

Supplementary Table 2: List of proteins exclusively identified in MDA-Exo.

ACTB_HUMAN Mass: 41736 **Score: 1424** Matches: 53(49) Sequences: 12(12) emPAI: 5.33

Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1

Query	Score	Peptide
364	47	R.DLTDYLMK.I
395	-46	R.DLTDYLMK.I + Oxidation (M)
528	-45	R.GYSFTTTAER.E
529	74	R.GYSFTTTAER.E
530	-49	R.GYSFTTTAER.E
531	-74	R.GYSFTTTAER.E
532	-46	R.GYSFTTTAER.E
533	-48	R.GYSFTTTAER.E
534	-51	R.GYSFTTTAER.E
536	-35	R.GYSFTTTAER.E
537	-54	R.GYSFTTTAER.E
538	-37	R.GYSFTTTAER.E
539	-50	R.GYSFTTTAER.E
540	-49	R.GYSFTTTAER.E
541	-36	R.GYSFTTTAER.E
542	-71	R.GYSFTTTAER.E
592	-52	K.EITALAPSTMK.I
593	81	K.EITALAPSTMK.I
594	-39	K.EITALAPSTMK.I
595	-42	K.EITALAPSTMK.I
610	-47	R.HQGVMVGMGQK.D
611	48	R.HQGVMVGMGQK.D
612	-35	R.HQGVMVGMGQK.D
629	-60	K.EITALAPSTMK.I + Oxidation (M)
630	-43	K.EITALAPSTMK.I + Oxidation (M)
631	-40	K.EITALAPSTMK.I + Oxidation (M)
654	48	R.AVFPSIVGRPR.H
983	-56	K.QEYDESGPSIVHR.K + Gln->pyro-Glu (N-term Q)
1001	44	K.IWHHTFYNELR.V
1003	-40	K.IWHHTFYNELR.V
1004	-52	K.QEYDESGPSIVHR.K
1008	57	K.QEYDESGPSIVHR.K
1010	-45	K.QEYDESGPSIVHR.K
1015	-44	K.QEYDESGPSIVHR.K
1362	-99	K.SYELPDGQVITIGNER.F
1363	118	K.SYELPDGQVITIGNER.F
1364	-109	K.SYELPDGQVITIGNER.F
1365	-72	K.SYELPDGQVITIGNER.F
1366	-63	K.SYELPDGQVITIGNER.F
1367	-89	K.SYELPDGQVITIGNER.F
1368	-83	K.SYELPDGQVITIGNER.F
1537	-64	R.VAPEEHPVLLTEAPLNPK.A
1538	93	R.VAPEEHPVLLTEAPLNPK.A
1539	-52	R.VAPEEHPVLLTEAPLNPK.A
1542	-65	R.VAPEEHPVLLTEAPLNPK.A
1545	-42	R.VAPEEHPVLLTEAPLNPK.A
1547	-50	R.VAPEEHPVLLTEAPLNPK.A
1734	-104	K.DLYANTVLSGGTTMYPGIADR.M

1746	117	K.DLYANTVLSGGTTMYPGIADR.M + Oxidation (M)
1780	134	R.KDLYANTVLSGGTTMYPGIADR.M
1781	-81	R.KDLYANTVLSGGTTMYPGIADR.M
1895	102	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
1896	-52	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L

ACTC_HUMAN Mass: 42019 **Score: 644** Matches: 26(25) Sequences: 7(7) emPAI: 1.62

Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1

Query	Score	Peptide
364	47	R.DLTDYLMK.I
395	-46	R.DLTDYLMK.I + Oxidation (M)
592	-52	K.EITALAPSTMK.I
593	81	K.EITALAPSTMK.I
594	-39	K.EITALAPSTMK.I
595	-42	K.EITALAPSTMK.I
610	-47	R.HQGVMVGMGQK.D
611	48	R.HQGVMVGMGQK.D
612	-35	R.HQGVMVGMGQK.D
629	-60	K.EITALAPSTMK.I + Oxidation (M)
630	-43	K.EITALAPSTMK.I + Oxidation (M)
631	-40	K.EITALAPSTMK.I + Oxidation (M)
654	48	R.AVFPSIVGRPR.H
1001	44	K.IWHHTFYNELR.V
1003	-40	K.IWHHTFYNELR.V
1362	-99	K.SYELPDGQVITIGNER.F
1363	118	K.SYELPDGQVITIGNER.F
1364	-109	K.SYELPDGQVITIGNER.F
1365	-72	K.SYELPDGQVITIGNER.F
1366	-63	K.SYELPDGQVITIGNER.F
1367	-89	K.SYELPDGQVITIGNER.F
1368	-83	K.SYELPDGQVITIGNER.F
1561	-41	K.YPIEHGIITNWDDMEK.I
1562	63	K.YPIEHGIITNWDDMEK.I
1563	-44	K.YPIEHGIITNWDDMEK.I
1589	-50	K.YPIEHGIITNWDDMEK.I + Oxidation (M)

TBB2C_HUMAN Mass: 49830 **Score: 381** Matches: 10(10) Sequences: 7(7) emPAI: 1.08

Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1

Query	Score	Peptide
556	65	K.LAVNMVPPFR.L
839	-83	R.IMNTFSVVPSPK.V
845	91	R.IMNTFSVVPSPK.V
872	-46	R.IMNTFSVVPSPK.V + Oxidation (M)
954	75	K.EVDEQMLNVQNK.N
960	-63	K.EVDEQMLNVQNK.N + Oxidation (M)
1129	77	R.AVLVDLEPGTMDSVR.S
1204	92	R.ALTVPELTQQMFDAK.N
1209	74	K.NSSYFVEWIPNNVK.T
1720	53	R.GRMSMKEVDEQMLNVQNK.N + 2 Oxidation (M)

HSP71_HUMAN Mass: 70051 **Score: 284** Matches: 9(8) Sequences: 7(7) emPAI: 0.50

Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Query	Score	Peptide
653	47	K.DAGVIAGLNVL.R
697	44	K.FGDPVVQSDMK.H
700	-36	K.VEIIANDQG.NR.T
701	-41	K.VEIIANDQG.NR.T
703	44	K.VEIIANDQG.NR.T
976	103	R.TTPSYVAFTDTER.L
1174	93	K.NQVALNPQNTVFDAK.R
1186	78	K.ATAGDTHLGGEDFDNR.L
1199	88	R.IINEPTAAAIAYGLDR.T

TBB3_HUMAN Mass: 50432 **Score: 279** Matches: 7(7) Sequences: 5(5) emPAI: 0.62
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2

Query	Score	Peptide
556	65	K.LAVNMVPPFR.L
839	-83	R.IMNTFSVVPSPK.V
845	91	R.IMNTFSVVPSPK.V
872	-46	R.IMNTFSVVPSPK.V + Oxidation (M)
925	55	K.EVDEQMLAIQSK.N
1204	92	R.ALTVPELTQQMFDK.N
1209	74	K.NSSYFVEWIPNNVK.V

CLH1_HUMAN Mass: 191612 **Score: 195** Matches: 7(7) Sequences: 7(7) emPAI: 0.16
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5

Query	Score	Peptide
720	47	K.TLQIFNIEMK.S
880	42	R.VVGAMQLYSVDR.K
1085	72	R.RPISADSAIMNPASK.V
1245	84	K.VSQPIEGHAASFAQFK.M
1529	69	K.LHIIIEVGTPTGNQPFPK.K
1779	55	R.RPISADSAIMNPASKVIALKAGK.T
1859	41	K.ADDPSSYMEVVQAANTSGNWEELVK.Y

UGDH_HUMAN Mass: 55023 **Score: 176** Matches: 5(5) Sequences: 5(5) emPAI: 0.45
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1

Query	Score	Peptide
471	79	K.LAANAFLAQR.I
510	39	R.VTVVDVNESR.I
914	43	R.VLIGGETPEGQR.A
971	86	K.ILTTNTWSELSK.L
1500	73	R.INAWNSPTLPIYEPGLK.E

K2C8_HUMAN Mass: 53704 **Score: 149** Matches: 7(7) Sequences: 7(7) emPAI: 0.70
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7

Query	Score	Peptide
366	53	R.LQAEIEGLK.G
475	39	R.QLYEEEIR.E
580	39	R.EYQELMNK.L
619	49	K.LVSESSDVLPK.-

893	57	R.ASLEAAIADAEQR.G
897	67	R.TEMENEFVLIK.K
940	69	R.LEGLTDEINFLR.Q

H2B1C_HUMAN Mass: 13906 **Score: 139** Matches: 5(3) Sequences: 4(3) emPAI: 2.10
Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4

Query	Score	Peptide
545	36	K.ESYSVYVYK.V
573	50	K.QVHPDTGISSK.A + Gln->pyro-Glu (N-term Q)
578	-35	K.QVHPDTGISSK.A + Gln->pyro-Glu (N-term Q)
757	62	R.KESYSVYVYK.V
1350	96	K.AMGIMNSFVNDIFER.I + 2 Oxidation (M)

AT1A3_HUMAN Mass: 111747 **Score: 125** Matches: 5(5) Sequences: 5(5) emPAI: 0.20
Sodium/potassium-transporting ATPase subunit alpha-3 OS=Homo sapiens GN=ATP1A3 PE=1 SV=3

Query	Score	Peptide
719	50	R.LNIPVSQVNPR.D
922	48	K.VIMVTGDHPITAK.A
1140	69	K.VDNSSLTGESEPQTR.S
1421	53	K.GVGIISEGNETVEDIAAR.L
1798	53	R.IISAHGCKVDNSSLTGESEPQTR.S

EPCAM_HUMAN Mass: 34932 **Score: 118** Matches: 1(1) Sequences: 1(1) emPAI: 0.12
Epithelial cell adhesion molecule OS=Homo sapiens GN=EPCAM PE=1 SV=2

Query	Score	Peptide
1489	118	K.TQNDVDIADVAYYFEK.D

STOM_HUMAN Mass: 31730 **Score: 115** Matches: 1(1) Sequences: 1(1) emPAI: 0.14
Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3

Query	Score	Peptide
1514	115	R.VQNATLAVANITNADSATR.L

4F2_HUMAN Mass: 67993 **Score: 109** Matches: 3(2) Sequences: 3(2) emPAI: 0.13
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3

Query	Score	Peptide
607	37	K.ADLLLSTQPGR.E
977	70	K.IKVAEDEAEAAAAAK.F
991	70	K.GQSEDPGSLLSLFR.R

GNAI3_HUMAN Mass: 40532 **Score: 109** Matches: 4(4) Sequences: 4(4) emPAI: 0.49
Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3

Query	Score	Peptide
447	69	K.LLLL GAGESGK.S
921	57	K.TTGIVETHFTFK.D
1100	40	K.LLLL GAGESGKSTIVK.Q
1325	52	R.ISQSNIPTQQDVL.R

ALDOA_HUMAN Mass: 39420 **Score: 104** Matches: 2(2) Sequences: 2(2) emPAI: 0.23

Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2

Query	Score	Peptide
870	85	K.GILAADESTGSIK.R
947	54	M.PYQYPALTPEQK.K

RS3_HUMAN Mass: 26688 **Score: 104** Matches: 1(1) Sequences: 1(1) emPAI: 0.16
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2

Query	Score	Peptide
943	104	R.ELAEDGYSGVEVR.V

RS8_HUMAN Mass: 24205 **Score: 103** Matches: 2(2) Sequences: 2(2) emPAI: 0.39
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2

Query	Score	Peptide
827	54	K.LTPEEEEILNK.K
1251	87	R.IIDVVYNASNELVR.T

RAI3_HUMAN Mass: 40251 **Score: 100** Matches: 1(1) Sequences: 1(1) emPAI: 0.11
Retinoic acid-induced protein 3 OS=Homo sapiens GN=GPRC5A PE=1 SV=2

Query	Score	Peptide
946	100	R.TNVNVFSELSAPR.R

HSPB1_HUMAN Mass: 22782 **Score: 99** Matches: 3(2) Sequences: 3(2) emPAI: 0.42
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2

Query	Score	Peptide
448	36	R.QLSSGVSEIR.H + Gln->pyro-Glu (N-term Q)
596	66	R.LFDQAFGLPR.L
1496	71	K.LATQSNEITIPVTFESR.A

K2C1_HUMAN Mass: 66038 **Score: 95** Matches: 2(2) Sequences: 2(2) emPAI: 0.13
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

Query	Score	Peptide
758	43	R.TNAENEFVTIK.K
964	90	R.FLEQQNQVLQTK.W

GNAS1_HUMAN Mass: 111023 **Score: 90** Matches: 3(3) Sequences: 3(3) emPAI: 0.12
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens
GN=GNAS PE=1 SV=2

Query	Score	Peptide
447	69	R.LLLLGAGESGK.S
1100	40	R.LLLLGAGESGKSTIVK.Q
1349	48	R.YTTPEDATPEPGEDPR.V

PPIA_HUMAN Mass: 18012 **Score: 89** Matches: 2(2) Sequences: 2(2) emPAI: 0.55
Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2

Query	Score	Peptide
581	39	K.FEDENFILK.H
992	87	K.VKEGMNIVEAMER.F

UBA1_HUMAN Mass: 117848 **Score: 86** Matches: 2(2) Sequences: 2(2) emPAI: 0.07
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Query	Score	Peptide
731	45	R.KPLLESGTLGTK.G
1484	78	R.NEEDAAELVALAQAVNAR.A

RSSA_HUMAN Mass: 32854 **Score: 85** Matches: 1(1) Sequences: 1(1) emPAI: 0.13
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4

Query	Score	Peptide
671	85	K.FAAATGATPIAGR.F

NDKA_HUMAN Mass: 17149 **Score: 83** Matches: 1(1) Sequences: 1(1) emPAI: 0.26
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1

Query	Score	Peptide
1355	83	R.VMLGETNPADSKPGTIR.G

HNRPK_HUMAN Mass: 50976 **Score: 82** Matches: 1(1) Sequences: 1(1) emPAI: 0.08
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1

Query	Score	Peptide
1352	82	R.TDYNASVSPDSSGPER.I

ARF1_HUMAN Mass: 20697 **Score: 82** Matches: 1(1) Sequences: 1(1) emPAI: 0.21
ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2

Query	Score	Peptide
1152	82	K.QDLPNAMNAAEITDK.L

RL7A_HUMAN Mass: 29995 **Score: 78** Matches: 1(1) Sequences: 1(1) emPAI: 0.14
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2

Query	Score	Peptide
894	78	R.AGVNTVTTLVENK.K

K1C18_HUMAN Mass: 48057 **Score: 73** Matches: 1(1) Sequences: 1(1) emPAI: 0.09
Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2

Query	Score	Peptide
941	73	R.QAQEYEALLNIK.V

RAN_HUMAN Mass: 24423 **Score: 71** Matches: 2(2) Sequences: 2(2) emPAI: 0.39
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3

Query	Score	Peptide
686	51	K.NLQYYDISAK.S
780	57	K.FNVWDTAGQEK.F

AAAT_HUMAN Mass: 56598 **Score: 70** Matches: 2(2) Sequences: 2(2) emPAI: 0.15
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2

Query	Score	Peptide
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557 55 R.STEPELIQVK.S
1717 51 K.SELPLDPLVPTEEGNPLLK.H

RS2_HUMAN Mass: 31324 **Score: 70** Matches: 2(1) Sequences: 2(1) emPAI: 0.14
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2

Query	Score	Peptide
414	36	R.GTGIVSAPVVK.K
961	70	K.SPYQEFTDHLVK.T

LAT1_HUMAN Mass: 55010 **Score: 69** Matches: 1(1) Sequences: 1(1) emPAI: 0.08
Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2

Query	Score	Peptide
1226	69	K.SADGSAPAGEGEGVTLQR.N

RAB1A_HUMAN Mass: 22677 **Score: 68** Matches: 1(1) Sequences: 1(1) emPAI: 0.19
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3

Query	Score	Peptide
830	68	K.LQIWDTAGQER.F

RS26_HUMAN Mass: 13015 **Score: 68** Matches: 1(1) Sequences: 1(1) emPAI: 0.35
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3

Query	Score	Peptide
1171	68	R.DISEASVFDAYVLPK.L

RS24_HUMAN Mass: 15423 **Score: 65** Matches: 1(1) Sequences: 1(1) emPAI: 0.29
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1

Query	Score	Peptide
1195	65	K.TTGFGMIYDSL DYAK.K

1A01_HUMAN Mass: 40845 **Score: 64** Matches: 1(1) Sequences: 1(1) emPAI: 0.10
HLA class I histocompatibility antigen, A-1 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1

Query	Score	Peptide
1837	64	R.DGEDQTQDTEL VETRPAGDGFQK.W

CLIC1_HUMAN Mass: 26922 **Score: 59** Matches: 1(1) Sequences: 1(1) emPAI: 0.16
Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4

Query	Score	Peptide
769	59	K.GVTFNVTTVDTK.R

K6PP_HUMAN Mass: 85595 **Score: 57** Matches: 1(1) Sequences: 1(1) emPAI: 0.05
6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2

Query	Score	Peptide
939	57	R.DLQSNVEHLTEK.M

RS6_HUMAN Mass: 28680 **Score: 55** Matches: 1(1) Sequences: 1(1) emPAI: 0.15
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1

Query	Score	Peptide
770	55	K.DIPGLTDTTVPR.R

LEG3_HUMAN Mass: 26152 **Score: 54** Matches: 1(1) Sequences: 1(1) emPAI: 0.17
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5

Query	Score	Peptide
761	54	R.GNDVAFHFNPR.F

ANXA6_HUMAN Mass: 75872 **Score: 52** Matches: 2(2) Sequences: 2(2) emPAI: 0.11
Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3

Query	Score	Peptide
501	41	R.SELDMLDIR.E + Oxidation (M)
626	49	R.DAFVAIVQSVK.N

RL17_HUMAN Mass: 21397 **Score: 51** Matches: 1(1) Sequences: 1(1) emPAI: 0.20
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3

Query	Score	Peptide
1145	51	K.EQIVPKPEEEVAQK.K

RL3_HUMAN Mass: 46108 **Score: 50** Matches: 1(1) Sequences: 1(1) emPAI: 0.09
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2

Query	Score	Peptide
890	50	K.NNASTDYDLSDK.S

MUC1_HUMAN Mass: 122101 **Score: 49** Matches: 1(1) Sequences: 1(1) emPAI: 0.03
Mucin-1 OS=Homo sapiens GN=MUC1 PE=1 SV=3

Query	Score	Peptide
779	49	K.NYGQLDIFPAR.D

PUR9_HUMAN Mass: 64615 **Score: 49** Matches: 1(1) Sequences: 1(1) emPAI: 0.07
Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3

Query	Score	Peptide
1130	49	R.DVSELTGFPEMLGGR.V

RS16_HUMAN Mass: 16445 **Score: 49** Matches: 1(1) Sequences: 1(1) emPAI: 0.27
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2

Query	Score	Peptide
495	49	K.LLEPVLLLGK.E

DDX5_HUMAN Mass: 69147 **Score: 47** Matches: 1(1) Sequences: 1(1) emPAI: 0.06
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1

Query	Score	Peptide
699	47	K.APILIATDVASR.G

K1C19_HUMAN Mass: 44105 **Score: 46** Matches: 1(1) Sequences: 1(1) emPAI: 0.10
Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4

Query	Score	Peptide
730	46	R.ALEAANGELEVK.I

PSD1_HUMAN Mass: 109541 **Score: 45** Matches: 1(1) Sequences: 1(1) emPAI: 0.04
PH and SEC7 domain-containing protein 1 OS=Homo sapiens GN=PSD PE=2 SV=2

Query	Score	Peptide
850	45	R.RSLSELADPNPK.V

EZRI_HUMAN Mass: 69412 **Score: 42** Matches: 1(1) Sequences: 1(1) emPAI: 0.06
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4

Query	Score	Peptide
500	42	K.IGFPWSEIR.N

H2A1B_HUMAN Mass: 14135 **Score: 42** Matches: 1(1) Sequences: 1(1) emPAI: 0.32
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Query	Score	Peptide
1516	42	R.VTIAQGGVLPNIQAVLLPK.K

RNF17_HUMAN Mass: 184641 **Score: 41** Matches: 1(1) Sequences: 1(1) emPAI: 0.02
RING finger protein 17 OS=Homo sapiens GN=RNF17 PE=1 SV=3

Query	Score	Peptide
863	41	K.KNNLNAAMNIAR.A

AT1B1_HUMAN Mass: 35061 **Score: 40** Matches: 1(1) Sequences: 1(1) emPAI: 0.12
Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1

Query	Score	Peptide
978	40	R.VAPPGLTQIPQIQK.T

PGK1_HUMAN Mass: 44614 **Score: 40** Matches: 1(1) Sequences: 1(1) emPAI: 0.10
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3

Query	Score	Peptide
1160	40	K.LGDVYVNDAFGTAHR.A

Proteins matching the same set of peptides:

PGK2_HUMAN Mass: 44796 **Score: 40** Matches: 1(1) Sequences: 1(1)
Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3

NQO1_HUMAN Mass: 30867 **Score: 40** Matches: 1(1) Sequences: 1(1) emPAI: 0.14
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1

Query	Score	Peptide
503	40	R.ALIVLAHSER.T

C1TC_HUMAN Mass: 101558 **Score: 39** Matches: 1(1) Sequences: 1(1) emPAI: 0.04

C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3

Query	Score	Peptide
660	39	K.TPVPSDIDISR.S

H2AV_HUMAN Mass: 13509 **Score: 39** Matches: 1(1) Sequences: 1(1) emPAI: 0.34

Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3

Query	Score	Peptide
512	39	R.GDEELDSLIIK.A

Proteins matching the same set of peptides:

H2AZ_HUMAN Mass: 13553 **Score: 39** Matches: 1(1) Sequences: 1(1)

Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2

FAS_HUMAN Mass: 273423 **Score: 39** Matches: 2(1) Sequences: 2(1) emPAI: 0.02

Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3

Query	Score	Peptide
439	39	K.AQVADVVSRSR.W
643	38	R.SDEAVKPFGLK.V

RL22_HUMAN Mass: 14787 **Score: 38** Matches: 1(1) Sequences: 1(1) emPAI: 0.31

60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2

Query	Score	Peptide
672	38	K.ITVTSEVPFSK.R

GBLP_HUMAN Mass: 35076 **Score: 38** Matches: 1(1) Sequences: 1(1) emPAI: 0.12

Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3

Query	Score	Peptide
1357	38	K.IIVDELKQEVISTSSK.A