

**Supplementary Table 1. List of identified 3FI-binding partner proteins and their basic characteristics**

Part I: List of 3FI-binding proteins identified from a band at ~70 kDa

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	Molecular Function	Cellular Component	Biological Process	# AAs	MW [kDa]	calc. pI
Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=2 - [FUBP1_HUMAN]	166.56	42.33	1	24	24	53	DNA binding; RNA binding	cytoplasm; nucleus; organelle lumen	metabolic process; regulation of biological process; transport	644	70.9	7.30
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [KGPP_HUMAN]	96.18	30.74	1	18	19	30	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; cytosol	metabolic process	784	85.5	7.55
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	39.28	13.51	1	8	10	13	catalytic/motor/receptor/structural molecule/transporter activity; protein binding	cytoskeleton; membrane	coagulation; defense response; development; metabolic process; regulation of biological process; response to stimulus; transport	644	66.0	8.12
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 - [NUFIP2_HUMAN]	37.70	21.87	1	10	10	12	protein binding; RNA binding	cytoplasm; nucleus; ribosome		695	76.1	8.70
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1 - [RAGP1_HUMAN]	36.64	23.51	1	11	11	13	enzyme regulator activity; protein binding	chromosome; cytoplasm; cytoskeleton; cytosol; membrane; nucleus	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	587	63.5	4.08
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	36.30	14.59	1	9	9	12	catalytic activity; nucleotide binding	cytoplasm; membrane; mitochondrion	metabolic process	795	87.2	7.12

P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2 - [K6PF_HUMAN]	30.60	17.69	1	9	10	12	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytosol; membrane	cell organization and biogenesis; cellular homeostasis; metabolic process	780	85.1	7.99
Q99567	Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2 - [NUP88_HUMAN]	29.97	19.70	1	9	9	9	transporter activity	cytoplasm; cytosol; membrane; nucleus; organelle lumen	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	741	83.5	5.69
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	25.56	20.33	1	9	9	10	DNA binding; RNA binding	cytoplasm; cytosol; nucleus; organelle lumen	metabolic process; regulation of biological process; transport	711	73.1	5.70
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	24.43	20.21	1	9	9	9	structural molecule activity	cytoplasm; cytoskeleton	cell differentiation; development; response to stimulus	584	58.8	5.21
C9JJE2	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=4 SV=2 - [C9JJE2_HUMAN]	22.98	12.89	2	5	5	8	metal ion binding; RNA binding	nucleus; organelle lumen		613	65.3	8.38
B4E2Z3	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1 - [B4E2Z3_HUMAN]	22.63	22.11	3	8	8	8	catalytic activity		metabolic process	511	55.9	5.17
P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	19.64	12.08	1	7	7	7	protein binding; structural molecule activity	cytoplasm; cytoskeleton; cytosol; membrane; nucleus; organelle lumen	cell communication; cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	745	81.7	6.14
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	18.56	8.61	1	3	5	6	structural molecule activity	cytoplasm; cytoskeleton; Golgi	cell differentiation; cell proliferation; cellular component movement; development	639	65.4	8.00

P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	15.00	12.36	1	6	6	6	6	6	6	623	62.0	5.24
F5H365	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=4 SV=1 - [F5H365_HUMAN]	12.85	7.88	2	4	4	4	4	4	736	82.9	7.46	
O95202	LETM1 and EF-hand domain- containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1 - [LETM1_HUMAN]	12.58	7.85	1	5	5	5	5	5	739	83.3	6.70	
O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	11.92	9.64	1	4	4	4	4	4	633	70.9	8.13	
Q9UHD2	Serine/threonine-protein kinase TBK1 OS=Homo sapiens GN=TBK1 PE=1 SV=1 - [TBK1_HUMAN]	10.26	8.09	1	4	4	4	4	4	729	83.6	6.79	
Q9H9E3	Conserved oligomeric Golgi complex subunit 4 OS=Homo sapiens GN=COG4 PE=1 SV=3 - [COG4_HUMAN]	9.89	7.39	1	4	4	4	4	4	785	89.0	5.19	
Q6PJG6	BRCA1-associated ATM activator 1 OS=Homo sapiens GN=BRAT1 PE=1 SV=2 - [BRAT1_HUMAN]	8.77	4.26	1	3	3	3	3	3	821	88.1	5.27	
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	8.39	5.13	1	3	3	3	3	3	819	93.4	5.72	

Q81Y67	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1 - [RAVR1_HUMAN]	7.24	6.60	2	2	2	2	2	2	2	nucleotide binding; RNA binding	cytoplasm; nucleus	606	63.8	8.48
Q96T51	RUN and FYVE domain-containing protein 1 OS=Homo sapiens GN=RUFY1 PE=1 SV=2 - [RUFY1_HUMAN]	6.26	4.52	1	3	3	3	3	3	3	metal ion binding; protein binding	cytoplasm; endosome; membrane	708	79.8	5.74
F5H6Z6	Transcription factor 12 OS=Homo sapiens GN=TCF12 PE=4 SV=1 - [F5H6Z6_HUMAN]	5.92	5.14	2	2	2	2	2	2	2			681	72.5	7.64
Q86U12	Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=1 - [Q86U12_HUMAN]	5.63	5.57	3	2	2	2	2	2	2	nucleotide binding; protein binding		413	49.3	5.41
Q9H6T0	Epithelial splicing regulatory protein 2 OS=Homo sapiens GN=ESRP2 PE=1 SV=1 - [ESRP2_HUMAN]	4.45	3.16	1	2	2	2	2	2	2	nucleotide binding; RNA binding	nucleus	727	78.4	6.71

Part II: List of 3FI-binding proteins identified from a band at ~200 kD

Q92616	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L1_HUMAN]	67.93	12.21	1	22	22	22	22	24	24	protein binding; RNA binding	cytoplasm; ribosome	2671	292.6	7.47
P35658	Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2 - [NUP214_HUMAN]	49.71	13.49	1	17	17	17	18	18	18	protein binding; transporter activity	cytoplasm; cytosol; membrane; nucleus; organelle lumen	2090	213.5	7.47

A5YKK6	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2 - [CNOT1_HUMAN]	46.07	8.75	1	17	17	17	17	17	17	protein binding	cytoplasm; cytosol; membrane	metabolic process; regulation of biological process	2376	266.8	7.11
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	43.65	19.57	1	10	11	14				catalytic activity; motor activity; protein binding; receptor activity; structural molecule activity; transporter activity	cytoskeleton; membrane	coagulation; defense response; development; metabolic process; regulation of biological process; response to stimulus; transport	644	66.0	8.12
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 - [GBF1_HUMAN]	28.02	7.80	1	10	10	10				enzyme regulator activity	cytoplasm; Golgi; membrane	cell communication; cell organization and biogenesis; regulation of biological process; response to stimulus; transport	1859	206.3	5.73
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	25.99	19.01	1	8	8	9				structural molecule activity	cytoplasm; cytoskeleton	cell differentiation; development; response to stimulus	584	58.8	5.21
F8VPD4	Dihydroorotase OS=Homo sapiens GN=CAD PE=3 SV=1 - [F8VPD4_HUMAN]	24.07	5.64	2	9	9	9				catalytic activity; metal ion binding; nucleotide binding		metabolic process	2162	235.9	6.55
G5E9S1	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=4 SV=1 - [G5E9S1_HUMAN]	23.83	8.76	6	8	8	8				DNA binding; enzyme regulator activity; protein binding; RNA binding	cytoplasm	metabolic process; regulation of biological process	1404	154.8	5.16
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	17.04	7.82	1	3	4	5				structural molecule activity	cytoplasm; cytoskeleton; Golgi	cell differentiation; cell proliferation; cellular component movement; development	639	65.4	8.00
C9JCN0	Myoferlin OS=Homo sapiens GN=MYOF PE=4 SV=2 - [C9JCN0_HUMAN]	11.59	3.02	3	5	5	5				protein binding	membrane		2051	233.3	6.04

Q14160	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4 - [SCRIB_HUMAN]	11.59	4.97	1	4	4	4	4	protein binding	cytoplasm; membrane	cell death; cell differentiation; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; reproduction; response to stimulus	1630	174.8	5.07
--------	--	-------	------	---	---	---	---	---	-----------------	------------------------	---	------	-------	------

### Definitions

<b>Accession:</b>	The unique protein accession number for the identification.
<b>Description:</b>	Protein Name
<b>Score:</b>	Sequest Score
<b>Coverage:</b>	Percent coverage of the protein observed.
<b># Proteins:</b>	Number of proteins matching the peptides identified. These are typically isoforms etc. which are difficult to differentiate.
<b># Unique Peptides:</b>	Unique peptides identified which only occur in the protein identified.
<b># Peptides:</b>	All unique peptide plus peptides that may be common between two or more proteins.
<b># PSMs:</b>	Peptide Spectral Matches. PSMs are roughly proportional to protein abundance. PSMs for the same protein in different samples can be used to compare changes in relative abundance.
<b>Molecular Function:</b>	From literature
<b>Cellular Component:</b>	From literature
<b>Biological Process:</b>	From literature
<b># Aas:</b>	Number of amino acids in the intact protein (theoretical)
<b>MW [kDa]:</b>	Molecular Weight of the intact protein (theoretical)
<b>calc. pI:</b>	Calculated PI of the intact protein (theoretical)

```

Human      691 -----GAUCAGUUUAUGGAUAAAUGGCAUCUCUAACCAUAACACAGGAGAAUUGGA 742
Mouse     749 ACA-CAGAGAAACCCUGUUUCGAAAACC-----CAAAAAA-UAGGUAGGAUUGGA 797
Rat       576 -CAGCAAGGAAAGCCCCAAAGAUAAACUG-----AAGGAUAA-AAUGUAGGAUUGGA 625
Cattle    693 -----GAUCAAUUGUGAGU-UAAAUGUCAUUUCACAAUAAACAUAGGAGAAUUGGA 743
Rabbit    733 -----GAAUGGUUAAGAUAUAAAUGAAAUCUCUAACCAUAA-----GAGAAUUGUA 779
Zebrafish -----
-----

Human      743 A-GGAGCCCUAAGUUGUCACUCAGUUUAAUUUCU-UUUAAUGGUUAGUUUAGCCUAAAGA 800
Mouse     798 A-GGGGCCUCAAUUCUUAACUAACAUUUGACUUUCAAUUA---UUUGUUAGCAUAGAAA 852
Rat       626 A-GAGGCCUUCGAUUCUAG---UUUGACUUUCAAUUA---UUUGUUGGCAUAGAAA 676
Cattle    744 A-AGAGCCAAA-----UCACUAAAUUUGAUUUUUCCUUAAAAUUAGUUUAGUUAUAAAGA 797
Rabbit    780 AGGGAGCACUAAGUUGUUUUAAGAUUUUGGCUUUUUCUGAA---AAUUUAGUACAAGA 835
Zebrafish 1 -----GAGG 4
                                         *

Human      801 UUUUUCUGCAUAUUCUUUUCCCAUGUGGCUCUACUCAUUUGCAACUGAAUUUUAUGUUA 860
Mouse     853 UUUCUCUAUU---UUUCUUUCCUUAUGUGUC-----UCAUUUAUAACCAAUUUUAUUA 904
Rat       677 UUUCUGCAUU---UUUU-UUCUU--AUGUC-----UCAUUUUAACCAAUUUUAUUA 725
Cattle    798 UUUUUCUGUAUAGUCUUUUGCUCGUGGCUGAACUUACUUGCAACU-----844
Rabbit    836 UUUUUCCAUAUGUUGUCUUUCCCAUGUGGCACAACUCAC-UGCAACUAAAUUUGGUUAUA 894
Zebrafish 5 -----UG-----UUUUAUUUGUAA-----A 19
                                         * * * *

Human      861 UAACUCAUCUAGUGAGACCAACUUAC--U-AA-AUUUUUAGUAUGCACUGAA----- 908
Mouse     905 AAA--AAACUAAUAAG---ACAAACACUGAAUAAUUUCACUGUGUAGUGAA----- 950
Rat       726 AAA--UAGCUAAUAAGCCAGACAUAACACUGAAUAAUUU-AGUACGCAAUGAA----- 774
Cattle    845 ----AAUGUAGGAAGAUAAACUUAC--U-AAAAUUUUUAGGAUGUAUCAA----- 888
Rabbit    895 UAAUUAAUCCAGUAAAACAGACUUAC--U-AAAGUUCUAAUAGGCACUGAA----- 943
Zebrafish 20 ACACUGCUCAGUAACACAG-CUUGCACAAAUCAACUU-CAGAAGUAUCAAGCCACAGC 77
          * * * * * * * * * *

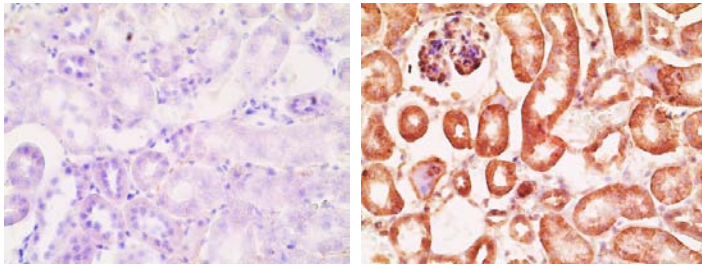
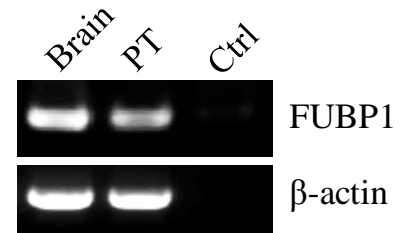
Human      909 ----AG---UUUUUAUCCAACAUAUUGUUAUUUUAAGCAAAAUUUUAAGAAAGUUUU 960
Mouse     951 ----AG---UUUUUAUCUCAUCAAUAUUGUACAUGGGAAGCAGUAUUUUUAAGAAAGUUUU 1002
Rat       775 ----AG---UUUUUAACUCAGCAAACAUGUACAUGCGAAGCAGUUUUUUAAGGAAGUUUU 826
Cattle    889 ----AG---UUUUGAUUCAGCAAUAACGUUUAUUUUAACGAAAUUUUAAGAAAU-UUG 939
Rabbit    944 ----AG---AUUUUACUCAGCAAUUGUGUCAUAAUAAAGCAAACUUUUUAU-----UUC 990
Zebrafish 78 CGCUAAGGUGAAAUAUGUCCUGCAAAAAGCUAUUUUAUUUGCGUUUCUUUAU-----AUU 131
          ** * * ** * * * **

Human      961 GAAAUUCAUA-----AAGCAUUUGGUUUUAAACUAUUUUUAAGAAUAUA 1003
Mouse     1003 GAGGUGCAUA-AAAGCUCUGUAAAAGUAGAGGUCUGGU-UUACGUUGUAUCUUGAAUAUU 1060
Rat       827 GAAGCAGUA-AAAGCCUGUAAAAGUAAAGGCUUGGU-UUGUGCUGUAUCUAGAAUAUA 884
Cattle    940 GAAAUUCGUUAAAUAUUUAAAACUAAGACUUGAGUUUUUAGACUGUUUUUAAGAAUACA 999
Rabbit    991 AGAAUUUUUAU--AAAGCAUUGUAAAACUGAAGCUUUGGUUUUUAUGCUGUCUUAAGG---UA 1045
Zebrafish 132 AAAGUUAUUC-AGGGCUUUUAAAAGAUAAAUUCAUG-----UA 168
          *

human      1004 GU-----ACUCGGUCAGGUUAGACGGCUCACGCCUGUAAUCCAGC 1044
Mouse     1061 CUUAAUAUCUAGAAUAUUCUUAAG---U-----CAUAUA--UCAGGA 1096
Rat       885 GU-----UCUCAAUAUUCUUA---U-----CUUGUAUUUCAGAA 917
Cattle    1000 GA-----ACUCAAUAUCUUGA---U-----CCUGCAUUUCAAA 1032
Rabbit    1046 AU-----UCUCAAUAUUCUUGG---U-----CUUAUAUUGCAGAA 1077
Zebrafish 169 GU-----UAUCAACACAGUU-----UCAGUAUUAAUUUCC--- 201
          * * * * *

```

**Supplementary Figure 1. Sequence alignment of PKD2 mRNA 3FI from indicated species.** National Center for Biotechnology Information accession number for sequences used here are NM\_000297.3 (Human), NM\_008861.3 (Mouse), NM\_001191934.1 (Rat), NM\_001046312.1 (Cattle), XM\_002717010.2 (Rabbit), and NM\_001002310.1 (Zebrafish). Identical residues among the species are indicated by “\*” and AUUUA signature sequences were highlighted with yellow. 3FI AU contents for different species are as follows: Human, 67.5% AU with two AUUUA sequences; Mouse, 70.4% AU with two AUUUA sequences; Rat, 67.8% AU with one AUUUA sequence; Cattle, 72.6% AU with one AUUUA sequence; Rabbit, 70% AU with three AUUUA sequences; Zebrafish, 66.2% AU with one AUUUA sequence.

**A****B**

**Supplementary Figure 2. Expression of FUBP1 in mouse normal kidney.** (A) Immunohistochemistry of kidney cortical sections from a 7-month adult mouse, showing expression of FUBP1 protein in various parts of kidney, including proximal and distal tubules. *Left panel*, Ctrl; *Right panel*, FUBP1 staining with antibody from AVIVA SYSTEMS BIOLOGY (#ARP35704\_P050). (B) mRNA signals obtained by RT-PCR showing expression of FUBP1 mRNA in proximal tubules (PT) from a 7-month adult mouse. The whole brain tissue from the same mouse was used as a positive control and “Ctrl” represents PT without reverse transcription.  $\beta$ -actin signals were detected as controls. The FUBP1 primers used in the assays are the same as those reported previously (Zhang et al, *Onkologie*, 36: 650-5, 2013). Two rounds of PCR each with 25 cycles were performed.