAGGCAAGCUGCCUT; FMRp#2: CCUCCUGUAGGUUAUAAUAUT, UAUUAUAACCUACAGGAGGUT; FMRp#3: GAACGUCUAAGAUCUGUUAUT, UAACAGAUCUUAGACGUUCUT; FMRp#4: ACAGGUACUUUGUCUAAGAUT, UCUUAGACAAAGUACCUGUUT; ctrl.: UUGUCUUGCAUUCGACUAAUT, UUAGUCGAAUGCAAGACAAUT. The siRNAs against TNRC6B and Ago1-4 were described before (Meister et al., 2004).

The following 2'OMe oligoribonucleotides were used: let-7a 2'OMe: 5'-AACTATACAACCTACTACCTCAT; BART5 2'OMe: 5'-CTATCAAGGAAACAAAACCACTGT. BART5 is a miRNA derived from the Epstein-Barr virus and used as a control for unspecific effects caused by the 2'-OMe oligoribonucleotides.

Tissue culture and transfection

HEK 293 cells were grown in Dulbecco's modified Eagle's medium (DMEM) (PAA) supplemented with 10% heat inactivated fetal bovine serum (Biochrom AG), 100 unit/ml penicillin and 100 μg/ml streptomycin (Gibco) at 37°C in 5% CO_2 atmosphere. Cells were transfected using calcium phosphate. Approximately 3h prior to transfection cells were plated at 30% confluency. Per 15 cm dish 15 μg plasmid DNA was diluted in 1082 μl H_2O and 153 μl 2M $CaCl_2$. 1250 μl 2× HEPES-buffered saline (274 mM NaCl, 1.5 mM Na_2HPO_4, 54.6 mM HEPES-KOH pH 7.1) were added drop-wise under gentle agitation. The transfection solution was then sprinkled onto the cells and extracts were generated 48 h after transfection. For luciferase assays, HeLa cells were transfected as described below.

Mass spectrometry (MS) and protein identification

After Coomassie Blue staining gel lanes with corresponding glycerol gradient fractions, were cut into pieces of similar size (23 splices), and subjected to in-gel trypsinization (Shevchenko et al., 1996) The extracted peptides were analyzed by liquid chromatography-coupled tandem

MS[LC-MS/MS] on a Q-ToF Ultima mass spectrometer (Waters). MSMS spectra of doubly and triply charged precursors were acquired for max. 3.3 sec (0.1 sec interscan time). The raw data were processed and transformed into a peaklist using MassLynx software 4.0 (Waters) with the following settings: i) Smoothing: smooth window (channels) 3.00, number of smooths 3 using Savitzky Golay algorithm; ii) Centroiding: min. peak width at half high: 4, centroid top, 80 %.

The peak list of fragment spectra was searched against the NCBI non-redundant database (NCBInr) with a mass accuracy of 0.2 Da for the parent ion (MS) and 0.2 Da for the fragment ions (MS/MS). Mascor was used as seaerch engine. The peptides were constrained to be tryptic with a maximum of 1 missed cleavage. Carbamidomethylation of cysteines was considered as a fixed modification whereas oxidation of methionine residues was considered as a variable modification. The highest scoring peptide from each protein as well as single hit peptides entry has been manually inspected to eliminate any false positives in the data-set.

Protein expression and antibody production

For the production of GST-fusion proteins, plasmids containing fragments of Ago1, Ago2, full length TRBP or full length SART-3 were transformed into E.coli strain BL21(DE3) and grown as over night cultures. GST-tagged proteins were purified using glutathione sepharose according to the maunfacturer's instructions (Amersham). For antibody production in rabbits, 200 μg of recombinant protein was repeatedly injected into rabbits. After 5 injections, rabbits were euthanized and the final serum was obtained. Lou/C rats were immunized subcutaneously and intraperitoneally with a mixture of Ago1-GST fusion protein (50 μg), 5 nmol CPG oligonucleotide (ODN 2006, TIB Molbiol, Berlin, Germany), 500μl PBS and 500 μl IFA. After a six-week interval a final boost without adjuvant was given three days before fusion of the rat spleen cells with the murine myeloma cell line P3X63-Ag8.653 (ZIT). Hybridoma supernatants were tested in an ELISA using bacterial extracts from E. coli

expressing either the Ago1 fusion protein or an irrelevant GST fusion protein. Monoclonal antibodies reacting with Ago1-GST fusion protein and not with an irrelevant GST fusion protein were analysed in western blotting. Ago1-4B8 (rat IgG2a) recognized the protein specifically in western blotting and was used for this study. The Ago1-4B8 antibody is commercially available form Ascenion (http://www.ascenion.de/).

Western blotting

For Western blotting, gradient fractions were separated by 10% SDS-PAGE and transferred to a nitrocellulose membrane (Amersham-Biosciences) by semi-dry electroblotting. The following primary antibodies were used: anti-HA (Upstate), anti-hnRNP-U, hnRNP-C1/2, anti-DDX5, anti-YB-1 (all from Abcam), anti-NF-90, anti-NF-45, anti-rpS6 (Cell signaling tech.), DDB1 (Serotec), anti-ZBP-1, anti-ZBP-3, anti-SART3 (see main text), anti-TRBP (see main text) anti-Ago1 (see main text) and anti-Ago2 (Upstate and see above). As secondary antibody, peroxidase-conjugated anti-mouse (Sigma), anti-goat (Abcam), anti-rat (Jackson labs) and anti-rabbit (Sigma) antibodies were used.

RT-PCR

For detection of miRNA association with Ago complexes, lysates from cells transfected with FLAG/HA-tagged Ago1 or Ago2 were separated on sucrose gradients as described. Ago complexes were immunoprecipitated from single fractions using FLAG beads. RNA was isolated and reverse transcription and semi-quantitative PCR was performed using mirVana qRT-PCR miRNA Detection Kit (Ambion) and miRVana qRT-PCR Primer Sets for the miRNAs let-7a and miRNA-16 (Ambion).

For qRT-PCR experiments a reporter construct containing the KRAS 3' UTR (Johnson et al., 2005) was transfected together with FLAG/HA-Ago1 into HEK 293 cells. Lysates were separated by gradient centrifugation and total RNA was extracted from each individual

fraction using phenol/chloroform. Extracted RNA was incubated with 1U DNaseI (Fermentas) and 20U RNasin (Promega) in 1x DNaseI buffer (Fermentas) for 30 min at 37°C followed by enzyme inactivation for 10 min at 70°C. Reverse transcription was performed using a first strand cDNA synthesis kit (Fermentas) according to manufacturer's instructions. The PCR reaction consisted of 2 µl cDNA, 5 nmol primer each and 1x LightCycler 480 SYBR Green I Master buffer (Roche). After initial activation (95°C, 10 min), the target sequence was amplified in 40 PCR cycles (95°C, 15 s; 55°C, 15 s; 72°C, 30 s). PCR Products were tested for specificity by melting point analysis. Quantification was carried out using the LightCycler 480 Basis Software (Roche).

For siRNA knockdown validation, HeLa cells were transfected with siRNAs using the conditions that were employed for the reporter assays. After 5d, total RNA was isolated using the PrepEase Kit (USB corporation, Cleveland, USA). Reverse transcription was performed with random hexamer primers using a first strand cDNA synthesis kit (Fermentas) according to manufacturer's instructions. qPCR was carried out using 500 nM primer each and 1x iQ SYBR Green supermix (Biorad). After initial activation (95°C, 3 min), the target sequence was amplified in 40 PCR cycles (95°C, 10 s; 55°C, 30 s) on a MYiQ (Biorad). Data were evaluated using the iQ5 software (Biorad). The levels of specific mRNAs were normalized to corresponding levels of GAPDH mRNA.

RNA cleavage experiments

In vitro transcribed cleavage substrates used in this study were described previously in (Landthaler et al., 2004; Meister et al., 2004). For RISC activity assays, the miR-19b substrate was ^{32}P-cap labeled as described (Martinez et al., 2002) and 10 μl of Ago complex-containing anti-FLAG beads were incubated in a 25 μl reaction containing 5 nM target RNA, 1 mM ATP, 0.2 mM GTP, 10 U/mL RNasin (Promega), 100 mM KCl, 1,5 mM $MgCl_2$ and 0,5 mM DTT for 1.5 h at 30°C. The reaction was stopped by adding 200 μl proteinase K buffer

followed by proteinase K treatment (0.2 mg/ml). RNA was isolated with Phenol/Chloroform and analysed by 8% denaturing RNA PAGE. Signals were detected by autoradiography. For Dicer activity assays, 10 μl of Ago complex-containing anti-FLAG beads were incubated in 20 μl phosphate buffered saline (PBS) containing 5 mM ATP, 7.5 mM $MgCl_2$, 10 U/ml RNasin (Promega) and about 100 counts of internally labeled Dicer for 1 h at 37ºC. Beads were treated as described above, and the RNA products were analyzed on a 15% denaturing RNA gel. Radioactive signals were detected as described above.

Northern Blotting

For Northern Blotting, HEK 293 cell lysates transfected with FLAG/HA-Ago2 were subjected to FLAG immunoprecipitation and incubated with or without RNase A treatment as described above. Beads were subjected to Proteinase K treatment as described above. RNA was isolated from the beads using Phenol/Chloroform and separated by 15 % denaturing RNA PAGE. Northern Blotting against miR-19b was performed as described before (Lagos-Quintana et al., 2001).

Luciferase reporter assays

HeLa cells were seeded in complete DMEM to 48 well plates 5hrs prior to transfection to give 50% confluency.

siRNAs were transfected at 10mM final concentration using Hiperfect (Qiagen), according to the manufacturer's instructions. After 2d, cells were passaged in a 1:3 ratio and seeded into a 48 well plate. On the following day, medium was changed to OptiMEM (Invitrogen). Cells were subsequently transfected with reporter plasmids using 0.5 μl/well Lipofectamine (Invitrogen) and 0.125 μg/well plasmid, according to the manufacturer's instructions. 24hrs later, lipofection complexes were removed and complete DMEM was added. Cells were lysed 1d later in 50 μl/well passive lysis buffer (Promega). Luminescence was measured in a

Mithras LB 940 luminometer (Berthold Technologies, Bad Wildbad, Germany), using firefly luciferase buffer (470 μM D-luciferin, 530 μM ATP, 270 μM coenzyme A, 33.3 mM DTT, 20 mM Tricine, 5.34 mM magnesium sulfate, 0.1 mM EDTA; pH adjusted to 7.8) and renilla luciferase buffer (1.43 μM Coelenterazine, 2.2 mM EDTA, 0.22 M potassium phosphate, 0.44 mg/ml BSA, 1.1 M NaCl, 1.3 mM NaN_3; pH adjusted to 5.0). Luciferase substrates were purchased from PJK crysosystems (Kleinblittersdorf, Germany). All samples were assayed in 4-6 replicates. For each siRNA, the firefly/renilla luminescence ratios of the miRNA reporter plasmids were normalized to the corresponding ratio of the empty reporter vector.

For miRNA inhibition experiments 40 pmol of the 2'-O-methyl oligoribonucleotides were pre-transfected into HeLa cells using EscortV (Sigma), according to the manufacturer's instructions. After 6hrs, the medium on the cells was exchanged and cells were transfected with reporter plasmids (0.1 μg DNA/well) using 1 μl/well EscortV (Sigma), according to the manufacturer's instructions. Cells were lysed 24hrs later in 50 μl/well passive lysis buffer (Promega) and luminescence was measured as described above. The firefly/renilla luminescence ratios of the miRNA reporter plasmids were normalized to the corresponding ratio of the empty reporter vector.

For over-expression experiments, cells were co-transfected with reporter plasmids (0.1 μg DNA/well) and FLAG/HA-tagged constructs as indicated using 1 μl/well EscortV (Sigma), according to the manufacturer's instructions. After 36 h, cells were lysed in 50 μl/well passive lysis buffer (Promega) and luminescence was measured as described above. Again, results were normalized to those of the empty vector.

Supplemental references

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Supplementary Figure legends

Supplementary Figure 1. Proteomic analysis of Ago complexes I, II and III. HEK 293 cells were transfected with FLAG/HA-Ago1 or FLAG/HA-Ago2. Lysates were separated by sucrose gradient centrifugation. Fractions 3-8 (complex I), 11-13 (complex II) and 15-17 (complex III) were pooled and subjected to immunoprecipitation using anti-FLAG antibodies. Immunoprecipitated FLAG/HA-Ago1 complexes (lanes 2, 4 and 6) or FLAG/HA-Ago2 complexes (lanes 8, 10 and 12) were separated by SDS PAGE and the proteins were analyzed

by ESI TOF mass spectrometry. Lanes 1, 3, 5, 7, 9 and 11 show molecular weight markers. IgG as well as FLAG/HA-Ago1 and –Ago2 bands are indicated.

Supplementary Figure 2. Proteomic analysis of control samples. Lysates from HEK 293 cells transfected with FLAG/HA-Ago2 were separated by gradient centrifugation and fractions were pooled as in S1. Immunoprecipitation using agarose coupled mouse IgG and proteomic analysis were preformed as described in S1. Lanes 2, 4 and 6 show immunoprecipitates from Ago complexes I, II and III, respectively, obtained with control antibody. IgG bands are denoted to the right, lanes 1, 3, 5 and 7 show molecular weight markers.

Supplementary Figure 3. Efficiency test of RNase treatment. (A) Total RNA from HEK 293 cells was incubated with (+) or without (-) RNase A, separated by RNA PAGE and stained with ethidium bromide. (B) Lysates from HEK 293 cells transfected with FLAG/HA-Ago2 were subjected to immunoprecipitation using FLAG beads. Beads were incubated with or without RNAse A. Northern Blot against miR-19b was performed with RNA isolated from these beads. As a loading control, 15% of the beads were used for Western blotting against the HA-tag.

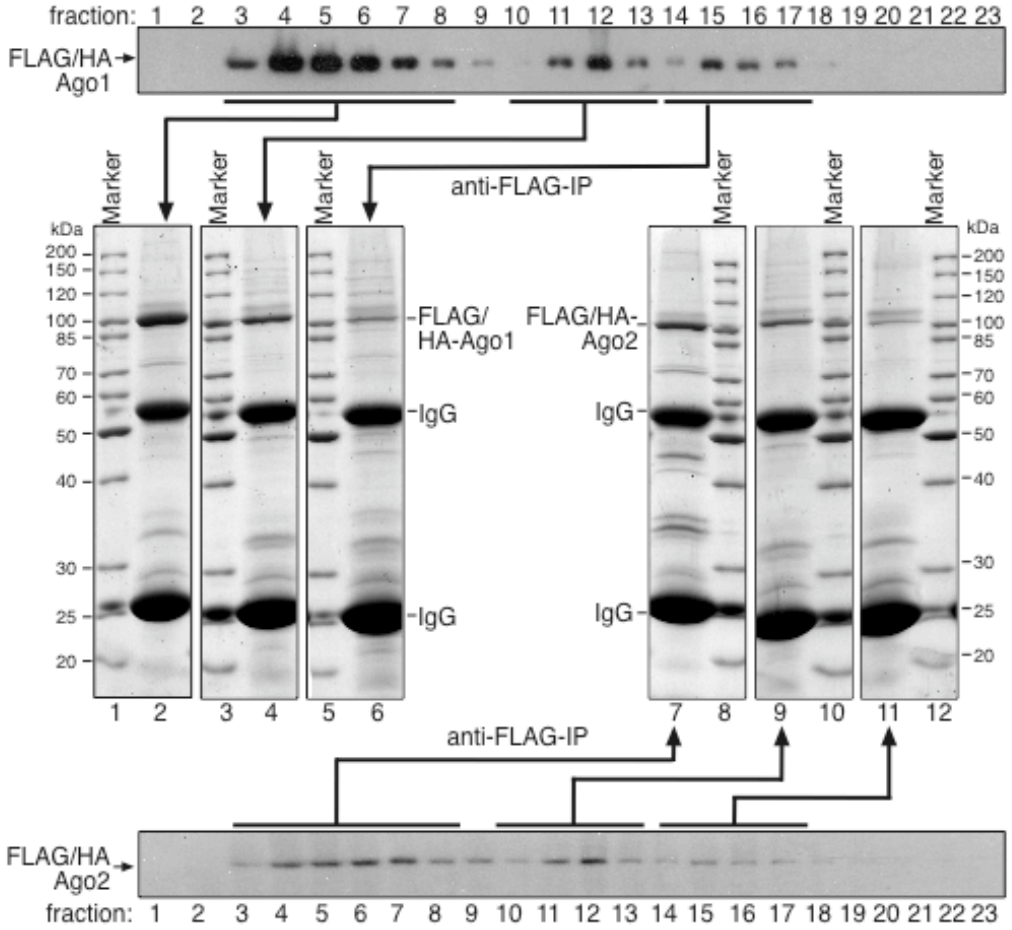
Supplementary Figure 4. SiRNA validation using qRT-PCR. Total RNA was reverse transcribed and cDNA was amplified by qPCR with primers specific to RBM4 (A), YB1 (B), ZBP3 (C) and FMRp (D). mRNA levels relative to GAPDH mRNA were normalized to control transfections. The error bars are derived from three different transfections.

Supplementary Figure 5. Mutant miR-21 cleavage construct shows no significant difference compared to empty vector. SiRNAs against the indicated proteins were pre-transfected into HeLa cells. After 48hrs, a luciferase reporter containing a mutated binding site for miR-21 or

a control vector lacking the miR-21 binding site were transfected. Luciferase assays were done in triplicates. Results from the mutated reporter construct were normalized to those of the empty vector.

Supplementary Figure 6. Overexpression of RBM4 interferes with miRNA-regulated gene silencing. The indicated amounts of plasmids encoding for RBM4 and ZBP3 (control) were co-transfected into HeLa cells together with the KRAS luciferase reporter plasmid. Luciferase assays were done in triplicates. KRAS data were normalized to those of the empty vector.

A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FLAG/HA-Ago2
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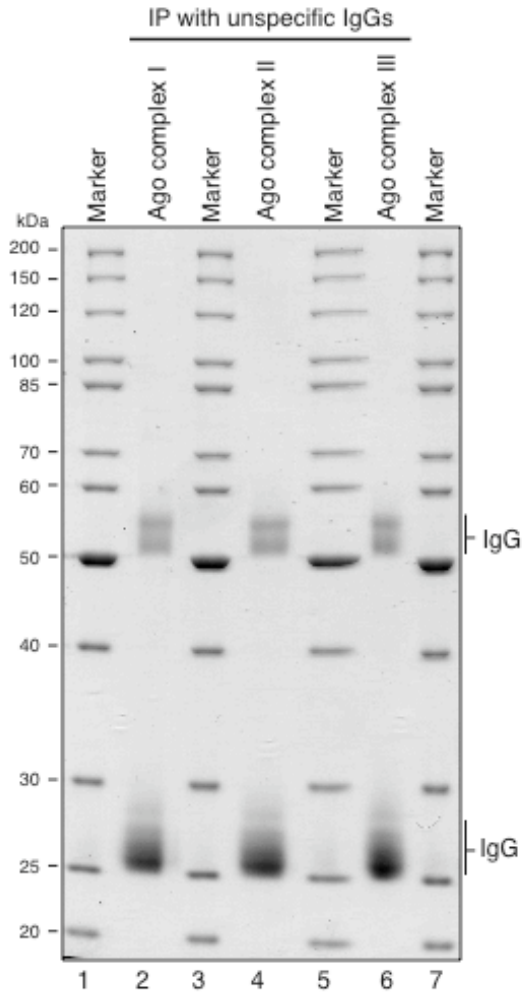
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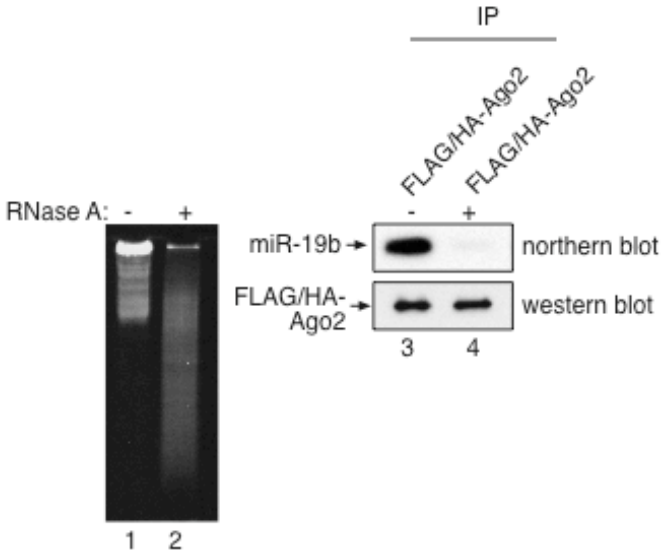
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FLAG/HA-Ago2
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- +
miR-19b
northern blot
FLAG/HA-Ago2
western blot
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3 4

A

miR-21 cleavage construct

CGGCCGGACCTCACGCATCCAGATTA**ATCGAATAGTCTGACTACAACT**CCGAATTTGTTCCACCGCTACTCGAG **- 5'**

5'- TAGCTTATCAGACTGATGTTGA

miR-21

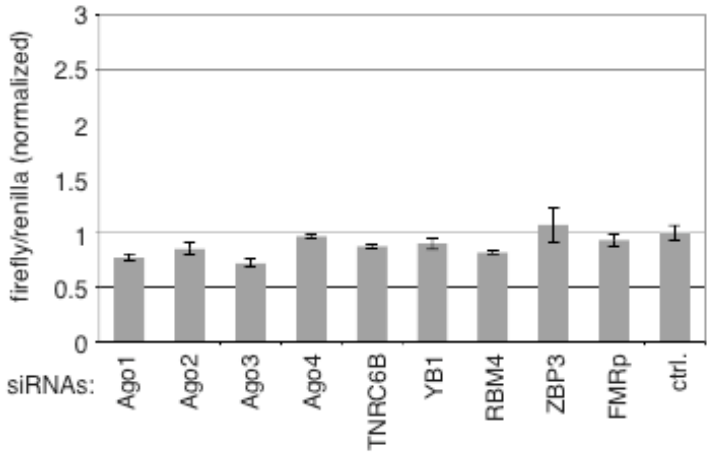
mutant cleavage construct

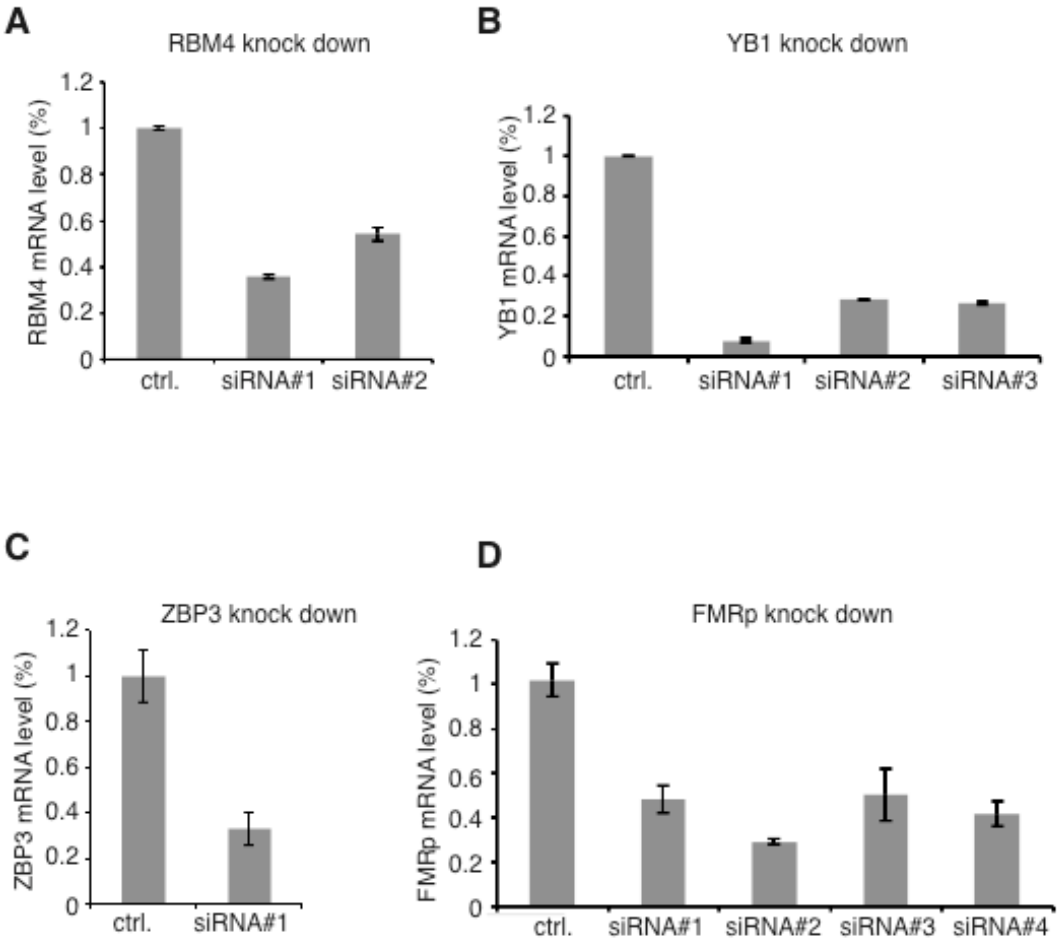
CGGCCGGACCTCACGCATCCAGATTA**AT ATCT TA CCAC GACTACAACT**CCGAATTTGTTCCACCGCTACTCGAG **- 5'**

5'- TAGCTTATCAGACTGATGTTGA

miR-21

B




A
RBM4 knock down
RBM4 mRNA level (%)
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0.6
0.4
0.2
0
ctrl.
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siRNA#2
B
YB1 knock down
YB1 mRNA level (%)
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1
0.8
0.6
0.4
0.2
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siRNA#1
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C
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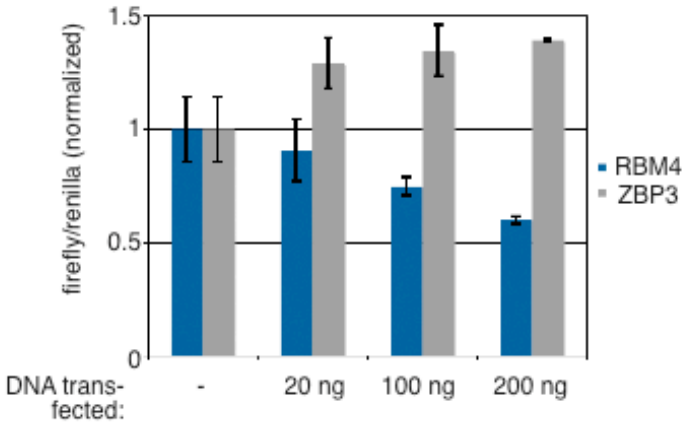
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1
0.5
0
firefly/renilla (normalized)
RBM4
ZBP3
DNA trans-
fected:
-
20 ng
100 ng
200 ng

Supplemental table 1: Protein composition of Ago1 complex 1

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
eukaryotic translation initiation factor 2C, 1 (Ago1) [Homo sapiens]	gi|6912352	97152	26	2058	58	87	-0,0038	K.NASYNLDPYIQEFGIK.V
Dicer	gi|21665773	217490	7	383	5	112	0,1540	K.SNAETATDLVVLDR.Y
squamous cell carcinoma antigen recognized by T cells 3 (SART3) [Homo sapiens]	gi|7661952	109865	6	158	6	40	0,0663	R.YSQYLDR.Q
Na+/K+ -ATPase alpha 1 subunit isoform a proprotein [Homo sapiens]	gi|21361181	112824	2	72	1	39	0,0775	R.LNIPVSQVNPR.D
unnamed protein product [Homo sapiens]	gi|34535987	148788	1	24	-	24	0,0190	K.EPLLHFR.R
DNA damage binding protein 1 (Damage-specific DNA binding protein 1) (DDB p127 subunit) (DDBa) (UV-damaged DNA-binding protein 1) (UV-DDB 1)	gi|418316	126901	4	92	3	50	0,0530	K.LLASINSTVR.L
sirtuin 1 [Homo sapiens]	gi|7657575	81630	1	68	1	68	0,0590	R.GDIFNQVVPR.C
HSPC273 [Homo sapiens]	gi|6841196	25891	1	66	4	66	0,0725	R.ELGENLDQILR.A
E1B-55kDa-associated protein (hnRNP U-like) [Homo sapiens]	gi|3319956	95750	1	48	0	48	0,0579	K.INEEISVK.H
programmed cell death 1 precursor [Homo sapiens]	gi|4826890	31687	1	20	2	20	0,0633	R.RTGQPLK.E
heat shock 90kDa protein [Homo sapiens]	gi|56204416	83212	12	686	24	61	0,0464	K.SIYYITGESK.E
Skb1Hs (PRMT5) [Homo sapiens]	gi|48145599	72638	12	749	25	75	0,0108	K.AAILPTSIFLTNK.K
aralar2 [Homo sapiens]	gi|6523256	74093	3	115	6	86	0,0492	K.TVELLSGVVDQTK.D
chaperonin (HSP60)	gi|306890	60986	7	374	21	55	0,0037	R.VTDALNATR.A
translation initiation factor eIF-2b delta subunit [Homo sapiens]	gi|6563202	57563	1	60	2	60	0,0320	R.VGTAQLALVAR.A
elongation factor Tu [Homo sapiens]	gi|31092	50095	5	194	10	54	0,0206	K.IGGIGTVPVGR.V
RuvB-like 2 [Homo sapiens]	gi|5730023	51125	2	89	4	47	0,0332	K.GTEVQVDDIKR.V
Dnj3/Cpr3 [Homo sapiens]	gi|2352904	46277	1	145	10	32	0,0337	R.ELYDRYGEQGLR.E
trans-activation-responsive RNA-binding protein - human (TRBP) (fragment)	gi|107904	38814	1	36	2	36	0,0358	R.FIEIGSGTSK.K
KIAA0115 [Homo sapiens]	gi|473947	50680	1	31	1	31	0,0317	K.SSLNPILFR.G
MEP50 protein (MEP50) [Homo sapiens]	gi|13559060	36701	5	390	22	93	0,0469	K.VWDLAQQVVLSSYR.A
signal sequence receptor, alpha [Homo sapiens]	gi|4507237	32163	1	44	3	44	0,0306	K.GEDFPANNIVK.F
solute carrier family 25 member 3 isoform a precursor [Homo sapiens]	gi|6031192	40069	1	54	3	54	0,0282	R.IQTQPGYANTLR.D
S3 ribosomal protein [Homo sapiens]	gi|7765076	26699	2	206	25	68	0,0322	R.ELAEDGYSGVEVR.V
solute carrier family 25, member 5 [Homo sapiens]	gi|4502099	32874	7	190	22	49	0,0239	K.LLLQVQHASK.Q
Solute carrier family 25, member A6 [Homo sapiens]	gi|15928608	32905	7	204	22	49/48	0,0239/0,0088	K.LLLQVQHASK.Q / R.GNLANVIR.Y
solute carrier family 25 member 4 variant [Homo sapiens]	gi|62089114	29328	3	131	11	47	0,0142	R.GNLANVIR.Y
transmembrane protein 33 [Homo sapiens]	gi|8922491	27933	1	56	4	56	0,0113	R.ALLANALTSALR.L
ribosomal protein L23 [Homo sapiens]	gi|4506605	14856	1	28	5	28	0,0137	K.NLYIISVK.G
Ribosomal protein S27-like protein [Homo sapiens]	gi|13277528	9472	1	58	9	58	0,0133	R.LTEGCSFR.R + Carb.
ribosomal protein L38 [Homo sapiens]	gi|3088356	4291	1	38	27	38	0,0253	K.QSLPPGLAVK.E
ribosomal protein S6	gi|225901	28633	1	28	3	28	0,0224	K.LIEVDDER.K

Supplemental table 2: Protein composition of Ago1 complex II

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
								K.LLANYFEVDIPK.I /
eukaryotic translation initiation factor 2C, 1 (Ago1) [Homo sapiens]	gi|6912352	97152	30	2142	62	76/76	0,0133/0,0398	K.NASYNLDPYIQEFGIK.V
	gi|38649144	97151	5	332	12	63	0,0179	R.VLPAPILQYGGR.N
splicing factor 3b, subunit 1 isoform 1 [Homo sapiens]	gi|54112117	145738	6	460	8	69	0,0353	R.GGDSIGETPTPGASK.R
Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit)	gi|2498883	97596	5	158	6	57	0,0227	R.AAVLLEQER.Q
RNA helicase A [Homo sapiens]	gi|1806048	140788	9	382	10	58	0,0264	R.GISHVIVDEIHER.D
KIAA0017 protein [Homo sapiens]	gi|40788938	139414	9	302	7	62	0,0263	R.SVAGGFVYTYK.L
DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 (Ddx30) [Homo sapiens]	gi|20336294	133854	4	189	6	44	0,0273	K.AIFQQPPVGVR.K
hnRNP U protein [Homo sapiens]	gi|32358	88890	4	286	5	110	0,0361	R.NFILDQTNVSAAAQR.R
squamous cell carcinoma antigen recognized by T cells 3 (SART3) [Homo sapiens]	gi|7661952	109865	4	151	5	58	0,0224	R.ALEYLKQEVEEER.F
spliceosomal protein SAP 155 [Homo sapiens]	gi|4033735	145723	1	51	0	51	0,0237	R.QQAADLISR.T
gemin4 [Homo sapiens]	gi|7657122	119913	1	45	-	45	0,0193	R.GLTQIQSR.I
F-box and leucine-rich repeat protein 13 [Homo sapiens]	gi|24432072	83887	1	35	2	17	0,0223	K.THFCTWRDIAR.T + Carb
KIAA1488 protein (Dhx36) [Homo sapiens]	gi|7959237	97766	1	27	1	27	0,0334	R.LGGIAYFLSR.L
RNA helicase Gu - human (fragment)	gi|2135315	89196	4	117	-	40	0,043	K.STYEQVDLIGK.K
transcription factor NF-AT 90K chain - human	gi|1082856	73293	3	114	-	52	0,0559	R.EDITQSAQHALR.L
ATP-dependent RNA helicase #46 [Homo sapiens]	gi|2996613	92770	1	112	3	44	0.06	R.YGVIILDEAHER.T
motor protein [Homo sapiens]	gi|516764	79659	2	88	3	46	0,0521	R.GVYSEETLR.A
hypothetical protein LOC55037 [Homo sapiens]	gi|38683855	78500	4	232	7	53	0,0595	K.DISEAALKER.I
ZNF326 protein [Homo sapiens]	gi|31807861	33426	2	109	7	61	0,0775	R.SGYGFNEPEQSR.F
NSAP1 protein [Homo sapiens]	gi|5031512	62617	2	102	4	60	0,0886	R.TGYTLDVTTGQR.K
Skb1Hs (PRMT5) [Homo sapiens]	gi|2323410	72740	3	90	5	32	0,0664	R.GPLVNASLR.A
mRNA-binding protein CRDBP [Homo sapiens]	gi|7141072	63417	3	145	6	50	0,1205	R.DQTPDENDQVIVK.I
poly(A) binding protein, cytoplasmic 1 [Homo sapiens]	gi|46367787	70626	4	128	-	66	0,0246	R.IVATKPLYVALAQR.K
E2IG3 [Homo sapiens]	gi|6457340	63528	1	35	1	35	0,084	K.GGIPNVEGAAK.L
ribosomal protein L4 [Homo sapiens]	gi|16579885	47667	1	153	6	56	0,0646	K.AAAAAAALQAK.S
heterogeneous nuclear ribonucleoprotein H2 (H') [Homo sapiens]	gi|6065880	49232	1	61	3	61	0,0995	K.HTGPNSPDTANDGFVR.L
DNA-binding protein B (Homo sapiens)	gi|181486	39954	9	538	28	115	0,1146	K.GAEAANVTGPGGVPVQGSK.Y
elongation factor Tu [Homo sapiens]	gi|31092	50095	4	130	9	37	0,0854	R.YEEIVKEVSTYIK.K
HNRPF protein [Homo sapiens]	gi|16876910	45671	1	66	3	66	0,0805	K.HSGPNSADSANDGFVR.L
Rev interacting protein Rip-1	gi|1326184	33263	2	60	6	37	0,0634	R.SVSFEQAVR.I
translation initiation factor (Ddx48) [Homo sapiens]	gi|496902	46803	1	13	3	13	0,1046	R.GIYAYGFEKPSAIQQR.A
NF45 protein	gi|532313	44669	2	117	5	65	0,0579	K.VLQSALAAIR.H
LYAR [Homo sapiens]	gi|49065522	43626	1	92	3	92	0,0949	R.ELLEQISAFDNVPR.K
KIAA0264 [Homo sapiens]	gi|1665795	47767	1	89	4	58	0,0533	R.LIDNISSR.E
MEP50 protein (MEP50) [Homo sapiens]	gi|13559060	36701	1	31	4	31	0,0842	R.YRSDGALLLGASSLSGR.C
mitochondrial ribosomal protein S5 [Homo sapiens]	gi|13994259	47976	2	105	5	73	0,0862	R.AIITCR.L + Carb
ionizing radiation resistance conferring protein - human	gi|7430427	43584	3	104	-	45	0,0508	R.NATDAVGIVLK.E
Mitochondrial ribosomal protein S22 [Homo sapiens]	gi|14424546	41254	2	169	12	30	0,0572	K.DQAAEGINLIK.V
60S acidic ribosomal protein P0 (L10E)	gi|3041728	33236	2	229	14	57	0,1075	R.GTIEILSDVQLIK.T
ribosomal protein L6 [Homo sapiens]	gi|36138	32841	3	99	10	46	0,0912	R.SVFALTNGIYPHK.L
Hypothetical protein PRO1855 [Homo sapiens]	gi|16877878	34909	2	42	7	28	0,152	K.LVTLPVSFAQLK.N
ribosomal protein S3a [Homo sapiens]	gi|4506723	29926	7	279	35	57	0,1812	R.EVQTNDLKEVVNK.L
prohibitin 2 [Homo sapiens]	gi|6005854	33276	2	143	12	74	0,1698	K.LLLGAGAVAYGVR.E
ribosomal protein S2 [Homo sapiens]	gi|15055539	31305	8	442	40	63	0,1102	R.GTGIVSAPVPK.K
mitochondrial ribosomal protein S2 [Homo sapiens]	gi|55958121	30460	1	32	2	32	0,1113	K.GIILFISR.N
ribosomal protein S6	gi|337514	28614	3	173	31	59	0,1626	L.LFNLSKEDDVR.E
S3 ribosomal protein [Homo sapiens]	gi|7765076	26699	6	350	33	72	0,1654	R.ELAEDGYSGVEVR.V
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform H (heart) precursor [Homo sapiens] ?alpha subunit found	gi|4885079	32860	1	106	8	67	0,1784	R.IYGLGSLALYEK.A
solute carrier family 25 member 3 isoform a precursor [Homo sapiens]	gi|6031192	40069	1	50	3	50	0,187	R.IQTQPGYANTLR.D
ribosomal protein S4	gi|227229	29664	4	208	18	64	0,1729	K.VNDTIQIDLETGK.I
ribosomal protein L7 [Homo sapiens]	gi|35903	29164	3	178	12	81	0,1303	R.IALTDNALIAR.S
ribosomal protein L14 [Homo sapiens]	gi|1620022	23788	1	49	5	49	0,1671	K.LVAIVDVIDQNR.A
unnamed protein product [Homo sapiens]	gi|34392	24191	1	33	3	33	0,11	K.ATFDAISK.T
prohibitin [Homo sapiens]	gi|4505773	29786	4	203	16	83	0,1505	R.FDAGELITQR.E
ADP,ATP translocase	gi|339721	28042	4	182	15	63	0,1574	R.AAYFGIYDTAK.G
ribosomal protein L13 [Homo sapiens]	gi|15431297	24247	1 / 2	101 / 79	11 / 8	67 / 46	0,2710 / 0,1869	K.STESLQANVQR.L / R.VATWFNQPAR.K
ribosomal protein L10 [Homo sapiens]	gi|5174431	24561	5	290	38	52	0,2486	R.GAFGKPQGTVAR.V
ribosomal protein L13a [Homo sapiens]	gi|6912634	23562	4	244	29	68	0,2626	K.YQAVTATLEEK.R
ribosomal protein S9	gi|550023	22558	4	123	16	48	0,2173	R.LFEGNALLR.R
mitochondrial ribosomal protein S23 [Homo sapiens]	gi|16554604	21757	2	55	11	37	0,3242	K.APIQDIWYHEDR.I
ribosomal protein L19 [Homo sapiens]	gi|4506609		1	56	4	56	0,1872	K.LLADQAEAR.R
mitochondrial ribosomal protein S15 [Homo sapiens]	gi|16554611	29823	1	46	3	46	0,2045	K.IVANPEDTR.S
ribosomal protein L29 [Homo sapiens]	gi|793843	17656	1	93	10	51	0,2829	K.AQAAAPASVPAQAPK.R
Ribosomal protein S5 [Homo sapiens]	gi|550021	22763	1	45	4	45	0,2053	R.QAVDVSPLR.R
Ribosomal protein L17 [Homo sapiens]	gi|42542645	21402	6	391	51	46	0,2477	R.YSLDPENPTK.S
ribosomal protein L24 [Homo sapiens]	gi|4506619	17768	3	327	30	62	0,2436	R.TDGKVFQFLNAK.C
ribosomal protein S7 [Homo sapiens]	gi|4506741	22113	2	36	8	18 / 18	0,1832 / 0,2003	R.ELNITAAK.E / K.HVVFIAQR.R
RPL21 protein [Homo sapiens]	gi|38649057	18553	1	36	9	36	0,3273	R.VYNVTQHAVGIVVNK.Q
FUS interacting protein (serine-arginine rich) 1 [Homo sapiens]	gi|55961039	22122	1	31	6	31	0,2568	R.YLRPPNTSLFVR.N
ribosomal protein L26	gi|292435	17278	4	169	28	43	0,1556	K.YVIYIER.V
ribosomal protein L11 [Homo sapiens]	gi|14719845	20112	3	152	19	77	0,2808	K.VLEQLTGQTPVFSK.A
ribosomal protein L23a [Homo sapiens]	gi|1574942	17629	2	117	13	68	0,2592	R.LAPDYDALDVANK.I
ribosomal protein L18a [Homo sapiens]	gi|11415026	20749	1	24	3	24	0,1656	K.NFGIWLR.Y
ribosomal protein L27a [Homo sapiens]	gi|4506625	16551	4	142	14	76	0,1704	K.TGAAPIIDVVR.S
ribosomal protein L28	gi|550019	15752	3	132	17	62	0,2314	K.QTYSTEPNNLK.A
ribosomal protein L35 [Homo sapiens]	gi|6005860	14543	2	122	21	49	0,2655	R.VLTVINQTQKENLR.K
Ribosomal protein S18 [Homo sapiens]	gi|75517276	17708	3	233	30	89	0,1868	R.AGELTEDEVER.V
ribosomal protein S26 [Homo sapiens]	gi|296452	12922	2	221	31	124	0,2636	R.DISEASVFDAYVLPK.L
ribosomal protein L23 [Homo sapiens]	gi|4506605	14856	2	148	30	34	0,1091	K.NLYIISVK.G
ribosomal protein homologous to yeast S24 [Homo sapiens]	gi|36142	14707	2	135	25	59	0,2588	K.HGYIGEFEIIDDHR.A
ribosomal protein S23 [Homo sapiens]	gi|3088342	6465	2	110	38	69	0,1774	K.VANVSLLALYK.G
PREDICTED: similar to ribosomal protein S27 [Homo sapiens]	gi|51463957	18745	1	86	-	41	0,2139	K.DLLHPSPEEEKR.K
ribosomal protein L38 [Homo sapiens]	gi|3088356	4291	2	79	59	51	0,2235	R.YLYTLVITDKEK.A
splicing factor 3B, 14 kDa subunit [Homo sapiens]	gi|7706326	14576	2	71	16	42	0,2498	R.GTAYVVYEDIFDAK.N
ribosomal protein L31 [Homo sapiens]	gi|1655596	14084	2	67	28	32	0,2614	K.LYTLVTYVPVTTFK.N
mitochondrial ribosomal protein S16 [Homo sapiens]	gi|7705626	15335	2	41	18	38	0,1442	K.LVALNLDR.I
ribosomal protein L35a [Homo sapiens]	gi|16117791	12530	1	36	13	28	0,1292	K.IEGVYAR.D
PHD-finger 5A [Homo sapiens]	gi|14249398	12397	1	33	6	33	0,1486	K.TDLFYER.K

Supplemental table 3: Protein composition of Ago1 complex III

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
eukaryotic translation initiation factor 2C, 1 (Ago1) [Homo sapiens]	gi|6912352	97152	24	1797	60	89	0.2587	K.LLANYFEVDIPK.I
Transcription factor (TFIIIC) alpha chain, partial [Homo sapiens]	gi|2342740	209464	2	105	1	43	0.1593	R.GYYSPGIVSTR.N
RNA helicase A -- human	gi|1082769	141984	20	1135	26	64	0.1842	K.LAQFEPSQR.Q
hnRNP U protein [Homo sapiens]	gi|32358	88890	12	401	16	95	0.2567	K.SSGPTSLFAVTVAPPGAR.Q
MYB binding protein 1a [Homo sapiens]	gi|7657351	148758	12	628	13	69	0.1538	K.ALVDILSEVSK.A
ubiquitin	gi|229532	8446	1	26	12	26	0.1429	R.TLSDYNIQK.E
Dicer [Homo sapiens]	gi|5019620	218673	2	62	0	62	0.1331	R.AQTASDAGVGVR.S
U5 snRNP-specific 200kD protein [Homo sapiens]	gi|3255965	194356	2	46	0	27	0.1184	R.TYTQLVR.L
polymerase (RNA) I polypeptide A, 194kDa [Homo sapiens]	gi|7661686	194068	1	32	-	32	0.1293	R.GYLTPTSAR.E
proliferation-inducing protein 32 [Homo sapiens]	gi|45643460	162923	11	421	9	84	0.2010	K.SLYDEVAAQGEVVR.K
PELP1 [Homo sapiens]	gi|21426922	136556	7	320	7	65	0.1701	R.LPSLGAGFSQGLK.H
coatomer protein [Homo sapiens]	gi|1002369	138244	6	247	6	53	0.1850	K.LVGQSIIAYLQK.K
DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 (Ddx30) [Homo sapiens]	gi|20336294	133854	14	662	16	76	0.2654	R.ENYLEENLLYAPSLR.F
regulator of nonsense transcript stability (RENT1) [Homo sapiens]	gi|1575536	123039	8	293	9	51 / 51	0.1395 / 0.1640	R.YGVIVGNPK.A / R.EAIIPGSVYDR.S
squamous cell carcinoma antigen recognized by T cells 3 (SART3) [Homo sapiens]	gi|7661952	109865						
Splicing factor 3B subunit 3 (Spliceosome associated protein 130) (SAP 130) (SF3b130) (Pre-	gi|19863446	135507	2	82	-	46	0.1859	R.FLAVGLVDNTVR.I
spliceosomal protein SAP 155 [Homo sapiens]	gi|4033735	145723	1	32	1	14	0.1482	K.TEILPPFFK.H
unnamed protein product [Homo sapiens]	gi|7023011	113841	3	84	2	52	0.1564	R.QSILNSLSR.G
novel S-100/ICaBP type calcium binding domain and EF hand domain containing protein	gi|12314268	24325	1	54	-	54	0.2037	R.SVTVIDVIFYK.Y
KIAA1488 protein (Dhx36) [Homo sapiens]	gi|7959237	97766	1	38	1	38	0.1752	R.LGGIAYFLSR.L
matrin 3 [Homo sapiens]	gi|6563246	95138	1	36	1	36	0.1478	K.SFQSSLSR.D
Chain A, Human Dna Topoisomerase I (70 Kda) In Non-Covalent Complex With A 22 Base	gi|3659924	69975	5	210	11	65	0.2323	R.TYNASITLQQQLK.E
gemin4 [Homo sapiens]	gi|7657122	119913	3	123	-	52	0.2582	R.LLETVIDVSTADR.A
Nucleolin (Protein C23)	gi|128841	76298	3	94	-	42	0.3323	R.SISLYYTGEKGQNQDYR.G
serine protein kinase SRPK1 -- human	gi|630737	74273	1	45	-	45	0.2781	K.SAEAYTETAEDEIR.L
RNA helicase Gu - human (fragment)	gi|2135315	89196	5	142	-	41	0.2663	K.STYEQVDLIGKK.T
NF-90 [Homo sapiens]	gi|5006602	82749	9	470	18	47	0.2972	K.AVSDWIDEQEK.G / R.IFVNDDR.H
nbla10363 [Homo sapiens]	gi|19911062	105622	3	132	4	41	0.1882	K.SLQATALR.I
fragile X mental retardation syndrome related protein 2 [Homo sapiens]	gi|4758410	74083	4	122	6	62	0.3632	K.AGYSTDESSSSSLHATR.T
novel protein [Homo sapiens]	gi|5578958	81192	1	50	3	31	0.3445	R.GLHSQNFTQALLER.M
DEAD (Asp-Glu-Ala-Asp) box polypeptide 50 [Homo sapiens]	gi|5596207	82514	2	48	4	27	0.2840	R.GVTYLFPIQVK.T
motor protein [Homo sapiens]	gi|516764	79659	1	41	1	41	0.3122	K.VVSGYHELVVQAR.D
90kDa heat shock protein	gi|306891	83242	1	37	1	37	0.2755	K.ADLINNLGTIAK.S
general transcription factor IIIC, polypeptide 4, 90kDa [Homo sapiens]	gi|6912400	91943	1	31	1	31	0.2307	K.QVDLIDLVR.W
RNA helicase (Ddx18) [Homo sapiens]	gi|1498229	68416	3	201	7	77	0.3234	K.LGNGINIIVATPGR.L
motor protein [Homo sapiens]	gi|516768	83626	3	117	5	52	0.2728	R.YSTSGSSGLTTGK.I
ZNF326 protein [Homo sapiens]	gi|4725447	57787	2	112	4	72	0.3989	R.ESVLTATSILNNPIVK.A
FMR1	gi|182673	74981	1	22	1	22	0.2391	R.LQIDEQLR.Q
polyadenylate binding protein II [Homo sapiens]	gi|693937	58481	16	808	39	66	0.2400	R.IVATKPLYVALAQR.K
putative G-binding protein [Homo sapiens]	gi|3153873	65375	2	78	4	52	0.2486	R.ADVDVQPYAFTTK.S
IGF-II mRNA-binding protein 1 (ZBP-1) [Homo sapiens]	gi|56237027	63441	10	499	21	92	0.3391	K.ITISSLQDLTLYNPER.T
IGF-II mRNA-binding protein 3 (ZBP-3) [Homo sapiens]	gi|30795212	63666	6	274	12	61	0.2814	R.DQTPDENDQVVVK.I
E2IG3 [Homo sapiens]	gi|6457340	63528	6	207	11	49	0.1862	K.GGIPNVEGAAK.L
PBK1 protein [Homo sapiens]	gi|3668141	58097	3	103	5	37	0.1655	R.LLPSLIGR.H
NSAP1 protein [Homo sapiens]	gi|5031512	62617	2	65	3	44	0.2641	R.NLANTVTEEILEK.A
hNoo56 [Homo sapiens]	gi|2230878	66807	2	62	3	39	0.1809	R.VVSLSEYR.Q
G22P1 [Homo sapiens]	gi|4947432	69829	1	53	1	53	0.2187	R.DSLIFLVDASK.A
KIAA1273 protein [Homo sapiens]	gi|6382028	68066	2	47	3	35	0.1802	R.QTVLESIR.T
Similar to ribophorin I [Homo sapiens]	gi|14124942	64542	1	31	1	31	0.1624	K.IILPEGAK.N
heterogeneous nuclear ribonucleoprotein L [Homo sapiens]	gi|11527777	64046	1	55	1	55	0.2128	R.SSSGLLEWESK.S
t-complex polypeptide 1 [Homo sapiens]	gi|36796	60356	1	37	1	37	0.1868	R.YPVNSVNILK.A
testis-specific poly(A)-binding protein [Homo sapiens]	gi|11610605	70072	1	33	2	33	0.2196	R.IVATKPLYVALAQR.K
ribophorin II precursor - human	gi|88567	69273	1	29	-	29	0.1694	R.YIANTVELR.V
Ost-I [Homo sapiens]	gi|4138665	102111	1	13	1	13	0.1875	R.HLCDQFSAEIAR.R + Carb.
ribosomal protein L4 [Homo sapiens]	gi|16579885	47667	5	279	19	43	0.1513	R.NIPGITLLNVSK.L
DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 1 [Homo sapiens]	gi|20149629	50615	2	85	5	43	0.1470	R.DIIGLAETGSGK.T
nuclear RNA helicase (Ddx39) [Homo sapiens]	gi|1905998	49046	1	45	2	45	0.1370	R.ILVATNLFGR.G
translation initiation factor (KIAA0111) [Homo sapiens]	gi|496902	46803	6	207	15	51	0.1949	R.ETQALILAPTR.E
Ribosomal protein P0 [Homo sapiens]	gi|12654583	34253	7	519	43	76	0.0606	K.TSFFQALGITTK.I
NF45 protein	gi|532313	44669	8	469	25	64 / 64	0.0115 / 0.0249	K.VLQSALAAIR.H / K.ILPTLEAVAALGNK.V
PAK/PLC-interacting protein 1 [Homo sapiens]	gi|14211689	44076	1	44	2	44	0.1426	K.LALSVGTDK.T
unnamed protein product [Homo sapiens]	gi|31092	50095	1	37	2	37	0.1690	K.IGGIGTVPVGR.V
KIAA1756 protein [Homo sapiens]	gi|12998057	116668	1	30	0	30	0.0590	R.AELEKVDLR.A
R32184_1 [Homo sapiens]	gi|3025445	47276	1	26	2	26	0.1660	K.SVLGGQDQLR.V
WS beta-transducin repeats protein [Homo sapiens]	gi|4704417	47537	1	24	2	24	0.1765	K.YLATCADDR.T + Carb.
HNRPC protein [Homo sapiens]	gi|13937888	33578	4	349	20	71	0.0539	R.VFIGNLNTLVVK.K
RNA polymerase I subunit isoform 2 [Homo sapiens]	gi|4759046	38623	2	93	5	49	0.0182	R.VVLGEFGVR.N
ribosomal protein L6 [Homo sapiens]	gi|36138	32841	7	265	22	50	0.0414	K.FVATSTK.I
EBNA1 binding protein 2 [Homo sapiens]	gi|5803111	34798	1	55	3	55	0.0383	R.ESYDDVSSFR.A
B23 nucleophosmin (280 AA) [Homo sapiens]	gi|825671	30919	2	109	7	57	0.0379	K.GPSSVEDIK.A
hnRNP-E2 [Homo sapiens]	gi|460773	38556	1	56	3	56	0.0448	K.IANPVEGSTDR.Q
HuR RNA binding protein	gi|1022961	36039	1	73	3	73	0.0541	R.VLVDQTTGLSR.G
putative dimethyladenosine transferase [Homo sapiens]	gi|3646270	17915	1	46	6	46	0.0453	K.SSAVQQLLEK.N
prohibitin 2 [Homo sapiens]	gi|6005854	33276	10	513	35	90	0.0478	K.FNASQLITQR.A
ribosomal protein S3a [Homo sapiens]	gi|4506723	29926	4	278	38	56	0.0516	R.EVQTNDLIKEVVNK.L
ribosomal protein S6	gi|337514	28614	2	289	16	73	0.0372	K.LIEVDDER.K
SMN-interacting protein 1 isoform alpha [Homo sapiens]	gi|4506961		1	32	2	32	0.0362	R.TPQEYLR.R
PREDICTED: hypothetical protein XP_499151 [Homo sapiens]	gi|51467206	12243	1	22	-	22	0.1148	K.VCSWPVDLDSK.G
distal-less homeobox 4 isoform a [Homo sapiens]	gi|20143962	26246	1	22	6	22	0.0799	-.MTSLPCPLPGRDASK.A + Oxid.
ribosomal protein L7a [Homo sapiens]	gi|4506961	29977	11	535	50	92	0.0422	R.AGVNTVTTLVENK.K
Ribosomal protein L8 [Homo sapiens]	gi|15341853	27993	7	311	27	76	0.0493	R.ASGNYATVISHNPETK.K
ribosomal protein S2 [Homo sapiens]	gi|15055539	31305	6	277	25	48	0.0565	K.TYSYLTPDLWK.E
S3 ribosomal protein [Homo sapiens]	gi|7765076	26699	3	165	18	67	0.0604	R.ELAEDGYSGVEVVR.V
solute carrier family 25 member 3 isoform a precursor [Homo sapiens]	gi|6031192	40069	1	50	3	50	0.0594	R.IQTQPGYANTLR.D
scar protein	gi|337930	27386	10	423	42	90	0.0455	K.VNDTIQIDLETGK.I
ribosomal protein L7 [Homo sapiens]	gi|35603	29164	6	304	36	83	0.0317	R.IALTDNAIAR.S
prohibitin [Homo sapiens]	gi|4505773	29786	6	308	23	89	0.0292	K.AAIISAEGDSK.A
ADP,ATP translocase	gi|339721	28042	2	79	9	42	0.0444	R.AAYFGIYDTAK.G
Unknown (protein for MGC:117326) [Homo sapiens]	gi|76779245	36999	10	440	27	98	0.0343	R.IALTDNALIAR.S
ribosomal protein S4	gi|227229	29664	2	82	9	57	0.0297	R.LSNIFVIGK.G
ribosomal protein S8 [Homo sapiens]	gi|5596108 0	2186	2	79	13	64	0.0221	K.ISSLLEEQFQQGK.L
60S ribosomal protein L13	gi|6831614	24378	1	72	5	72	0.0266	K.STESLQANVQR.L
ribosomal protein L13 [Homo sapiens]	gi|15431297	24247	2	139	16	72	-0.0036	K.STESLQANVQR.L
ribosomal protein L14 [Homo sapiens]	gi|1620022	23788	1	86	5	86	0.0163	K.LVAIVDVIDQNR.A
ribosomal protein L19 [Homo sapiens]	gi|4506609		1	72	4	72	-0.0192	K.LLADQAEAR.R
ribosomal protein L18 [Homo sapiens]	gi|4506607	21621	7	453	41	103	-0.0268	K.ILTFDQLALDSPK.G
ribosomal protein L13a [Homo sapiens]	gi|6912634	23562	4	237	28	68	-0.0100	K.YQAVTATLEEK.R
ribosomal protein L15 [Homo sapiens]	gi|15431293	24131	4	140	18	65	-0.0128	R.SLQSVAEER.A
ribosomal protein S9	gi|550023	22558	9	373	39	49	0.0154	R.LGVLDEGK.M
ribosomal protein L10 [Homo sapiens]	gi|5174431	24561	2	83	17	35	-0.0132	R.GAFGKPQGTVAR.V
Ribosomal protein S5 [Homo sapiens]	gi|15929961	22862	1	51	4	51	-0.0091	R.QAVDVSPLR.R
ribosomal protein L29 [Homo sapiens]	gi|793843	17656	2	130	15	56	-0.0696	K.AQAAAPASVPAQAPKR.T
ribosomal protein S7 [Homo sapiens]	gi|4506741	22113	5	196	18	46	-0.0254	K.VETFSGVYK.K
Ribosomal protein L17 [Homo sapiens]	gi|42542645	21402	3	198	23	51	-0.0285	R.YSLDPENPTK.S
L21 ribosomal protein	gi|619788	17646	2	80	17	43	-0.0441	R.VYNVTQHAVGIVVNK.Q
ribosomal protein L24 [Homo sapiens]	gi|4506619	17768	3	191	21	45	-0.0534	R.TDGKVFQFLNAK.C
ribosomal protein L18a [Homo sapiens]	gi|11415026	20749	2	43	30	43	-0.0278	R.IFAPNHVVAK.S
ribosomal protein L11 [Homo sapiens]	gi|14719845	20112	7	363	31	97	-0.0372	K.VLEQLTGQTPVFSK.A
ribosomal protein L26 [Homo sapiens]	gi|4506621	17248	3	243	26	33	-0.0321	K.DDEQVVR.G
ribosomal protein L12 [Homo sapiens]	gi|55665101	17808	3	165	24	65	-0.0607	K.HSGNITFDEIVNIAR.Q
ribosomal protein L23a [Homo sapiens]	gi|1574942	17629	2	108	13	59	-0.0328	R.LAPDYDALDVANK.I
ribosomal protein L27a [Homo sapiens]	gi|4432754	3706	1	57	32	57	-0.0284	K.TGAAPIIDVVR.S
ribosomal protein L28	gi|550019	15752	5	338	43	52 / 52	-0.0343 / -0.0738	K.VVVVKR.R / K.GTYSTEPNNLVQR.L
ribosomal protein L11 [Homo sapiens]	gi|495126	20103	3	215	16	55	-0.0786	K.VLEQLTGQTPVFSKAR.Y
ribosomal protein S13 [Homo sapiens]	gi|553640	13313	4	101	24	50	-0.0420	K.GLTPSQIGVILR.D
PREDICTED: similar to 60S ribosomal protein L32 [Homo sapiens]	gi|51467067	52271	1	64	-	39	-0.0630	R.AAQLAIRVTNPNAR.Q
ribosomal protein L35 [Homo sapiens]	gi|6005860	14543	2	142	21	47	-0.0744	R.VLTVINQTQKENLR.K
ribosomal protein S28 [Homo sapiens]	gi|296452	12922	2	168	31	73	-0.0614	R.DSEASVFDAYVLPK.L
ribosomal protein L23 [Homo sapiens]	gi|4506605	14856	2	247	51	39	-0.0393	K.GSAITGPVAK.E
Ribosomal protein S15a [Homo sapiens]	gi|12804561	14770	3	209	60	74	-0.0769	K.HGYIGEFEIIDDHR.A
ribosomal protein L37a [Homo sapiens]	gi|4506643	10268	1	132	39	102	-0.0533	K.TVAGGAWTYNTTSAVTVK.S
PREDICTED: similar to ribosomal protein S27 [Homo sapiens]	gi|51463957	18745	1	94	-	41	-0.0609	K.DLLHPSPEEEKR.K
Mov10	gi|14424568	43599	6	52	6	52	0.06	R.ITGNPVVTNP.I

Supplemental table 4: Protein composition of Ago2 complex I

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
eukaryotic initiation factor 2C2 (Ago2) [Homo sapiens]	gi|29171734	97146	12	1104	40	91	0,0204	R.SVSIPAPAYYAHLVAFR.A
solute carrier family 25 member 3 isoform a precursor [Homo sapiens]	gi|6031192	40069	5	217	14	62	0,0382	R.IQTQPGYANTLR.D
Dicer [Homo sapiens]	gi|5019620	218673	6	353	5	112	0,0632	K.SNAETATDLVVLDR.Y
KIAA1093 protein [Homo sapiens]	gi|14133235	183156	3	169	3	74	0,0779	K.TGSVGSWGAAR.G
HsGCN1 [Homo sapiens]	gi|2282576	211377	1	41	0	41	0,0405	K.ASLLDPVPEVR.T
Na+,K+ ATPase [Homo sapiens]	gi|1359715	111901	1	122	3	47	0,0305	R.LNIPVSQVNPR.D
RNA-binding protein 10 (RNA-binding motif protein 10) (DXS8237E)	gi|12644371	103396	1	40	1	40	0,0326	R.DGLGSDNIGSR.M
HSPC273 [Homo sapiens]	gi|6841196	25891	1	95	10	74	0,1177	R.ELGENLDQILR.A
importin 4 [Homo sapiens]	gi|18700635	118642	1	70	1	41	0,0912	R.ELLLPDTER.I
DNA damage binding protein 1 (Damage-specific DNA binding protein 1) (DDB p127 subunit) (DDBa) (UV-damaged DNA-binding protein 1) (UV-DDB 1)	gi|418316	126901	1	31	2	24	0,1030	K.VTLGTQPTVLR.T
importin 8 [Homo sapiens	gi|53759103	119861	1	30	0	30	0,1061	K.IINFAPSLLR.I
eukaryotic translation initiation factor 2C, 3 (Aqo3) [Homo sapiens]	gi|56204478	71165	12	1104	16	91	0,0204	R.SVSIPAPAYYAHLVAFR.A
Heat shock protein 90 [Homo sapiens]	gi|56204416	83212	8	520	13	81	0,0209	R.GVVDSEDLPLNISR.E
PREDICTED: similar to liver phosphofructokinase isoform b; 6-phosphofructokinase, liver type; liver-type 1-phosphofructokinase; phosphofructokinase 1	gi|55657570	85437	1	53	-	48	0,0934	R.FDEATQLR.G
initation factor 4B [Homo sapiens]	gi|288100	69183	1	32	2	32	0,1246	R.AASIFGGAKPVDTAAR.E
MTHSP75	gi|292059	73734	2	25	6	33	0,0469	R.QAVTNPNNTFYATKR.L
Skb1Hs [Homo sapiens]	gi|82581643	72520	10	710	25	66	0,1128	K.YSQYQQAIYK.C
aralar2 [Homo sapiens]	gi|6523256	74093	2	100	2	61	0,1153	R.LQVAGEITTGPR.V
proteasome subunit p58 [Homo sapiens]	gi|2656092	60968	1	44	2	44	0,0964	R.VYEFLDKLDVVR.S
glycoprotein-associated amino acid transporter hb0,+AT1 [Homo sapiens]	gi|5823978	53436	1	32	1	32	0,0358	K.VLSYISVRR.L
Chaperonin [Homo sapiens]	gi|49522865	61016	5	348	10	79	0,0927	K.NAGVEGSLIVEK.I
mitogen-activated protein kinase kinase kinase 7 interacting protein 1 isoform alpha [Homo sapiens]	gi|5174703	54610	1	64	2	64	0,1068	K.YGYTDIDLLSAAK.S
TATA binding protein interacting protein 49 kDa [Homo sapiens]	gi|4506753	50196	1	61	2	61	0,0746	K.QAASGLVGQENAR.E
elongation factor Tu	gi|556301	50132	4	196	10	65	0,0505	K.THINIVVIGHVDSGK.S
RuvB-like 2 [Homo sapiens]	gi|5730023	51125	2	140	4	82	0,0451	R.GLGLDDALEPR.R
trans-activation-responsive RNA-binding protein - human (TRBP) (fragment)	gi|107904	38814	1	46	2	46	0,0250	R.FIEIGSGTSK.K
unnamed protein product [Homo sapiens]	gi|31092	50095	3	88	6	39	0,0260	K.IGGIGTVPVGR.V
HNRPF protein [Homo sapiens]	gi|16876910	45671	1	64	4	51	0,0328	R.YIEVFKSSQEEVR.S
26S proteasome regulatory chain 4 [validated] - human	gi|345717	49210	1	46	-	46	0,0247	K.GVILYGPPGTGK.T
MEP50 protein (MEP50) [Homo sapiens]	gi|13559060	36701	4	343	21	89	0,0813	K.VWDLAQQVVLSSYR.A
brain tumor associated protein LRRC4 [Homo sapiens]	gi|14495561	72671	1	47	1	47	0,0122	R.MAELKCR.T
otopetrin 2 [Homo sapiens]	gi|30039714	62195	1	43	1	43	0,0044	R.EAVAIVSTPR.S
Cl channel	gi|228672	25872	1	92	5	92	0,0186	K.GLGTGTLYIAESR.L
7-dehydrocholesterol reductase [Homo sapiens]	gi|3171089	53073	1	38	1	38	0,0129	R.YTAAVPYR.L
oxidase (cytochrome c) assembly 1-like [Homo sapiens]	gi|4826880	55262	1	37	1	37	0,0062	R.NQLELAAR.G
[Human pre-mRNA splicing factor SF2p32, complete sequence.], gene product	gi|338043	30888	4	469	33	81	0,0706	R.EVSFQSTGESEWK.D
emerin [Homo sapiens]	gi|4557553	28976	1	40	3	40	0,0357	R.APGAGLGQDR.Q
Solute carrier family 25, member A6 [Homo sapiens]	gi|15928608	32905	12	420	33	66	0,0461	K.LLLQVQHASK.Q
solute carrier family 25, member 5 [Homo sapiens]	gi|4502099	32874	11	362	32	71	0,0513	K.DFLAGGVAAAISK.T
transmembrane protein 33 [Homo sapiens]	gi|8922491	27933	2	90	8	60	0,0839	R.ALLANALTSALR.L
ADP,ATP translocase	gi|339721	28042	1	25	4	25	0,0780	R.AAYFGIYDTAK.G
signal sequence receptor, delta [Homo sapiens]	gi|5454090	18987	1	87	13	44	0,0744	R.FFDEESYSLLR.K
ribosomal protein S20 [Homo sapiens]	gi|3088340	6853	1	38	20	38	0,0502	R.LIDLHSPSEIVK.Q
ribosomal protein L23 [Homo sapiens]	gi|4506605	14856	2	86	20	35	0,0407	K.GSAITGPVAK.E
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa [Homo sapiens]	gi|75517917	9364	2	52	22	37	0,0487	K.FYSVNVDYSK.L
ribosomal protein S27 [Homo sapiens]	gi|4432748	7686	1	49	17	49	0,0437	-.DLLAPSPEEEKR.K
ribosomal protein L38 [Homo sapiens]	gi|3088356	4291	1	29	27	29	0,0371	K.QSLPPGLAVK.E
c-myc binding protein [Homo sapiens]	gi|1785851	11945	1	24	10	24	0,0610	K.LAQYEPPQEEK.R

Supplemental table 5: Protein composition of Ago2 complex II

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
eukaryotic translation initiation factor 2C, 2 (Ago2) [Homo sapiens]	gi|29171734	97146	20	1819	53	86	0.0231	R.SVSIPAPAYYAHLVAFR.A
ubiquitin	gi|229532	8446	1	30	12	30	-0.0019	R.TLSDYNIQK.E
proliferation-inducing protein 32 [Homo sapiens]	gi|45643460	162923	3	224	4	65	-0.008	K.LTVAENEAETK.L
hornerin [Homo sapiens]	gi|28557150	48569	1	48	3	48	-0.0294	R.GPYESGSGHSSGLGHR.E
RNA helicase A [Homo sapiens]	gi|1806048	140788	7	444	11	87	-0.0199	R.ELDALDANDELTPLGR.I
splicing factor 3b, subunit 1 isoform 1 [Homo sapiens]	gi|54112117	145738	2	133	3	47	-0.0142	R.ATVNTFGYIAK.A
Splicing factor 3B subunit 3 (Spliceosome associated protein 130) (SAP 130) (SF3b130) (Pre-mRNA splicing factor SF3b 130 kDa subunit) (STAF130)	gi|19863446	135507	6	222	-	53	-0.0221	R.FLAVGLVDNTVR.I
coatomer protein [Homo sapiens]	gi|1002369	138244	2	85	2	39	-0.0162	R.TLDLPIYVTR.V
Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit)	gi|2498883	97596	1	62	1	62	-0.0147	R.AAVLLEQER.Q
hnRNP U protein [Homo sapiens]	gi|32358	88890	9	390	13	96	-0.0305	R.NFILDQTNVSAAAQR.R
DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 (Ddx30) [Homo	gi|20336294	133854	5	257	7	46	-0.0193	K.AIVLAAIFR.C
RNA-binding protein 10 (RNA-binding motif protein 10) (DXS8237E)	gi|12644371	103396	1	63	1	63	-0.0462	R.ESATADAGYAILEKK.G
gemin4 [Homo sapiens]	gi|7657122	119913	2	81	-	57	-0.0126	R.LLETVIDVSTADR.A
DHX36 protein (KIAA1488) [Homo sapiens]	gi|23243423	111426	1	70	2	61	-0.0344	R.LGGIAYFLSR.L
RNA helicase Gu - human (fragment)	gi|2135315	89196	3	142	-	59	0.0074	R.AAVIGDVIR.V
NF-90	gi|1082856	73293	2	118	-	47	0.0057	R.IFVNDDR.H
ATP-dependent RNA helicase #46 [Homo sapiens]	gi|2696613	92770	1	81	2	38	0.0033	R.YGVIILDEAHER.T
hypothetical protein LOC55037 [Homo sapiens]	gi|38683855	78500	3	129	3	45	0.0180	R.SPALQVLR.E
polyadenylate binding protein II [Homo sapiens]	gi|693937	58481	7	262	20	66	0.0315	R.IVATKPLYVALAQR.K
Skb1Hs (PRMT 5) [Homo sapiens]	gi|2323410	72740	3	166	4	65	0.0228	R.GPLVNASLR.A
thyroid autoantigen 70kDa (Ku antigen) [Homo sapiens]	gi|57165052	69799	1	36	2	36	0.0367	K.NIYVLQELDNPGAK.R
E2IG3 [Homo sapiens]	gi|6457340	63528	1	36	1	36	0.005	K.GGIPNVEGAAK.L
sodium bicarbonate cotransporter-like protein [Homo sapiens]	gi|10567590	118582	1	20	1	20	0.0657	K.FEEKVEEGGER.W
DNA-binding protein B (YB-1)	gi|181486	39954	4	222	11	87	-0.1458	K.GAEAANVTGPGGVPVQGSK.Y
RuvB-like 2 [Homo sapiens]	gi|12653319	51125	2	69	4	44	-0.0949	R.GLGLDDALEPR.Q
Ribosomal protein L4 [Homo sapiens]	gi|12655035	47667	1	68	4	32	-0.1009	R.NIPGITLLNVSK.L
unnamed protein product [Homo sapiens]	gi|31092	50095	1	55	2	55	-0.0852	K.IGGIGTVPVGR.V
KIAA0115 [Homo sapiens]	gi|473947	50680	1	45	1	45	-0.0815	K.SSLNPILFR.G
nuclear RNA helicase (Ddx39) [Homo sapiens]	gi|1905998	49046	1	18	2	18	-0.1250	R.ILVATNLFGR.G
NF45 protein	gi|532313	44669	4	258	12	70	-0.0847	K.VLQSALAAIR.H
ribosomal protein L3	gi|337580	45440	2	89	7	38	-0.08	R.HGSLGFLPR.K
KIAA1756 protein [Homo sapiens]	gi|12698057	116668	1	38	0	38	-0.1676	R.AELEKVLR.A
MRPS27 protein [Homo sapiens]	gi|38014602	25008	2	105	10	55	-0.0913	R.EALDVLGAVLK.A
HNRPC protein [Homo sapiens]	gi|13937888	33578	3	184	12	71	-0.1095	R.VFIGNLNTLVVK.K
7-dehydrocholesterol reductase [Homo sapiens]	gi|3171089	53073	1	38	1	38	-0.0803	R.YTAAVPYR.L
protein translation initiation factor 2C2: EIF2C2 [Homo sapiens]	gi|6468775	42502	1	29	0	29	-0.0889	R.ELLIQFYK.S
Mitochondrial ribosomal protein S22 [Homo sapiens]	gi|14424546	41254	2	98	6	60	-0.1498	K.ILTPIIFKEENLR.T
ribosomal protein L6 [Homo sapiens]	gi|36138	32841	2	79	5	45	-0.0726	K.FVIATSTK.I
fibrillarin	gi|182592	33797	1	51	3	51	-0.1100	R.TNIIPVIEDAR.H
ribosomal protein S2 [Homo sapiens]	gi|15055539	31305	6	475	35	54	-0.1249	K.TYSYLTPDLWK.E
hypothetical protein LOC84319 [Homo sapiens]	gi|14150167	31792	1	31	3	31	-0.0925	K.QGGLNLSPLK.F
prohibitin 2 [Homo sapiens]	gi|6005854	33276	6	389	29	78	-0.1100	K.FNASQLITQR.A
ribosomal protein S3a [Homo sapiens]	gi|4506723	29926	6	245	28	52	-0.0928	K.LITEDVQGK.N
ribosomal protein S6	gi|337514	28633	4	182	25	58	-0.09	K.LIEVDDR.K
S3 ribosomal protein [Homo sapiens]	gi|7765076	26699	12	725	65	75	-0.1272	R.ELAEDGYSGVEVER.V
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform H (heart) precursor [Homo sapiens]	gi|4885079	32860	2	160	12	59	-0.0931	K.SEVATLTAAGK.E
Ribosomal protein L8 [Homo sapiens]	gi|15341853	27993	1	49	4	49	-0.0799	R.AVVGVVAGGGR.I
solute carrier family 25 member 3 isoform a precursor [Homo sapiens]	gi|6031192	40069	1	27	1	27	-0.0692	R.TVEALYK.F
scar protein	gi|337930	27386	7	330	32	64	-0.1010	K.DANGNSFATR.L
prohibitin [Homo sapiens]	gi|4505773	29786	5	159	19	62	-0.0952	K.AAIISAEGDSK.A
PREDICTED: similar to SLC25A5 protein [Homo sapiens]	gi|51460683	40069	3	127	-	50	-0.1368	R.VKLLLQVQHASK.Q
Solute carrier family 25, member A6 [Homo sapiens]	gi|15928608	32905	3	126	10	47	-0.1097	R.AAYFGVYDTAK.G
Similar to ribosomal protein S8 [Homo sapiens]	gi|13542987	9277	3	161	41	99	-0.1323	K.ISSLLEEQFQQGK.L
ribosomal protein S9	gi|550023	22558	9	351	36	52	-0.0945	R.LFEGNALLR.R
ribosomal protein S5	gi|550021	22763	1	147	14	58	-0.0871	R.QAVDVSPLR.R
ribosomal protein L24 [Homo sapiens]	gi|4506619	17768	2	197	26	50	-0.1190	R.QINWTVLYR.R
ribosomal protein L29 [Homo sapiens]	gi|793843	17656	1	38	9	38	-0.1299	K.AQAAAPASVPAQAPK.R
ribosomal protein L13a [Homo sapiens]	gi|6912634	23562	1	31	3	31	-0.0735	R.KFAYLGR.L
Ribosomal protein L17 [Homo sapiens]	gi|42542645	21402	4	231	34	59	-0.1090	R.YSLDPENPTK.S
homology to rat ribosomal protein L23	gi|306549	16730	2	99	14	68	-0.1240	R.LAPDYDALDVANK.I
ribosomal protein L27a [Homo sapiens]	gi|4432754	3706	1	76	32	76	-0.0830	K.TGAAPIIDVVR.S
ribosomal protein L26	gi|292435	17278	3	186	26	47	-0.1496	K.ANGTTVHVGIHPSK.V
ribosomal protein L27a [Homo sapiens]	gi|4506625	16551	4	170	29	76	-0.1032	K.TGAAPIIDVVR.S
ribosomal protein L11 [Homo sapiens]	gi|495126	20103	1	111	7	111	-0.1332	K.VLEQLTGQTPVFSK.A
Ribosomal protein S18 [Homo sapiens]	gi|75517910	17708	1	90	11	70	-0.0951	R.VLNTNIDGR.R
ribosomal protein L31 [Homo sapiens]	gi|1655596	14084	2	46 / 32	11 / 7	46 / 32	-0.1070 / -0.1004	K.LYTLVTYVPVTTFK.N / R.SAINEVVTR.E
ribosomal protein S26 [Homo sapiens]	gi|296452	12922	2	147	20	100	-0.1180	R.DISEASVFDAYVLPK.L
Ribosomal protein S15a [Homo sapiens]	gi|12804561	14770	1	92	20	45	-0.0610	K.IVVNLTGR.L
ribosomal protein L35 [Homo sapiens]	gi|6005860	14543	2	78	18	45	-0.0876	R.VLTVINQTQK.E
histone H2A.5 - human	gi|70686	14047	1	68	12	56	-0.0626	R.AGLQFPVGR.V
pro-ubiquitin	gi|340062	17434	2	43	21	26	-0.136	K.CCLTYCFNKPEDK.- + Carb.
Ring finger protein 149 [Homo sapiens]	gi|32425835	43151	1	15	2	15	-0.1652	K.GREILELVQK.G
Gemin3	gi|14209614	92163	1	30	0	30	1.2	K.EGLEKPVEIIR.H

Supplemental table 6: Protein composition of Ago2 complex III

protein	Acc.No.	Mass	Queries matched	Proteinscore	Seq cov %	Peptidescore	Pep delta	Pep sequence
eukaryotic translation initiation factor 2C, 2 (Ago2) [Homo sapiens]	gi|29171734	97146	17	1170	40	62	-0.0935 (-0.147)	K.AVQVHQDTLR.T (R.SVSIPAPAYYAHLVAFR.A)
ubiquitin	gi|229532	8446	2	56	21	56 / 21	-0.1095 / -0.0765	K.TITLEVEPSDTIENVK.A / R.TLSDYNIQK.E
Dicer [Homo sapiens]	gi|5019620	218673	1	46	0	36	-0.0649	R.YTAVVLNR.L
MYB binding protein 1a [Homo sapiens]	gi|7657351	148758	1	36	2	40	-0.0738	R.SPSLLQSGAK.K
proline and glutamic acid rich nuclear protein isoform [Homo sapiens]	gi|3168604	109069	1	51	1	51	-0.1009	R.TGSAVAPVHPPNR.S
RNA helicase A	gi|1082769	141984	4	146	3	39	-0.0787	K.VFDPVPVGVTK.V
DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 (Ddx30)[Homo	gi|20336294	133854	2	33	1	18	-0.0661	K.NLLNSVIGR.A
Splicing factor 3B subunit 3 (Spliceosome associated protein 130) (SAP 130) (SF3b130) (Pre-mRNA splicing factor SF3b 130 kDa subunit) (STAF130)	gi|19863446	135507	1	27	-	27	-0.0797	R.FLAVGLVDNTVR.I
hnRNP U protein [Homo sapiens]	gi|32358	88890	4	213	6	52	-0.1008	K.LLEQYKEESK.K
matrin 3 [Homo sapiens]	gi|6563246	95138	1	39	1	39	-0.0686	K.SFQQSSLSR.D
gemin4 [Homo sapiens]	gi|7657122	119913	3	150	-	75	-0.1312	K.VLQPHPVTPSDTETR.W
hect domain and RLD 5 [Homo sapiens]	gi|7705931	116773	1	54	-	54	-0.0795	K.FLVFLTGTDR.L
polyadenylate binding protein II [Homo sapiens]	gi|693937	58481	9	414	24	66	-0.1173	R.IVATKPLYVALAQR.K
Skb1Hs [Homo sapiens]	gi|2323410	72740	1	41	1	41	-0.0820	R.EFIQEPAK.N
mRNA-binding protein CRDBP [Homo sapiens]	gi|7141072	63417	2	118	5	52	-0.1047	R.DQTPDENDQVIVK.I
Ribosomal protein L4 [Homo sapiens]	gi|12655035	47667	4	287	21	50	-0.2030	R.QPYAVSELAGHQTSAESWGTGR.A
Y box-binding protein [Mus musculus]	gi|55451	35822	3	158	11	85	-0.1388	R.SVGDGETVEFDVVEGEK.G
unnamed protein product [Homo sapiens]	gi|31092	50095	1	47	2	47	-0.0860	K.IGGIGTVPVGR.V
ribosomal protein L3	gi|337580	45440	4	218	14	57	-0.1166	K.NNASTDYDLSDK.S
KIAA1756 protein [Homo sapiens]	gi|12698057	116668	1	33	0	33	-0.1734	R.AELEKVLR.A
NF45 protein	gi|532313	44669	2	134	9	53	-0.0943	K.VLQSALAAIR.H
HNRPC protein [Homo sapiens]	gi|14250048	33578	2	106	8	45	-0.0822	R.VPPPPPIAR.A
ribosomal protein L6 [Homo sapiens]	gi|36138	32841	4	169	11	60	-0.0788	K.FVIATSTK.I
Stomatin (EPB72)-like 2 [Homo sapiens]	gi|14603403	38494	1	43	2	43	-0.1070	R.ATVLESEGTR.E
EBNA1 binding protein 2 [Homo sapiens]	gi|5803111	34798	1	36	3	36	-0.0823	R.QAQAAVLAVLPR.L
HNRPC protein [Homo sapiens]	gi|13937888	33578	3	152	12	58	-0.0926	K.SDVEAIFSK.Y
B23 nucleophosmin	gi|190238	9189	1	40	10	40	-0.0821	K.GPSSVEDIK.A
RNA binding motif protein 4 isoform 1 [Homo sapiens]	gi|4506445	40914	1	32	-	32	-0.0791	R.AEDAVEAIR.G
Ribosomal protein P0 [Homo sapiens]	gi|12654583	34253	5	310	21	61	-0.1265	R.GTIEILSDVQLIK.T
fibrillarin	gi|182592	33797	1	35	3	35	-0.1090	R.TNIIPVIEDAR.H
prohibitin 2 [Homo sapiens]	gi|6005854	33276	1	41	3	41	-0.0566	R.VLPSIVNEVLK.S
ribosomal protein S6	gi|225901	28633	2	64 / 38	4 / 3	64 / 38	-0.0725 / -0.0504	K.DIPGLTDTTVPR.R / K.LIEVDDER.K
ribosomal protein L7a [Homo sapiens]	gi|4506661	29977	6	236	21	73	-0.0820	R.AGVNTVTTLVENK.K
Ribosomal protein L8 [Homo sapiens]	gi|15341853	27993	5	187	21	80	-0.1253	R.ASGNYATVISHNPETK.K
S3 ribosomal protein [Homo sapiens]	gi|7765076	26699	3	177	14	57	-0.0749	R.TEIIILATR.T
unnamed protein product [Homo sapiens]	gi|34392	24191	1	39	4	39	-0.0797	K.TYSYLTPDLWK.E
ribosomal protein S4	gi|227229	29664	1	52	3	52	-0.0589	R.LSNIFVIGK.G
ADP,ATP translocase	gi|339721	28042	2	77	8	43	-0.1026	R.YFPTQALNFAFK.D
Ribosomal protein L7 [Homo sapiens]	gi|14250762	29207	5	228	20	61	-0.0853	R.IALTDNALIAR.S
ribosomal protein L10a [Homo sapiens]	gi|15431288	24816	2	84	13	37	-0.0633	R.DTLYEAVR.E
ribosomal protein S9	gi|550023	22558	4	139	18	47	-0.0619	R.LFEGNALLR.R
ribosomal protein L18 [Homo sapiens]	gi|4506607	21621	2	126	13	74	-0.0864	K.TAVVVGTITDDVR.V
ribosomal protein L13a [Homo sapiens]	gi|6912634	23562	1	70	9	54	-0.0788	K.YQAVTATLEEK.R
ribosomal protein L10	gi|414587	23903	1	42	4	42	-0.0652	R.SLQSVAEER.A
L21 ribosomal protein	gi|619788	17646	1	35	9	35	-0.1089	R.VYNVTQHAVGIVVNK.Q
ribosomal protein L24 [Homo sapiens]	gi|4506619	17768	1	109	14	52	-0.0820	R.QINWTVLYR.R
unnamed protein product [Homo sapiens]	gi|527578	16582	(1)	77	9	77	-0.1049	R.DLTTAGAVTQCYR.D + Carb:
ribosomal protein L11 [Homo sapiens]	gi|495126	20103	1	95	11	77	0.0258	K.VLEQLTGQTPVFSK.A
ribosomal protein L27a [Homo sapiens]	gi|4432754	3706	1	76	32	76	0.0092	K.TGAAPIIDVVR.S
amino acid starvation-induced protein	gi|202990	13865	1	30	11	30	-0.1136	K.EQIVPKPEEEVAQK.K
ribosomal protein L12 [Homo sapiens]	gi|55665101	17808	2	163	24	42	-0.0017	K.IGPLGLSPK.K
ribosomal protein L26 [Homo sapiens]	gi|4506621	17248	2	59	10	36	0.0115	K.DDEVQVVR.G
ribosomal protein S26 [Homo sapiens]	gi|456351	13035	1	78	13	78	-0.1098	R.DISEASVFDAYVLPK.L
ribosomal protein L28	gi|550019	15752	1	32	8	32	-0.1066	K.QTYSTEPNNLK.A
ribosomal protein S13	gi|553640	13313	3	129	34	54	-0.0858	K.GLTPSQIGVILR.D
ribosomal protein L35 [Homo sapiens]	gi|6005860	14543	2	123	21	48	-0.1371	R.VLTVINQTQKENLR.K
ribosomal protein L27 [Homo sapiens]	gi|4506623	15788	2	109	20	45	-0.0541	K.VVLVLAGR.Y
ribosomal protein S16 - mouse	gi|70920	16319	2	89	-	49	-0.0849	K.GPLQSVQVFGR.K
RPL23 protein [Homo sapiens]	gi|38571606	14875	1	83	18	37	-0.0601	K.NLYIISVK.G
60S ribosomal protein L34	gi|132910	13499	2	69	12	36	-0.0671	R.AFLIEEQK.I
acidic ribosomal phosphoprotein P1 [Homo sapiens]	gi|31979223	11392	1	53	14	53	-0.1187	K.AAGVNVEPFWPGLFAK.A
ribosomal protein L35a [Homo sapiens]	gi|16117791	12530	1	47	14	21	-0.0686	K.AIFAGYKR.G
ribosomal protein homologous to yeast S24 [Homo sapiens]	gi|36142	14707	1	47	6	47	-0.0634	K.IVVNLTGR.L
Ribosomal protein S27-like protein [Homo sapiens]	gi|13277528	9472	(1)	42	9	42	-0.0701	R.LTEGCSFR.R + Carb:
ribosomal protein S20 [Homo sapiens]	gi|3088340	6853	1	33	20	33	-0.1046	R.LIDLHSPSEIVK.Q
RPL37A protein [Homo sapiens]	gi|34783045	10137	(1)	28	8	28	-0.0723	K.YTCSFCGK.T + Carb:
unnamed protein product [Homo sapiens]	gi|32111	14164	1	27	27	27	-0.0586	R.AGLQFPVGR.V
Mov10	gi|144244568	43599	7	23	5	23	0.8	R.ITGNPVVTNP.I
FXR1	gi|1730139	69649	10	40	15	41	0.04	R.LQIDEQLR.Q